

**GENETIC ANALYSIS OF DROUGHT TOLERANCE IN
GROUNDNUT (*Arachis hypogaea*. L)**

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**GENETIC ANALYSIS OF DROUGHT TOLERANCE IN
GROUNDNUT (*Arachis hypogaea*. L)**

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In

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By

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CERTIFICATE

This is to certify that the thesis entitled "GENETIC ANALYSIS OF DROUGHT TOLERANCE IN GROUNDNUT (*Arachis hypogaea*. L)" submitted by Mrs. SRIVALLI POTHULA for the degree of DOCTOR OF PHILOSOPHY in GENETICS AND PLANT BREEDING to the University of Agricultural Sciences, Dharwad, is a record of research work done by her during the period of her study in this University, under my guidance and supervision and the thesis has not previously formed the basis of the award of any degree, diploma, associateship, fellowship or other similar titles.

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CONTENTS

Sl. No.	Chapter Particulars
	CERTIFICATE
	ACKNOWLEDGEMENT
	LIST OF TABLES
	LIST OF FIGURES
	LIST OF PLATES
	LIST OF APPENDIX
1.	INTRODUCTION
2.	REVIEW OF LITERATURE
	2.1 Evaluation for traits related to drought tolerance
	2.2 Genetic variability, Heritability and Genetic Advance
	2.3 Correlation studies
	2.4 Molecular markers and genetic mapping in groundnut for various traits
	2.5 QTL mapping approach
3.	MATERIAL AND METHODS
	3.1 Experimental material
	3.2 Experimental site
	3.3 Soil moisture content and meteorological condition
	3.4 Climate and weather
	3.5 Methods
	3.6 Statistical analysis
	3.7 Assigning parental polymorphism and genotyping for linkage map construction and QTL analysis
4.	RESULTS
	4.1 Phenotyping for quantitative, physiological, oil quality and foliar disease resistance traits in RILs of TMV-2 x GM 6-1 evaluated during summer 2012-13 and summer 2013-14
	4.2 Phenotyping for root traits in RILs of TMV-2 x GM 6-1 during summer 2012-13 and summer 2013-14
	4.3 Multilocation yield trials of selected lines during <i>kharif</i> 2014-15
	4.4 Construction of genetic linkage map
	4.5 QTL mapping for traits related to drought tolerance and quality traits

5.	DISCUSSION
	5.1 Mean performance for quantitative, physiological, root, oil quality and foliar disease resistance traits
	5.2 Genetic variability for quantitative, physiological, root, oil quality and foliar disease resistance traits
	5.3 Correlation analysis for quantitative, physiological, root, oil quality and foliar disease resistance traits
	5.4 Construction of genetic linkage map
	5.5 QTL mapping for traits related to drought tolerance and quality traits
6.	SUMMARY AND CONCLUSIONS
	REFERENCES
	APPENDICES

LIST OF TABLES

Table No.	Title
1	Literature showing the variability studies of various quantitative traits in groundnut
2	Review of reports on genotypic coefficient of variation and phenotypic coefficient of variation for some quantitative characters in groundnut
3	Reports on degree of heritability for some quantitative characters in groundnut
4	Review of reports on genetic advance as per cent of mean for some quantitative characters in groundnut
5	Literature showing the variability studies of various quality traits in groundnut
6	Review of reports on genotypic coefficient of variation and phenotypic coefficient of variation for quality characters in groundnut
7	Reports on degree of heritability for some quality characters in groundnut
8	Review of reports on genetic advance as per cent of mean for some quality characters in groundnut
9	Nature of correlation reported between pod yield and other component traits in groundnut
10	Reports on inter correlation between quantitative traits in groundnut
11	Summary of the review on intercorrelations between quality traits and other quantitative traits in groundnut
12	Details of some major genetic maps constructed in <i>Arachis</i> species
13	List of QTLs identified for some economically important traits in groundnut
14	Modified 9-point scale used for field-screening groundnut genotypes for resistance to late leaf spot (Subbarao <i>et al.</i> , 1990)
15	Modified 9 scale used for field screening groundnut genotypes for rust resistance (Subbarao <i>et al.</i> , 1990)
16	PCR reactions for the targeted microsatellites loci used for genotyping of TMV-2 x GM 6-1 population
17	Touch- Down PCR profiles for the targeted microsatellite loci used for genotyping of TMV-2 x GM 6-1 population

18	Analysis of variance for pod yield and its component traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
19	Analysis of variance for pod yield and its component traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
20	Pooled analysis of variance for pod yield and its component traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad
21	Mean and range for quantitative traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
22	Genetic parameters for quantitative traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
23	Analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
24	Analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
25	Pooled analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad
26	Mean and range for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
27	Genetic parameters for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
28	Analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
29	Analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
30	Pooled analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad

31	Mean and range for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
32	Genetic parameters for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
33	Analysis of variance for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
34	Analysis of variance for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
35	Pooled analysis of variance for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad
36	Mean and range for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
37	Genetic parameters for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad
38	Estimates of phenotypic and genotypic correlation coefficients for pod yield and its component traits in WW block during the two seasons of summer 2012-13 and summer 2013-14
39	Estimates of phenotypic and genotypic correlation coefficients for pod yield and its component traits in WS block during the two seasons of summer 2012-13 and summer 2013-14
40	Estimates of phenotypic and genotypic correlation coefficients for physiological traits in WS block during the two seasons of summer 2012-13 and summer 2013-14
41	Pooled estimates of phenotypic correlation coefficients between pod yield and physiological traits in WS block over two seasons of summer 2012-13 and summer 2013-14
42	Estimates of phenotypic and genotypic correlation coefficients for oil quality traits in WW block during the two seasons of summer 2012-13 and summer 2013-14
43	Estimates of phenotypic and genotypic correlation coefficients for oil quality traits in WS block during the two seasons of summer 2012-13 and summer 2013-14
44	Estimates of phenotypic and genotypic correlation coefficients for foliar

	disease resistance traits in WW block during the two seasons of summer 2012-13 and summer 2013-14
45	Estimates of phenotypic and genotypic correlation coefficients for foliar disease resistance traits in WS block during the two seasons of summer 2012-13 and summer 2013-14
46	Analysis of variance for root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
47	Analysis of variance for root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
48	Mean, range and genetic parameters of root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad
49	Mean, range and genetic parameters of root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad
50	Estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block during the two seasons of summer 2012-13 and summer 2013-14
51	Estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block during summer 2013-14
52	Pooled estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block over two seasons of summer 2012-13 and 2013-14
53	Pooled performance of selected recombinant inbred lines in multilocation yield trials at Annigeri and Bijapur during Kharif 2014-15
54	General features of genetic map of groundnut (<i>Arachis hypogaea</i> L.) developed using SSR markers based on 299 RILs developed from the cross TMV-2 x GM 6-1
55	QTLs associated with quantitative traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14
56	QTLs associated with physiological traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14
57	QTLs associated with root traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14
58	QTLs associated with oil quality traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

59	QTLs associated with foliar disease resistance traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14
60	Superior RILs for pod yield under WS condition along with its component traits, physiological and root traits under WW and WS conditions pooled over the two seasons of summer 2012-13 and 2013-14
61	Comparison of DTI for pod yield and DTI for other important attributes among drought tolerant and drought susceptible RILs identified across the seasons
62	Superior RILs for DTI (pod yield) along with other component traits under WW and WS conditions pooled over the two seasons
63	Superior RILs for increased root length under WS condition
64	Stable QTLs identified for various traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14
65	Major QTLs identified for various traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WS condition during summer 2012-13 and summer 2013-14
66	Important QTL regions mapped for various traits at common positions

LIST OF FIGURE

Figure No.	Title
1a	Weather parameters during crop growth period of field evaluation during summer 2012-13
1b	Weather parameters during crop growth period of field evaluation during summer 2013-14
1c	Weather parameters during crop growth period of raised bed evaluation during summer 2012-13
1d	Weather parameters during crop growth period of raised bed evaluation during summer 2013-14
2	Soil moisture content in field and raised bed evaluation of summer 2012-13 and summer 2013-14
3	The modified 9-point scale for field evaluation of rust of groundnut
4	The modified 9-point scale for field evaluation of late leaf spot of groundnut
5	Identification of superior RILs for pod yield under WS condition along with traits associated with drought tolerance under WS conditions pooled over the two seasons of summer 2012-13 and 2013-14
6	Comparison of drought tolerant and drought susceptible RILs for traits associated with drought tolerance
7	Identification of superior RILs for DTI along with other component traits under WW and WS conditions pooled over the two seasons
8	Identification of superior RILs for increased root length under WS condition

LIST OF PLATES

Plate No.	Title
1	Variation for root length and pegging pattern between the parents TMV-2 and GM 6-1
2	Development of TMV-2 x GM 6-1 mapping population
3	General view of RILs at 30 days after stress in WW and WS condition of field and raised bed evaluation
4	Parental polymorphism for some of the markers
5a	Genotyping with markers Seq 15F12-V and TC7C06-NT in the RIL population on capillary electrophoresis ABI 3730 XL genetic analyzer
5b	Genotyping with markers TC 5D06-P and m13-AHGS2960-V in the RIL population on capillary electrophoresis ABI 3730 XL genetic analyzer
6	Genetic linkage map of TMV-2 x GM 6-1
7	Variation observed among the genotypes at 15 days after water stress with in WS condition of field evaluation
8	Variation observed among the genotypes at 30 days after water stress with in WS condition of field evaluation
9	Comparison of drought tolerant (RIL 101) and drought susceptible (RIL 59) RILs for pod yield under WW and WS conditions of field evaluation
10	Comparison of checks for pod yield under WW and WS conditions of field evaluation
11	Comparison of drought tolerant and drought susceptible lines during field evaluation of summer 2012-13
12	Superior RILs for higher root length under WS condition of raised bed evaluation
13	LOD peak for various traits on LG-3 between m13TC39C01V-Gm2215-F in TMV-2 x GM 6-1 mapping population of groundnut

LIST OF APPENDICES

Appendix No.	Title
I	Meteorological data during the crop growth periods of field and raised bed evaluation during summer 2012-13
II	Meteorological data during the crop growth periods of field and raised bed evaluation during summer 2013-14
III	List of polymorphic SSR primers between the parents TMV-2 x GM 6-1 in groundnut
IV	Meteorological data at Annigeri during <i>kharif</i> 2014-15
V	Meteorological data at Bijapur during <i>kharif</i> 2014-15
VI	Mean air temperature and Rainfall at Bijapur and Annigeri from the years 2011-2014
VII	Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for pod yield and oleic acid under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14
VIII	Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for important physiological traits under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14
IX	Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for root traits under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an important legume grown for the extraction of edible oil and used as a nutritional ingredient of human and animal foods. It is a native of South America and grown in six continents but mainly in Asia, America and African countries. It is one of the main sources of protein in Africa and Asia (Savage and Keenan, 1994). It ranks fifth in the world among oilseeds with an area of 24.48 million hectares, production of 42.74 million tonnes (with shell) and productivity of 1.68 tonnes/hectare (Anon., 2013). China, India and USA are the major producers of the crop, of which India accounts for area of 5.24 million hectares with 9.47 million tonnes of production (Anon., 2013). Though, India is a leading producer of the crop but its productivity is lower (1804 kg/ha) compared to USA (4496 kg/ha) and China (3658 kg/ha). Of the five principal groundnut producing states in the country, in Karnataka it is grown on an area of 0.59 million hectares with production of 0.40 million tonnes and productivity of 671 kg/ha (Anon., 2013).

The cultivated tetraploid groundnut ($2n = 4x = 40$, AABB) (Stebbins, 1957; Stalker and Dalmacio, 1986) is a self-pollinating crop with ten basic chromosomes. It is a member of genus *Arachis* and belongs to the family *Leguminosae*, subfamily *Fabaceae*, tribe *Aeschynomeneae* and subtribe *Stylosanthenae* (Krapovickas and Gregory, 1994). Groundnut is believed to have originated in the Bolivian region of South America where the greatest diversity is found (Krapovickas, 1969; Gregory and Gregory, 1976). The origin of cultivated groundnut was probably through a single hybridization event between two diploid wild species, *A. duranensis* (AA genome) and *A. ipaensis* (BB genome), followed by a spontaneous chromosome duplication (Halward *et al.*, 1991).

Among oilseed crops, groundnut is unique in consumption pattern that can be consumed directly as an item of food and also utilized in diverse ways. Groundnut is an important source of vegetable oil (48 %) and protein (25 %) in tropical and subtropical regions of the world. It also provides vitamins such as thiamine, riboflavin and niacin and minerals like phosphorous, iron and zinc (Savage and Keenan, 1994). A large number of food products are prepared from groundnuts; which include boiled nuts,

roasted nuts, salted nuts, groundnut milk, groundnut yogurt, groundnut bars, groundnut butter, groundnut cheese, bakery products etc. It is a cash crop and useful rotation crop, easy to grow, withstands drought to some extent and so a choice crop for dry farming. It is resistant to soil erosion, can fix atmospheric nitrogen and maintains soil fertility. In addition, the plant stalks (haulms), shell and hay are fed to cattle. Groundnut cake obtained after oil extraction is a good feed for livestock and it is also used as manure. It has all the potential to be used as a highly economical food supplement to fight malnutrition that occurs due to deficiencies of nutrients in the cereal grains like wheat and rice. Although India is a leading producer of groundnut, low productivity is attributed to the crop loss due to biotic and abiotic stresses.

Drought is by far the most important abiotic stress contributing to crop yield loss in the semi-arid tropics (SAT) characterized by low and erratic rainfall. Therefore, identification of genotypes that have a better ability to use limited available water is important to enhance crop productivity in the SAT. More than half of the production area, that accounts for 70 per cent of the groundnut growing area fall under arid and semi-arid regions, where crop is frequently subjected to drought stresses for different duration and intensities (Reddy *et al.*, 2003). Unpredictable and intermittent periods of water deficit commonly occur during its growth period (Vorasoot *et al.*, 2003). Drought stress has depressive effects on groundnut productivity (Nageswara Rao *et al.*, 1989; Nautiyal *et al.*, 2002, Nigam *et al.*, 2005, Songsri *et al.*, 2008a). The depressive effect of drought on growth and yield components depends on the time, the intensity and the duration of drought stress (Nautiyal *et al.*, 2002; Nigam *et al.*, 2005).

Drought is a meteorological term and is commonly defined as a period without significant rainfall. Generally drought stress occurs when the available water in the soil is reduced and atmospheric conditions cause continuous loss of water by transpiration or evaporation. Groundnut typically experiences a range of stresses and effect on yield is highly dependent on the stage when the stress occurs and the available water to the crops at that stage (Ratnakumar *et al.* 2009).

Imposition of pre-flowering drought resulted in an increase in yield of 13-57 per cent in some genotypes (Nautiyal *et al.*, 1999; Puangbut *et al.*, 2010). Yield reductions of 56–85 per cent were recorded when groundnut was exposed to

intermittent drought at flowering and seed-formation stages (Del Rosario and Fajardo, 1988), and yield reduction of 24 per cent was reported when the crop was subjected to end of season drought (Boontang *et al.*, 2010). Water uptake is crucial during key stages like flowering and kernel filling (Boyer and Westgate 2004; Vadez *et al.*, 2007), and small differences in water uptake at these stages can bring large yield benefits in groundnut (Boote *et al.*, 1982; Ratnakumar *et al.*, 2009). Intermittent drought, which is an episodic water deficit during plant growth, is the most prevalent drought type affecting groundnut production and productivity in the rain-fed regions of SAT, which is estimated to 500 million US\$ every year (Sharma and Lavanya, 2002). Therefore, breeding for drought adaptation is an important strategy in alleviating drought effects on groundnut productivity.

Drought is perhaps the most complex stress, and the equally complex and varied adaptive mechanisms evolved by plants have made the task of improving drought tolerance a formidable challenge. Therefore, improving drought tolerance by improving productivity under water limited conditions as well as use of trait-based breeding approach is being suggested as the most suitable strategy. Simple analytical crop models can provide an attractive framework for understanding genotypic variation in yield and the effect of environment on physiological processes contributing to yield. Such models lead to the identification of relevant traits that warrant exploitation. The model proposed by Passioura (1977) describes yield (Y) as a product of total transpiration (T), WUE (defined as the biomass produced per unit of water transpired) and harvest index (HI; defined as the proportion of economic yield in total biomass).

Among a large number of traits that have relevance for drought tolerance, those traits that contribute to the maintenance of better tissue water relations of the plants have the greatest relevance. Traits associated with water mining from deeper soil profiles (root traits), efficiency of water use for biomass production (WUE), water conservation strategies associated with epicuticular waxes and regulation of stomatal movement, and superior intrinsic tolerance at the cellular level are a few of the most relevant traits that deserve exploitation.

Breeding progress for drought resistance in groundnut on basis of yield as a sole selection criterion is slow due to large and uncontrollable genotype $\times$ environment

(G × E) interactions. Breeding approaches using physiological traits having high heritability and low G × E interactions can improve selection efficiency for superior drought tolerant genotypes and supplement the selection on basis of yield (Blum, 1988).

Drought resistance might be enhanced by improvement of soil water extraction capability or improvements in water use efficiency (WUE), or integration of both (Wright and Nageswara Rao, 1994). Improvement of WUE could potentially lead to increased yield under limited moisture availability (Passioura, 1986). However, WUE is not easy to measure and may not be a feasible selection criterion in large segregating breeding populations. Putative selection criteria that could be used as indirect selection to increase WUE in groundnut have long been identified (Nageswara Rao and Wright, 1994; Nageswara Rao *et al.*, 2001 and Upadaya, 2005).

Although stable isotope ratios are accurate surrogates, progress in breeding for physiological traits can be hindered severely by the cost of a mass spectrometer and limited accessibility. Thus, simpler yet accurate alternatives are essential, at least as initial screening strategies. For drought resistance breeding, Water Use Efficiency (WUE) is an important parameter that is correlated with SPAD chlorophyll meter reading (SCMR) and specific leaf Area (SLA).

Biomass accumulation in plants is always a function of total water transpired. Thus, water mining (Angus and Herwardeen, 2001; Passioura, 1986) from deeper soil profiles as associated with a deep root system is a very important trait to sustain the water requirement for transpiration, thereby enhancing biomass (Li *et al.*, 2005). Roots could play an important role for yield increase in response to intermittent drought in groundnut. Information on the responses of root characteristics of diverse groundnut genotypes to intermittent drought under field conditions is still lacking and further investigations are necessary. Further, the mechanisms underlying yield responses of the groundnut genotypes have not been well understood because there was no information on root traits under these conditions. The results reported so far have been limited to experiments under greenhouse conditions and with only a few genotypes. There is an immediate need to study the mechanism of response of root traits for the pod yield under drought stress in field conditions.

The complex nature of physiological traits associated with drought tolerance and the difficulties associated with their measurements in large segregating populations inhibited their use in developing water-use efficient genotypes in breeding programs in the past. Even at the present scenario, studies on selective evaluation of advanced breeding lines for drought tolerance is scarce and is very much required to identify drought tolerant genotypes which can help the farming community especially in rainfed ecosystems of our country. Furthermore, selected new plant varieties must have an array of biotic stress resistances, while still retaining product quality traits which are required for the farmers' adoption of any new cultivar.

Among the biotic stresses, the two major foliar diseases viz. late leaf spot (*Phaeoisariopsis personata* [(Berk. and Curt.) Deighton] and rust (*Puccinia arachidis* Speg.) are widespread and economically most important. They often occur together and cause yield loss up to 50-70 per cent in groundnut (Subrahmanyam *et al.*, 1984).

About 80 per cent of total groundnut production in India is crushed for oil extraction, thus improvement in oil content and quality is of interest to plant breeders and millers. Oleic and linoleic acids are the primary fatty acids in groundnut oil accounting for 80 per cent of fatty acid composition (Andersen and Gorbet, 2002). Maintaining quality is a concern where low quality and short storability are generally associated with rancidity of the kernels. High oleic acid groundnut has much longer shelf life and flavor stability than normal-oleic groundnut (O'Keefe *et al.*, 1993; Mugendi *et al.*, 1998). High oleic oil may provide health benefits since it has been associated with lowered blood serum cholesterol especially with low density lipoproteins (LDL) in humans (O'Byrne *et al.*, 1997).

Genetic variability for economic traits is the pre-requisite for any successful breeding programme as the degree of response to selection depends on the quantum of variability. Besides variation, the accurate reflection of phenotype on genotype is essential as the phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and also environment. So it is necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameter such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. The selection of one character leads to correlated

response in other trait as a result of complex relationship existing among different traits is well known. Many characters including yield are complex and polygenically inherited traits are highly influenced by a large number of factors and their interactions. Hence information on association of component characters with yield and among themselves and extent to which they are influenced by environment is necessary to bring desirable genetic changes.

Conventional breeding for developing drought tolerant varieties is time consuming and labor intensive due to the quantitative nature of drought tolerance and difficulties in selection for drought tolerance (Ribaut *et al.*, 1997). Recent advances in the area of crop genomics have offered tools to assist breeding (Varshney *et al.*, 2005, 2006). Molecular markers and molecular genetic linkage maps are the pre-requisites for undertaking molecular breeding activities in any crop. Such tools would then simply speed up the process of introgression of beneficial traits into preferred varieties, especially for complex traits such as drought. Identification of genomic regions associated with drought tolerance would also enable breeders to develop improved cultivars with increased drought tolerance using marker-assisted selection (MAS) (Ribaut *et al.*, 1996).

Even though several studies have reported the importance of trait based breeding approach, comparison of the progenies developed through trait-based and empirical (selections for yield under drought) breeding approaches, for enhanced pod yield of groundnut across environments, have shown that the trait-based selections did not demonstrate clear superiority over the empirical selections for yield under drought (Nigam *et al.*, 2005). This has prompted the need for the development of a component-trait approach using molecular marker tools, to characterize the parents precisely for component traits related to drought tolerance and to identify relevant QTLs for them that could be used in subsequent marker-assisted selection. Preliminary studies indicated that two genotypes, TMV-2 and GM 6-1, differed significantly for root and other component traits of drought tolerance which prompted the use of recombinant inbred line population developed using these two parents for purpose of genetic mapping.

Based on these cited facts, it was proposed in this study to evaluate the genetic variability in recombinant inbred lines of groundnut derived from diverse parents (TMV-2 and GM-6-1) for drought tolerance and root traits and their correlated response to yield contributing traits under irrigated and water stress conditions; and to develop a genetic map and identify the QTLs for the above traits by using SSR markers.

Keeping the above facts in view, the present study was proposed with the following objectives.

1. Phenotyping the recombinant inbred lines (RILs) of the mapping population developed from the cross TMV-2 x GM 6-1 for drought tolerance under field conditions.
2. Phenotyping the RILs of the mapping population developed from the cross TMV-2 x GM 6-1 for root traits in raised beds.
3. Identification of drought tolerant RILs from the mapping population based on the correlated response for drought tolerance traits, root traits as well as yield component traits.
4. Screening of parents and RILs with SSR DNA markers to map and identify QTLs for important drought tolerance related traits, yield and its component traits, quality traits and foliar disease resistance.

2. REVIEW OF LITURATURE

Drought is a complex syndrome, involving several climatic, edaphic and agronomic factors. Unpredictable rainfall, high temperatures, high levels of solar radiation and poor soil characteristics prevalent in groundnut-growing tropical areas make it extremely hard to predict the time of occurrence, duration and intensity of drought stress. Further, plant responses to drought stress are species-specific and show significant phenological variation.

When phenotypic selection was the only tool available to improve yield under drought, the improvements in crop yield observed were likely due to an increase in yield potential through the unconscious pyramiding of yield-related traits or loci. While the direct selection for yield can be effective for specific adaptation but its application in larger breeding programmes catering for a wider range of environments is becoming increasingly limited and it depends on a comprehensive understanding of the nature and extent of G x E interactions for the physiological traits contributing to yield, especially under water-limited environments (Ludlow and Muchow, 1990; Sheshshayee *et al.*, 2003).

In recent years, crop physiology and genomics have led to new insights in drought tolerance providing breeders with new knowledge and tools for plant improvement (Tuberosa and Salvi, 2006). Use of molecular markers has accelerated plant breeding in a number of areas including disease resistance and drought tolerance. The availability of consensus genetic maps has facilitated localization of genes controlling both simple and complex traits, mapping of QTLs of agronomic interest in many crops and marker assisted selection (Paterson *et al.*, 1991; Winter and Kahl, 1995). The present study was initiated to understand the combinations of morphological, physiological, and phenological traits required for optimal adaptation to drought stress and to develop a molecular genetic map of groundnut using the cultivated x cultivated mapping population using SSR markers. Furthermore the application of this genetic map was demonstrated for mapping QTLs for the traits related to yield improvement in groundnut under water limited conditions.

The literature pertaining to the present topic is reviewed and presented under following subheadings.

2.1 Evaluation for traits related to drought tolerance

2.1.1 Physiological traits in relation to drought tolerance

2.1.2 Root traits in relation to drought tolerance

2.2 Genetic variability, Heritability and Genetic Advance

2.2.1 Quantitative traits

2.2.2 Physiological traits

2.2.3 Root traits

2.2.4 Quality traits

2.2.5 Foliar disease resistance

2.3 Correlation studies

2.3.1 Correlation between yield and yield components

2.3.2 Correlation between yield and physiological traits related to drought tolerance

2.3.3 Correlation between yield and root traits related to drought tolerance

2.3.4 Correlation between oil quality traits

2.3.5 Correlation between yield and foliar disease resistance

2.4 Molecular markers and genetic mapping in groundnut for various traits

2.5 QTL mapping approach

2.1 Evaluation for traits related to drought tolerance

2.1.1 Physiological traits in relation to drought tolerance

The genotype $\times$ environment (G $\times$ E) interaction for yield in groundnut under drought, as it occurs in many other crops, indeed complicates selection and slows down the breeding progress (Wright *et al.*, 1996; Mothilal *et al.*, 2010). Information on physiological traits contributing to high yield under drought stress might reveal the underlying mechanism from which improved strategies could be developed to enhance the effectiveness and progress in breeding for drought tolerance in groundnut (Pimratch *et al.*, 2008; Songsri *et al.*, 2009). Some physiological characters such as relative water content (RWC), specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) are related to drought tolerance in groundnut.

Leaf water status affects numerous physiological processes which contribute to plant growth and yield. Relative Water Content is considered as a more useful integrator of plant water balance than leaf water potential and significant decrease in RWC seemed in close accordance with soil water availability that was related to rain distribution before the application of water deficit (Clavel *et al.*, 2005).

RWC of leaves is higher in the initial stages of leaf development and declines as the as the dry matter accumulates (Jain *et al.*, 1997). It showed large diurnal variation with high values in the morning when solar radiation and vapour pressure deficits are low, followed by low values around midday and gradual increase after midday (Erickson and Ketring, 1985).

Relative Water Content (RWC) values in well watered groundnuts are typically in a range of 85-98 per cent (Bhagasari *et al.*, 1976; Bennett *et al.*, 1981). Under drought conditions, RWC was as low as 29 per cent (Bhagasari *et al.*, 1976) indicating that groundnut has a very low lethal water status. This attribute should contribute to high level of dehydration tolerance and leaf survival in groundnut during intermittent drought stress.

Water stressed plants have lower RWC than non- stressed plants where it ranged from 85-90 per cent in non-stressed plants while it was as low as 30 per cent in the

stressed plants (Babu and Rao 1983). Drought tolerant cultivars had lower water potential but higher RWC than drought susceptible cultivars (Joshi *et al.*, 1988).

Painwadee *et al.* (2009) indicated that RWC was sensitive in identifying drought stress even in same groundnut genotypes with appropriate stress level. In case of mild drought stress, the use of RWC would not be appropriate because there was no significant difference between the stressed and non-stressed treatments. This is possibly due to slow response of groundnut to declining water level. Whereas, the response to water depletion was more acute in the soil than in the groundnut plants.

For drought resistance breeding, Water Use Efficiency (WUE) is an important parameter that is correlated with SPAD chlorophyll meter reading (SCMR) and specific leaf weight (SLA). These two traits, SCMR and SLA, can be used as surrogate traits for selecting for WUE. In order to improve SCMR and SLA, and in turn WUE in groundnut, a good knowledge of the genetic system controlling the expressions of these traits is essential for the selection of the most appropriate and efficient breeding procedure.

In a field experiment conducted at Khon Kaen University using split plot design during 2010-11 and 2011-12, Koolachart *et al.* (2013) revealed that the groundnut genotypes with high SCMR, RWC, leaf area index and stomatal conductance, and low SLA and canopy temperature and high drought tolerant index (DTI) for number of pods per plant, DTI for number of seeds per pod and DTI for 100-seed weight could maintain high pod yield under drought conditions. They also suggested that ability to maintain physiological traits and yield components could aid groundnut genotypes in sustaining high pod yield under stress conditions and identified the genotypes viz., ICGV 98324, ICGV 98348 and Tifton 8 for water stress conditions

Studies by Wright *et al.* (1994) and Nageswara Rao & Wright (1994) demonstrated a positive correlation between specific leaf area (SLA, ratio of leaf area to leaf dry weight) and $\Delta^{13}C$ ($r^2 = 0.90-0.93^{**}$) in groundnut and a negative relationship between SLA and TE, suggesting that SLA can be used as a rapid alternate to estimate genetic variability in TE among groundnut genotypes. Although a close correlation between SLA and $\Delta^{13}C$ (and thus with TE) has been established in controlled experiments, the strength of correlation varied with 'r' ranging from 0.71 to 0.94 over a

range of groundnut genotypes and environments (Wright *et al.*, 1994). It can therefore be inferred that SLA might be influenced by factors such as time of sampling, leaf age (Wright & Hammer, 1994; Nageswara Rao *et al.*, 1995, 2001) as well as accuracy of the measurement.

Richardson *et al.* (2002) revealed that thicker leaves (low SLA) usually have higher chlorophyll per unit area and hence have a greater photosynthetic capacity compared with thinner leaves.

The light absorbance and/or transmittance characteristics of a leaf can be exploited to determine the leaf chlorophyll content (Balasubramanian *et al.*, 2000; Takebe *et al.*, 1990). The ability to maintain chlorophyll density under water deficit condition has been suggested as drought tolerance mechanism in groundnut (Arunyanark *et al.* 2008; Sheshshayee *et al.* 2006). The SCMR is an indicator of the photo-synthetically active light transmittance characteristic of the leaf which is dependent on the unit amount of chlorophyll per unit leaf area.

A significant positive relationship between SCMR and chlorophyll content has been reported in many crop species including groundnuts (Rao *et al.*, 2001; Sheshshayee *et al.*, 2006). Further, Dwyer *et al.* (1995) and Chapman & Barreto (1997) demonstrated that SCMR is related to the leaf nitrogen status. Therefore, the close relationships observed among SCMR, SLA and SLN (Nageswara Rao *et al.*, 2001) implied that SCMR could be used as a rapid, low cost and in situ technique to screen for TE in large breeding populations.

Nigam and Aruna (2008) reported that SCMR and SLA had low G x E interaction, indicating that these traits are stable across a wide range of environments. These findings are in accordance with Songsri *et al.* (2008).

Songsri *et al.* (2009) showed that the relationship between SLA and SCMR were constant under different water regimes. Groundnut genotypes having ability to maintain high SCMR and lower SLA under drought stress should be more tolerant to drought and hence maintain higher WUE under severe drought conditions.

Upadhyaya *et al.* (2011) evaluated two crosses viz., ICG 72439 x ICG 9418 and ICG 67669 x Chico, and their reciprocals to determine the gene action controlling the

inheritance of SCMR and SLA. They revealed importance of additive effects in both the crosses for SCMR at 80 DAS whereas predominance of dominance effects with duplicate epistasis for SCMR at 60 DAS and SLA at both stages in both the crosses suggesting that selection could be effective even in early generations for SCMR at 80 DAS, whereas, selection to later generations for SCMR at 60 DAS and SLA at both stages in both crosses.

Boontang *et al.* (2010) in a split plot design consisting of ten groundnut genotypes and two water regimes viz., field capacity and 1/3 available water, identified the released cultivar KGU-60 as the drought tolerant genotype by using SCMR, SLW and pod yield as selection criteria.

Thakur *et al.* (2013) evaluated twenty five groundnut genotypes in a randomized complete block design in three replications and identified the genotypes viz., ICGV-99171, ICGV-98089, ICGV-97100, Baidehi, ICGV-00440 and B-4 for drought tolerance with high pod yield by using the traits such as SCMR, SLA, root to shoot ratio and drought tolerance score. They also suggested that these genotypes could be used as parents in breeding programmes for developing drought tolerant groundnut cultivars.

2.1.2 Root traits in relation to drought tolerance

The maximization of water uptake is essential for the growth and production under limited water resource. Drought resistance may be enhanced by improving the ability of the crop to extract water from the soil (Wright and Nageswara Rao 1994). In several crops, adaptation to drought is closely associated to root development, which provides a better water extraction ability to plants (Jongrunklang *et al.* 2011). Roots are expected to play an important role in adaptation to drought in groundnut where relation between root depth and pod yield under drought condition has been established (Robertson *et al.* 1980). Since the root traits had big contributions on yield in crop, they received increasing attention by crop breeders (Steele *et al.*, 2006).

Quantitative inheritance of many root characteristics was revealed by O'Toole and Bland (1987). Deep rooting, root length density (RLD) and root distribution have been identified as drought adaptive traits (Passioura 1983, Turner 1986, Ludlow and Muchow 1990, Matsui and Singh 2003, Taiz and Zeiger, 2006) that can be used as

selection criteria for drought resistance. However, such observation was based upon few studies involving only few genotypes.

The status of water in plants represents an integration of atmospheric demand, soil water potential, rooting density and its distribution and could be used as a true measure of drought tolerance in plants (Kramer, 1983).

There appears to be some controversy on the response of the root to stress. Root growth was reported to increase upon water deficit (Allen *et al.* 1976), in particular rooting depth (Ketrin and Reid 1993). Songsri *et al.* (2008, 2013) found that the groundnut genotypes with higher root length density (RLD) under drought could maintain high pod yield. By contrast, Robertson *et al.* (1980) did not find any RLD differences at shallow soil depths between well irrigated and water stressed condition.

Meisner and Karnok (1992), who investigated root growth of a groundnut genotype in a rhizotron chamber, found that the root growth rate was significantly reduced during stress from 20 to 50 days after planting (DAP) compared to non-stressed conditions under sufficient irrigation. After recovery, early drought-stressed groundnut had more root growth than the non-stressed groundnut of the control treatment.

In fact, Ketrin and Reid (1993) found that groundnut was able to establish both a deep and laterally spreading root system fairly early during the growing cycle, providing the adaptation to drought occurrence during later stage in the season.

Ability for drought resistance in groundnut genotypes was exhibited through maximum water uptake through improving the capacity of root system to acquire water and optimization of water use for yield production (Subbarao *et al.*, 1995).

Rucker *et al.* (1995) found that some groundnut genotypes that had a large root system (root dry weight) under non-stress conditions produced a higher yield under drought conditions and they suggested that these genotypes could possess drought avoidance traits.

Awal and Ikeda (2002), who studied only one groundnut genotype grown in containers, reported that drought significantly enhanced the root to shoot ratio which accelerated post-stress recovery. Therefore, it appears that the seasonal dynamics of

water use are crucial and the question is still open about the study of root growth alone in relation to pod yield.

Root traits such as root length density, rooting depth and root distribution have been identified as drought resistance (Matsui and Singh, 2003).

Puangbut *et al.* (2009) reported that root dry weight had a contribution to TE under well-watered and drought conditions, especially under drought condition while, SCMR and SLA had smaller contributions to TE under well-watered and early season drought conditions. From this study they concluded that root dry weight was an important trait for TE under early season drought.

Puangbut *et al.* (2010) evaluated groundnut in a split-plot design with two watering regimes as main-plots, and 12 groundnut genotypes as sub-plots. They found that imposition of pre flowering drought (PFD) followed by recovery resulted in an average increase in yield of 24 per cent with a range from 10 per cent to 57 per cent and 12 per cent with a range from 2 per cent to 51 per cent in the field and glasshouse experiments, respectively. A combination of N₂ fixation, leaf area and root growth accounted for a major portion of the genotypic variation in yield ($r = 0.68\text{--}0.93$) suggesting that these traits could be used as selection criteria for identifying genotypes with rapid recovery from PFD.

Jongrunklang *et al.* (2011) conducted a split-plot experiment with two water management treatments as the main plots, i.e. field capacity and pre-flowering stress, and six groundnut genotypes as the sub-plots for investigating the root dry weight and root length density along with their relationships with pod yield. They categorized groundnut genotypes into three groups based on their responses to drought for pod yield, e.g. increasing, decreasing and non-responsive groups. The genotypes of each group showed a differential response for root quantity and distribution and concluded that increasing pod yield group had more root dry weight and root length density in the deeper soil layers during pre-flowering stress compared to the non-stress treatment.

A recent modelling study with soybean indicated that a faster rate of root growth had a negative effect on yield as a result of rapid use of soil water (Sinclair *et al.*, 2010). Recent studies in chickpea (Zaman-Allah *et al.*, 2011a) and groundnut (Ratnakumar *et*

et al., 2009) bring experimental evidence to this by showing the importance of temporal patterns of water use rather than root development per se and profuse rooting. Zaman-Allah *et al.* (2011a, b) found that slower shoot growth in chickpea resulted in water saving during vegetative stages (2011b) and this was critical in making water available during grain filling (2011a).

Root characters such as root dry weight and root length density were defined as important traits for response to early season drought in groundnut and also contributed to yield (Jongrunklang *et al.*, 2011).

Koolachart *et al.* (2013) evaluated five groundnut genotypes in a split plot design and revealed that the genotypes with large root system and high stomatal conductance, WUE and biomass could maintain higher pod yield under terminal drought. Further, they concluded that percent root length density could be useful as a selection criterion for improving resistance to drought.

To investigate the mechanism of drought tolerance, Jongrunklang *et al.* (2013) evaluated six groundnut genotypes in a split-plot experiment under different levels of pre-flowering drought (PFD) conditions. Based on the response of ICGV 98305 to PFD, they reported that high water uptake of the root systems could provide sufficient water for normal transpiration which induce the improvement of groundnut pod growth rate in pod filling stage due to the change of assimilate proportion, resulting in increasing pod yield to PDF comparing with adequate water conditions. In contrast, with the response of ICGV 98330, they reported that pre-flowering drought can increase the ability of groundnut to save more water by reduction of transpiration, where rooting traits were not changed, by which the plant can conserve more water by reducing transpiration to maintain high RWC. Finally they concluded that increase in groundnut productivity to pre-flowering drought was contributed by the improvement of assimilate proportion to economic part in reproductive phase.

2.2 Genetic variability, Heritability and Genetic Advance

The basic key to bring about the genetic upgrading in a crop is to utilize the available or created genetic variability. Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of

selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. The genetic coefficient of variability gives a useful measure of the magnitude of genetic variance present in the population. The degree of success depends on the magnitude of heritability [$h^2(b)$] as it measures the relative amount of the heritable portion of variability. Genetic advance (GA) under selection gives an idea about how much of the genetic gain obtained was due to selection. Hence, the estimates of genetic variability, heritability and genetic advance had an immense value in identifying the superior genotypes. A brief review of work done on variability, heritability and genetic advance in groundnut is presented hereunder.

2.2.1 Quantitative traits

Sharma and Varshney (1995) noticed high GCV, PCV, heritability and genetic advance for harvest index and its component traits *viz.*, pod yield per plant, number of branches per plant, 100-seed weight and sound mature kernel per cent.

Varman and Raveendran (1996) observed high heritability for plant height, number of branches per plant, number of mature pods per plant, number of pegs per plant and 100-kernel weight. They also revealed low genetic advance for harvest index and kernel yield per plant and low heritability for shelling out turn and oil content. They further noted that kernel weight and number of mature pods as the most important traits contributing to pod yield and oil content, respectively.

Naik *et al.* (2000) revealed high GCV for pod weight per plant, 100-kernel weight and plant height suggesting that selection for these characters would be more effective. They observed low GCV for number of primaries per plant, number of pods per plant, shelling percentage and sound mature kernel percentage. They found high heritability in broad sense [$h^2(b)$] for 100-kernel weight and number of primary branches indicating that they were least influenced by environment. They also recorded medium heritability values for plant height and pod weight per plant and high genetic advance as per cent of mean for pod weight per plant and 100-kernel weight.

Vijayasekhar (2002) reported high GCV, PCV, heritability and genetic advance as per cent of mean for harvest index, 100-seed weight, kernel yield per plant and

shelling percentage. On contrary, low estimates of variability, heritability and genetic advance were revealed for primary branches per plant, days to maturity, plant height, pods per plant, mature pods per plant and oil content.

A field evaluation with 48 diverse large seeded groundnut genotypes by Parameshwarappa *et al.* (2005) revealed higher genetic variability for number of primary branches, pod yield per plant, kernel yield and plant height. They noticed considerable variability for number of pods, 100-kernel weight, seed size and protein content and low variability for oil content and sound mature kernels. High heritability coupled with high genetic advance was noticed in respect of kernel yield, sound mature kernels and 100-kernel weight indicating the genetic control of additive genes for these characters. They further reported low genetic advance for kernel size and oil content indicating that these traits were influenced by environment.

Suneetha *et al.* (2005) reported high heritability coupled with high genetic advance as per cent of mean for number of mature pods and number of immature pods while, high heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50 per cent flowering, height of the main axis, 100-seed weight and pod yield per plant. On contrary, they observed high heritability coupled with low genetic advance as per cent of mean for number of primary branches and shelling percentage.

Singh (2005) studied genetic variability, heritability and genetic advance in 163 genotypes of groundnut for pod yield and its attributes. They observed high heritability and high percentage of GAM for number of pods and pod yield per plant indicating the involvement of additive genes in their genetic control and improvement in yield could be brought about by selection based on phenotypic superiority.

Korat *et al.* (2009) tested 80 diverse genotypes of bunch groundnut during summer 2006 for 14 yield contributing characters and observed high PCV, GCV and heritability coupled with high genetic advance as per cent of mean for number of secondary branches per plant indicating that this trait is mainly governed by additive gene action and responsive to selection for further improvement.

Wunna *et al.* 2009 evaluated ninety lines in the $F_{4:5}$ generation from four groundnut crosses under field capacity and one third available water. They reported high heritability for biomass production, pod yield number of pods per plant and 100 seed weight for all crosses under both water regimes.

Raut *et al.* (2010) evaluated six crosses of F_2 population along with nine parental lines in groundnut and reported high estimates of GCV, PCV and genetic advance for days to flowering, number of primary branches per plant, plant height, number of mature pods per plant, number of immature pods per plant, kernel yield per plant and pod yield per plant in most of the crosses indicating the influence of additive gene action and scope for improvement through simple selection.

Shinde *et al.* (2010) observed highly significant differences among the genotypes for all the yield contributing characters except number of primary branches per plant. They registered high estimates of GCV and PCV for pod yield per plant, number of immature pods per plant, number of mature pods per plant and biological yield per plant indicating the large extent of genetic variability and less role of environment in the expression of these traits. They found high GCV, high heritability coupled with high genetic advance for pod yield per plant and number of mature pods per plant. They concluded that these characters were mainly under the influence of additive gene action indicating the ample scope for improvement in these traits through simple selection.

Pradhan and Patra (2011) evaluated 460 genotypes of groundnut germplasm in four different seasons for estimation of phenotypic variation, heritability and genetic advance among pod yield and yield components. They observed low GCV for shelling percentage and moderate GCV for hundred pod weight and hundred kernel weight. They noticed high heritability coupled with high genetic advance as per cent of mean for hundred pod weight and hundred kernel weight.

Jogloy *et al.* (2011) studied 200 lines of ten crosses (F_6 generation) in groundnut to evaluate heritability for pod yield and its attributes. High heritability estimates were found for days to maturity and harvest index while, low to moderate heritability was observed for pod yield.

Zaman *et al.* (2011) evaluated 34 genotypes during *rabi* 2009-2010 for estimation of genetic variability and genetic parameters for 11 morphological characters and observed highly significant variations among the genotypes for all the characters studied. The highest GCV was observed for kernel yield per hectare followed by kernel yield per plant, branches per plant, immature and mature nuts per plant, 100 kernel weight and plant height. The highest heritability was observed for kernel yield per plant (95.08%), followed by kernel yield per hectare (94.38%), 100-kernel weight (87.01%), immature and mature nuts per plant (82.24% and 80.32%), and branches per plant (79.54%) while, high values of genetic advance were recorded for all the characters except days to maturity and days to 50 per cent flowering.

A review of literature on variability for quantitative characters in groundnut indicates the existence of high degree of variability for most of characters studied. Though there were reports of high genetic variability for plant height, shelling per cent, pod yield per plant, reports contradicting the above and quoting low or medium variability for these characters were also available which are listed in Table 1. Some of the reports on genotypic coefficient of variation and phenotypic coefficient of variation for some quantitative characters in groundnut are given in Table 2.

High heritability for plant height, pod yield per plant, shelling per cent, number of primary branches, kernel yield, 100-seed weight were reported. However, contradicting reports stating moderate to low heritability for plant height, pod yield per plant, shelling per cent, were also indicated by many workers (Table 3).

High genetic advance was reported for plant height, number of primary branches, and pod yield per plant, kernel yield, sound mature kernels, and 100-kernel weight. However, for shelling per cent and 100-kernel weight contrasting reports stating medium to low heritability were also available and are presented in Table 4.

2.2.2 Drought tolerance traits

Efficient utilization of the physiological traits for improving drought resistance in a breeding program requires an understanding of the inheritance and genetic relationships of the trait that is available for selection. Series of experiment were conducted to estimate the heritability of physiological traits for drought resistance under

Table 1: Literature showing the variability studies of various quantitative traits in groundnut

Sl. No.	Characters	Status of genetic variability	Authors
1	Days to 50% flowering	High	Sumathi and Ramanathan (1995a), Uddin <i>et al.</i> (1995), John <i>et al.</i> (2008), Raut <i>et al.</i> (2010)
		Low	Ganesan and Sudhakar (1995), Korat <i>et al.</i> (2009), Vishnuvardhan <i>et al.</i> (2012)
2	Plant height (cm)	High	Habib <i>et al.</i> (1985), Alam <i>et al.</i> (1985a), Kandaswamy <i>et al.</i> (1986), Patil and Bhaskar (1987), Reddy <i>et al.</i> (1987), Kale and Dhoble (1988), Prasanthi <i>et al.</i> (1990), Mishra and Yadava (1992), Sumathi and Ramanathan (1995a), Uddin <i>et al.</i> (1995), Apte <i>et al.</i> (2008), John <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Raut <i>et al.</i> (2010), Shinde <i>et al.</i> (2010)
		Medium	Ganesan and Sudhakar (1995), Naik <i>et al.</i> (2000), Korat <i>et al.</i> (2009), Mothilal (2004)
		Low	Badwal <i>et al.</i> (1967), Wynne and Rawling (1978), Joshi <i>et al.</i> (1981)
3	Primary branches per plant	High	Uddin <i>et al.</i> (1995), Thaware <i>et al.</i> (2008), Raut <i>et al.</i> (2010)
4	Pod yield per plant	High	Deshmukh <i>et al.</i> (1986), Kandaswami <i>et al.</i> (1986), Reddy <i>et al.</i> (1986), Reddy <i>et al.</i> (1987), Lu <i>et al.</i> (1988), Patil and Bhaskar (1987), Manoharan <i>et al.</i> (1990), Vaddoria and Patel (1990), Reddy and Gupta (1992), Bansal <i>et al.</i> (1992), Mishra and Yadava (1992), Pathirana (1993), Sharma and Varshney (1995), Varman and Raveendran (1996), Gowda <i>et al.</i> (1996), Bashir <i>et al.</i> (1998), Yadav <i>et al.</i> (1998), Rudraswamy <i>et al.</i> (1999), Abhay <i>et al.</i> (2002), John <i>et al.</i> (2007), Jatti <i>et al.</i> (2008), John <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Savaliya <i>et al.</i> (2009), Raut <i>et al.</i> (2010)
		Medium	Kale and Dhoble (1988), Uddin <i>et al.</i> (1995), Naik <i>et al.</i> (2000), Mothilal (2004), Korat <i>et al.</i> (2009)
		Low	Badwal <i>et al.</i> (1967), Wynne and Rawling (1978)
5	Kernel yield	High	Wang <i>et al.</i> (1987), Lu <i>et al.</i> (1988), Mishra and Yadava (1992), Reddy and Gupta (1992), Sumathi and Ramanathan (1995a), Uddin <i>et al.</i> (1995), John <i>et al.</i> (2007), Jatti <i>et al.</i> (2008), Raut <i>et al.</i> (2010)
		Moderate	Sharma and Gupta (2011), Shoba <i>et al.</i> (2009)

Sl. No.	Characters	Status of genetic variability	Authors
6	Shelling per cent	High	Manoharan <i>et al.</i> (1990), Varman and Paramashivam (1992), Reddy and Gupta (1992), Bhat (1995), Uddin <i>et al.</i> (1995), Singh and Singh (1998), Rudraswamy <i>et al.</i> (1999), Singh <i>et al.</i> (1996), Mather and Manivel (2000), Abhay <i>et al.</i> (2002)
		Moderate	Reddy (1994)
		Low	Reddy <i>et al.</i> (1986), Nadaf and Habib (1987), Sumathi and Ramanathan (1995a), Gowda <i>et al.</i> (1996), Sarala and Gowda (1998), Yogendraprasad <i>et al.</i> (2002)
7	100 seed weight	High	Alam <i>et al.</i> (1985b), Reddy <i>et al.</i> (1986), Deshmukh <i>et al.</i> (1986), Patil and Bhaskar (1987), Vaddoria and Patel (1990), Manoharan <i>et al.</i> (1990), Varman and Paramasivam (1992), Mishra and Yadava (1992), Yadava (1992), Sumathi and Ramanathan (1995a), Uddin <i>et al.</i> (1995), Bhat (1995), Sharma and Varshney (1995), Singh <i>et al.</i> (1996), Singh and Singh (1998), Vasanthi <i>et al.</i> (1998a), Yadav <i>et al.</i> (1998), Venkataramana <i>et al.</i> (2001), Apte <i>et al.</i> (2008), John <i>et al.</i> (2008), Thaware <i>et al.</i> (2008)
		Moderate	Mothilal (2004), Korat <i>et al.</i> (2009)

Table 2: Review of reports on genotypic coefficient of variation and phenotypic coefficient of variation for some quantitative characters in groundnut

Sl. No.	Characters	GCV	PCV	Authors
1	Days to 50 per cent flowering	High	High	Raut <i>et al.</i> (2010)
		Medium	Medium	Sunday and Omolayo (2013)
		Low	Low	Venkateshmurthy (2005), Channayya (2009), Korat <i>et al.</i> (2009), John <i>et al.</i> (2011), Zaman <i>et al.</i> (2011), Rao <i>et al.</i> (2012), Vishnuvardhan <i>et al.</i> (2012)
		Low	-	Thaware <i>et al.</i> (2008)
		Low	High	Thakur <i>et al.</i> (2011),
2	Days to maturity	Low	Low	Makhan <i>et al.</i> (2003), Channayya (2009), Korat <i>et al.</i> (2009), John <i>et al.</i> (2011), Thakur <i>et al.</i> (2011), Zaman <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012), Rao <i>et al.</i> (2012)
		Medium	Medium	Sunday and Omolayo (2013)
3	Plant height	High	-	Suryanarayanareddy <i>et al.</i> (2001), Thaware <i>et al.</i> (2008),
		-	High	Kale and Dhoble (1988), Nath and Alam (2002)
		High	High	Kandswamy <i>et al.</i> (1986), Makhan <i>et al.</i> (2003), Venkateshmurthy (2005), John <i>et al.</i> (2007), Apte <i>et al.</i> (2008), Korat <i>et al.</i> (2009), Raut <i>et al.</i> (2010), Sudha <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Medium	Medium	Venkateshmurthy (2005), John <i>et al.</i> (2006), Kavera (2008), Channayya (2009), Zaman <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012), Rao <i>et al.</i> (2012),
		Low	Medium	Kavera (2008), Sarvamangala (2009), John <i>et al.</i> (2011)
		Low	High	Thakur <i>et al.</i> (2011)
4	Primary branches per plant	High	-	Kuriakose and Joseph (1986a)
		-	High	Nath and Alam (2002)
		High	High	Raut <i>et al.</i> (2010), Sudha <i>et al.</i> (2012)
		Medium	Medium	Channayya (2009), Korat <i>et al.</i> (2009), Vishnuvardhan <i>et al.</i> (2012)
		Low	Medium	John <i>et al.</i> (2011)
		-	Low	Rudraswamy <i>et al.</i> (1999)
5	Secondary branches per plant	High	-	Alam <i>et al.</i> (1985a), Chuahan and Shukla (1985)
		High	High	Korat <i>et al.</i> (2009), John <i>et al.</i> (2011),
		High	High	John <i>et al.</i> (2007), Sudha <i>et al.</i> (2012), Vishnuvardhan <i>et al.</i> (2012)
		-	Low	Rudraswamy <i>et al.</i> (1999)

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Sl. No.	Characters	GCV	PCV	Authors
6	Pod yield per plant	High	-	Chuahan and Shukla (1985)
		High	High	Kandswamy <i>et al.</i> (1986), Sharma and Varshney (1995), Makhan <i>et al.</i> (2003), Venkateshmurthy (2005), John <i>et al.</i> (2006), John <i>et al.</i> (2007), Kavera (2008), Raut <i>et al.</i> (2010), Zaman <i>et al.</i> (2011), Jonah <i>et al.</i> (2012), Sudha <i>et al.</i> (2012), Rao <i>et al.</i> (2012), Sunday and Omolayo (2013)
		-	High	Kale and Dhoble (1988), Nath and Alam (2002)
		-	Low	Rudraswamy <i>et al.</i> (1999)
		Low	Medium	John <i>et al.</i> (2011)
		Medium	High	Venkateshmurthy (2005), Kavera (2008), Sarvamangala (2009), Azharudheen (2010), Vishnuvardhan <i>et al.</i> (2012)
		Medium	Medium	Korat <i>et al.</i> (2009)
		Medium	Low	Azharudheen (2010)
7	Kernel yield per plant	High	-	Venkataramana <i>et al.</i> (2001)
		High	High	John <i>et al.</i> (2007), Kavera (2008), Raut <i>et al.</i> (2010), Rao <i>et al.</i> (2012)
		Low	Low	Apte <i>et al.</i> (2008)
		Low	Medium	John <i>et al.</i> (2011)
		Medium	Medium	Jonah <i>et al.</i> (2012)
		High	Medium	Venkateshmurthy (2005)
8	Shelling percentage	-	Low	Rudraswamy <i>et al.</i> (1999)
		Low	Medium	Vishnuvardhan <i>et al.</i> (2012)
		High	High	Kandswamy <i>et al.</i> (1986)
		Medium	Medium	Zaman <i>et al.</i> (2011)
		Low	Low	Venkateshmurthy (2005), Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat <i>et al.</i> (2009), Azharudheen (2010), John <i>et al.</i> (2011), Thakur <i>et al.</i> (2011), Jonah <i>et al.</i> (2012), Rao <i>et al.</i> (2012)
9	100 Seed weight	High	-	Joshi <i>et al.</i> (1981), Kuriakose and Joseph (1986a), Suryanarayana Reddy <i>et al.</i> (2001), Venkataramana <i>et al.</i> (2001), Thaware <i>et al.</i> (2008)
		High	High	Deshmukh <i>et al.</i> (1986), Sharma and Varshney (1995), Venkateshmurthy (2005), Apte <i>et al.</i> (2008), Thakur <i>et al.</i> (2011), Jonah <i>et al.</i> (2012), Rao <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Medium	Medium	Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat <i>et al.</i> (2009), Azharudheen (2010), Zaman <i>et al.</i> (2011)
		-	Low	Rudraswamy <i>et al.</i> (1999)
		Low	Low	John <i>et al.</i> (2011),

Table 3: Reports on degree of heritability for some quantitative characters in groundnut

Sl. No.	Characters	Degree of heritability	Authors
1	Days to 50 per cent flowering	High	Nadaf and Habib (1987), Yadava (1992), Ganesan and Shudhakar (1995), Venkateshmurthy (2005), Korat <i>et al.</i> (2009), John <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012), Rao <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Medium	Vaddoria and Patel (1990), Thakur <i>et al.</i> (2011), Zaman <i>et al.</i> (2011)
		Low	Venkateshmurthy (2005), Channayya (2009)
2	Days to maturity	High	Makhan <i>et al.</i> (2003), Thaware <i>et al.</i> (2008), Korat <i>et al.</i> (2009), John <i>et al.</i> (2011), Thakur <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Medium	Channayya (2009), Zaman <i>et al.</i> (2011), Rao <i>et al.</i> (2012)
		Low	Channayya (2009)
3	Plant height (cm)	High	Kandaswamy <i>et al.</i> (1986), Basu <i>et al.</i> (1986), Kale and Dhoble (1988), Manoharan <i>et al.</i> (1990), Mishra and Yadava (1992), Ganesan and Sudhakar (1995), Uddin <i>et al.</i> (1995), Varman and Raveendran (1996), Nath and Alam (2002), Makhan <i>et al.</i> (2003), Venkateshmurthy (2005), John <i>et al.</i> (2006), John <i>et al.</i> (2007), Apte <i>et al.</i> (2008), John <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Kavera (2008), Channayya (2009), Korat <i>et al.</i> (2009), Zaman <i>et al.</i> (2011), Sudha <i>et al.</i> (2012), Rao <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Moderate	Alam <i>et al.</i> (1985a), Prasanthi <i>et al.</i> (1990), Sumathi and Ramanathan (1995a), Suryanarayan Reddy <i>et al.</i> (2001), Thakur <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
		Low	Sarvamangala (2009), John <i>et al.</i> (2011)
4	Primary branches per plant	High	Kulkarni and Albuquerque (1967), Dixit <i>et al.</i> (1970), Raman and Sreerangaswamy (1970), Kandaswamy <i>et al.</i> (1986), Kuriakose and Joseph (1986), Ganeshan and Sudhakar (1995), Channayya (2009), Korat <i>et al.</i> (2009), Sudha <i>et al.</i> (2012)
		Medium	John <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
5	Secondary branches per plant	High	Alam <i>et al.</i> (1985), Reddy (1986), Dixit <i>et al.</i> (1970), Chauhan and Shukla (1985), Kandaswamy <i>et al.</i> (1986), Reddy <i>et al.</i> (1987), John <i>et al.</i> (2007), John <i>et al.</i> (2011), Sudha <i>et al.</i> (2012)
		Low	Vishnuvardhan <i>et al.</i> (2012),

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Sl. No.	Characters	Degree of heritability	Authors
6	Pod yield per plant	High	Reddy (1986), Bansal <i>et al.</i> (1992), Mishra and Yadava (1992), Yadava (1992), Reddy and Gupta (1992), Sharma and Varshney (1995), Varman and Raveendran (1996), Singh and Singh (1998), Prakash <i>et al.</i> (2000), Venkataraman <i>et al.</i> (2001), Yogendraprasad <i>et al.</i> (2002), Nath and Alam (2002), Venkateshmurthy (2005), John <i>et al.</i> (2006), John <i>et al.</i> (2007), Apte <i>et al.</i> (2008), John <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), Kavera (2008), Korat <i>et al.</i> (2009), Savaliya <i>et al.</i> (2009), Raut <i>et al.</i> (2010), Zaman <i>et al.</i> (2011), Rao <i>et al.</i> (2012), Jonah <i>et al.</i> (2012), Sudha <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Moderate	Basu <i>et al.</i> (1986a), Sumathi and Ramanathan (1995a), Singh (1998), Kavera (2008), Vishnuvardhan <i>et al.</i> (2012)
		Low	Wang <i>et al.</i> (1987), Manoharan <i>et al.</i> (1990), Reddy and Gupta (1992), Bhat. (1995), Ntrae and Waliyar (1999), Painawadee <i>et al.</i> (2009), Sarvamangala (2009), Azharudheen (2010), John <i>et al.</i> (2011)
7	Kernel yield per plant	High	Bansal <i>et al.</i> (1992), John <i>et al.</i> (2007), Kavera (2008), Rao <i>et al.</i> (2012)
		Low	John <i>et al.</i> (2011)
8	Shelling per cent	High	Bernard (1960), Sandhu and Khehra (1977), Labana <i>et al.</i> (1980), Quadri and Kunti (1982), Xiang <i>et al.</i> (1984), Reddy <i>et al.</i> (1987), Reddy and Gupta (1992), Uddin <i>et al.</i> (1995), Vasanthi <i>et al.</i> (1998b), Varman and Raveendram (1996), Singh <i>et al.</i> (1998), Ntare and Waliyar (1999), Yogendraprasad <i>et al.</i> (2002), Nath and Alam (2002), Venkateshmurthy (2005), John <i>et al.</i> (2007), Kavera (2008), Channayya (2009), Savaliya <i>et al.</i> (2009), Korat <i>et al.</i> (2009), Zaman <i>et al.</i> (2011), Jonah <i>et al.</i> (2012)
		Moderate	Venkateshmurthy (2005), Thakur <i>et al.</i> (2011), Rao <i>et al.</i> (2012), Vishnuvardhan <i>et al.</i> (2012)
		Low	Swamy Rao <i>et al.</i> (1988), Manoharan <i>et al.</i> (1990), Varman and Raveendran (1996), Sarvamangala (2009), Azharudheen (2010), John <i>et al.</i> (2011)
9	100 seed weight	High	Sangha and Sandhu (1970), Dixit <i>et al.</i> (1970), Khangura and Shandhu (1973), Kumar and Yadav (1979), Rao <i>et al.</i> (1983), Labana <i>et al.</i> (1980), Quadri and Khunti (1982), Alam <i>et al.</i> (1985a and b), Chauhan and Shukla (1985), Reddy <i>et al.</i> (1986), Kuriakose and Joseph (1986), Nadaf and Habib (1987), Wang <i>et al.</i> (1987), Vaddoria and Patel (1990), Mishra and Yadava (1992), Uddin <i>et al.</i> (1995), Sharma and Varshney (1995), Varman and Raveendran (1996b), Vasanthi <i>et al.</i> (1998b), Ayub <i>et al.</i> (2000), Suryanarayan Reddy <i>et al.</i> , (2001), Venkataraman (2001), Yogendraprasad <i>et al.</i> (2002), Makhan <i>et al.</i> (2003), Venkateshmurthy (2005), John <i>et al.</i> (2007), Apte <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Kavera (2008), Channayya (2009), Savaliya <i>et al.</i> (2009), Korat <i>et al.</i> (2009), Azharudheen (2010), Thakur <i>et al.</i> (2011), Zaman <i>et al.</i> (2011), Rao <i>et al.</i> (2012), Jonah <i>et al.</i> (2012), Sunday and Omolayo (2013)
		Moderate	Alam <i>et al.</i> (1985a), Sarvamangala (2009)
		Low	Kandaswami <i>et al.</i> (1986), Swamy Rao <i>et al.</i> (1988), John <i>et al.</i> (2011)

Table 4: Review of reports on genetic advance for some quantitative characters in groundnut

Sl. No.	Characters	Genetic advance	Authors
1	Days to 50 per cent flowering	Low	Monoharan <i>et al.</i> (1990), Vaddoria and Patel (1990, Venkateshmurthy (2005), Channayya (2009), John <i>et al.</i> (2011), Thakur <i>et al.</i> (2011), Zaman <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012), Rao <i>et al.</i> (2012)
		High	Korat <i>et al.</i> (2009), Raut <i>et al.</i> (2010), Zaman <i>et al.</i> (2011) , Vishnuvardhan <i>et al.</i> (2012)
2	Days to maturity	High	Makhan <i>et al.</i> (2003), Thaware <i>et al.</i> (2008), Thakur <i>et al.</i> (2011), Rao <i>et al.</i> (2012)
		Low	Channayya (2009), John <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
3	Plant height	High	Deshmukh <i>et al.</i> (1986), Kandaswamy <i>et al.</i> (1986), Reddy <i>et al.</i> (1987), Kale and Dhoble (1988), Manoharan <i>et al.</i> (1990), Uddin <i>et al.</i> (1995), Varman and Raveendran (1996), Suryanarayanareddy <i>et al.</i> (2001), Nath and Alam (2002), Apte <i>et al.</i> (2008), John <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Raut <i>et al.</i> (2010), Rao <i>et al.</i> (2012)
		Low	Venkateshmurthy (2005), Channayya (2009), John <i>et al.</i> (2011), Thakur <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
4	Primary branches per plant	High	Kuriakose and Joseph (1986), Ganeshan and Sudhakar (1995), Uddin <i>et al.</i> (1995), Raut <i>et al.</i> (2010)
		Low	Channayya (2009), John <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
5	Secondary branches per plant	High	Reddy <i>et al.</i> (1987a)
		Low	John <i>et al.</i> (2011), Vishnuvardhan <i>et al.</i> (2012)
6	Pod yield per plant	High	Chauhan and Shukla (1985), Alam <i>et al.</i> (1985a), Deshmukh <i>et al.</i> (1986), Kandaswami <i>et al.</i> (1986), Reddy <i>et al.</i> (1987), Kale and Dhoble (1988), Vaddoria and Patel (1990), Manoharan <i>et al.</i> (1990), Mishra and Yadava (1992), Reddy and Gupta (1992), Yadava (1992), Sharma and Varshney (1995), Ganesan and Sudhakar (1995), Sarala and Gowda (1998), Nath and Alam (2002), Bashir <i>et al.</i> (1998), Prakash (2000), Apte <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), John <i>et al.</i> (2008), Savaliya <i>et al.</i> (2009), Raut <i>et al.</i> (2010), John <i>et al.</i> (2011), Rao <i>et al.</i> (2012)
		Medium	Venkateshmurthy (2005)
		Low	Venkateshmurthy (2005), John <i>et al.</i> (2006), Vishnuvardhan <i>et al.</i> (2012)

Sl. No.	Characters	Genetic advance	Authors
7	Kernel yield per plant	High	Reddy <i>et al.</i> (1987), Kale and Dhoble (1988), Sumathi and Ramanathan (1995a), John <i>et al.</i> (2008), Raut <i>et al.</i> (2010), Rao <i>et al.</i> (2012)
		Medium	Jonah <i>et al.</i> (2012)
		Low	Varman and Raveendran (1996), Venkateshmurthy (2005), John <i>et al.</i> (2011)
8	Shelling per cent	High	Reddy <i>et al.</i> (1986), Reddy and Gupta (1992), Nath and Alam (2002), Savaliya <i>et al.</i> (2009), John <i>et al.</i> (2007)
		Moderate	Reddy <i>et al.</i> (1987), Uddin <i>et al.</i> (1995)
		Low	Venkateshmurthy (2005), Channayya (2009), John <i>et al.</i> (2011), Jonah <i>et al.</i> (2012), Vishnuvardhan <i>et al.</i> (2012), Rao <i>et al.</i> (2012)
		Low	Badwal <i>et al.</i> (1967), Nadaf and Habib (1987), Alam <i>et al.</i> (1985a), Swamy Rao <i>et al.</i> (1988) Prashanthi <i>et al.</i> (1990), Manoharan <i>et al.</i> (1990), Vaddoria and Patel (1990), Sumathi and Ramanathan (1995a), Uddin <i>et al.</i> (1995), Varman and Raveendran (1996), Rudraswamy <i>et al.</i> (1999), Yogendraprasad <i>et al.</i> (2002), Thakur <i>et al.</i> (2011)
9	100 seed weight	High	Alam <i>et al.</i> (1985a and b), Deshmukh <i>et al.</i> (1986), Reddy <i>et al.</i> (1986), Nadaf and Habib (1987), Prasanthi <i>et al.</i> (1990), Vadodaria and Patel (1990), Sharma and Varshney (1995), Varman and Raveendran (1996), Vasanthi <i>et al.</i> (1998a), Singh and Singh (1998), Prakash <i>et al.</i> (2000), Suryanarayanareddy <i>et al.</i> (2001), Yogendraprasad <i>et al.</i> (2002), Apte <i>et al.</i> (2008), Jatti <i>et al.</i> (2008), John <i>et al.</i> (2008), Thaware <i>et al.</i> (2008), Savaliya <i>et al.</i> (2009), Rao <i>et al.</i> (2012)
		Moderate	Vasanthi <i>et al.</i> (1988b), Ghizan and Nor (1994), Venkateshmurthy (2005), Channayya (2009), Thakur <i>et al.</i> (2011)
		Low	Swamy Rao <i>et al.</i> (1988), Channayya (2009), John <i>et al.</i> (2011)

different drought conditions (Cruickshank *et al.*, 2004; Hubick *et al.*, 1988; Ntare and Williams, 1998a, 1998b; Nigam *et al.*, 2005; Puangbut *et al.*, 2011; Songsri *et al.*, 2008).

Hubick *et al.* (1988) reported that heritability estimates were high for transpiration efficiency (TE) and especially for carbon isotope discrimination (Δ) and there was no significant G $\times$ E interaction for Δ . There are numerous reports on groundnut response to drought but most studies have been limited to small numbers of groundnut genotypes (e.g. Vorasoot *et al.*, 2003). Other studies have used larger number of germplasm (e.g. thirty six, sixty, and one hundred twenty in Ndunguru *et al.*, 1995; Jongrungsklang *et al.*, 2008 and Painawadee *et al.*, 2009, respectively) and revealed a significant genotypic variation in drought tolerance.

Nautiyal *et al.* (2002) reported significant variation in DTI in the field experiments conducted under three soil moisture regimes of adequate irrigation (W_1), drought simulated under rain-out-shelter (W_2) and rain-fed (W_3) conditions. They also reported that low SLA types have heritability. Surihan *et al.*, 2005 showed predominance of additive gene effects in determining the expression of SLA and HI in all the three crosses viz., ICGV 86388 $\times$ IC 10, ICGV 86388 $\times$ KK 60-1 and IC 10 $\times$ KK 60-1 accounting for 80-95% of total genetic variability for SLA and 63-73% for HI.

Songsri *et al.* (2008) found that heritability estimates of physiological traits for drought resistance in groundnut were high ($h^2 > 0.50$) under drought and well-watered conditions.

Painwadee *et al.* (2009) conducted pot experiments for 128 progenies in the F_3 generation derived from the cross ICGV 98324 $\times$ KK-4 in randomized complete block design with four replications and revealed that heritability estimates in broad sense were low to intermediate, ranging from 0.27 to 0.59 for root and drought resistance traits.

Nandini *et al.* (2011) reported a moderate GCV and heritability and high GAM for number of SLA while, a low GCV, medium heritability and medium GAM for SPAD chlorophyll meter reading.

Puangbut *et al.* (2011) reported high heritability estimates for SLA and SCMR under early season drought and recovery conditions indicated that selection for these traits after recovery could be achieved and also indicated their importance in contributing for the pod yield.

Girdthai *et al.* 2012 evaluated 140 groundnut lines in the F4:6 and F4:7 generations developed from four crosses (ICGV 98348 × Tainan 9, ICGV 98348 × KK60-3, ICGV 98353 × Tainan 9, and ICGV 98353 × KK60-3) under well-watered and terminal drought conditions. They reported that higher heritability estimates for physiological traits compared to agronomic traits. The heritability for HI, SCMR, and SLA ranged from 0.55 to 0.85, 0.72 to 0.91, and 0.61 to 0.90, respectively with in the four crosses.

A remarkable level of variability was revealed by Thakur *et al.* 2013 for drought tolerance among the groundnut varieties which is very essential in improving its performance under rainfed conditions.

2.2.3 Root traits

Genetic analysis revealed that most root traits showed low heritability and were controlled by multiple genes and gene interaction occurred in some root traits. The inherent difficulty of measuring root traits, their interactions with the below-ground environment and a lack of understanding of the rhizosphere have all rendered breeding for root traits impractical (O'Toole and Soemartono, 1981). Further, genetic improvement of root traits by conventional breeding methods has been rather difficult.

Despite of the difficulty in improvement of the root traits as cited above efforts have been made to assess the genetic variability in root traits in groundnut and other crops which were reviewed as given below

Significant genetic variation was reported by Serraj *et al.* (2003) among the RIL population of chick pea derived from a cross ICC 4958 × Annigeri for root length density, root dry weight and shoot dry weight at 35 days after sowing and for shoot biomass and seed yield at maturity. They also observed high heritability ($h^2=0.49$) for shoot dry weight compared to moderate heritability for root dry weight and root length density at the same stage. They revealed high heritability for seed weight in both years

(0.829 in 2000–2001 and 0.617 in 2001–2002). Similarly considerable genetic variability was reported for root traits in wheat by Reynolds *et al.* (2007).

Kashiwagi *et al.*, 2005 reported high heritability estimates for plant dry weight to root length density in mini-core germplasm collection of ICRISAT using a cylinder culture system during two consecutive growth seasons.

Kashiwagi *et al.*, 2008 reported additive and additive x additive interaction effects in governing the root length density and root dry weight. The direction of the additive gene effects was consistent and towards increasing the root growth. They also concluded that delaying selections to later generations and generating larger populations for selections were proposed as strategies for improving root systems of chickpea to exploit additive additive interaction.

Ren *et al.* 2006 in their heritability analysis of eleven quantitative traits of root in RIL population of groundnut revealed low heritability estimates for most of the traits except, for dry weight of lateral root ($h(n) = 0.569$) and number nodules of lateral root ($h(n) = 0.545$) and number of lateral root ($h(n) = 0.542$). They also indicated that all groundnut root characters are quantitative traits genetically controlled by polygenes.

Ren *et al.* 2007 revealed high heritability estimates for most of the traits in RIL population. They reported polygenic control of root traits i.e. 10 genes controlling nodule number of lateral and axial root and dry weight of lateral root, while about 5~8 genes in other root related characters.

2.2.4 Quality traits

2.2.1 Oil content

The improvement kernel protein or oil content requires a thorough knowledge of the existing genetic variation among cultivars. Larger genetic variation is available for these quality traits in the groundnut germplasm (Norden *et al.*, 1987; Branch *et al.*, 1990; Upadhyaya *et al.*, 2005).

The oil content of groundnut produced in India may vary from 42 to 55 per cent. A wide range of variability of (42.3 to 56.5 %) oil content was reported by Rao *et al.*

(1965), a variation of (46.50 to 63.10 %) for wild species and (43.6 to 55.50 %) for the cultivars was reported by Cherry (1977) and (35.80 to 54.20 %) and average near 45 per cent (Jambunathan *et al.*, 1985 and Dwivedi *et al.*, 1990), similar reports of high genetic variability was observed by Rudraswamy *et al.* (1999), Venkataramana *et al.* (2001). A narrow difference between PCV and GCV values for oil content was observed in bunch and spreading types of groundnut by Velu and Gopalkrishna (1985).

However, a low variability for oil content in parents and progeny lines was reported by Chiow and Wynne (1983), Nadaf and Habib (1987) and Prakash *et al.* (2000), and in F₉ generation of cross TG-26 x GPBD-4 by Sarvamangala *et al.* (2011).

Tai *et al.* (1975) reported that oil content is quantitatively inherited, while Martin (1967) estimated that only two pairs of major genes control oil content in groundnut seeds. Martin (1967) obtained high heritability estimates for oil content.

Similarly a high estimates of heritability with high genetic advance for oil percentage indicating the presence of additive gene action by Venkataramana *et al.* (2001), Varman and Raveendran (1996).

Noubissie *et al.* 2012 evaluated 12 promising groundnut (*Arachis hypogaea* L.) genotypes, in randomized complete block design with six replicates and revealed moderate to high broadsense heritability values of 0.52 for oil content and 0.64 for protein content whereas, low values of expected genetic advance, 3.70 % for oil and 4.70 % for protein indicating the preponderance of non-additive gene effects.

Oil content influenced by maturity i.e. increases (Nagaraj *et al.*, 1987), season i.e. higher oil content in summer than in rainy season (Nagaraj and Chauhan, 1987).

2.2.3 Protein content

The groundnut kernels contain high quality protein than meat, eggs and most of other vegetables. Hence, it is important for children, women and people eating more meatless meals (Misra, *et al.*, 1992). In absence of adequate carbohydrate and fat in diets, dietary proteins are broken down to provide energy (4 Kcal/g). The development of nutritionally balanced foods to feed the growing population of dietary deficiencies of proteins is receiving increasing attention of the food scientist and nutritionists, oilseeds

are used to manufacture and market high protein foods at reasonably low prices (Bookwaltes *et al.*, 1979).

A large variation of 22 per cent to 30 per cent and 16.10 per cent to 34.0 per cent of crude protein content was reported by (Pancholy *et al.*, 1978; Singh *et al.*, 1998 respectively) in spanish bunch groundnuts which is generally influenced by genotype and environment and a higher variation of 21 per cent to 37 per cent in *kharif* and 24 per cent to 36 percent in summer but pooled analysis showed less variation in a study conducted by Sarvamangala *et al.* (2011) indicate there is significant effect of environment on the genotype.

Ajay *et al.* (2008) reported that GPBD-4 has a high protein content (30.33%) which is a desirable trait for the confectionary food items among the 17 groundnut varieties. A very high heritability (>80%) was observed in both summer and *kharif* environments but the pooled data heritability was lower (<50%) indicate that significant effect of environment on trait by Sarvamangala *et al.* (2011).

2.2.2 Oil quality

A total of 75 to 80 per cent of total fatty acid content was oleic and linoleic acid in groundnut seeds reported by (Cobb and Johnson, 1973; Bruner *et al.*, 2001; Lopez *et al.*, 2001) and 55-65 per cent of monounsaturated fatty acids (MUFA), 26-28 per cent polyunsaturated fatty acids (PUFA) and 17-18 per cent saturated fatty acids (SFA) in groundnut oil by Ory *et al.*, 1992. In a study conducted by stalker *et al.* (1989) who surveyed 75 *Arachis* species accessions, representing 5 and 7 sections of genus and compared with 4 cultivars for fatty acid composition found an average ratio of (0.35 - 0.45) oleic to linoleic acid ratio in sections *Extranervosae* and *Triseminalae* respectively, to 1.32 in diploid species of section *Arachis*.

Oil content heritability is rather high, and has been estimated to be 0.65–0.70 by Fick (1975) and 0.57 by Mokrani *et al.* (2002). Mokrani *et al.* (2002) reported that genetic gain (the difference between the best parents and the mean of 10% of selected RILs) is significant for oil content.

Hammond *et al.* (1997) observed a variation in fatty acid composition when Groundnut plant introductions were analyzed and found that Palmitate ranged from 8.2

to 15.1 per cent, stearate from 1.1 to 7.2 per cent, oleate from 31.5 to 60.2 per cent, linoleate from 19.9 to 45.4 per cent, arachidate from 0.8 to 3.2 per cent, eicosenoate from 0.6 to 2.6 per cent, behenate from 1.8 to 5.4 per cent and lignocerate 0.5 to 2.5 per cent.

Similarly Treadwell *et al.* (1983) observed a variation in fatty acid composition ranged from palmitic acid (7.54%-11.90%), stearic acid (1.46%-3.26%), oleic acid (39.29%-56.56%), linoleic acid (25.95%-38.90%), arachidic acid (1.02%-1.63%), eicosenoic acid (0.89% - 1.74%), behenic acid (2.39%-4.04%) and lignoceric acid (1.21%-2.52%) in 40 groundnut cultivars.

The O/L ratio ranged from 1.24-1.78 among four varieties of groundnut (Sadhanakumari and Snehalatha, 1998). The majority of groundnut cultivars average 55 per cent oleic acid and 25 per cent linoleic acid (Knauff *et al.*, 1993). In India, early maturing Spanish Bunch varieties cover major area (70 %) but they have poor oil quality with O/L ratio of ~ 1.0 (Raheja *et al.*, 1987; Bandyopadhyaya and Desai (2000).

Motagi *et al.* (2005) reported fatty acid composition in seven Spanish Bunch ruling cultivars in India and O/L ratio varied from 0.97 to 1.65. Wide range in fatty acid composition, especially in oleic and linoleic acid, was found among groundnut genotypes in the Florida breeding programme. Two closely related spontaneous mutants (435-2-1 and 435-2-2) had 80 per cent oleic acid and 2 per cent linoleic acid, with O/L ratio of 10:1 and iodine value of 74 per cent (Norden *et al.*, 1987). The oleic acid content of the different experimental lines ranged from 37 to 80 per cent, and the linoleic acid content from 2 per cent to 43 per cent. These two high oleic acid genotypes were derived from a Florispan parental stock. In seven years (1968-1974) of oil quality tests, the parental stock had 50.8 ± 1.3 per cent oleic acid and 26.2 ± 1.2 per cent linoleic acid in its oil composition with iodine value of 91.3 ± 1.3 . The high oleic and low linoleic levels in these two 435 groundnut lines may have occurred as a result of natural mutation. Groundnut mutant derivatives TG-8, TG-9, TG-17 and TG-18 induced by gamma- irradiation differed in fatty acid composition from their parent Spanish Improved.

A broad range of variation for oleic acid (29-65%), linoleic acid (16-47%) and O/L ratio (0.63-3.93) for oil quality by Sarvamangala *et al.* (2011) and oleic acid (33.6-73.54%) in the mini core collections of ICRISAT found that *A.hypogaea ssp hypogaea*

had more oleic acid (54.16%) and O/L ratio of (2.75-6.93) than *A.hypogaea ssp fastigiata* (45.70%) and O/L ratio (1.51-3.80) by Ganapathi *et al.* (2012) and a range of oleic acid (35%-56%); linoleic acid (27.8%-42.47%) by Ajay *et al.* (2012) and in mutant ranged from 48.9 per cent to 61.4 per cent with O/L ratio of 1.74-3.16 in Spanish bunch types by (Sharma *et al.*, 1985), an oleic acid (40-48%) and O/L ratio (1.50-1.70) with high unsaturated fatty acid content (78.80%) in GPBD-4 reported by Motagi *et al.* (2005), and the improvement in oleic acid and corresponding decrease in linoleic ranged for 14.66 per cent from gamma rays treatment in GPBD-4 and TPG 41 mutant population by Kavera (2008). Details of variability, heritability and GAM for quality traits was given in the Tables 5, 6, 7 and 8.

2.2.4 Resistance to foliar disease

A high PCV of (21.71%-33.55%) at different stages and environments revealed substantial variation for LLS and Rust was reported by Khedikar *et al.*, 2008 and similar reports of high variability reported by Anderson *et al.* (1991), Bhat (1995), and a significantly higher difference between PCV and GCV was reported by Venkataravana *et al.* (2008) indicating that there is much effect of environment and in contrast to this a narrow difference between PCV and GCV for late leaf spot and rust severity reported that disease severity was largely controlled by additive gene action by Vasanthi *et al.* (1998b).

Pensuk *et al.* (2003) evaluated the groundnut cultivars in a Randomized Complete Block Design (RCBD) with four replications and found significant genotypic differences for all resistance parameters. Genotypes differed significantly in mean disease score, wherein NC 17135 recorded the lowest disease score while Tainan 9 and Lampang registered the highest disease score. They revealed that differences in sporulation between genotypes were significant. The genotype NC 17135 recorded the lowest sporulation while the two susceptible cultivars, NC 9 and Chico, recorded the highest indices. They reported NC 17135 as the most resistant genotype against late leaf spot.

In their studies on genetic parameters for 64 groundnut genotypes (39 germplasm and 25 advanced breeding lines) for pod yield, maturity and foliar disease resistance characters, Venkataravana and Injeti (2008) observed high amount of phenotypic and genotypic coefficients of variation for late leaf spot, rust and pod yield.

Table 5: Literature showing the variability studies of quality traits in groundnut

Sl. No.	Characters	Status of Genetic variability	Authors
1	Oil content	High	Bovi (1983), Velu and Gopalkrishnan (1985), Norden <i>et al.</i> (1987), Vaddoria and Patel (1990), Mishra <i>et al.</i> (1992), Dwivedi <i>et al.</i> (1994), Nazar Ali <i>et al.</i> (2000), Venkataraman (2001), Jatti <i>et al.</i> (2008), Asibuo <i>et al.</i> (2008)
		Low	Chiw and Wynne (1983), Nadaf and Habib (1987), Prakash <i>et al.</i> (2000), Yogendraprasad <i>et al.</i> (2002), koarat <i>et al.</i> (2009), Sarvamangala <i>et al.</i> (2011)
2	Protein content	High	Gupta <i>et al.</i> (1982), Chiow and Wynne (1983), Kale <i>et al.</i> (1988), Mishra <i>et al.</i> (1992), Dwivedi <i>et al.</i> (1993), Singh (1998), Sarvamangala <i>et al.</i> (2011) Sharma and Gupta (2011)
3	Oleic acid	High	Norden <i>et al.</i> (1987), Andersen <i>et al.</i> (1998), Asibuo <i>et al.</i> (2008), Ganapati <i>et al.</i> (2012)
		Moderate	Sarvamangala <i>et al.</i> (2010)
4	Linoleic acid	High	Norden <i>et al.</i> (1987), Andersen <i>et al.</i> (1998), Asibuo <i>et al.</i> (2008), Ganapati <i>et al.</i> (2012)
		Moderate	Sarvamangala <i>et al.</i> (2010)
5	O/L ratio	High	Norden <i>et al.</i> (1987), Andersen <i>et al.</i> (1998), Asibuo <i>et al.</i> (2008), Ganapati <i>et al.</i> (2012)
		Moderate	Sarvamangal <i>et al.</i> (2010)
6	Palmitic acid	High	Ganapati <i>et al.</i> (2012)
		Moderate	Sarvamangala <i>et al.</i> (2010)
7	Iodine value	High	Norden <i>et al.</i> (1987), Andersen <i>et al.</i> (1998), Asibuo <i>et al.</i> (2008), Ganapati <i>et al.</i> (2012)
		Moderate	Sarvamangala <i>et al.</i> (2010)
8	LLS and Rust score/ severity	High	Khedikar <i>et al.</i> (2010), Sawargaonkar <i>et al.</i> (2010), Reddy and Gupta (1992), Bashir <i>et al.</i> (1998), Salara and Gowda (1998)
		Moderate	Vishnuvardhan <i>et al.</i> (2012)

Table 6: Review of reports on genotypic coefficient of variation and phenotypic coefficient of variation for quality traits in groundnut

Sl. No.	Characters	GCV	PCV	Authors
1	Oil content	High	-	Venkataramana <i>et al.</i> (2001)
		Low	Low	Venkateshmurthy (2005), Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat <i>et al.</i> (2009), Azharudheen (2010)
2	Protein	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010), John <i>et al.</i> (2011)
3	Palmitic acid	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
4	Stearic acid	Moderate	High	Kavera (2008)
		Low	Moderate	Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		Moderate	Low	Azharudheen (2010)
		Moderate	Moderate	Channayya (2009)
5	Oleic acid	High	High	Kavera (2008)
		Moderate	Moderate	Kavera (2008)
		Low	Low	Channayya (2009), Sarvamangala (2009), Azharudheen (2010),
6	Linoleic acid	Moderate	Moderate	Kavera (2008), Channayya (2009)
		Moderate	High	Channayya (2009)
		Low	Low	Sarvamangala (2009), Azharudheen (2010)
7	Arachidic acid	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		Moderate	Moderate	Channayya (2009)
8	Behenic acid	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
9	Eicosenoic acid	Low	Low	Kavera (2008), Channayya (2009), Azharudheen (2010)
		Low	Moderate	Sarvamangala (2009)
10	Lignoceric acid	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
11	O/L ratio	High	High	Kavera (2008), Channayya (2009)
		Moderate	Moderate	Kavera (2008), Channayya (2009), Sarvamangala (2009)
12	U/S ratio	Low	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
13	P/S ratio	Moderate	Moderate	Kavera (2008)
14	IV	Low	Low	Kavera (2008), Sarvamangala (2009)
15	% SFA	Low	Low	Channayya (2009), Sarvamangala (2009)
16	LLS and Rust score/ severity	High	High	Venkataramana and Injeti (2008), Giri <i>et al.</i> (2009), Vishnuvardhan <i>et al.</i> (2012)

Table 7: Reports on degree of heritability for quality traits in groundnut

Sl. No.	Characters	Degree of heritability	Authors
1	Oil content	High	Alam <i>et al.</i> (1985a), Varman and Raveendran (1996), Naazar Ali <i>et al.</i> (2000) Venkateshmurthy (2005), Korat <i>et al.</i> (2009), Venkataramana <i>et al.</i> (2001), Kavera (2008), Channayya (2009), Sarvamangala (2009)
		Medium	Venkateshmurthy (2005), Azharudheen (2010),
		Low	Chio and Wynne (1983), Varman and Raveendran (1996a), Parmar <i>et al.</i> (2000), Singkham <i>et al.</i> (2010)
2	Protein Content	High	Chio and Wynne (1983), Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		Medium	Kavera (2008)
		Low	John <i>et al.</i> (2011)
3	Palmitic acid	High	Kavera (2008), Channayya (2009), Sarvamangala (2009)
		Medium	Channayya (2009), Azharudheen (2010)
		Low	Kavera (2008)
4	Stearic acid	High	Kavera (2008)
		Medium	Channayya (2009), Sarvamangala (2009), Azharudheen (2010),
		Low	Azharudheen (2010)
5	Oleic acid	High	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010), Singkham <i>et al.</i> (2010)
		Medium	Kavera (2008), Sarvamangala <i>et al.</i> (2010)
6	Linoleic acid	High	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010), Singkham <i>et al.</i> (2010)
		Medium	Channayya (2009), Sarvamangala <i>et al.</i> (2010)
		Low	Channayya (2009)
7	Arachidic acid	Medium	Kavera (2008), Channayya (2009), Azharudheen (2010)
		High	Channayya (2009)
		Low	Sarvamangala (2009), Azharudheen (2010)
8	Behenic acid	Medium	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		High	Kavera (2008), Channayya (2009)
9	Eicosenoic acid	High	Kavera (2008)
		Medium	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		Low	Azharudheen (2010)
10	Lignoceric acid	Medium	Kavera (2008), Sarvamangala (2009), Azharudheen (2010)
		Medium	Kavera (2008)
11	O/L ratio	High	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		Medium	Kavera (2008), Channayya (2009), Sarvamangala <i>et al.</i> (2010)
		Low	Kavera (2008)
12	U/S ratio	High	Kavera (2008), Channayya (2009), Sarvamangala (2009)
13	P/S ratio	High	Kavera (2008)
14	IV	High	Kavera (2008), Sarvamangala (2009)
		Medium	Sarvamangala <i>et al.</i> (2010)
15	% SFA	High	Channayya (2009), Sarvamangala (2009)
16	LLS and rust score/ severity	High	Khedikar <i>et al.</i> (2008), Vishnuvardhan <i>et al.</i> (2012), Sawargaonkar <i>et al.</i> (2010), Venkataravana <i>et al.</i> (2008), Venkataravana and Injethi (2008), Giri <i>et al.</i> (2009), Narshimulu <i>et al.</i> (2012)

Table 8: Review of reports on genetic advance as per cent of mean for some qualitative characters in groundnut

Sl. No.	Characters	Genetic advance as per cent mean	Authors
1	Oil content	Low	Kavera (2008), Channayya (2009), Korat <i>et al.</i> (2009), Sarvamangala (2009), Azharudheen (2010)
2	Protein	Low	Channayya (2009), John <i>et al.</i> (2011)
		Medium	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
3	Palmitic acid	High	Channayya (2009)
		Medium	Kavera (2008), Channayya (2009)
		Low	Kavera (2008), Sarvamangala (2009), Azharudheen (2010)
4	Stearic acid	High	Kavera (2008)
		Medium	Sarvamangala (2009)
		Low	Azharudheen (2010)
5	Oleic acid	Medium	Kavera (2008), Channayya (2009), Sarvamangala (2009),
		Low	Channayya (2009), Azharudheen (2010)
6	Linoleic acid	High	Kavera (2008), Channayya (2009)
		Medium	Sarvamangala (2009)
7	Arachidic acid	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		High	Channayya (2009)
8	Behenic acid	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
		High	Channayya (2009)
9	Eicosenoic acid	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
10	Lignoceric acid	Low	Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010)
11	O/L ratio	High	Kavera (2008), Channayya (2009), Sarvamangala (2009)
		Medium	Azharudheen (2010)
12	U/S ratio	High	Kavera (2008), Channayya (2009)
		Medium	Kavera (2008)
		Low	Channayya (2009), Sarvamangala (2009)
13	P/S ratio	High	Kavera (2008)
		Low	Kavera (2008)
14	IV	High	Kavera (2008)
		Low	Kavera (2008), Sarvamangala (2009)
15	% SFA	Low	Channayya (2009), Sarvamangala (2009)
16	LLS and rust score/ severity	High	Venkataravana <i>et al.</i> (2008), Venkataravana and Injethi (2008), Giri <i>et al.</i> (2009), Sawargaonkar <i>et al.</i> (2010), Vishnuvardhan <i>et al.</i> (2012)

They also noticed high heritability coupled with high genetic variation for pod yield, late leaf spot and rust resistance, indicating that additive gene action plays a major role in their inheritance. Based on the *per se* mean performance they listed the genotypes ICGV-05033, ICGV-03037, ICGV-05099, ICGX-020063-P11, ICGV-04093, ICGV-03016, PAFRGVT-60, ICGV-04071, ICGV-86031 and ICGV-03157 as superior ones for these characters indicating that they could be used for further improvement of pod yield, earliness and disease resistance characters.

Venkataravana *et al.* (2008) studied 30 germplasm accessions at Agricultural Research Station, Chintamani for three consecutive years during *kharif* 2001-2003 along with the checks (JL-24 and K-134) in RBD with three replications and evaluated for PCV, heritability and genetic advance for resistance to late leaf spot and rust. They reported high values of PCV, heritability and genetic advance for late leaf spot and rust resistance.

Giri *et al.* (2009) conducted variability studies for yield and disease resistance traits in groundnut and noticed high estimates of PCV, GCV, heritability and GAM for late leaf spot severity, kernel yield per plant and pod yield per plant indicating the role of additive gene action in their genetic control.

Gowda *et al.* (1996) in a study involving F_4 generation of two single crosses of groundnut (TMV 2 x PI 393516 and JL 24 x PI 393516) evaluated the variability and association of late leaf spot resistance and productivity of two crosses of and reported high variability for leaf area affected by the disease, pod yield and pod number.

Genetic studies on LLS and rust resistance suggest that resistance to these fungal diseases is complex and polygenic in nature and probably controlled by several recessive genes (Sharief *et al.*, 1978; Nevill *et al.*, 1982; Green, 1986; Motagi, 2001; Dwivedi *et al.*, 2002). Furthermore, additive genetic variance seems to contribute predominantly to the resistance (Kornegay *et al.*, 1980; Hamid *et al.*, 1981; Anderson *et al.*, 1986; Jogloy *et al.*, 1987).

A high heritability was observed for both late leaf spot and rust in RIL population by Khedikar *et al.*, 2008 and a high heritability coupled with high GAM for late leaf spot severity and rust severity observed by Vishnuvardhan *et al.* (2012) in F_2

population are in conformity with the reports of Venkataravana *et al.* (2008), Venkataravana and Injeti (2008) and Giri *et al.* (2009).

Ashish (2014) evaluated 816 RILs developed out of the cross GPBD-4 X GM4-3 in a randomized block design with two replications during *kharif*, 2011 at MARS, Dharwad. They reported high genotypic and phenotypic coefficient of variation for rust and for late leaf spot scores indicating presence of high genetic variability for the trait. They also found high heritability coupled with high genetic advance for both rust and late leaf spot disease scores indicating the effectiveness of direct selection for the traits.

2.3 Association studies

Grain yield in any crop depends on many component characters that influence yield either jointly or singly and either directly or indirectly through other related characters. Direct selection for yield *Per se* is often not effective because of lower heritability. Therefore, indirect selection for yield using traits with high heritability and strongly correlated with yield is often practiced for productivity improvement in crop plants and groundnut is not exception to this.

The correlation between characters may exists due to various reasons such as pleiotrophy, and genetic linkage. An understanding of the direction and extent of association of the component characters with economic yield is an essential prerequisite for formulating best selection strategy in groundnut breeding programmes.

2.3.1 Correlation between yield and yield components

Jaswal and Gupta (1966) suggested that primary and secondary branches contributed to the yield in Spanish types. Increase in the branch number and node number resulted in the increased peg number and yield in the case of Spanish mutants (Prasad *et al.*, 1984).

Alam *et al.* (1985a) in a study of 20 groundnut varieties found that pod yield per plant recorded a positive correlation with the number of pods per plant, days to maturity and number of secondary branches per plant.

Alam *et al.* (1985b) in a study of eighteen genotypes of groundnut found that pod yield per plant registered positive association with the number of pods per plant, days to maturity, number of primary branches per plant and plant height. They also revealed that days to maturity was positively associated with plant height, number of primary branches per plant and number of pods per plant.

Abraham (1990) reported significant positive correlation of kernel yield with pods per plant, kernels per plant, 100-kernel weight and shelling per cent in a study involving 42 bunch type ground nut varieties.

Reddi *et al.* (1991) reported a strong and positive correlation of pod yield with kernel yield, sound mature kernels and 100-kernel weight in 32 diverse groundnut genotypes grown in three environments arising due to three different dates of sowing.

Correlation studies in 18 varieties of groundnut indicated significant and positive correlation of pod yield with pods per plant, shelling per cent, kernel weight and HI (Sharma and Varshney, 1995).

In a study involving 35 groundnut genotypes, a strong positive correlation of pod yield with 100-kernel weight but weak negative association with shelling per cent was reported (Vasanthi *et al.*, 1998a).

Plant height, number of primary branches, pod yield per plant, shelling per cent, kernel yield, sound matured kernels, 100-kernel weight, seed size, protein content, number of developed pods, harvest index and days to 50 per cent flowering showed positive correlation with yield. However, low positive correlation has been recorded for plant height with yield by (Shobhakuparani, 1999).

Pod yield had significant positive correlation with plant height, number of branches per plant, number of mature pods per plant, shelling per cent, 100-kernel weight and kernel yield per plant at genotypic and phenotypic level (Venkataravana *et al.*, 2000).

Number of pods per plant, 100-kernel weight, 100 pod weight, shelling per cent and days to 75 per cent flowering was positively and significantly correlated with yield per plant in groundnut (Roy *et al.*, 2003).

In a study involving 15 Valencia groundnut genotypes showed significant positive association of pod yield and kernel yield with kernels per plant, 100- kernel weight and biomass yield was recorded (Kavani *et al.*, 2004).

Mahalakshmi *et al.* (2005) evaluated fifty seven groundnut genotypes and observed significant and positive association of kernel yield per plant with days to 50 per cent flowering, plant height, number of secondary branches, number of immature pods, number of mature pods, sound mature kernel (SMK) weight, total number of pods, shelling percentage and pod yield.

Giri *et al.* (2009) found positive and significant association of pod yield with days to 50% flowering, days to maturity, kernel yield and test weight. They also observed negative and significant association of pod yield with late leaf spot severity indicating that they could be used as selection criteria for developing high yielding as well as late leaf spot disease resistant varieties.

Dhaliwal *et al.* (2010) reported that dry pod yield had significant positive association with days to flowering, days to maturity, haulm yield per plant and kernel yield per plant. They further revealed that at genotypic level also these traits displayed high positive correlation with dry pod yield.

Jogloy *et al.* (2011) evaluated 200 lines of 10 crosses in a Randomized Complete Block Design with two replications under fully-irrigated conditions and observed negative correlation of days to maturity with pod yield and harvest index, suggesting the possibility to select for early maturing genotypes without detrimental effect on pod yield and harvest index.

Pradhan and Patra (2011) evaluated 460 genotypes of groundnut germplasm in four different seasons for estimation of correlation coefficients among pod yield and its components. They observed consistently positive association for unfilled pods per plant with number of branches per plant and hundred pod weights with hundred kernel weight in all the seasons. They revealed that *rabi* and *kharif* performance of yield and yield contributing characters were positively correlated except unfilled pods per plant and plant height. They concluded that selection for high yield in groundnut could be made

by inclusion of pod weight, shelling percentage and hundred kernel weight as selection criteria along with plant height.

The correlation study conducted by Narasimhulu *et al.* (2012) in 18 selected groundnut genotypes revealed that pod yield per plant had significant positive association with kernel yield per plant, shelling percentage and SMK percent at both genotypic and phenotypic levels.

Many agronomically important traits in groundnut are quantitatively inherited (Murthy and Reddy, 1993). Association studies revealed significant positive correlation for pod yield per plant with number of pods per plant, 100-seed weight, oil yield and it was negatively correlated with shelling percentage at both genotypic and phenotypic levels (Sah *et al.*, 2000 and Lakshmiddevamma *et al.*, 2004).

Highest pod yield per plant was reported in *hypogaea* group with a range of 6.68 g to 11.49 g followed by *fastigiata* group (3.69 to 8.76 g) (Mallikarjuna Swamy *et al.*, 2003). They also reported that pod yield per plant had a significant negative correlation with oil content and positive correlation with test weight. Upadhyaya (2003) reported higher shelling percentage among *fastigiata* types over *hypogaea* types from a study consisting groundnut core collection.

In a study to determine the variability in reproductive response of groundnut genotypes subjected to pre-flowering drought (PFD) and their contributions to yield Puangbut *et al.* 2013 evaluated 11 groundnut genotypes in a split-plot design with four replications for two seasons. They indicated that genotypes differed in their response to PFD, and also revealed that PFD increased number of flowers, number of pegs, number of pods and number of mature pods per plant in many genotypes. They concluded that number of mature pods were the most important component contributing to high yield under PFD conditions.

A detailed review of literature on nature and directions of correlation between pod yield and its components along with their inter correlations was presented in the table 9 and 10.

Table 9: Nature of correlation reported between pod yield and other component traits in groundnut

Sl. No.	Characters	Nature of association	Authors
1	Days to 50 % flowering	Positive	Nagabushanam (1981), Phaokantarokorn and Waranyawat (1986)
		Negative	Deshmukh (1986), Venkateshmurthy (2005)
2	Primary branches per plant	Positive	Yadava <i>et al.</i> (1984), Alam <i>et al.</i> (1985b), Vaddoria and Patel (1992), Uddin <i>et al.</i> (1995), Nikram <i>et al.</i> (2008), Kavera (2008), Channayya (2009)
3	Secondary branches per plant	Positive	Lakshmaiah <i>et al.</i> (1983), Alam <i>et al.</i> (1985b)
4	Plant height	Positive	Alam <i>et al.</i> (1985a), Manoharan <i>et al.</i> (1990), Pushkaran and Nair (1993), Wu (1993), Uddin <i>et al.</i> (1995), Ursal <i>et al.</i> (1995), Rosemary and Ramalingam (1997), Moinuddin (1997), Jayaramaiah and Thimmegowda (1998), Venkateshmurthy (2005), Apte <i>et al.</i> (2008), Sunday and Omolayo (2013)
		Negative	Manoharan <i>et al.</i> (1990), Rao <i>et al.</i> (2012)
5	Days to maturity	Positive	Alam <i>et al.</i> (1985a), Uddin <i>et al.</i> (1995), Mohan <i>et al.</i> (2003)
		Negative	Wu (1993), Korat <i>et al.</i> (2010), Sunday and Omolayo (2013)
6	Shelling percentage	Positive	Yadava <i>et al.</i> (1984), Abraham (1990), Manoharan <i>et al.</i> (1990), Prasanthi <i>et al.</i> (1990), Reddy and Gupta (1992), Vaddoria and Patel (1992), Bhagat <i>et al.</i> (1993), Pushkaran and Nair, 1993, Sharma and Varshney (1995), Ursal <i>et al.</i> (1995), Vasanthi <i>et al.</i> (1998a), Sah <i>et al.</i> (2000), Bentur (2001), Abhay <i>et al.</i> (2002), Kalmeshwar (2004), Venkateshmurthy (2005), Channayya (2009), Rao <i>et al.</i> (2012)
		Negative	Uddin <i>et al.</i> (1995), Moinuddin (1997), Vasanthi <i>et al.</i> (1998b), Sah <i>et al.</i> (2000)

Contd...

Sl. No.	Characters	Nature of association	Authors
7	100 seed weight	Positive	Yadava <i>et al.</i> (1984), Alam <i>et al.</i> (1985a), Alam <i>et al.</i> (1985b), Deshmukh <i>et al.</i> (1986), Swamyrao <i>et al.</i> (1988), Sahu and Roy (1989), Abraham <i>et al.</i> (1990), Manoharan <i>et al.</i> (1990), Raddy and Gupta (1992), Bhagat <i>et al.</i> (1993), Vaddoria and Patel (1992), Ursal <i>et al.</i> (1995), Sumathi and Ramanathan (1995b), Sarala and Gowda (1998), Ramesh <i>et al.</i> (1998), Vasanthi <i>et al.</i> (1998a), Sah <i>et al.</i> (2000), Bentur (2001), Nagda <i>et al.</i> (2001), Abhay <i>et al.</i> (2002), Venkateshmurthy (2005), John <i>et al.</i> (2007), Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat <i>et al.</i> (2010), Rao <i>et al.</i> (2012)
		Negative	Uddin <i>et al.</i> (1995), Moinuddin (1997), Jayaramaiah and Timmegowda (1998), Vasanthi <i>et al.</i> (1998b)
8	Kernel yield	Positive	Phaokantarokorn and Waranyawat (1986), Abraham (1990), Prasanthi <i>et al.</i> (1990), Mishra and Yadava (1992), Nagabhushanam and Prasad (1992), Reddy <i>et al.</i> (1992), Reddy and Gupta (1992), Pathirana (1993), Baydar and Bayraktar (1994), Uddin <i>et al.</i> (1995), Rosemary and Ramalingam (1997), Sah <i>et al.</i> (2000), Venkateshmurthy (2005), John <i>et al.</i> (2008), Rao <i>et al.</i> (2012)
		Negative	Ayub <i>et al.</i> (2000)
9	Oil content	Positive	Dwivedi <i>et al.</i> (1998), Ramesh <i>et al.</i> (1998), Nazar Ali <i>et al.</i> (2000), Sah <i>et al.</i> (2000), Ursal <i>et al.</i> (1995), Venkateshmurthy (2005)
		Negative	Chow and Wynne (1983), Alam <i>et al.</i> (1985a), Swamyrao <i>et al.</i> (1988), Nadaf and Habib (1990), Rosemary and Ramalingam (1997) and Bentur (2001)
10	Protein content	Positive	Khangura and Sandhu (1972)
		Negative	Keneni <i>et al.</i> (1998), Bentur (2001)
11	LLS and Rust score/severity	Negative	John <i>et al.</i> (2005)

Table 10: Reports on inter correlation between quantitative traits in groundnut

Sl. No.	Characters	Nature of correlation	Character	Authors
1	Days to 50 per cent flowering	Negative	Plant height	Channayya (2009)
		Positive	100 kernel weight	Channayya (2009)
			Days to maturity	Rao <i>et al.</i> (2012),
		Positive	Kernel weight	Zaman <i>et al.</i> (2011)
		Positive	Shelling per cent	Zaman <i>et al.</i> (2011)
		Positive	Days to maturity, Plant height	Channayya (2009)
		Negative	Oil content	Channayya (2009)
		Negative	Protein	Channayya (2009)
2	Days to maturity	Positive	Plant height	Alam <i>et al.</i> (1985b)
		Positive	Primary branches	Alam <i>et al.</i> (1985b)
		Positive	100 kernel weight	Alam <i>et al.</i> (1985b)
		Positive	Plant height, Shelling per cent, Pod yield per plant, Protein	Channayya (2009)
		Negative	100 kernel weight	Channayya (2009)
3	Plant height	Positive	50 per cent flowering	Sunday and Omolayo (2013)
		Positive	Days to maturity	Sunday and Omolayo (2013)
		Positive	Primary branches per plant, protein	Channayya (2009)
		Positive	100 kernel weight	Sarvamangala (2009)
		Negative	Shelling per cent	Zaman <i>et al.</i> (2011), Rao <i>et al.</i> (2012),
		Negative	100 kernel weight	Channayya (2009), Rao <i>et al.</i> (2012)
		Negative	Seed yield per plant	Rao <i>et al.</i> (2012)
4	Primary branches per plant	Positive	Kernel yield per plant	Kavera (2008)
		Positive	Secondary branches per plant	Channayya (2009)
		Positive	Pod yield per plant, protein	Channayya (2009)
		Negative	100 kernel weight	Channayya (2009)
5	Shelling percentage	Positive	Oil content	Rao <i>et al.</i> (1983)
		Positive	Pod yield per plant	Channayya (2009)
		Negative	100 kernel weight	Rao <i>et al.</i> (1983) and Alam <i>et al.</i> (1985a)
		Negative	Plant height	Sarvamangala (2009)
		Negative	Pod yield per plant	Sarvamangala (2009)
		Negative	Rust	Azharudheen (2010)
		Positive	Rust	Azharudheen (2010)
6	100 seed weight	Positive	50 per cent flowering	Sunday and Omolayo (2013)
		Positive	Days to maturity	Sunday and Omolayo (2013)
		Positive	Shelling percentage	Channayya (2009), Azharudheen (2010), Zaman <i>et al.</i> (2011)
		Positive	Number of pods	Ursal <i>et al.</i> (1995)
		Positive	Kernel yield per plant	Kavera (2008), Zaman <i>et al.</i> (2011)
		Positive	Oil content	Sandhu and Khehra (1977)
		Positive	Pod yield per plant	Channayya (2009), Azharudheen (2010)
		Negative	Protein	Channayya (2009)

Contd...

Sl. No.	Characters	Nature of correlation	Character	Authors
7	Kernel yield	Positive	50 per cent flowering	Zaman <i>et al.</i> (2011)
		Positive	100 seed weight	Nagabhushanam (1981), Venkataraman <i>et al.</i> (2001), John <i>et al.</i> (2007), Channayya (2009), Zaman <i>et al.</i> (2011)
		Positive	Oil content	Venkataraman <i>et al.</i> (2001)
		Positive	Primary branches per plant	Channayya (2009)
		Positive	Pod yield per plant	Channayya (2009)
		Negative	100 kernel weight	O'fori (1998),
		Positive	Shelling per cent	Channayya (2009), Rao <i>et al.</i> (2012),
8	Oil content	Positive	100 seed weight	Kale <i>et al.</i> (1988)
		Positive	Eicosenoic, Lignoceric	Sarvamangala (2009)
		Negative	Stearic acid, Arachidic acid, Behenic acid	Sarvamangala (2009)
		Negative	Plant height	Alam <i>et al.</i> (1985a)
			Days to maturity	Alam <i>et al.</i> (1985a)
			Pod yield per plant	Alam <i>et al.</i> (1985a)
		Negative	Days to 50 per cent flowering	Channayya (2009),
		Negative	Protein content	Dwivedi <i>et al.</i> (1990), Sarvamangala <i>et al.</i> (2010)
		Negative	LLS	Azharudheen (2010)
9	Protein	Positive	Plant height, Days to maturity	Channayya (2009)
		Negative	Oil content	Channayya (2009)
10	Rust	Negative	Oil content, Protein, Pod yield per plant, Shelling per cent, 100 seed weight	Sarvamangala (2009)
		Negative	Oil content, Protein	Azharudheen (2010)

2.3.2 Correlation between yield and physiological traits related to drought tolerance

Roy Stephen (1995) evaluated 21 selected groundnut genotypes in three moisture regimes viz., rainfed, irrigated and moisture stress condition and observed that SLA was lower in moisture stress condition compared to that in irrigated conditions in pot culture experiment. The relationship of SLA with WUE was negative and significant, whereas $\Delta^{13}C$ was positively related to SLA in both field and pot culture experiments. SLA had significant inverse relationship with SCMR and total chlorophyll content (project report, UAS-B, 1996).

Bindu Madhava *et al.* (2003) provided evidence that the relationship between TE and SLA was predominantly due to strong association between SLA and SLN.

Sheshashayee *et al.* (2006) reported the significant positive relationship between SCMR and transpiration efficiency. They also found significant inverse relationship between SCMR and $\Delta^{13}C$. They opined that SLA is an indirect measure of leaf expansion. Higher SLA indicates higher leaf area per unit biomass and hence larger surface area for transpiration.

Songsri *et al.* (2008) expressed that harvest index (HI), specific leaf area (SLA) and SCMR had high heritability and positive correlation with pod yield under long duration drought and identified the genotypes viz., ICGV 98300, ICGV 98303, ICGV 98305 as drought-avoiding genotypes as they exhibited high DTI (RLD40 to 100 cm) which may explain their high pod yield, DTI (PY) and DTI (HI).

Wunna *et al.* 2009 evaluated ninety lines in the $F_{4:5}$ generation from four groundnut crosses under field capacity and one third available water. They revealed positive and significant genotypic correlation (r_g) between nodule dry weight and biomass production (BM); BM and pod yield, while moderate r_g between BM and 100 seed weight; BM and SCMR at 60 DAE. They also reported significant correlation between BM in FC and early drought conditions indicating that for this trait could be done under both water regimes.

SCMR under drought conditions was positively correlated with pod number per plant (Puangbut *et al.*, 2011; Painawadee *et al.*, 2009; Wunna *et al.*, 2009). However, Boontang *et al.* (2010) found that SCMR was not related to number of pods per plant, number of seeds pod⁻¹ and seed size.

Recently, Boontang *et al.* (2010) reported that for pod yield of groundnut, high potential under well watered conditions alone gave significant contribution to maintaining high pod yield under drought. However, Talebi *et al.* (2009) found that the grain yield under irrigated conditions was adversely correlated with rain-fed condition and suggested that high potential yield of wheat under optimal conditions does not necessarily result in improved yield under stress conditions.

Puangbut *et al.* (2011) showed that harvest index had high genetic correlation (r_g) with pod yield and number of mature pods under early season drought (ESD) conditions while SCMR had moderate r_g with number of mature pods. They also indicated that these traits are useful for indirect selection for pod yield under ESD conditions to improve the breeding process.

Hamidou *et al.* (2011) evaluated 247 lines belonging to the reference collection under the intermittent drought for two years and reported a close relationship between yield and pod growth rate ($r^2 = 0.51$), and partition ($r^2 = 0.33$) under water stress (WS) conditions, whereas no significant relationship between yield under WS and SCMR, or specific leaf area (SLA).

Sadeghi *et al.* (2012) revealed highly significant positive correlation of 100-seed weight, total no. of kernels per plant, total no. of pods per plant and biomass with seed yield under both drought stress and irrigated conditions. Through path analysis they also reported high positive direct effects of total no. of kernels per plant, 100-seed weight and total no. of pods per plant on seed yield in irrigated condition while in drought stress condition 100-seed weight, total no. of kernels per plant, total no. of pods per plant and biomass had high positive direct effects on seed yield.

Girdthai *et al.* (2012) evaluated 140 groundnut lines in the $F_{4:6}$ and $F_{4:7}$ generations developed from four crosses (ICGV 98348 × Tainan 9, ICGV 98348 × KK60-3, ICGV 98353 × Tainan 9, and ICGV 98353 × KK60-3) under well-watered and

terminal drought conditions. They revealed significant positive between HI and SCMR while inverse correlation of SLA with SCMR, HI and other agronomic traits. They also indicated that HI, SLA, and SCMR could be useful as indirect selection traits for terminal drought resistance.

2.3.3 Correlation between yield and root traits related to drought tolerance

Nageswara Rao *et al.* (1989) assumed that the promotion of root growth during drought stress was an important character contributing to the increased yield.

A strong correlation between root dry weight and shoot dry weight has been reported in groundnut grown under greenhouse (Ketring 1984) and field conditions (Wright *et al.* 1994).

Rucker *et al.* (1995) found that some groundnut genotypes with large root system (root dry weight) under non-stress conditions gave higher yield under drought conditions. Moreover, root dry weight was highly correlated to shoot dry weight, leaf area and number of leaves (Ketring, 1984).

Rucker *et al.* (1995) demonstrated that large root systems of groundnut under well watered conditions were positively correlated with pod yield of groundnut grown under drought in field trials.

Serraj *et al.* (2003) revealed that the RIL population of chick pea derived from a cross ICC 4958 x Annigeri exhibited a range of combinations of root size and seed yield, with a few RILs showing large root systems and high seed yield. They reported linear correlation ($r^2=0.23$) between root and the shoot dry weights and significant positive correlation for harvest index and seed weights of RILs between the years ($r^2=0.38$ and 0.67 respectively). They also concluded that, there was no general correlation between seed yield and root size, where contribution to high seed yield of the RILs was through high shoot biomass and harvest index.

Some positive relationships between the depth of rooting and seed yield of crops subjected to terminal drought have indeed been shown in chickpea (e.g. Kashiwagi *et al.*, 2005).

Root system is an important organ of plants for absorbing water and nutrition and synthesizing chemicals like hormones. It plays an important role in the development of aboveground organs and yield formation (de Dorlodot *et al.*, 2007). Although, the root system has long been noticed and studied, progress remains slow and limited as compared with aboveground organs due to a massive volume of work and limitations of research methods. So far, studies on the root system of groundnut have been mostly focused on variation in root morphology under different environments, root characteristics among different varieties and inheritance of root traits (Meisner and Karnok, 1992; Liao *et al.*, 2000, 1992; Ren *et al.*, 2006a, 2007).

Ren *et al.* (2007) found significant correlation between dry weight of axial and lateral root, thickness of root base, fresh weight of axial and lateral root. They also reported significant correlation between root volume and thickness of root base, fresh and dry weight of lateral root.

Junjittakarn *et al.* (2013) conducted a factorial experiment with four replicates where factor A consisted of two water regimes (field capacity and 1/3 available water at 80 d after planting to harvest), and factor B comprised of 11 groundnut genotypes. They found that terminal drought significantly decreases root characteristics (0.83-1.03 g plant⁻¹ of root dry weight) and groundnut yield (7.98-8.89 g plant⁻¹ of pod dry weight). They also indicated that yield responses to terminal drought were not correlated with root traits except root length and root volume ($r = 0.71^{**}$ and 0.83^{**} , respectively). They reported differential response of varieties for maintaining the pod yield under terminal drought conditions.

Higher yield and improved drought resistance have been shown to be associated with larger and deeper root system in rice (Nemoto *et al.* 1998, Kondo *et al.* 2003), pearl millet (Zegada-Lizarazu and Iijima 2005), chickpea (Kashiwagi *et al.* 2006) and cowpea (Matsui and Singh, 2003).

Ren *et al.* (2006) revealed significant correlation between dry weight of axial root, dry weight of lateral root and thickness of root base (1 cm), thickness of root base (3 cm) and root volume. They also reported that root volume was significantly correlated with thickness of root base (3 cm) while there was no correspondence in relation to root volume between fresh weight of axial fresh and weight of lateral root.

Painwadee *et al.* (2009) reported positive correlation among root characters such as root length, root dry weight and root volume and these traits were positively correlated with biomass production. They also observed negative correlation was observed among drought resistance traits such as RWC, SLA and SCMR in their pot experiments with 128 progenies in the F_3 generation derived from the cross ICGV 98324 x KK-4 under long duration drought.

Hong *et al.* (2012) reported that correlations between root traits and aboveground traits at the fruiting stage were different with those at the flowering stage. Root biomass was significantly correlated with aboveground biomass and total biomass, but was not correlated with the other aboveground traits. In addition, no significant correlations were found between root traits (root volume and root activity) and any aboveground traits. Contrary to the correlation analysis at the flowering stage, root/shoot ratio at the fruiting stage was significantly and positively correlated with green leaf number on the main culm. They also found that root activity at the fruiting stage still maintained a significant positive correlation ($r = 0.700$) with yield.

Jongrunklang *et al.* (2014) reported significant positive correlations between drought tolerance index (DTI) for root surface area at deeper soil layer and DTI for pod yield in both seasons Under PFD conditions, but the correlations were not significant for root diameter and root volume.

2.3.4 Correlation between yield, physiological traits and quality traits

Oil yield is a complex and poly genetically controlled highly environmental influenced trait governed by the interaction of many variables and selection if based merely on yield is not effective. The relationships between oil yield and reproductive characters may be altered by drought. So far, important characters determining oil yield under drought and those affecting the response of groundnut genotypes to drought as far as reproductive characters and oil yield are concerned are not well understood(Knauft and Wynne, 1995; Reddy *et al.*, 2003; Habibullah *et al.*, 2007).

Mane *et al.* (2008) revealed that 100-kernel weight showed the highest but non-signification correlation with oil yield. Path coefficient analysis indicated that 100-

kernel weight had the highest direct effect on oil yield followed by number pods per plant and number seeds per pod and SMK %.

Sharma and Dashora (2009) reported that only number of mature pods per plant was positively and significantly correlated with oil yield. Path analysis showed that 100 pods weight had height positive direct effect on oil yield.

Korat *et al.* (2010) revealed that oil yield had signification positive association with shelling percentage, and 100 kernel weight, while day to maturity had negative correlation with oil yield. The direct and indirect effect obtained from path analysis revealed that oil yield was positively associated with 100-kernel weight and shelling percentage, while days to maturity and sound mature kernel percent (SMK%) had negative association with oil yield.

Sadeghi *et al.* 2012 revealed significant positive correlation of seed yield, total no. of kernels per plant, plant height and 100- seed weight with oil yield under both drought stress and irrigated conditions conditions. They also revealed greatest positive direct effects of 100-seed weight, seed yield and biomass on seeds yield in drought stress condition.

Noubissie *et al.* 2012 evaluated 12 promising groundnut (*Arachis hypogaea* L.) genotypes, in randomized complete block design with six replicates and revealed positive correlation of oil content with kernel weight ($r = 0.67$), while negative correlation of protein level with oil content ($r = -0.51$) and physical properties investigated.

Detailed review on nature of correlation between quality traits and quantitative traits was given in the Table 11.

2.3.5 Correlation between yield and foliar disease resistance

Iroume and Knauft (1987) observed negative genetic correlations between yield and leaf spot severity. They suggested that expected progress in increasing resistance of groundnut genotypes through selection for yield (30 to 40% of the response from direct selection for resistance) can be achieved through selection for yield under disease

Table 11: Summary of the review on intercorrelations between quality traits and other quantitative traits in groundnut

Sl. No.	Character s	Nature of correlation	Characters	Authors
1	Palmitic acid	Positive	SFA, Linoleic acid, Eicosenoic acid	Raheja <i>et al.</i> (1987), Lukange <i>et al.</i> (2007)
		Positive	Lignoceric acid	Noelle <i>et al.</i> (2011)
		Positive	Behenic, Linoleic, TSFA	Channayya (2009)
		Positive	Linoleic acid, P/S, IV, Protein	Kavera (2008)
		Positive	Linoleic, Behenic, Lignoceric, IV, %S	Sarvamangala(2009)
		Negative	Oleic, Eicosenoic, O/L, USFA, SFA	Sarvamangala (2009)
		Negative	Oleic, O/L, U/S	Kavera (2008)
		Negative	Oleic, Eicosenoic, Lignoceric, O/L, U/S	Channayya (2009)
2	Stearic acid	Significant positive	Oleic, SFA	Anderson <i>et al.</i> (1998), Anderson and Gorbet (2002), Lukange <i>et al.</i> (2007)
		Positive	Linoleic, Arachidic, Behenic acid, TSFA	Channayya (2009)
		Positive	Arachidic acid, , Behenic, %S	Channayya (2009)
		Positive	Arachidic, O/L, Oleic, Behenic	Kavera (2008)
		Positive	Behenic, TSFA	Channayya (2009)
		Negative	Oleic acid	Lajara <i>et al.</i> (1990), Shaikh <i>et al.</i> (1998)
		Negative	Eicosenoic acid, Lignoceric, U/S	Channayya (2009), Sarvamangala (2009)
		Negative	Linoleic, P/S	Kavera (2008)
3	Oleic acid	Significant negative	Palmitic, Linoleic	Bovi (1983), Raheja <i>et al.</i> (1987), Miller <i>et al.</i> (1987), Badwal <i>et al.</i> (1993), Anderson <i>et al.</i> (1998), Rathe <i>et al.</i> (1998), Anderson and Gorbet (2002)
		Negative	SFA, Iodine value	Anderson <i>et al.</i> (1998), Anderson and Gorbet (2002)
		Negative	Palmitic, Behenic acid, Lignoceric acid, IV, %S	Sarvamangala (2009)
		Positive	Lignoceric acid, Eicosenoic acid, O/L, U/S	Sarvamangala (2009)
		Positive	O/L ratio	Asibuo <i>et al.</i> (2008)
		Positive	O/L, U/S, Eicosenoic acid, 100 seed weight	Kavera (2008)
		Positive	Eicosenoic acid, Lignoceric, O/L, U/S	Channayya (2009)
		Positive	Eicosenoic acid, U/S	Andersen <i>et al.</i> (1998)
		Negative	Palmitic acid, Iodine value	Andersen <i>et al.</i> (1998)
		Negative	Linoleic acid	Asibuo <i>et al.</i> (2008), Singkham <i>et al.</i> (2010)
		Negative	Linoleic, Behenic acid, TSFA	Channayya (2009)
		Negative	Linoleic acid, P/S, IV, Protein & Oil content	Kavera (2008)

Contd...

Sl. No.	Characters	Nature of correlation	Characters	Authors
4	Linoleic acid	Positive	Eicosenoic	Anderson <i>et al.</i> (1998)
		Positive	U/S, P/S, IV, Oil content	Kavera (2008)
		Positive	Behenic, TSFA	Channayya (2009)
		Positive	Arachidic acid, Behenic, TSFA	Channayya (2009)
		Negative	Arachidic acid, O/L, Lignoceric, 100 seed weight	Kavera (2008)
		Negative	Arachidic acid, Eicosenoic acid, O/L, U/S	Channayya (2009)
		Negative	Oleic, Eicosenoic acid, Lignoceric acid, O/L, U/S ratio	Channayya (2009)
5	Arachidic acid	Negative	Eicosenoic acid	Hammond <i>et al.</i> (1997), Sarvamangala (2009)
		Negative	U/S, P/S, IV	Kavera (2008)
		Negative	O/L, U/S	Channayya (2009)
		Positive	Lignoceric acid	Kavera (2008)
		Positive	Lignoceric acid, SFA	Channayya (2009)
		Positive	Behenic, TSFA	Channayya (2009)
6	Eicosenoic acid	Positive	Lignoceric	Hammond <i>et al.</i> (1997)
		Positive	Behenic, Lignoceric, O/L, U/S	Kavera (2008)
		Positive	Lignoceric, O/L, U/S	Channayya (2009)
		Negative	P/S, IV	Kavera (2008)
		Negative	SFA	Channayya (2009)
7	Behenic acid	Positive	Lignoceric acid	Holley and Hammons (1968), Hammond <i>et al.</i> (1997)
		Positive	P/S ratio	Kavera (2008)
		Positive	TSFA	Channayya (2009)
		Negative	U/S ratio	Kavera (2008)
		Negative	O/L, U/S	Channayya (2009)
8	Lignoceric acid	Negative	U/S ratio	Kavera (2008)
		Negative	Stearic, Linoleic acid	Channayya (2009)
		Negative	TSFA	Channayya (2009)
		Positive	Oleic, Eicosenoic acid	Channayya (2009)
		Positive	O/L, U/S ratio	Channayya (2009)
9	O/L ratio	Significant positive	Oil stability	O'Keefe <i>et al.</i> (1993), Sharma <i>et al.</i> (1985), Jambunathan <i>et al.</i> (1993)
		Positive	U/S, Oleic, Eicosenoic acid	Channayya (2009)
		Significant negative	Iodine value, P/S, TLC SFA	Mercer <i>et al.</i> (1990)
		Negative	Oil content, 100 seed weight, Pod yield per plant	Kavera (2008)
		Negative	Palmitic, Linoleic, Behenic, SFA	Channayya (2009)
10	U/S ratio	Negative	TSFA, Palmitic, Stearic, Linoleic, Behenic acid	Channayya (2009)
		Positive	Oleic, O/L	Channayya (2009)
11	TSFA	Positive	Palmitic, Stearic, Linoleic, Behenic acid	Channayya (2009)
		Negative	Oleic, Eicosenoic, O/L, U/S, TFA	Channayya (2009)

pressure which could be advantageous for developing high yielding leaf spot tolerant genotypes.

Giri *et al.* (2009) found positive and significant association of pod yield with days to 50% flowering, days to maturity, kernel yield and test weight. They also observed negative and significant association of pod yield with late leaf spot severity indicating that they could be used as selection criteria for developing high yielding as well as late leaf spot disease resistant varieties.

Khedikar *et al.* (2010) revealed highly significant and positive correlation between stages in each of the environment for LLS ($r = 0.37-0.87$; $P < 0.01$) and rust ($r = 0.37-0.98$; $P < 0.01$). They revealed that correlations were high even across the environments in LLS, but negative correlation was observed between LLS and rust.

Sarvamangala and Gowda (2010) observed positive association between the stages and seasons for both the diseases i.e., rust and leaf spot, indicating the usefulness of population for mapping and tagging for these two diseases using appropriate molecular markers.

Hamasselbe *et al.* (2011) showed that cercospora severity and fodder yield at harvest had high and significant genotypic correlation coefficients of $+0.74^{**}$ and -0.61^{*} , respectively with percent defoliation indicating that these characters were governed by the same genes (pleiotropy). They further suggested that selection could be carried out on disease severity and fodder yield at harvest to improve resistance to Cercospora leaf spots in groundnut.

Varsha *et al.* (2013) reported significant positive association between stages and seasons for both the diseases, indicating consistency across seasons. They also reported negative correlation between rust and LLS, revealing antagonistic nature of the diseases.

2.4 Development of genetic linkage maps in groundnut

Although efforts were initiated towards developing genetic maps as early as 1993, genome mapping in groundnut has significantly increased since 2005. Initial genetic maps were developed based on mapping populations derived from the diverse parental genotypes.

For instance, Halward *et al.* (1993) reported first RFLP based genetic linkage map of groundnut using both random genomic and cDNA clones of DNA library constructed using groundnut cultivar GK 7 subsps *hypogaea* var *hypogaea*. They evaluated 100 genomic and 300 cDNA clones on F_2 populations derived from the interspecific cross between *A. stenosperma* and *A. cardenasii*. Fifteen genomic and 190 cDNA clones revealed polymorphism among the mapping parents. Of the 132 markers analysed for segregation, 117 were distributed into 11 linkage groups with a total map distance of approximately 1063 cM. Burow *et al.* (2001) reported a RFLP based tetraploid genetic linkage map, originating from a cross between Florunner and a synthetic amphidiploid $[(A. batizocoi \text{ K9J84} \times (A. cardenasii \text{ (KI 10017)} \times A. diogeni \text{ (GKP 10602)})]$, consisting of 370 RFLP loci spread into 23 linkage groups with a total map distance of 2210 cM.

Subsequently, a backcross population (78 BC₁F₁ lines) generated from the cross of TxAG-6, a synthetic amphidiploid line $[(A. batizocoi \times (A. cardenasii \times A. diogeni)]4x$ and Florunner was used to develop the genetic map with 370 RFLP loci onto 23 linkage groups and 2,210 cM genome coverage (Burow *et al.* 2001). The common markers mapped in both the crosses showed a high degree of co-linearity between the diploid and tetraploid chromosomes (Burow *et al.* 2001; Jesubatham and Burow, 2006).

However, RFLP is labor intensive and not very suitable for use in breeding programs. Therefore, several research groups have developed microsatellite or simple sequence repeat (SSR) markers but to date, these SSR markers have only been integrated into a diploid *Arachis* AA genome map (Moretzsohn *et al.*, 2005).

In terms of the second generation genetic maps based on SSR markers, an F_2 population obtained from a cross between two diploid species with AA genome (*A. duranensis* and *A. 12 stenosperma*) was used. As a result, the AA-genome map comprised of 170 SSR loci on 11 linkage groups covering 1,231 cM was developed (Moretzsohn *et al.* 2005). This map was saturated further and the current map based on this population has 369 marker loci (Leal-Bertioli *et al.*, 2009).

In parallel, a high density AA-genome genetic map (*A. duranensis* and *A. duranensis*) has also been developed with 2,319 markers (971 SSRs, 221 single stranded DNA conformation polymorphism (SSCP) markers and 1,127 SNPs) mapped

on 10 linkage groups (Nagy *et al.* 2010). For the BB- genome, a genetic map with 149 SSR loci on 11 linkage groups covering 1, 294 cM genome coverage has been developed based on a F₂ population (93 lines) derived from the cross between *A. ipaensis* (KG30076) and *A. magna* (KG30097).

Although low genetic diversity in the cultivated groundnut gene pool was a serious bottleneck until recently in developing the genetic maps using mapping populations of cultivated groundnut lines, availability of large numbers of SSR markers facilitated the development of the first SSR-based genetic map based on a RIL population derived from TAG 24 × ICGV 86031 (Varshney *et al.* 2009). They identified a total of 144 (12.6%) polymorphic markers amplifying a total of 150 loci, among which, total of 135 SSR loci were mapped into 22 linkage groups (LGs). They also identified 2–5 QTLs for each trait *viz.*, transpiration, transpiration efficiency, specific leaf area and SPAD chlorophyll meter reading where, the phenotypic variation explained by these QTLs was in the range of 3.5–14.1%.

This map was further saturated with more markers and the current map based on the above mapping population has 191 SSR loci onto 20 linkage groups with 1, 785 cM genome coverage (Ravi *et al.* 2011). Subsequently, several other genetic maps for cultivated groundnut have become available recently. With an objective of estimating the marker order for a maximum number of marker loci based on a single map, a composite map comprising of 175 marker loci has been developed by Hong *et al.* (2010).

Details of some major genetic maps constructed in *Arachis* species was given in the Table 12.

Consensus map

As compared to individual genetic maps, consensus maps offer several advantages such as:

- (i) Mapping of a large number of marker loci onto a single map.
- (ii) Determining relative position of common markers across the mapping populations.

Table 12: Details of some major genetic maps constructed in *Arachis* species

Population	Population size	Marker loci mapped	References
A-genome genetic maps			
<i>A. stenosperma</i> × <i>A. cardenasii</i>	F2	117 RFLPs	Halward <i>et al.</i> 1993
<i>A. kuhlmanni</i> × <i>A. diogoi</i>	179 F2	102 AFLPs	Milla 2003
<i>A. stenosperma</i> × (<i>A. stenosperma</i> × <i>A. cardenasii</i>)	44 BC1F1	167 RAPDs	Garcia <i>et al.</i> 2005
<i>A. duranensis</i> × <i>A. stenosperma</i>	F2	170 SSRs	Moretzsohn <i>et al.</i> 2005
<i>A. duranensis</i> × <i>A. stenosperma</i>	93F2	369 markers (SSR, AFLP, SNP, RFLP, SCAR)	Leal-Bertioli <i>et al.</i> 2009
<i>A. duranensis</i> × <i>A. duranensis</i>	94 F2	2,319 markers (1,127 SNPs, 971 SSRs, 221 SSCPs)	Nagy <i>et al.</i> 2010
B-genome genetic maps			
<i>A. ipaensis</i> × <i>A. magna</i>	93 F2	149 SSRs	Gobbi <i>et al.</i> 2006, Moretzsohn <i>et al.</i> 2009
<i>A. batizocoi</i> PI 298639 × <i>A. batizocoi</i> PI 468327	94 F2	449 SSRs	Guo <i>et al.</i> 2010
AB genome genetic maps			
<i>A. hypogaea</i> × <i>A. cardenasii</i>	46 F10C9	RAPDs	Garcia <i>et al.</i> 1995
<i>A. hypogaea</i> × (<i>A. batizocoi</i> × (<i>A. cardenasii</i> × <i>A. diogoi</i>))	78 BC1F1	370 RFLPs	Burow <i>et al.</i> 2001
ICG 12991 × ICGV-SM 93541	200 F2	12 AFLPs	Herselman <i>et al.</i> 2004
TAG 24 × ICGV 86031	318 RILs	191 SSRs	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
<i>A. duranensis</i> × (<i>A. ipaensis</i> × <i>A. duranensis</i>)	88 BC1F1	298 SSRs	Foncéka <i>et al.</i> 2009
Yueyou 13 × Zhen Zhuhei	142 RILs	132 SSRs	Hong <i>et al.</i> 2010
Yueyou 13 × FU 95-5	84 RILs	109 SSRs	Hong <i>et al.</i> 2010
Yueyou 13 × J 11	136 RILs	46 SSRs	Hong <i>et al.</i> 2010
TAG 24 × GPBD 4	266 RILs	188 SSRs	Khedikar <i>et al.</i> 2010, Sujay <i>et al.</i> 2011
ICGS 44 × ICGS 76	188 RILs	82 SSRs	Gautami <i>et al.</i> 2011
ICGS 76 × CSMG 84-1	176 RIL	119 SSRs	Gautami <i>et al.</i> 2011
TG 26 × GPBD 4	146 RILs	181 SSRs	Sarvamangala <i>et al.</i> 20011, Sujay <i>et al.</i> 2011
SunOleic 97R × NC94022	190 RILs	170 SSR, 2 CAPS	Chen <i>et al.</i> 2010
Tifrunner × GT-C20	158 RILs	238 SSR, 1 CAPS	Chen <i>et al.</i> 2010

- (iii) Determining stability of marker locus position across the genome.
- (iv) Provides evidence for chromosomal rearrangements (Beavis and Grant, 1991), gene duplication (Kianian *et al.*, 1992; Gentzbittel *et al.*, 1995) and assists in the assignment of linkage groups to chromosome.
- (v) Provides the basic information for comparative genomic studies among related species and subspecies and
- (vi) Provides genetic information for greater genomic coverage (Sewell *et al.*, 1999).
Because of above mentioned features, consensus genetic maps have been developed in many crop species like maize (Sharopova *et al.*, 2002; Falque *et al.*, 2005), wheat (Somers *et al.*, 2004) barley (Varshney *et al.*, 2007; Marcel *et al.*, 2007), soybean (Song *et al.*, 2004; Choi *et al.*, 2007) and pigeonpea (Bohra *et al.*, 2012).

QTL analysis in new mapping populations involves development of new genetic maps. Based on common markers mapped on genetic maps for different mapping populations, it is possible to develop the consensus map (Ablett *et al.*, 2003).

Goutami *et al.*, 2014 provided an international reference consensus genetic map comprised of 897 marker loci based on 11 mapping populations for tetraploid groundnut spanning a map distance of 3, 863.6 cM with an average map density of 4.4 cM and could be useful for selecting highly informative and uniformly distributed markers for developing new genetic maps, background selection, diversity analysis and QTL analysis in a multi-populations design, evaluating the genetic background effect on QTL expression.

2.5 QTL mapping

However in recent years due to availability of advanced mapping populations such as RILs and relatively large number of molecular markers, linkage-mapping based marker analysis has been undertaken to identify the QTLs for various traits (Table 13) such as resistance to foliar disease (Khedikar *et al.*, 2010; Sujay *et al.*, 2011) and nutritional quality traits (Sarvamangala *et al.*, 2011). By using multi-environment phenotyping data for drought tolerance traits, 153 main-effect and 25 epistatic QTLs

Table 13: List of QTLs identified for some economically important traits in groundnut

Trait	QTLs identified	Phenotypic variance explained (%)	References
Biotic stress			
Late leaf spot (LLS)	39	1.70-67.98	Khedikar <i>et al.</i> 2010, Sujay <i>et al.</i> 2011
Leaf rust	27	1.70-82.96	Khedikar <i>et al.</i> 2010, Sujay <i>et al.</i> 2011
Resistance to <i>Aspergillus flavus</i> invasion	6	6.2-22.7	Liang <i>et al.</i> 2009a
Aphid vector of groundnut rosette disease	8	1.18-76.16	Herselman <i>et al.</i> 2004
Abiotic stress			
Transpiration (T)	15	4.36-18.17	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011, Gautami <i>et al.</i> 2011
Transpiration efficiency (TE)	14	4.47-18.12	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011, Gautami <i>et al.</i> 2011
Specific leaf area (SLA)	13	3.48-13.29	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Leaf area (LA)	4	7.24-11.51	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
SPAD chlorophyll meter reading (SCMR)	29	5.72-19.53	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Biomass	7	4.25-20.32	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Canopy conductance (ISC)	7	3.28-22.24	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Total dry matter (TDM)	7	4.34-22.39	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011, Gautami <i>et al.</i> 2011
Agronomic traits			
Shoot dry weight (ShDW)	11	5.03-22.09	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011, Gautami <i>et al.</i> 2011
Pod weight (PW)	7	4.17-8.73	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Seed weight (SW)	5	4.18-8.22	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Haulm weight (HW)	6	3.78-33.66	Varshney <i>et al.</i> 2009, Ravi <i>et al.</i> 2011
Harvest index (HI)	3	6.39-40.10	Gautami <i>et al.</i> 2011
Pod mass/plant	3	13.1-18.3	Liang <i>et al.</i> 2009
Mature pods/plant	3	11.9-12.3	Liang <i>et al.</i> 2009
Number of branches	7	8.1-17.3	Liang <i>et al.</i> 2009
Number of fruit branches	1	17.5	Liang <i>et al.</i> 2009
Height of main axis	7	8.2-12.8	Liang <i>et al.</i> 2009
Stem diameter	4	7.8-24.1	Liang <i>et al.</i> 2009
Leaf length, width and length /width ratio	7	12.4-18.9	Liang <i>et al.</i> 2009
Yield parameters	5	9.19-17.69	Selvaraj <i>et al.</i> 2009
Oil content	7	1.5-9.5	Liang <i>et al.</i> 2009, Selvaraj <i>et al.</i> 2009, Sarvamangala <i>et al.</i> 2011
Oil quality	10	1-4-9.7	Sarvamangala <i>et al.</i> 2011
Protein content	10	1.5-13.4	Liang <i>et al.</i> 2009, Sarvamangala <i>et al.</i> 2011

were identified (Varshney *et al.*, 2009; Ravi *et al.*, 2011; Gautami *et al.*, 2011). On the other hand, one major QTL each for leaf rust (55.2 % PVE, Khedikar *et al.*, 2010; 82.96% PVE, Sujay *et al.*, 2011) and LLS (67.98 % PVE, Sujay *et al.*, 2011) was detected. Although in some cases like resistance to nematode (Nagy *et al.*, 2010b), leaf rust (Khedikar *et al.*, 2010), LLS (Sujay *et al.*, 2011) and high-oleate trait (Chu *et al.*, 2009, Chen *et al.*, 2010) diagnostic molecular markers are available for deployment in molecular breeding, tightly linked molecular markers for are yet to be identified for several other important traits like ELS, GRD, etc.

Several studies have reported identification of QTL for drought tolerance in groundnut and also other crops; however, in the case of groundnut, QTL study for drought tolerance traits has been conducted based on only one mapping population TAG-24 x ICGV-86031 (Varshney *et al.*, 2009). Comprehensive QTL analysis led to the identification of a total of 117 small main-effect QTL (M-QTL) and 23 epistatic QTL (E-QTL) for drought-related traits (Ravi *et al.* 2011).

But recently, with the aim of understanding the genetic basis and identification of quantitative trait loci (QTL) for drought tolerance, two new recombinant inbred line (RIL) mapping populations, namely ICGS 76 9 CSMG 84-1 (RIL-2) and ICGS 44 9 ICGS 76 (RIL-3) were used to develop a consensus map with 293 SSR loci distributed over 20 linkage groups, spanning 2, 840.8 cM. QTL analysis identified 153 main effect QTL (M-QTL) and 25 epistatic QTL (EQTL) for drought-tolerance-related traits and the localization of these QTL on the consensus map provided 16 genomic regions that contained 125 QTL (Gauthami *et al.*, 2012).

Several studies were conducted in the past that reported identification of QTLs for drought tolerance or related traits in other crops also. For instance, in soybean, 5 QTLs were identified for WUE in an F2 population with 14–20% phenotypic variation explained (PVE) (Mian *et al.* 1998). In case of wheat, Dashti *et al.* (2007) identified five QTLs for drought tolerance with 13–34% PVE. In another study, 47 QTLs for different plant stress indicators in rice with 5–59% PVE were identified.

3. MATERIAL AND METHODS

The complexity of drought tolerance mechanisms explains the slow progress in yield improvement in drought prone environments. Further, plant responses to drought stress are species-specific and show significant phenological variation. The understanding of the full interaction of a complex collection of drought adaptation traits is much more difficult than understanding the functioning of each individual trait. The accurate assessment of a cultivars drought adaptation may not be possible from a single season evaluation. Similarly, there generally is no single trait that breeders can deploy to improve the productivity of a given crop under water-limiting conditions. Development of overall drought adaptation for a plant is most generally the result of the collective expression of many plant characteristics in the appropriate environment. By taking these things into consideration in the present study, an attempt was made to identify the superior RILs derived from a cross TMV-2 x GM 6-1 based on evaluation for high yield along with physiological, root and quality traits under different water regimes.

3.1 Experimental material

The experimental material for the present study consisted of RILs in F_8 generation derived from the TMV-2 x GM 6-1 cross. A total number of 299 RILs were available for present study, which were evaluated along with the parents and checks for quantitative, physiological and quality traits in field and for root traits in raised bed. Further 14 superior drought tolerant RILs, identified across the two seasons from 299 RILs were evaluated in multilocation yield trials.

3.1.1 Salient features of the parental material

TMV-2 a Spanish bunch type variety derived through mass selection from Gudhiatham bunch (Ah 32) is a popular high yielding cultivar with medium sized pods and good kernel features. It contains low oleic acid (39-42 %) and is susceptible to drought as well as late leaf spot and rust diseases.

GM 6-1 a Spanish bunch variety and high oleic mutant derived from GPBD-4 by gamma rays irradiation (Ganapati *et al.*, 2012). It has the desirable features of drought tolerance, high oleic acid (68-72 %) and resistance to late leaf spot and rust diseases. Variation between parents TMV-2 x GM 6-1 for root length and pegging pattern is indicated in Plate 1.

3.1.2 Development of mapping population

The mapping population was developed at University of Agricultural Sciences, Dharwad. F_1 s derived from the cross between TMV-2 x GM 6-1 were selfed to produce F_2 and advanced through Single Seed Descent (SSD) method till F_8 generation. Schematic representation of development of mapping population was given in the Plate 2.

3.2 Experimental site

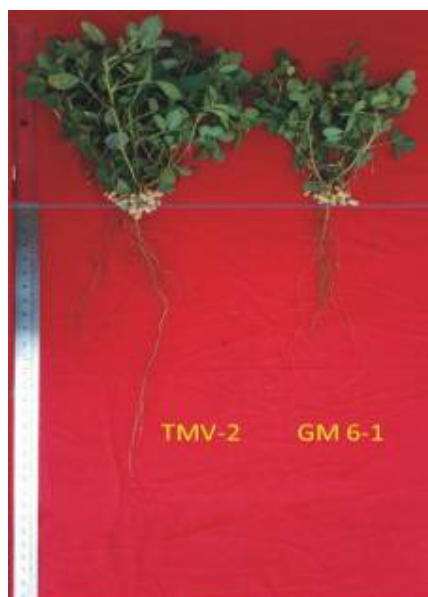
The experiments were carried out during summer 2012-13 and summer 2013-14 at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad to evaluate RILs for quantitative traits, physiological traits, root traits and quality traits. Multilocation yield trials (MLT) for selected lines were conducted during *kharif* 2014-15 at Annigeri and Bijapur.

3.3 Soil moisture content and meteorological condition

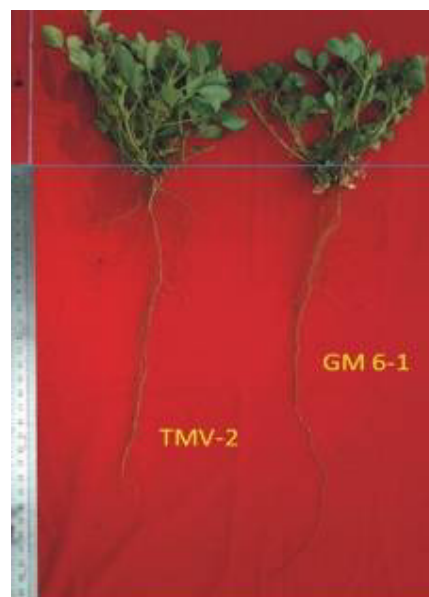
Soil moisture content was determined using gravimetric method at a depth of 0–15 cm during 30, 45 and 60 DAS to verify level of moisture content in well watered (WW) and water stress (WS) conditions. Rainfall, relative humidity (RH), vapour pressure, maximum and minimum temperature were recorded daily from sowing until harvest at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad at a distance of 100 m from the experimental field.

3.4 Climate and weather

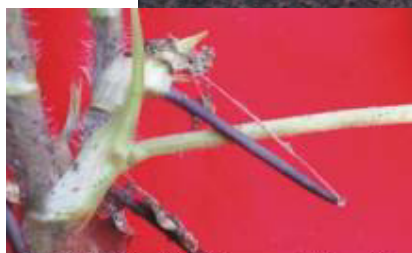
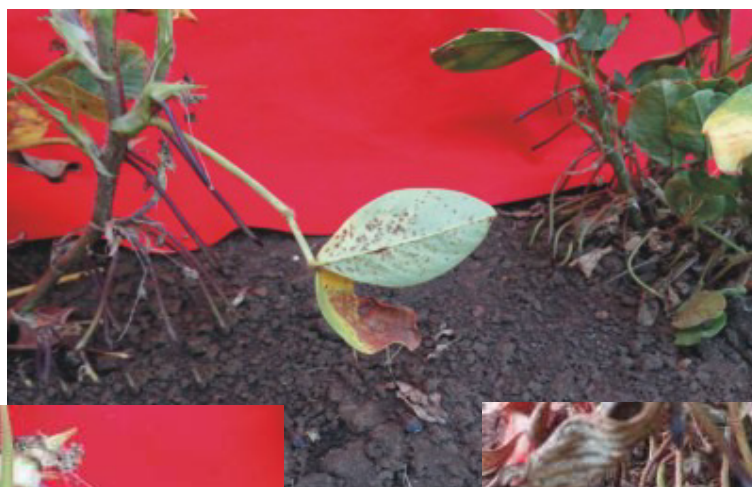
Geographically, Main Agricultural Research Station, Dharwad is located at a latitude of $15^{\circ}12'1''$ N of $75^{\circ}07'1''$ and an altitude of 678 m above mean sea level. It received an average rainfall of 740.40 mm in the year 2013 with one peak in June-July



WW condition (WW)



WS condition (WS)

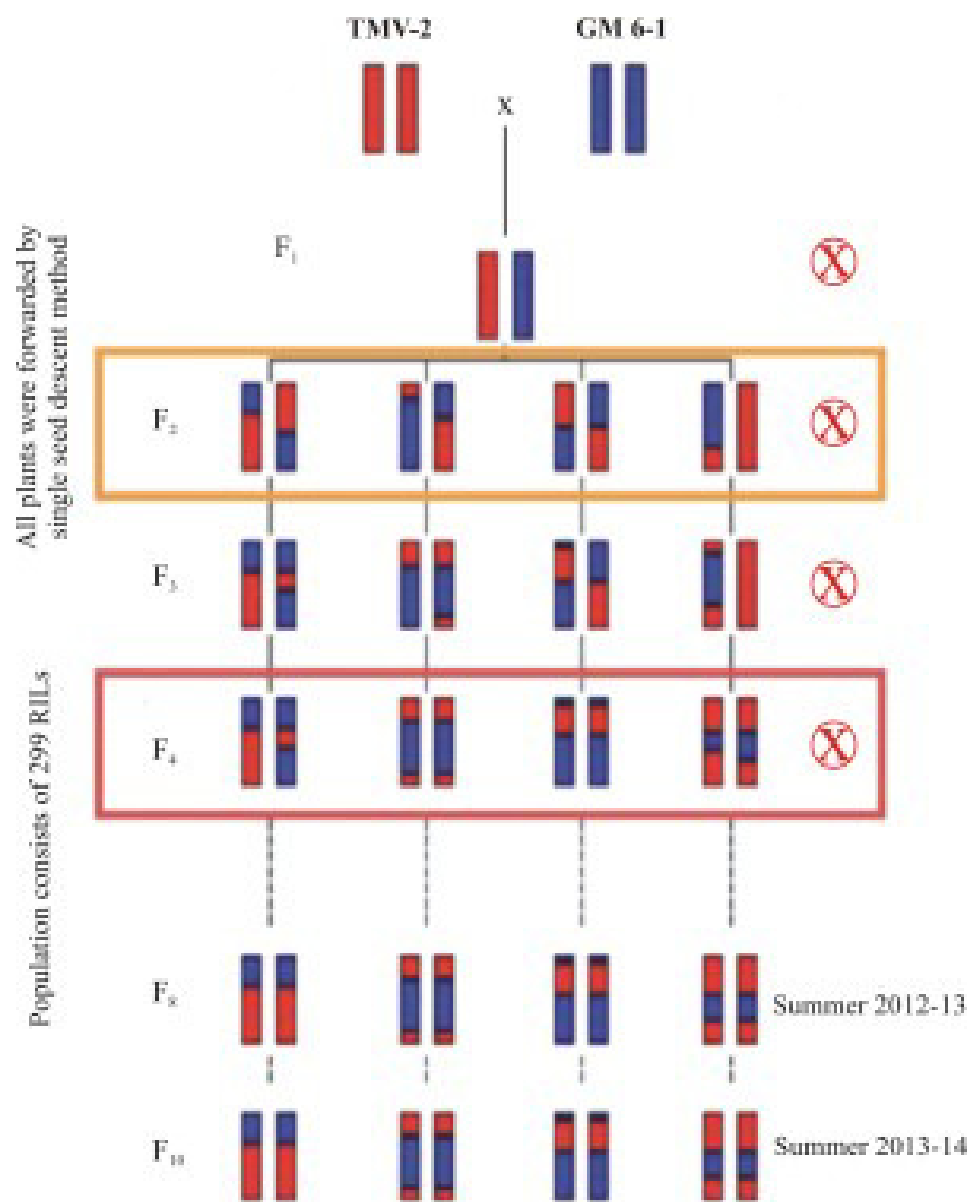


TMV-2 (WS condition)



GM 6-1 (WS condition)

Plate 1a Variation for root length and pegging pattern between the parents TMV-2 and GM 6-1



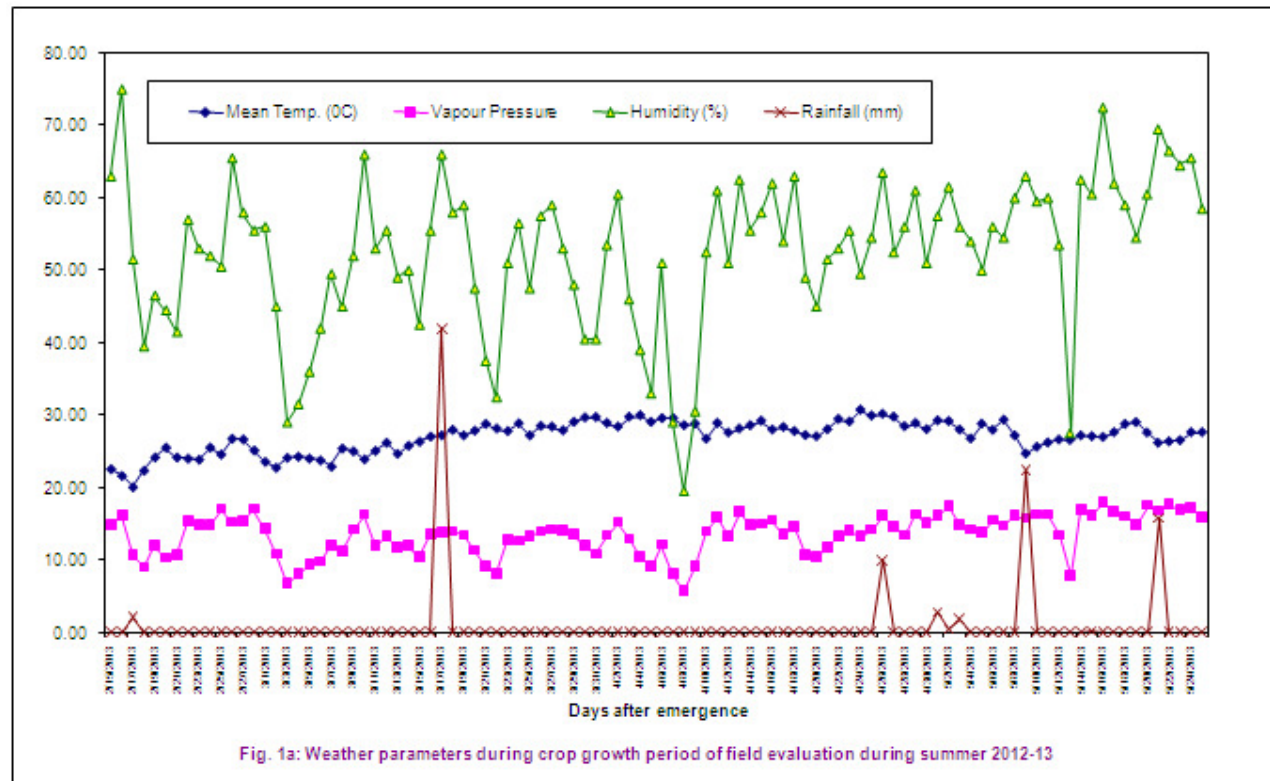
and 887.20 mm in 2014 with one peak two peaks in June-July and another in August-September. About 97.60 mm of total rain fall received in summer 2012-13 (February-May) while rainfall received was 108.10 mm during summer 2013-14 (January-April). The mean temperature varied from 19.45°C to 40.89°C in 2013 and 19.50°C to 30.70°C in 2014. The relative humidity recorded in 2013 was highest with 96.50 per cent during the month of July and the lowest of 29 per cent during the month of April. It ranged from 31 to 97 per cent in the year 2014 (Appendix I and II). Variation with respect to mean daily temperature (°C), vapour pressure, relative humidity (%) and rainfall during crop growth periods of field and raised bed evaluation of summer 2012-13 and summer 2013-14 are depicted in the Fig. 1a, 1b, 1c and 1d. Selected regions for multilocation yield trials had low rainfall during past 25 years. Meteorological data at Annigeri and Bijapur during *kharif* 2014-15 along with mean maximum and minimum air temperatures along with the rainfall during the years from 2011-2014 are presented in Appendix IV-VI.

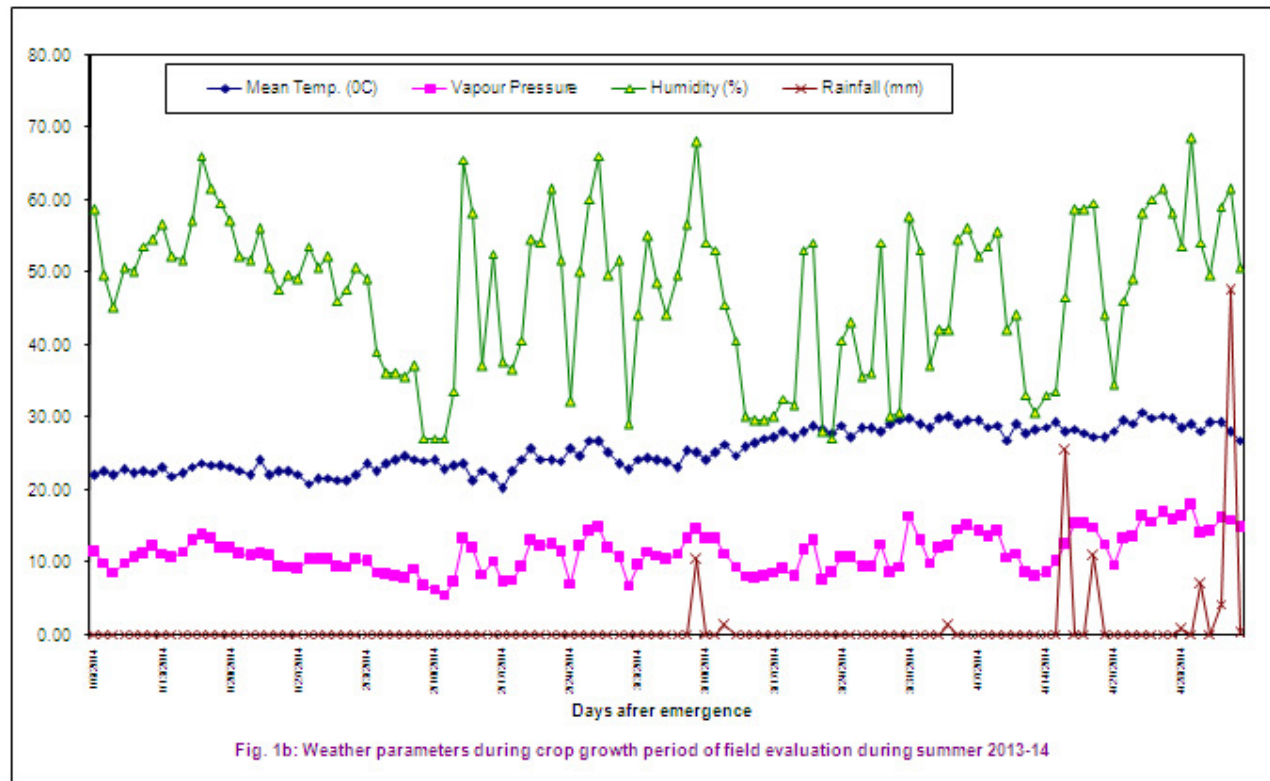
3.5 Methods

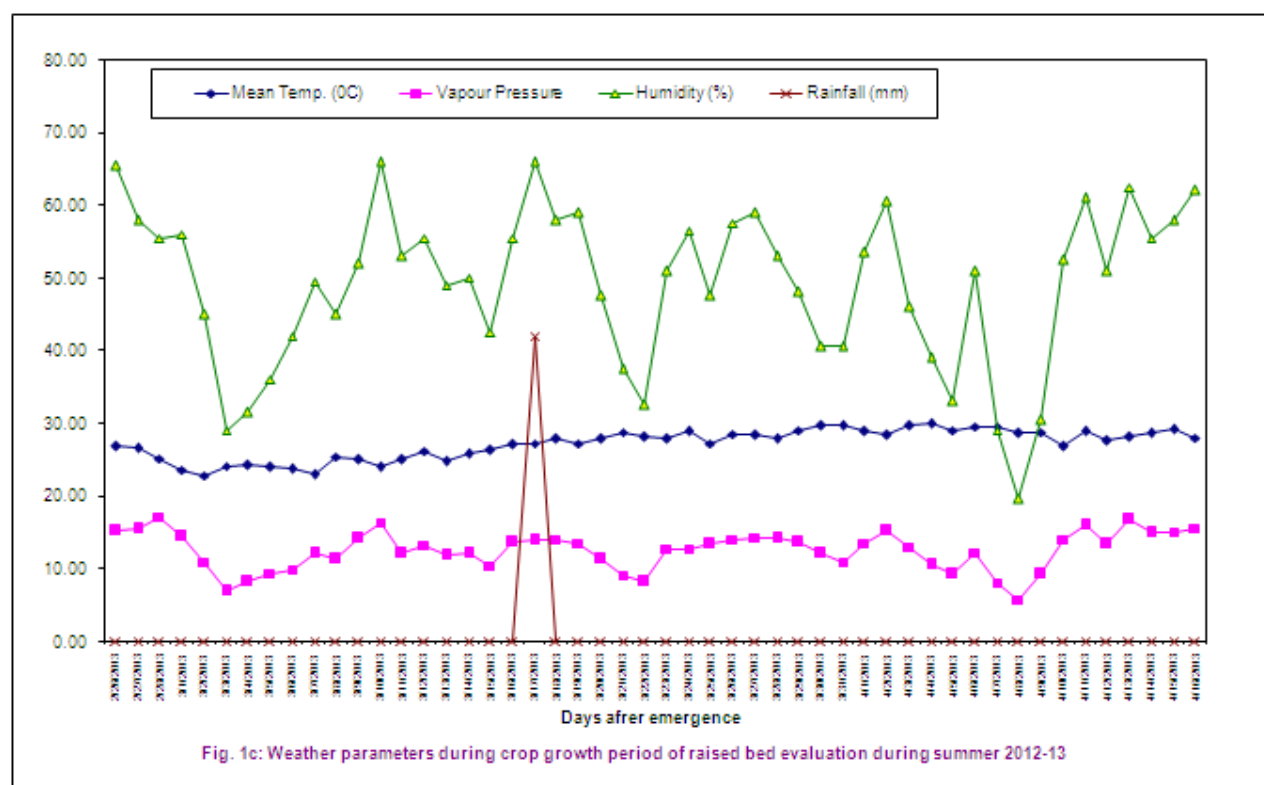
3.5.1 Phenotyping for drought tolerance, quantitative and quality traits

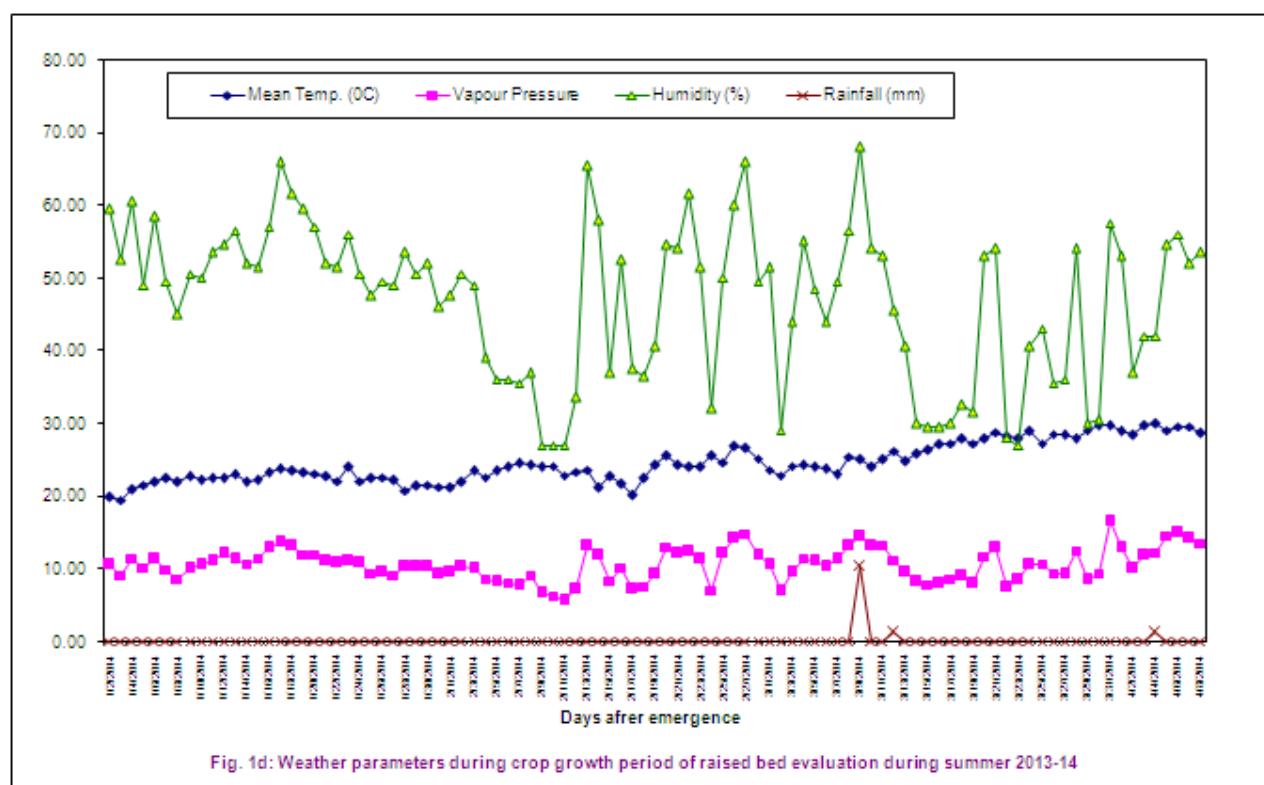
The RIL population in F_8 generation developed out of the two genotypes *viz.*, TMV-2 and GM 6-1 with distinct difference in root length and physiological traits under water stress condition along with the parents and checks were phenotyped for yield contributing traits, physiological traits and quality traits under normal as well as water stress conditions during summer seasons of 2012-13 and 2013-14.

A factorial experiment was planned in a randomized complete block design (RCBD) with two replications. The two water regimes of Well Watered (WW) and Water Stress (WS) conditions were assigned as Factor A, whereas the genotypes (2 parents + 299 RILS + 8 checks) were considered as Factor B. All the entries were sown on 15-02-2013 during summer season of 2012-13 and on 06-01-2014 during summer 2013-14. In both the seasons sowing was done in one row of 1m length with a spacing of 30 cm between rows and 10 cm between the plants. The recommended packages of practices were followed for raising a good crop.









3.5.1.1 Management of irrigation for treatment application

The plants were exposed to intermittent stress in the WS plot from the time of flowering (on 21-03-13 during summer 2012-13 and on 16-02-2014 during summer 2013-14) until pod initiation stage (on 28-04-2013 during summer 2012-13 and on 20-03-2014 during summer 2013-14) in field. In the field drought stress was imposed by irrigating both the plots (WW and WS) equally upto the time of flowering. Imposition of stress was initiated after the flowering for WS plot while, irrigation was supplied to the WW plot at 7-10 days interval. Irrigation to the WS plot was supplied based only when the wilting score of a majority of WS plots reached a value of 4. The scoring of wilting symptoms was recorded on a visual score of 1-5 where, 1 = no wilting symptoms, score 2 = few leaves wilted in a few plants from the plot, score 3 = a majority of plants in a plot have wilted leaves, but none has reached permanent wilting, score 4 = few of plants show at least partial symptoms of permanent wilting and score 5 = most plants show symptoms of permanent wilting (Ratnakumar *et al.*, 2009). Harvesting was done in both the plots at physiological maturity stage. Field view of RILs at 30 days after stress in WW and WS condition during summer 2013-14 is indicated in Plate 3.

3.5.1.2 Recording of observations

Observations were recorded on five randomly tagged plants for different characters in each entry in both the replications. The mean value for the treatment was computed by taking average of five plants. The characters studied and techniques adopted to record the observations are given below.

3.5.1.2.1 Soil moisture content

Average soil moisture from 0 to 15 cm was measured by using a micro auger at different stages of estimating RWC. Soil sample of about 50-100 gm was collected and weight of the soil was recorded as wet weight. Sample was placed in the oven at 80°C for 24 hours. Weight of the dried soil sample was recorded as dry weight. Variation in soil moisture content in field and raised bed evaluation of summer 2012-13 and summer 2013-14 are depicted in the Fig. 2.



WW condition



WS condition

Field evaluation during summer 2013-14



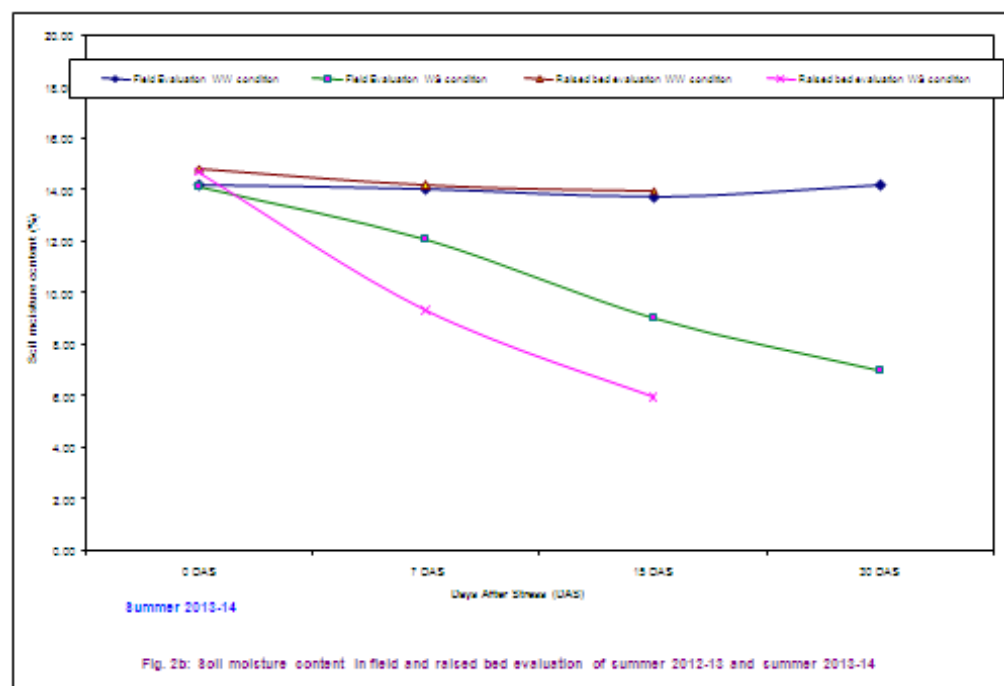
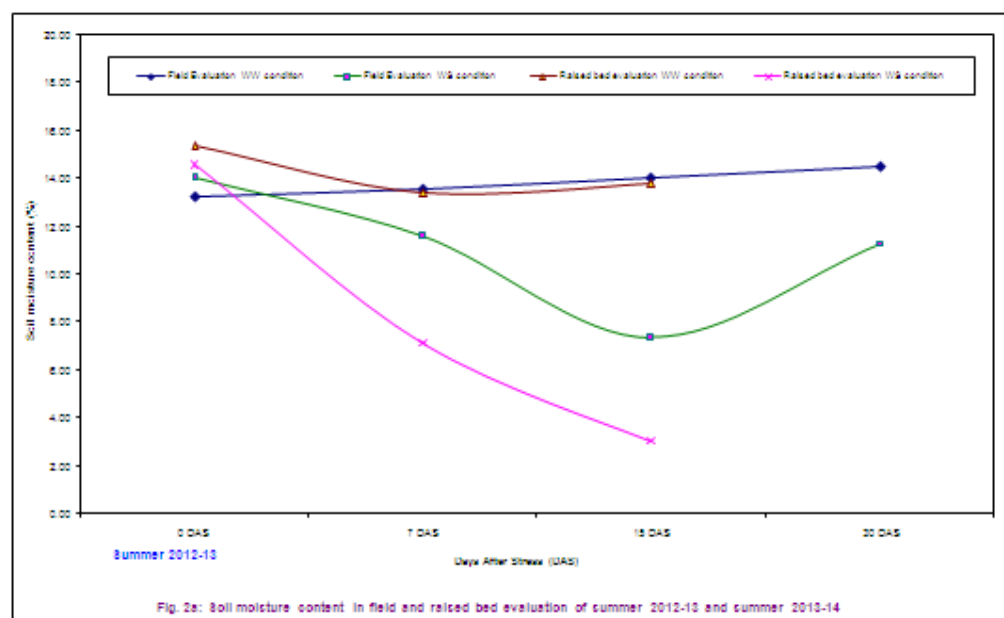
WW condition



WS condition

Raised bed evaluation during summer 2013-14

Plate 3: General view of RILs at 30 days after stress in WW and WS condition of field and raised bed evaluation



The moisture content in dry weight basis can be calculated using the following formula (Black 1965).

$$\text{Soil moisture content (\%)} = \frac{\text{Wet weight of the soil (gm)} - \text{Dry weight of the soil (gm)}}{\text{Dry weight of the soil (gm)}} \times 100$$

3.5.1.2.2 Quantitative traits

In summer 2012-13 and 2013-14, observations were recorded on randomly chosen five competitive plants in each genotype in each replication for most of the quantitative traits viz., plant height, number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant on random five plants of the treatment while pod yield per plant, kernel yield per plant, shelling percentage, 100 seed weight, sound mature kernel percentage except for days to 50 per cent flowering and days to maturity, which were recorded on per plot basis.

Days to 50 per cent flowering (DFF)

Number of days taken from the date of sowing to the date on which 50 per cent of plants in each treatment flowered was recorded as days to 50 per cent flowering.

Days to maturity (DM)

Number of days taken from date of sowing to physiological maturity of the plant was recorded as days to maturity.

Plant height (PH)

Plant height (cm) of the main axis from ground level to the apical leaflet was measured in cm and mean of 5 random plants was recorded at maturity.

Number of primary branches per plant (NPBP)

Numbers of n + 1 branches on main axis were counted and mean of 5 random plants was recorded.

Number of secondary branches per plant (NSBP)

Numbers of $n + 2$ branches on main axis were counted and mean of 5 random plants was recorded.

Number of pegs per plant (NPPP)

The total number of pegs were counted and mean of 5 random plants was recorded at the time of harvest.

Number of mature pods per plant (NMPP)

The total number of matured pods were counted and mean of 5 random plants was recorded at the time of harvest.

Number of immature pods per plant (NIPP)

The total number of immatured pods were counted and mean of 5 random plants was recorded at the time of harvest.

Pod yield per plant (PYP)

Dry pod weight of all the plants in each treatment was recorded and mean pod yield per plant was recorded in grams.

Kernel yield per plant (KYP)

Dry kernel weight of all the plants in each treatment after shelling was recorded and mean kernel yield per plant was recorded in grams.

Shelling per cent (SP)

Shelling per cent (%) was determined as the ratio of weight of kernels to weight of pods by shelling 100 g dried cleaned pods from each treatment.

Sound mature kernel percentage (SMK %)

The proportion of weight of sound mature kernels to the total kernel weight of the plant was calculated.

Hundred seed weight (HSW)

Hundred seed weight was computed by weighing random 100 kernels taken from each genotypes and weight was recorded in grams.

3.5.1.2.3 Physiological traits

Relative Water Content (RWC)

RWC was recorded during both seasons at three stages viz., 7, 15 and 30 days after stress (DAS). Ten plants in each plot were randomly chosen and the second fully expanded leaves from the top of the main stems were used for determination of relative water content. Leaf discs of one cm diameter were punched and fresh weight (FW) was recorded. The leaf disc samples were then soaked in distilled water for 4-5 hrs and blotted for surface drying and water saturated leaf weight was determined as turgid weight (TW). The samples were oven-dried at 80 °C until reaching constant weight and leaf dry weight (DW) could be determined. RWC was calculated based on the formula suggested by Gonzalez and Gonzanlez-Vilar (2001) as follows.

$$\text{RWC (\%)} = \frac{\text{Fresh weight} - \text{Dry weight}}{\text{Turgid weight} - \text{Dry weight}} \times 100$$

Specific leaf area (SLA)

For recording of SLA, the second fully expanded leaves were detached from the ten chosen plants were in kept in butter paper bags for recording observations. Leaf discs were punched from the selected leaves and leaf area was measured. Leaves were dried in an oven at 80°C for at least 48 h to determine the leaf dry weight. Immediately after drying, the leaves were weighed and the SLA was derived as leaf area per unit leaf dry weight (cm² g⁻¹). The SLA was calculated using the following formula (Evans, 1972).

$$\text{SLA} = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Leaf dry weight (g)}}$$

SPAD chlorophyll meter reading (SCMR)

The SPAD chlorophyll meter (Minolta SPAD-502 m, Tokyo, Japan) reading was recorded on each leaflet of the tetrafoliate leaf of five selected plants along the midrib during 60 DAS. In recording the SCMR, care was taken to ensure that the SPAD meter sensor fully covered the leaf lamina and that interference from veins and midribs was avoided.

Drought tolerance index (DTI)

Drought tolerance index was computed for pod yield by comparing means under water stress treatment to means for the field capacity treatment as suggested by Nautiyal *et al.* (2002) (more than 1 = increased, less than 1 = decreased).

$$\text{DTI (for pod yield)} = \frac{\text{Pod yield of WS condition}}{\text{Pod yield of WW condition}}$$

3.5.1.2.4 Quality traits

Oil content (%)

Oil content of recombinant inbred lines and checks were estimated by using Near Infrared Reflectance Spectrometer (NIRS) (Model 6500 Foss NIR systems, France)

Protein content (%)

Protein content of recombinant inbred lines and checks were estimated by using NIRS.

3.5.1.2.5 Fatty acid analysis

Fatty acid analysis of the advanced breeding lines and checks were carried out by NIRS analysis. The methodology involved in NIRS analysis for the determination of fatty acid composition is described below.

Near infrared spectroscopy (NIRS)

Near infrared spectroscopy either in reflectance (NIRs) or transmittance mode (NITS) is a multi-trait technique of large application in the analysis of quality traits in food and agricultural commodities.

Principle

The detection and measurement of chemical composition of biological material in NIRS is based on the vibrational responses of chemical bonds to NIR radiations.

Spectral measurements

NIR diffused reflectance spectra were collected by a monochromator NIR spectrometer model 6500 (Foss NIR systems, France) with the range from 400-2500 nm, which consisted of a light source of tungsten halogen lamps of 50w 12 volts. The spectrometer was equipped with silicon detector. For NIR analysis, the seeds were placed in a special adapter about 3 mm thick, with a diameter of 37 mm and central hole of 6 mm. For NIR scanning, the adapter was inserted in a NIRS standard ring up (IH-0325, infrasoftware international, LLC, France) and single seed was placed in the central hole. Before spectra acquisition, a reference spectrum was collected from a standard check cell (IH-032 HA, Infrasoftware International LLC, France). The instrument diagnostics was carried out to test the response of instrument, wave length and NIR repeatability to avoid the effect of surrounding environment on the instrument performance. The absorbance spectra ($10\log 1/R$) from 400 to 2500 nm were recorded at intervals. The method permitted the analysis of about 40 single seeds per hour. Mathematical procedures on the spectral information were carried out with WINISI II project manager software, version 1.50 (Infra Soft International, LLC).

Calibration

Before using NIR spectrometer for any quantitative analysis, it has to be calibrated first using chemical reference method with the application of multivariate regression models to interpret chemical information encoded in the spectral data (Shenk *et al.*, 1995). Original reflectance spectra were corrected prior to calibration by applying first and second derivative transformation, standard normal variate transformation and de-trend scatter correction, and four passes were used to eliminate outliers. Second derivative was calculated from $\log(1/R)$ spectra of six data points and a smoothing over segments of four data points. This combination was selected after having tested six additional math treatments (1, 4, 4, 1; 1, 10, 10, 1; 2, 10, 10, 1; 3, 10, 10, 1; 4, 10, 10, 1

and 2, 5, 5, 1) with and without spectral corrections and data pre-treatments. The 2, 6, 4, 1 treatment was either equal or superior in all cases based on standard error of cross-validation and 1-Vr (1 minus the ratio of unexplained variance to total variance) statistics. The calibration equations were developed using principal component regression (PCR), partial least square (PLS) and modified partial least square (mPLS) regression models. Wavelengths at interval of 8 nm across the entire visible-plus-near infrared spectrum (visible: 408-1092 nm; near infrared: 1108-2492 nm) were used for calibration. The standard error of calibration (SEC), standard error of cross-validation (SECV), correlation coefficient (r) and 1-VR statistics were used to select the best calibration equations.

Validation of calibration statistics

The performance of the calibration equations were monitored using the cross validation and external validation set of samples ($n = 100$). SECV, standard error of prediction (SEP) and r were used to determine the accuracy of prediction. The best equation for determining the fatty acid composition was developed and used for the subsequent analysis of fatty acid profile. The fatty acid contents obtained for the eight major fatty acids were used to compute various oil quality parameters as follows:

1. Palmitic acid (%)
2. Stearic acid (%)
3. Oleic acid (%)
4. Linoleic acid (%)
5. Arachidic acid (%)
6. Behenic acid (%)
7. Eicosenoic acid (%)
8. Lignoceric acid (%)

9. Oleic/Linoleic acid ratio (O/L ratio)

The higher ratio of oleic acid to linoleic acid ratio imparts oil stability with many health advantages (Holley and Hammons, 1968).

$$\text{O/L ratio} = \frac{\text{Oleic acid}}{\text{Linoleic acid}}$$

10. Total saturated fatty acid (SFA)

Saturated fatty acids are associated with health risks and higher levels of saturated fatty acids are undesirable for oil stability and nutrition. The reduction of the saturated fatty acid of groundnut is also important for the production of biodiesel as reduced saturated fatty acids content would improve winter operability of biodiesel (Korbitz, 2003).

$$\text{TSFA} = \text{Palmitic acid} + \text{Stearic acid} + \text{Arachidic acid} + \text{Behenic acid} + \text{Lignoceric acid}$$

11. Total Unsaturated fatty acid (UFA)

$$\text{TUSFA} = \text{Oleic acid} + \text{Linoleic acid} + \text{Eicosenoic acid}$$

12. Polyunsaturated/saturated fatty acid ratio

$$\frac{\text{L}}{\text{S}} = \frac{(\text{Linoleic acid})}{(\text{palmitic acid} + \text{stearic acid} + \text{arachidic acid} + \text{behenic acid} + \text{lignoceric acid})}$$

13. Unsaturated/saturated fatty acid ratio

$$\frac{\text{U}}{\text{S}} = \frac{(\text{oleic acid} + \text{linoleic acid} + \text{eicosenoic acid})}{(\text{palmitic acid} + \text{stearic acid} + \text{arachidic acid} + \text{behenic acid} + \text{lignoceric acid})}$$

14. Calculated iodine value

The iodine value is a common measure of the unsaturation of fats and oils and is widely used in the groundnut industry as an indicator of the relative storage life of groundnut products (Holley and Hammons, 1968).

$$\text{CIV} = (\text{Oleic acid} \times 0.8601) + (\text{Linoleic acid} \times 1.7321) + (\text{Eicosenoic acid} \times 0.7854)$$

15. Oleic acid desaturation ratio

Understanding enzymatic and genetic control of desaturation has allowed breeders to select for specific fatty acid profiles in groundnut. Oleic acid desaturation ratio was used to measure the activity of desaturase enzyme (Velasco *et al.*, 1997).

$$\text{ODR} = \frac{\text{Oleic acid}}{(\text{Oleic acid} + \text{Linoleic acid})}$$

3.5.1.2.5 Foliar disease resistance

Rust and Late leaf spot disease scores

The modified 9-point scale for rust (Table 14 and Fig. 3) and late leaf spot (Table 15 and Fig. 4) diseases was given by Subrahmanyam (1985) was used for screening RILs. Genotypes were scored 70 (stage 1), 80 (stage 2) and 90 (stage 3) days after sowing for both rust and late leaf spot.

3.5.2. Phenotyping for root traits

Phenotyping of RILS along with parents and checks for root traits was being carried out under well watered as well as water stress conditions during two seasons of summer 2012-13 and summer 2013-14. A raised bed (1.5 m height) of 5 m x 3 m with 28 rows was used, where sowing was done to accomplish one seedling per hill for each accession on the raised bed. The seeds were sown on 26-02-2014 and 02-01-2014 during summer 2012-13 and summer 2013-14 respectively. All the entries were sown with a spacing of 20 cm between the rows and 10 cm within the row.

During summer 2012-13, all the entries (2 parents + 299 RILS + 14 checks) were laid out in an augmented design (Federer, 1956, 1961, 1991) with two blocks and 14 checks. Entries are assigned to these plots in the form of an incomplete block design. During summer 2013-14, a factorial experiment was planned in a randomized complete block design (RCBD) with two replications. The two water regimes of Well Watered (WW) and Water Stress (WS) conditions were assigned as Factor A, whereas the genotypes (2 parents + 299 RILS + 8 checks) were considered as Factor B. The recommended packages of practices were followed for raising a good crop.

Table 14: Modified 9-point scale used for field-screening groundnut genotypes for resistance to late leaf spot (Subbarao *et al.*, 1990)

Disease score	Description	Disease severity (%)
1	No disease	0
2	Lesions present largely on lower leaves; no defoliation	1-5
3	Lesions present largely on lower leaves, very few on middle leaves; defoliation of some leaflets evident on lower leaves	6-10
4	Lesions on lower and middle leaves but sever on lower leaves, defoliation of some leaflets evident on lower leaves	11-20
5	Lesions present on all lower and middle leaves, over 50 per cent defoliation of lower leaves	21-30
6	Sever lesions on lower and middle leave; lesions present but less severe on top leaves; extensive defoliation of lower leaves; defoliation some leaflets evident on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and some middle leaves	41-60
8	Defoliation of all lower and middle leaves; sever lesions on top leaves; some defoliation of top leaves evident	61-80
9	Almost all leaves defoliated, leaving bare stems; some leaflets may remain, but show sever leaf spots	81-100

Table 15: Modified 9-scale used for field screening groundnut genotypes for rust resistance (Subbarao *et al.*, 1990)

Disease score	Description	Disease Severity (%)
1	No disease	0
2	Pustules sparsely distributed, largely on lower leaves	1-5
3	Many pustules on lower leaves, necrosis evident, very few pustules on middle leaves	6-10
4	Number of pustules on lower and middle leaves, severe necrosis of lower leaves	11-20
5	Severe necrosis for lower and middle leaves, pustules may be present on top leaves but less severe	21-30
6	Extension of damage of lower leaves, middle leaves, necrosis with dense distribution of pustules on top leaves	31-40
7	Severe damage of lower and middle leaves, pustules Densely distributed on top leaves	41-60
8	100 per cent damage to lower and middle leaves, pustules on top leaves	61-80
9	Almost all leaves withered, bare stems seen	81-100

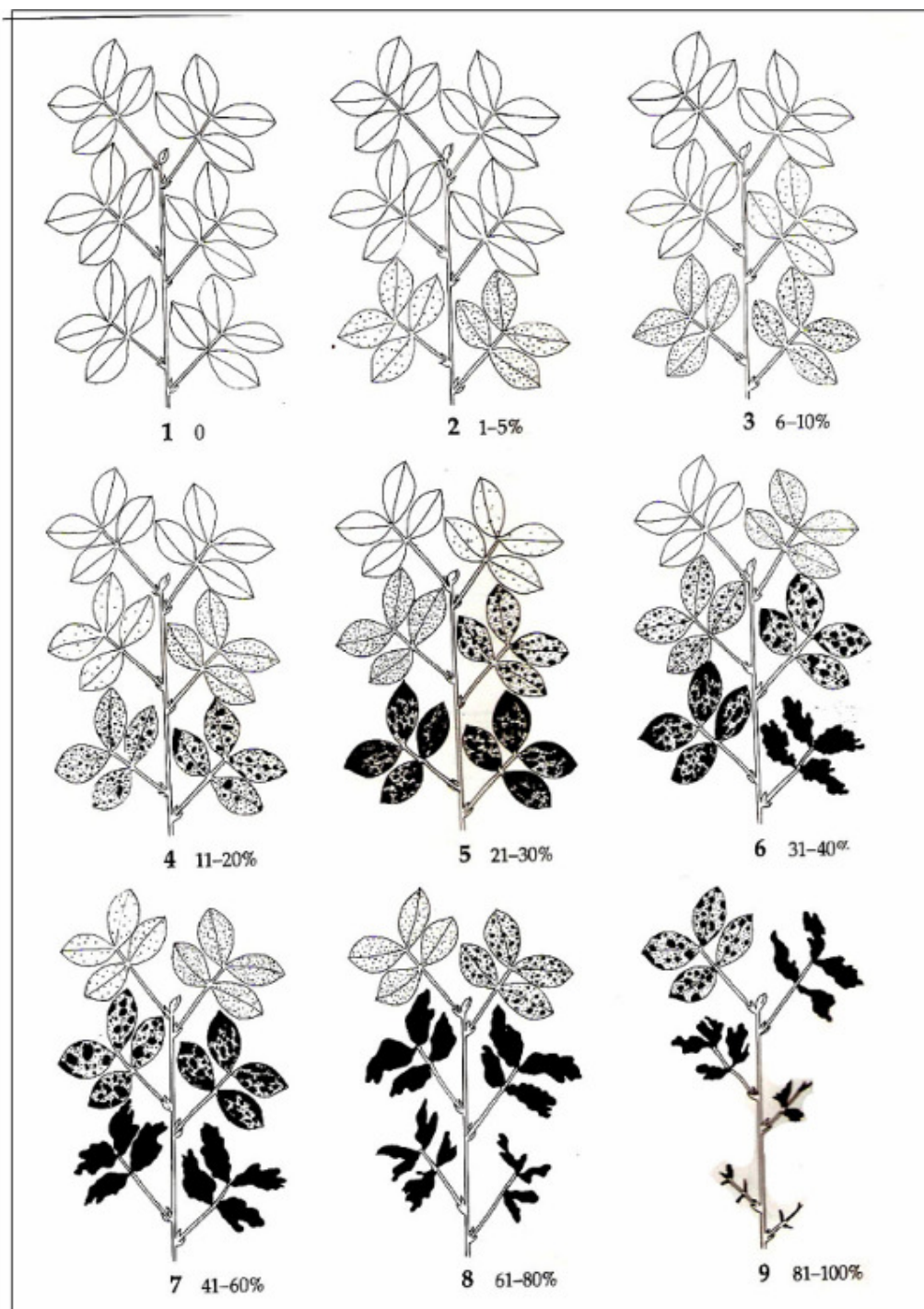


Fig. 3: The modified 9-point scale for field evaluation of rust of groundnut

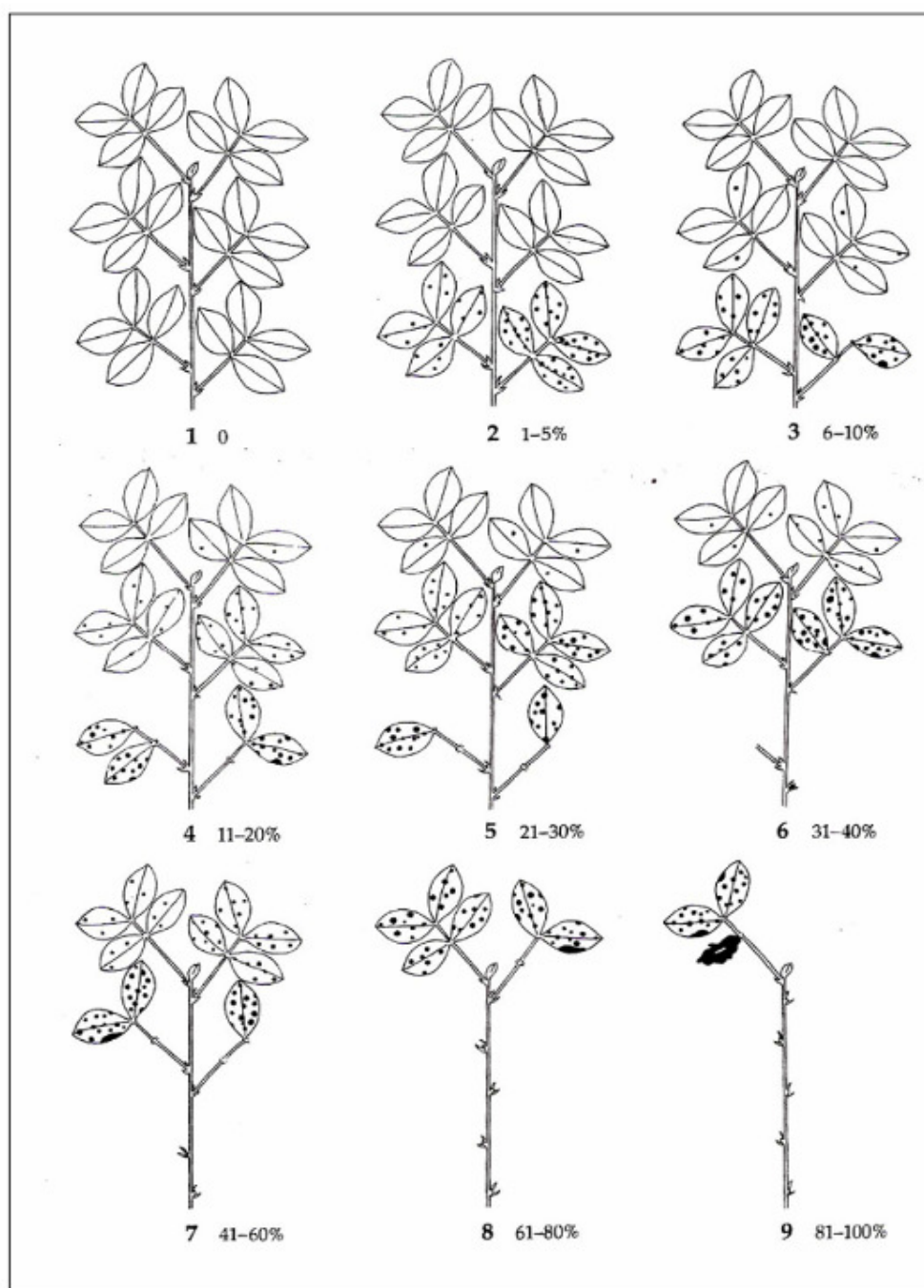


Fig. 4: The modified 9-point scale for field evaluation of late leaf spot of groundnut

3.5.2.1 Management of irrigation for treatment application

In the raised beds, both WW and WS conditions were fully irrigated until flowering time (on 24-03-2013 and 05-02-2014 of summer 2012-13 and 2013-14 respectively) by supplying a constant amount of water on daily basis. During imposition of stress, WS condition was maintained as rain out shelter to protect from rain. Similar scoring of wilting symptoms as given in the section 3.5.1.1 was followed to supply irrigation in the WS condition when the wilting score was severe in WS plots. Harvesting of the individual plants in both blocks for recording of root traits was done at 75 DAS during first season while in the second season harvesting was done at 90 DAS sowing. Plants were thoroughly washed manually with tap water to remove the soil and debris for recording the root traits. General view of RILs in raised bed evaluation at 30 days after stress in WW and WS condition during summer 2012-13 is indicated in Plate 3.

3.5.2.2 Recording of observations

3.5.2.2.1 Soil moisture content

Average soil moisture from 0 to 15 cm was measured by using a micro auger at 7 and 15 days after stress. Soil sample of about 50-100 gm was collected and weight of the soil was recorded as wet weight. Sample was placed in the oven at 80°C for 24 hours. Weight of the dried soil sample was recorded as dry weight.

The moisture content in dry weight basis can be calculated using the following formula (Black 1965).

$$\text{Soil moisture content (\%)} = \frac{\text{Wet weight of the soil (gm)} - \text{Dry weight of the soil (gm)}}{\text{Dry weight of the soil (gm)}} \times 100$$

3.5.2.2.2 Root traits

Roots are expected to play an important role in adaptation to drought in groundnut where relation between root depth and pod yield under drought condition has been established (Robertson *et al.* 1980). Since the root traits had big contributions on yield in crop, they received increasing attention by crop breeders (Steele *et al.*, 2006).

Root traits studied in the present investigation and the method of their measurement was given below.

Root length (RL)

Root length from ground level to the tip of the seminal root was measured in cm at the time of harvest.

Shoot length (SL)

Shoot length of main axis from ground level to the apical leaflet of each plant was measured in cm at the time of harvest

Root/Shoot ratio (RSR)

The proportion of root length to the shoot length of the plant was calculated.

Root dry weight (RDW)

Roots were washed, separated and oven-dried at 80°C for 48 h before recording the dry weight in gms.

Shoot dry weight (SDW)

Shoots were washed, separated and oven-dried at 80°C for 48 h before recording the dry weight in gms.

3.5.3 Multilocation yield trials of selected lines during *Kharif* 2014-15

All the entries (14 RILs, two parents and five checks) were sown in three rows of 3 m length with a spacing of 30 cm between rows and 10 cm between the plants on 24th and 25th July 2014. Observations were recorded on podyield and its components along with the physiological traits.

3.6 Statistical analysis

3.6.1 Mean

On the basis of individual plant observations, the mean for each character in all the treatments in two water regimes was computed as follows.

$$\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$$

Where, $\bar{y}$ = Population mean

y_i = Individual value

n = Number of observations

3.6.2 Range

The minimum and maximum value on the basis of individual plant observations were used to indicate the range for a given character under two water regimes.

3.6.3 Coefficient variation

The coefficient of variation (CV) is a normalized measure of dispersion of a probability distribution or frequency distribution. The coefficient of variation (CV) is defined as the ratio of the standard deviation to the mean where the standard deviation was computed as the square root of the mean of the squared deviation of the individuals from their mean.

$$\text{Standard Deviation} = \sigma = \sqrt{\frac{\sum (X - \mu)^2}{N}}$$

$$\text{CV (\%)} = \frac{\text{Standard deviation}}{\bar{X}} \times 100$$

3.6.5 Analysis of Variance (ANOVA)

3.6.5.1 ANOVA for Factorial RBD

The analysis of variance for different characters as given by Yates (1937) was carried out using mean data in order to assess the genetic variability among genotypes.

The level of significance was tested at 5 per cent and 1 per cent using F test. The model of ANOVA for factorial RBD used is presented below.

Source of variation	Degrees of freedom (DF)	Sum of Squares (SS)	Mean Sum of Squares (MSS)	F ratio
Replication	$r-1$	rSS	rMSS	
Treatment				
A	$a-1$	aSS	aMSS	aMSS/EMSS
B	$b-1$	bSS	bMSS	bMSS/EMSS
A * B	$(a-1)(b-1)$	abSSA	abMSS	abMSS/EMSS
Error	$(r-1)(ab-1)$	ESS	EMSS	
Total	$rab-1$	TSS		

r = number of replications, a = number of levels in factor A, b = number of levels in factor B

3.6.5.2 ANOVA for Augmented design

Analysis of variance (ANOVA) for augmented design-II as per Federer (1961) was as follows.

Source of Variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	F ratio
Blocks	$(b-1)$	bSS	bMSS	bMSS/EMS
Entries	$(e-1)$	eSS	eMSS	eMSS/EMS
Checks	$(c-1)$	cSS	cMSS	cMSS/EMS
Genotypes	$(v-1)$	vSS	vMSS	vMSS/EMS
Checks Vs Genotypes	1	cvSS	cvMSS	cvMSS/EMS
Error	$(c-1)(b-1)$	ESS	EMSS	
Total	$N-1$	TSS		

Where,

b = Number of blocks.

v = Number of lines

e = number of entries.

c = number of checks.

The significance of “F” value was tested by comparing the computed value with the table value as given by Fisher. Further, standard error of means (S.E_m±), critical difference (C.D) and co-efficient of variation (C.V) were worked out using appropriate formulae to facilitate the comparison of means of the genotypes.

$$SEd_1 = \frac{\sqrt{\frac{2 \text{ EMS}}{2}}}{2} \quad (\text{between checks})$$

$$SEd_2 = \sqrt{2 \text{ EMS}} \quad (\text{between genotypes})$$

$$SEd_3 = \sqrt{\text{EMS} (1 + 1/b + 1/c + 1/bc)} \quad (\text{between checks and genotypes})$$

$$CD = SEd_1 \times 't' \text{ at } 5\%$$

3.6.6 Estimation of genetic parameters

In order to assess and quantify the genetic variability among the genotypes, different parameters were estimated as given below:

3.6.6.1 Variance

Genotypic and phenotypic components of variance were computed with the help of following formulae.

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS}_{\text{Treatment}} - \text{MSS}_{\text{Error}}}{R}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \text{MSS (error)}$$

3.6.6.2 Coefficient of Variability

Both genotypic and phenotypic coefficients of variability were estimated as per the method suggested by Burton and Devane (1953).

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic Variance}}}{\text{Grand mean}} \times 100$$

$$\text{GCV (\%)} = \frac{\sqrt{\text{Genotypic Variance}}}{\text{Grand mean}} \times 100$$

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973).

GCV and PCV values	Classification
0-10	Low
10-20	Medium
20 and above	High

3.6.4.3 Heritability ($h^2_{(b.s.)}$)

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Heritability (broad sense) estimates were categorized into high, moderate and low by Robinson *et al.* (1949).

Heritability (%)	Classification
5-10	Low
10-30	Medium
30-60	High
>60	Very high

3.6.4.4 Genetic advance (GA)

Genetic advance was estimated by using the formula given by Johnson *et al.* (1955).

$$GA = h^2 \times k \times \sigma_p$$

Where,

h^2 = heritability estimate

σ_p^2 = Phenotypic standard deviation

K = Selection differential at 5% is equal to 2.06 of selection (Lush, 1940)

3.6.4.5 Genetic advance as per cent of mean (GAM)

This was computed by the following formula.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Grand mean of the trait

GA = Genetic advance

The Genetic Advance as per cent of Mean (GAM) was categorized by Johnson *et al.*, 1955).

GAM (%)	Classification
0-10	Low
10-20	Medium
20 and above	High

3.6.5 Correlation coefficient (r)

The correlation coefficients among all possible character combinations at phenotypic (r_p) level were estimated by employing the following formula of Weber and Moorthy (1952).

$$\text{Phenotypic correlation (\%)} = r_{xy}(p) = \frac{\text{Cov}(XY)_p}{\sigma^2(X)_p \times \sigma^2(Y)_p} \times 100$$

Where,

COV_{xy} - phenotypic covariances between x and y characters,

σ^2_x - phenotypic variances of x character and

σ^2_y - phenotypic variances of character y

The test of significance for association between characters was done by comparing calculated 'r' values with table 'r' values at (n-2) error degrees of freedom, where n is the number of pairs of observations.

3.7 Assigning parental polymorphism and genotyping for linkage map construction and QTL analysis

3.7.1 DNA extraction from parents and mapping populations

From young leaves of parents and F_{11} population, DNA extraction was done using "cetyl trimethyl ammonium bromide (CTAB)" method (Saghai-Maroo *et al.*, 1984) with some modifications as identified below

DNA extraction procedure

1. Young leaves (about 1-2 g) of each genotype was ground to a fine powder using pestle and mortar in the presence of liquid nitrogen and transferred to a sterile polypropylene tube (2ml) containing 1 ml of preheated (65°C) CTAB extraction buffer (1M Tris-HCL buffer pH 8, 4M NaCl, 0.5M ethylene diaminetetraacetic acid (EDTA) with pH 8, 10 per cent hexadecyltrimethyl ammonium bromide, 1ml mercaptoethanol and 100mg polyvinyl pyrrolidone.)
2. The contents were incubated at 65°C for 30-45 min in a water bath with occasional shaking during incubation.
3. The tubes were cooled to room temperature. The tubes were spinned at 13, 000 r.p.m. at 4°C for 8 min in refrigerated centrifuge and the supernatant was transferred to another tube (2 ml).
4. An equal quantity of chloroform: amyl alcohol (24:1) was added to each tube and they were firmly capped and shaken vigorously.
5. The tubes were spinned at 13, 000 r.p.m. at 4°C for 8 min in a refrigerated centrifuge.
6. The aqueous phase was transferred to another 1.5 ml eppendorf tubes and DNA was precipitated using 700 µl pre chilled Iso-propenol alcohol. Tubes were kept at -20°C for overnight.
7. The precipitate was rinsed with 70 per cent ethanol, and re-spin to pelletize DNA. Supernatant was poured off and the tubes were kept inverted on paper towel for several minutes to air-dry the pellet. The pellet was then redissolved in 200 µl of T10E1 (10 mM Tris pH 8.0 at 25°C: 1 mM EDTA).
8. Add 1-2 µl of RNase (10 mg/ml) and incubate at 37°C for 40-45 min
9. Stored at -20°C

3.7.2 DNA quality and quantity estimation

$$\text{DNA } (\mu\text{g/ml}) = \text{OD}_{260} \times \text{dilution factor} \times 50 \mu\text{g}$$

OD₂₆₀/ OD₂₈₀ ratio has been used to assess the purity of DNA wherein, a ratio of 1.6 to 1.8 indicates pure DNA, while 1.6 or less indicates the presence of proteins and/or other UV absorbers. The ratio higher than 2.0 indicates that the sample is being contaminated with chloroform or phenol.

Quantification of DNA

DNA quality was checked and quantified on 0.8% agarose gel with known concentration of uncut lambda DNA standard.

3.7.3 PCR (Polymerase Chain Reaction)

Polymerase Chain Reactions (PCR) were performed by using a Touch - Down PCR profile and an amplification protocol appropriate for pair of primers. DNA amplification was performed in 10 μl reaction mixture the contents of the reaction mixture is given in Table 16. The reaction mixture contained 5ng/ μl template DNA, 2 pM / μl SSR primer pair (Forward and Reverse), 50 mM MgCl_2 (Qiagen), 2 mM dNTP's, 10X PCR buffer (Qiagen) and 5U/ μl Taq DNA polymerase. The thermo profile for the PCR reaction was set as shown in Table 17. After the completion of the PCR, the products were stored at 4°C until the gel-electrophoresis was done.

3.7.4 Electrophoresis

The amplified products from each tube along with 2 μl of loading dye were separated capillary electrophoresis method by using the instrument ABI3730 xl.

3.7.5 Construction of linkage map and tagging of genes and QTLs

3.7.5.1 Phenotypic evaluation of mapping population

Mapping population was developed as mentioned in the section 3.1. To identify the QTLs for yield and drought related traits totally 299 RILS were evaluated for physiological, root, quality and yield related traits for two seasons of summer 2012-13

Table 16: PCR reactions for the targeted microsatellites loci used for genotyping of TMV-2 x GM 6-1 population

Components	Concentration per μl	PCR Reaction (10 μl)
Primers (F + R)	2 pM	1 of each primer
dNTP's	2 mM	1
MgCl ₂	50mM	0.50
Taq polymerase	5U/ μ L	0.05
Double distilled water	-	4.45
Template	5 ng/ μ L	2

Table 17: Touch- Down PCR profiles for the targeted microsatellite loci used for genotyping of TMV-2 x GM 6-1 population

S.No	Steps	Temperature ($^{\circ}\text{C}$)		Time	
		60-55 (56)	65-60 (59)		
1	Initial denaturation	95	95	15 min	5 cycles
2	Denaturation	94	94	20 sec	
3	Annealing	60	65	20 sec	
4	Primer extension	72	72	30 sec	40 cycles
5	Denaturation	94	94	20 sec	
6	Annealing	56	59	20 sec	
7	Primer extension	72	72	30 sec	
8	Final extension	72	72	20 sec	
9	Store at ($^{\circ}\text{C}$)	4	4		

and summer 2013-14 under irrigated and water stress conditions. Phenotyping for all traits was done in mapping population as mentioned in the subsection 3.5.1 and 3.5.2.

3.7.5.2 Assessment of parental polymorphism

Initially the parents TMV-2 and GM 6-1 were screened for polymorphism using a total of 453 SSR primers. Out of 453 primers, 71 primers were found polymorphic between the parents (Appendix III).

3.7.5.3 Marker analysis of mapping population

DNA was isolated as per the procedure mentioned in the section 3.7.1 from 299 RILs. Totally 71 polymorphic SSR markers between the parents were selected to screen against the 299 RILs. DNA quality check and polymerase chain reaction was carried out as per the procedure mentioned in the sub section 3.7.2. Obtained PCR products were run on horizontal electrophoresis with 4% metaphore agarose gel to assure the clear band appearance. The marker data generated represents the alleles, and were scored as follows.

1. "A" or 2 - Homozygote at marker locus as that of recurrent parent (TMV-2).
2. "B" or 0 - Homozygote at marker locus as that of donor parent (GM 6-1).
3. "U" or -1 - Missing data for the individual at the locus

3.7.5.4 Construction of genetic linkage map

Using genotyping data on 299 RILs, linkage map was constructed with the help of software QTL IciMapping v4.0 (Wang *et al.*, 2014). For the map construction, markers were assigned to the linkage group using a LOD threshold of 3 and the maximum distance between markers of 50 cM. Commands 'group', 'order' and 'ripple' were used to organize markers on linkage groups. Linkage groups were oriented by checking markers against known marker positions on genetic maps constructed by Shirasawa *et al.* (2011), Shirasawa *et al.* (2012) Koilkonda *et al.* (2012), Moretzsohn *et al.* (2005).

3.7.5.5 QTL analysis

Phenotypic data on all traits was combined with genotyping data and linkage map in order to identify the QTLs associated with these traits. For the QTL analysis, Inclusive Composite Interval (ICM-ADD) method was used in QTL IciMapping v.4.0. Significant QTL for individual traits were determined by the location of the peak LOD score at a genome wide based on 1000 permutation tests, with a walking step of 1cM, probability in stepwise regression of 0.05, and the type I error of 0.05. Composite interval mapping combines the approaches of interval mapping (IM) and single marker analysis (SMA) in multiple regression frameworks. The point at which the LOD score had the maximum value in the interval was taken as the estimated QTL position. The coefficient of determination also known as coefficient of variance (R^2) explained by the QTL was used as a measure of the magnitude of association and it is estimated as the square of the partial correlation coefficient. Estimates of the additive effect of each detected QTL, the total LOD score, the total proportion of phenotypic variance explained by all the detected QTLs were obtained by fitting a multiple linear regression model that simultaneously included all the detected QTLs for the traits in question. The additive effect was calculated as half the differences between genotypic values of two homozygotes (Falconer, 1989).

4. EXPERIMENTAL RESULTS

In an effort to improve groundnut for drought tolerance, the present investigation was carried out during 2012-13 and 2013-14 summer seasons at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad to assess the extent of genetic variability for quantitative characters, physiological traits, root traits, oil quality traits and foliar disease resistance traits and to identify superior recombinant inbred lines for traits related to drought tolerance and other quality traits among 299 RILs derived from the cross TMV-2 x GM 6-1. The mapping population was genotyped with SSR markers at ICRISAT, Hyderabad to construct a genetic linkage map and to identify QTLs for the traits studied. The results on phenotypic and genotypic evaluation of the RIL population and QTL detection are presented.

Results obtained from the present investigation are presented under the following headings

- 4.1 Phenotyping for quantitative, physiological, oil quality and foliar disease resistance traits in RILs of TMV-2 x GM 6-1 evaluated during summer 2012-13 and summer 2013-14
 - 4.1.1 Genetic variability for quantitative traits
 - 4.1.2 Genetic variability for physiological traits
 - 4.1.3 Genetic variability for oil quality traits
 - 4.1.4 Genetic variability for foliar disease resistance traits
 - 4.1.5 Correlation analysis for yield and yield component traits
 - 4.1.6 Correlation analysis for physiological traits under WS condition
 - 4.1.7 Correlation analysis for oil quality traits
 - 4.1.8 Correlation analysis for foliar disease resistance traits
- 4.2 Phenotyping for root traits in RILs of TMV-2 x GM 6-1 during summer 2012-13 and summer 2013-14

4.2.1 Genetic variability for root traits

4.2.2 Correlation analysis for root traits

4.3 Multilocation yield trials of selected lines during *Kharif* 2014-15

4.4 Construction of genetic linkage map

4.5 QTL mapping for traits related to drought tolerance and quality traits

4.1 Phenotyping for quantitative, physiological, oil quality and foliar disease resistance traits in RILs of TMV-2 x GM 6-1 during summer 2012-13 and summer 2013-14

4.1.1 Genetic variability for quantitative traits

4.1.1.1 Analysis of variance (ANOVA)

Analysis of variance for individual seasons of summer 2012-13 and 2013-14 (Table 18 and 19) indicated that genotypes included in the study differed significantly for all traits in each season. Irrigation level (well watered and water stress conditions) and genotypes* irrigation levels had significant effect on all the traits studied except days to 50 per cent flowering during summer 2012-13. Pooled ANOVA across the two seasons (Table 20) indicated significant difference among genotypes, seasons, irrigation levels and also their interactions for all the traits studied.

4.1.1.2 Mean, range and components of variation

Mean and range of quantitative traits under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 are presented in the Table 21. The nature and magnitude of variation for quantitative traits was assessed by phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance for the two seasons of summer 2012-13 and summer 2013-14 are presented in Table 22.

During summer 2012-13, days to 50 per cent flowering recorded low GCV (2.14), PCV (2.54) and high heritability (71.2 %) with low genetic advance as per cent

Table 18: Analysis of variance for pod yield and its component traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Source of Variation	df	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No of Primary branches/plant	No of Secondary branches/plant	No of Pegs per plant	No of Mature pods/plant	No of Immature pods/plant	Pod yield per plant	Kernel yield per plant	Shelling Per cent	Sound Mature Kernel per cent (%)	Hundred Seed Weight
Replication	1	0.10	0.32	0.10	0.29	1.14	6.60	0.03	8.45	2.23	0.28	8.08	100.2	0.04
Genotypes	308	1.26**	1.68**	56.84**	2.12**	5.03**	252.85**	133.35**	39.97**	15.91**	6.96**	132.74**	392.30**	143.80**
Irrigation Level	1	334.51**	419.42**	12520.05**	290.29**	183.47**	21534.23**	12907.47**	1624.05**	7289.86**	4414.74**	74541.83**	136835.40**	15522.99**
Genotypes * Irrigation Level	308	0.10	0.31**	33.28**	1.79**	9.15**	622.95**	293.35**	16.46**	11.24**	5.27**	99.35**	647.90**	35.72**
Error	617	0.11	0.13	22.12	1.20	0.49	7.61	4.27	3.46	0.90	0.38	22.74	37.1	6.46
Total	1235	0.66	0.90	43.67	1.81	3.93	239.66	119.00	17.12	13.12	6.82	129.61	390.90	60.57
General Mean		23.81	97.88	29.90	6.26	3.50	19.60	15.60	10.11	6.38	4.11	60.59	55.72	27.45
S.Em		0.163	0.181	2.352	0.548	0.349	1.379	1.033	0.930	0.474	0.308	2.384	4.31	1.271
CD 5%		0.45	0.50	6.53	1.52	0.97	3.83	2.87	2.58	1.32	0.86	6.62	11.97	3.53
C.V %		1.37	0.37	15.73	17.52	19.97	14.08	13.25	18.40	14.86	14.98	7.87	10.9	9.26

** Significance at 1%, * Significance at 5%

Table 19: Analysis of variance for pod yield and its component traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Source of Variation	df	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No of Primary branches/plant	No of Secondary branches/plant	No of Pegs per plant	No of Mature pods/plant	No of Immature pods/plant	Pod yield per plant	Kernel yield per plant	Shelling Per cent	Sound Mature Kernel per cent (%)	Hundred Seed Weight
Replication	1	0.18	0.1	3.52	1.57	0.06	2.95	0.25	0.06	2.16	0.01	2554.80**	7.0	4.15
Genotypes	308	1.43**	1.56**	62.22*	2.54**	1.63**	284.70**	77.38**	17.31**	14.37**	6.64**	25.69**	554.7**	189.39**
Irrigation Level	1	1578.97**	117.44**	53594.92*	77.25**	16.20**	40461.45	45963.50	236.71**	11392.78	6097.50*	23612.68*	204427.3*	121844.70
Genotypes * Irrigation Level	308	0.90**	0.65**	36.79*	2.51**	1.73**	257.34**	64.30**	10.84**	9.75**	4.60**	21.53	449.8**	122.32**
Error	617	0.16	0.16	14.09	0.59	0.16	7.13	3.52	1.07	1.03	0.42	19.63	26.7	6.14
Total	1235	1.94	0.72	75.13	1.62	0.93	171.51	74.31	7.75	15.76	7.95	42.77	437.5747	179.47
General Mean		37.18	107.75	21.43	4.83	2.19	17.37	14.55	5.64	5.92	3.98	64.93	63.52	26.12
S.Em		0.198	0.198	1.877	0.384	0.203	1.335	0.937	0.518	0.507	0.326	2.215	3.66	1.238
CD 5%		0.55	0.55	5.21	1.07	0.56	3.71	2.6	1.44	1.41	0.9	6.15	10.15	3.44
C.V %		1.06	0.37	17.51	15.92	18.54	15.37	12.89	18.38	17.13	16.37	6.82	8.10	9.48

** Significance at 1%, * Significance at 5%

Table 20: Pooled analysis of variance for pod yield and its component traits in groundnut RILS of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad

Source of Variation	df	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No of Primary branches/ plant	No of Secondary branches/ plant	No of Pegs per plant	No of Mature pods/ plant	No of Immature pods/ plant	Pod yield per plant	Kernel yield per plant	Shelling Per cent	Hundred seed weight
Season	1	110507.60**	60220.23**	44316.23**	1269.07*	1061.78*	3058.15*	682.29*	12380.67*	128.908**	11.44	11634.2	1092.53*
Genotype	308	1.43**	1.92**	58.19**	2.50**	3.37**	292.78**	115.99**	30.14**	21.70**	9.90**	78.10**	185.34**
Irrigation Level	1	1683.49**	490.37**	58961.37**	333.52**	154.35**	60515.74**	53792.68**	310.36**	18454.59**	10444.46**	91031.19**	112174.00**
Season * Irrigation Level	1	229.98**	46.49**	7153.60**	34.02**	45.32**	1479.94**	5078.30**	1550.40**	228.05**	67.78**	7123.32**	25193.68**
Season * Genotype	308	1.26**	1.32**	60.87**	2.16**	3.29**	244.77**	94.73**	27.14**	8.57**	3.70**	80.33**	147.85**
Irrigation Level * Genotype	308	0.48**	0.49**	36.57**	1.94**	5.56**	458.44**	176.77**	13.80**	11.44**	5.57**	59.53**	83.19**
Season* Irrigation Level * Genotype	308	0.52**	0.46**	33.50**	2.36**	5.31**	421.85**	180.88**	13.50**	9.55**	4.30**	61.36**	74.85**
Pooled Error	1234	0.13	0.14	18.11	0.9	0.33	7.37	3.89	2.27	0.96	0.4	21.19	6.3
General Mean		30.496	102.814	25.667	5.545	2.843	18.482	15.074	7.873	6.147	4.046	62.757	26.783
CD 5%		0.355	0.372	4.174	0.929	0.56	2.663	1.936	1.477	0.962	0.622	4.515	2.462
C.V %		1.187	0.368	16.578	17.08	20.092	14.685	13.09	19.126	15.961	15.667	7.334	9.371

** Significance at 1%, * Significance at 5%

Table 21: Mean and range for quantitative traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS , Dharwad

Character	Mean of WW		Mean of WS		Range in WW condition			Range in WS condition		
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2012-13	S 2013-14	S 2013-14
Days to 50% flowering	24.33	38.31	23.29	36.05	23 - 26	37 - 41	22 - 25	33 - 38		
Days to maturity	98.46	108.06	97.3	107.44	97 - 102	106 - 112	96 - 99	106 - 109		
Plant height (cm)	33.08	28.02	26.72	14.85	13 - 55	8.5 - 54	10 - 51	0.5 - 37		
No of primary branches/ plant	6.75	5.08	5.78	4.58	4 - 12	2.4 - 12.2	3 - 10	1.7 - 9.5		
No of secondary branches/ plant	3.88	2.3	3.11	2.07	0.4 - 13.2	0 - 9.0	1 - 9	0 - 6.5		
No of pegs per plant	23.77	23.09	15.42	11.65	0 - 98.3	3.4 - 86.4	0 - 50	1 - 83		
No of mature pods/ plant	18.83	20.65	12.37	8.45	1.9 - 76.4	2 - 39.6	2 - 31	0 - 35		
No of immature pods/plant	8.96	6.07	11.26	5.2	2 - 21	0.4 - 21.0	1 - 24	0 - 21.6		
Pod yield per plant (g)	8.8	8.95	3.95	2.88	0.9 - 19.5	1.4 - 20.8	0.15 - 10.45	0 - 8.6		
Kernel yield per plant (g)	6	6.2	2.22	1.76	0.6 - 13.24	1.05 - 14.5	0 - 6.41	0.06 - 5.13		
Shelling per cent	68.35	69.3	52.63	60.56	64.26 - 77.86	64.37 - 83.7	0 - 75.56	13.8 - 75.33		
Sound mature kernel per cent	66.22	76.67	44.63	50.35	14.15 - 95.93	39.29 - 97.79	0.73 - 86.15	3.78 - 93.53		
Hundred seed weight (g)	30.99	36.04	23.9	16.18	14.64 - 58.09	11.81 - 64.07	8.74 - 47.23	0.16 - 54.07		

Table 22: Genetic parameters for quantitative traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	PCV (%)		GCV (%)		h ² (Broad Sense)		GA		GAM	
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14
Days to 50% flowering	2.54	2.61	2.14	2.39	71.02	83.43	0.89	1.67	3.72	4.49
Days to maturity	0.63	0.71	0.51	0.61	65.96	73.34	0.84	1.16	0.86	1.07
Plant height (cm)	18.79	20.71	10.28	11.06	29.92	28.51	3.46	2.61	11.58	12.16
No of primary branches/ plant	19.11	25.42	7.63	19.81	15.96	60.76	0.39	1.54	6.28	31.81
No of secondary branches/ plant	44.09	37.99	39.3	33.16	79.48	76.19	2.53	1.3	72.18	59.62
No of pegs per plant	49.79	51.42	47.76	49.06	92.01	91.07	18.49	16.75	94.37	96.45
No of mature pods/ plant	35.55	39.8	32.99	37.65	86.11	89.51	9.84	10.68	63.07	73.39
No of immature pods/plant	42.6	47.64	38.43	43.96	81.35	85.11	7.22	4.71	71.39	83.54
Pod yield per plant (g)	31.04	23.4	27.25	15.93	77.08	46.39	3.14	1.32	49.28	22.36
Kernel yield per plant (g)	31.61	21.54	27.84	13.99	77.56	42.22	2.08	0.75	50.51	18.73
Shelling per cent	18.43	8.46	16.66	5	81.75	34.93	18.8	3.95	31.03	16.09
Sound mature kernel per cent	33.22	24.3	31.36	22.9	89.16	88.78	33.99	28.23	61.01	44.44
Hundred seed weight (g)	25.55	32.69	23.81	31.28	86.85	91.58	12.55	16.11	45.71	61.67

of mean (3.72 %). Range of days taken for 50 per cent flowering in WW condition was 23.00 to 26.00 days while it ranged from 22.00 to 25.00 days in WS condition with mean of 24.33 and 23.29 days, respectively. Similarly, during summer 2013-14, low PCV (2.61), GCV (2.39) and high heritability (83.43 %) with low genetic advance as per cent of mean (4.49) were recorded for days to 50 per cent flowering. Range of days taken for 50 per cent flowering in WW (37.00 to 41.00 days) and WS conditions (33.00 to 38.00 days) was higher compared to previous season with mean of 38.31 and 36.05 days, respectively.

Days to maturity recorded low GCV (0.51, 0.61), PCV (0.63, 0.71) and high heritability (65.96 %, 73.34 %) with low genetic advance as per cent of mean (0.86 %, 1.07 %) during the two seasons, respectively. During 2012-13 range of days taken for maturity in WW condition was from 97.00 to 102.00 days, while it ranged from 96.00 to 99.00 days in WS condition with mean of 98.46 and 97.30 days, respectively. During summer 2013-14, range of days taken for maturity in WW (106.00-112.00 days) and WS conditions (106.00-109.00 days) was higher compared to previous season with mean of 108.06 and 107.44 days, respectively.

Moderate GCV (10.28, 11.06), PCV (18.79, 20.71), GAM (11.58, 12.16) and low heritability (29.92, 28.51) were recorded for plant height in both seasons respectively. Mean plant height was higher during summer 2012-13 compared to 2013-14 in both WW (33.08 and 28.02) and WS (26.72 and 14.85) treatments respectively. Wide range for this trait was recorded during both seasons in WW (13.00-55.00 and 8.50-54.00) and WS (10.00-51.00 and 0.50-37.00) treatments.

During summer 2012-13, number of primary branches per plant recorded moderate PCV (19.11) but low GCV (7.63), heritability (15.96 %) and genetic advance as per cent of mean (6.28 %). In contrast, moderate GCV (19.81) but high PCV (25.42), heritability (60.76 %) and GAM (31.81) was recorded for this trait during summer 2013-14. Wide range for this trait was recorded in both water regimes during both seasons. Mean number of primary branches per plant in WW condition (6.75, 5.08) was higher compared to WS condition (5.78, 4.58) in both seasons, respectively.

High PCV, GCV and heritability with high GAM were recorded for most of the quantitative traits viz., number of secondary branches per plant, number of pegs per

plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, kernel yield per plant, sound mature kernel per cent and 100 seed weight except shelling per cent for which moderate GCV and PCV was recorded during summer 2012-13. During summer 2013-14, high PCV, GCV and heritability with high GAM were recorded for the traits *viz.*, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, sound mature kernel per cent and 100 seed weight except pod yield per plant, kernel yield per plant and shelling per cent. Wide range of variation was recorded for all the above traits in both the irrigation levels in each season.

During summer 2012-13, mean number of secondary branches per plant ranged from 0.40 to 13.20 per plant in WW condition and 1.00 to 9.00 per plant in WS condition with mean of 3.88 and 3.11 secondary branches per plant, respectively. The range of variation in the WW (0.00-9.00) and WS (0.00-6.50) during 2013-14 was less compared to previous season with mean of 2.30 and 2.07 secondary branches per plant in two irrigation levels, respectively.

Mean number of pegs per plant recorded high range of variation during both seasons of summer 2012-13 and 2013-14 in WW (0.00-98.30; 3.40-86.40) and WS (0.00-50.00; 1.00-83.00) conditions, respectively. Mean number of pegs per plant in WW condition (23.77, 23.09) was higher compared to WS condition (15.42, 11.65) in both 2012-13 and 2013-14 summer seasons, respectively.

Number of mature pods per plant recorded wide range during summer 2012-13 in WW condition (1.90-76.40) compared to WS condition (2.00-31.00) with mean of 18.83 and 12.37, respectively. During summer 2013-14, it ranged from 2.00 to 39.60 per plant in WW and from 0.00 to 35.00 per plant in WS condition with mean of 20.65 and 8.45 mature pods per plant in two seasons, respectively.

During summer 2012-13, number of immature pods per plant ranged from 2.00 to 21.00 in WW condition and from 1.00 to 24.00 in WS condition with mean of 8.96 and 11.26 respectively. Similar range of variation was observed in the WW (0.40-21.00) and WS (0.00-21.60) during 2013-14 with mean of 6.07 and 5.20 in WW and WS conditions, respectively.

Wide variation was recorded for pod yield per plant in WW condition in both seasons (0.90-19.50 gm and 1.40-20.80 gm) compared with WS (0.15-10.45 gm and 0.00-8.60 gm) condition. Mean pod yield of 8.80 gm and 8.95 gm per plant was recorded in WW condition while in WS condition, a mean of 3.95 gm and 2.88 gm per plant was observed during each season, respectively.

During 2012-13, range of kernel yield per plant in WW condition was from 0.60 to 13.24 gm, while WS condition it ranged from 0.00 to 6.41 gm per plant with an average of 6.00 gm and 2.22 gm respectively. During summer 2013-14, it ranged from 1.05 gm to 14.50 gm per plant in WW condition and from 0.06 gm to 5.13 gm per plant in WS condition with mean of 6.20 gm and 1.76 gm per plant, respectively.

In contrast to the above traits, shelling per cent recorded low to moderate GCV, PCV; moderate to high heritability and moderate to high GAM in two seasons. It has shown wide variation in the WS condition (0.00-75.86 and 13.80-75.33) during two seasons compared to the WW condition (64.26-77.86 and 64.37-83.70). Mean shelling per cent of 68.35 and 69.30 per plant in WW condition, while in the WS condition mean of 52.63 and 60.56 per cent recorded during summer 2012-13 and 2013-14, respectively.

Sound mature kernel per cent had wide range of variation in WW (14.15-95.93 % and 39.29-97.79 %) and WS (0.73-86.15 % and 3.78-93.53 %) treatments during two seasons of summer 2012-13 and 2013-14 respectively. During summer 2012-13, there was low mean of 66.22 and 44.63 % in WW and WS conditions while in summer 2013-14 there was higher mean of 76.67 and 50.35 % in respective water regimes.

Similarly, hundred seed weight had wide range of variation in WW (14.64-58.09 gm and 11.81-64.07 gm) and WS (8.74-47.23 gm and 0.16-54.07 gm) conditions during two seasons respectively. The mean of hundred seed weight were 30.99 gm and 36.04 gm in WW conditions and 23.90 gm and 16.18 gm in WS conditions in summer 2012-13 and summer 2013-14, respectively.

4.1.2 Genetic variability for physiological traits

4.1.2.1 Analysis of variance (ANOVA)

Analysis of variance of physiological traits for individual seasons of summer 2012-13 and 2013-14 (Table 23 and 24) indicated that genotypes included in the study differed significantly for all the traits studied in each season. Irrigation level (well watered and water stress conditions) and Genotypes * irrigation level had significant effect on all the traits studied. Pooled ANOVA across the two seasons (Table 25) indicated significant differences among the genotypes, seasons, irrigation level and also their interactions for most of the traits studied except RWC at 30 days after stress (DAS) for which effect of seasons was found to be non-significant.

4.1.2.2 Mean, range and components of variation

Mean and range of physiological traits for WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 are presented in the Table 26. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean are presented in the Table 27. Low PCV and GCV were recorded by all the traits during both the seasons.

RWC at seven days after stress (RWC at 7 DAS) recorded moderate to high heritability (72.99 and 52.86 %) and low GAM (6.30 and 5.43 %) during two seasons respectively. The range of variation was from 73.07 to 91.73 per cent in WW condition and from 68.56 to 91.80 per cent in WS condition during summer 2012-13 with mean of 82.51 per cent and 82.18 per cent in WW and WS conditions, respectively. During summer 2013-14, it ranged from 74.71 to 93.52 per cent in WW condition and from 64.40 to 90.01 per cent in WS condition with mean of 83.21 per cent and 79.06 per cent, respectively.

Moderate heritability (55.99 % and 51.14 %) and low GAM (4.70 and 8.87 %) was recorded for RWC at 15 DAS during consecutive seasons. During summer 2012-13, wide variation was recorded for RWC at 15 DAS in both WW (68.02-85.06) and WS (55.34-74.22) conditions with mean of 76.75 per cent and 67.00 per cent respectively. Similarly it had wide variation in WW (57.83-90.95) and WS

Table 23: Analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Source of Variation	df	RWC at 7 DAS	RWC at 15 DAS	RWC at 30 DAS	SLA at 7 DAS	SLA at 15 DAS	SLA at 30 DAS	SCMR
Replication	1	9.44	12.51	12.01	0.35	3.02	0.00	43.14
Irrigation level	1	41.42 ^{**}	29388.75 ^{**}	545479.40 ^{**}	6.81 [*]	8685.43 ^{**}	9598.84 ^{**}	5121.97 ^{**}
Genotypes	308	18.82 ^{**}	14.77 ^{**}	25.83 ^{**}	63.94 ^{**}	20.79 ^{**}	8.74 ^{**}	22.91 ^{**}
Genotypes * Irrigation Level	308	19.01 ^{**}	14.27 ^{**}	23.69 ^{**}	71.63 ^{**}	19.87 ^{**}	8.18 ^{**}	22.13 ^{**}
Error	617	3.21	3.78	12.82	1.25	2.67	2.43	12.5
Total	1235	11.08	32.93	481.67	34.44	18.51	13.20	21.66
General Mean		82.33	71.87	51.54	62.61	50.63	43.52	39.43
S.Em		0.90	0.97	2.54	0.56	0.82	0.78	1.77
CD 5%		2.49	2.70	7.02	1.55	2.27	2.16	4.91
C.V %		2.18	2.70	7.00	1.79	3.23	3.58	8.98

^{**} Significance at 1%, ^{*} Significance at 5%

RWC: Relative Water Content, SLA: Specific Leaf Area, SCMR: SPAD Chlorophyll Meter Reading, DAS: Days After Stress

Table 24: Analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Source of Variation	df	RWC at 7 DAS	RWC at 15 DAS	RWC at 30 DAS	SLA at 7 DAS	SLA at 15 DAS	SLA at 30 DAS	SCMR
Replication	1	2.82	0.06	2.74	0.74	1.92	0.34	0.97
Genotypes	308	18.40**	34.27**	22.69**	88.45**	61.07**	19.03**	28.58**
Irrigation Level	1	4220.70**	139038.10**	417283.00**	1795.16**	20151.69**	43676.49**	13787.99**
Genotypes * Irrigation Level	308	25.01**	34.68**	26.44**	92.53**	49.12**	18.63**	29.58**
Error	617	7.72	15.37	7.17	1.21	2.46	1.93	6.81
Total	1235	19.81	137.46	353.71	47.2	45.03	45.72	29.07
General Mean		81.13	66.63	52.22	61.96	49.61	39.05	49.13
S.Em		1.96	1.96	1.338	0.551	0.783	0.694	1.305
CD 5%		5.46	5.44	3.72	1.53	2.18	1.93	3.62
C.V %		3.40	5.88	5.13	1.78	3.16	3.55	5.31

** Significance at 1%, * Significance at 5%

Table 25: Pooled analysis of variance for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad

Source of Variation	df	RWC at 7 DAS	RWC at 15 DAS	RWC at 30 DAS	SLA at 7 DAS	SLA at 15 DAS	SLA at 30 DAS	SCMR
Season	1	23730.07 [*]	17013.58 [*]	283.293	265.96 ^{**}	637.57 ^{**}	12398.98 ^{**}	58607.43 [*]
Genotype	308	20.18 ^{**}	24.59 ^{**}	25.47 ^{**}	73.90 ^{**}	43.50 ^{**}	13.42 ^{**}	25.33 ^{**}
Irrigation level	1	32568.58 ^{**}	148136.50 ^{**}	977264.30 ^{**}	790.44 ^{**}	27648.30 ^{**}	47113.11 ^{**}	17858.65 ^{**}
Season * Irrigation level	1	29366.5 ^{**}	20290.39 ^{**}	5628.14 ^{**}	1011.53 ^{**}	1188.82 ^{**}	6162.22 ^{**}	1051.31 ^{**}
Season* Genotype	308	20.75 ^{**}	24.45 ^{**}	26.05 ^{**}	78.49 ^{**}	38.35 ^{**}	14.34 ^{**}	26.17 ^{**}
Irrigation Level * Genotype	308	21.12 ^{**}	23.51 ^{**}	26.90 ^{**}	76.94 ^{**}	35.20 ^{**}	13.99 ^{**}	27.40 ^{**}
Season * Irrigation Level * Genotype	308	19.25 ^{**}	25.44 ^{**}	27.93 ^{**}	87.22 ^{**}	33.79 ^{**}	12.83 ^{**}	24.31 ^{**}
Pooled Error	1234	5.47	9.57	12.99	1.23	2.56	2.18	9.65
General Mean		81.732	69.248	51.882	62.284	50.118	41.284	44.265
CD 5%		2.294	3.035	3.536	1.089	1.57	1.447	3.048
C.V %		2.951	4.467	6.947	1.783	3.194	3.573	7.019

^{**} Significance at 1%, ^{*} Significance at 5%

Table 26: Mean and range for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	Mean of WW		Mean of WS		Range in WW condition		Range in WS condition	
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14
RWC at 7 DAS	82.51	83.21	82.18	79.06	73.07 - 91.73	74.71 - 93.52	68.56 - 91.8	64.4 - 90.01
RWC at 15 DAS	76.75	77.23	67	56.02	68.02 - 85.06	57.83 - 90.95	55.34 - 74.22	40.61 - 83.06
RWC at 30 DAS	72.16	70.59	30.15	33.85	45.87 - 79.93	61.3 - 80.19	20.23 - 43.07	14.97 - 44.12
SLA at 7 DAS	62.73	63.16	62.55	60.75	49.34 - 71.51	33.61 - 79.11	47.23 - 75.18	48.22 - 73.39
SLA at 15 DAS	53.28	53.65	47.97	45.57	45.46 - 66.99	42.62 - 75.03	40.55 - 58.44	35.83 - 56.97
SLA at 30 DAS	46.31	44.99	40.74	33.1	30.45 - 52.6	30.27 - 60.54	34.81 - 49.6	28.64 - 39.04
SCMR	37.41	45.79	41.43	52.47	21.3 - 46.2	33 - 62.04	28.76 - 54.13	41.82 - 68.57

Table 27: Genetic parameters for physiological traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	PCV (%)		GCV (%)		h ² (Broad Sense)		GA		GAM	
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14
RWC at 7 DAS	4.19	4.98	3.58	3.62	72.99	52.86	5.19	4.3	6.3	5.43
RWC at 15 DAS	4.08	8.41	3.05	6.02	55.99	51.14	3.38	5.91	4.7	8.87
RWC at 30 DAS	8.33	8.18	4.53	6.39	29.69	60.81	2.6	5.36	5.09	10.26
SLA at 7 DAS	9.3	10.67	9.12	10.53	96.31	97.23	11.55	13.25	18.45	21.39
SLA at 15 DAS	5.05	10.59	3.88	10.12	59.09	91.13	3.11	9.87	6.14	19.9
SLA at 30 DAS	5.12	4.15	3.66	2.15	51.16	26.84	2.35	0.9	5.4	2.3
SCMR	9.69	7.53	3.65	5.35	14.16	50.33	1.11	3.84	2.83	7.81

(40.61-83.06) conditions during summer 2013-14, with mean of 77.23 per cent and 56.02 per cent, respectively.

Low heritability (29.69 %) along with low GAM (5.09 %) and wide variation in WW (45.87-79.93 %) and WS (20.23-43.07 %) treatments was recorded for RWC at 30 DAS during summer 2012-13 with mean of 72.16 per cent and 30.15 per cent in respective irrigation levels. In contrast to previous season, during summer 2013-14, high heritability (60.81 %) and moderate GAM (10.26 %) were recorded for this trait. In WW condition it ranged from 61.30 to 80.19 with mean of 70.59 per cent while in WS condition it ranged from 14.97 to 44.12 with mean of 33.85 per cent.

High heritability (96.31 % and 97.23 %) and moderate to high GAM (18.45 % and 21.39) was recorded during consecutive seasons for SLA at 7 DAS. During summer 2012-13, wide range of variation was recorded in both WW (49.34-71.51) and WS (47.23-75.18) condition with mean SLA of 62.73 and 62.55 respectively. Similarly wide variation was recorded in WW (33.61-79.11) and WS (48.22-73.39) conditions during summer 2013-14 with mean SLA of 63.16 and 60.75 respectively.

Moderate heritability (59.09 %) along with low GAM (6.14 %) and wide variation in WW (45.46-66.99) and WS (40.55-58.44) conditions was recorded for SLA at 15 DAS during summer 2012-13, with mean SLA of 53.28 and 47.97 in respective irrigation levels. During summer 2013-14, high heritability (91.13 %) and moderate GAM (19.90 %) was recorded for this trait. In WW condition it ranged from 42.62 to 75.03 with mean SLA of 53.65 while in WS condition it ranged from 35.83 to 56.97 with mean SLA of 45.57.

SLA at 30 DAS recorded low to moderate heritability (51.16 % and 26.84 %) and low GAM (5.40 % and 2.30 %) during two seasons respectively. It ranged from 30.45 to 52.60 in WW condition and from 34.81 to 49.60 in WS condition during summer 2012-13 with mean SLA of 46.31 and 40.74 in respective irrigation level. During summer 2013-14, it ranged from 30.27 to 60.54 in WW condition and from 28.64 to 39.04 in WS condition with mean of SLA 44.99 and 33.10, respectively.

During summer 2012-13, low heritability (14.16 %) along with low GAM (2.83) and wide variation in WW (21.30-46.20) and WS (28.76-54.13) treatments was recorded for SPAD chlorophyll meter reading during summer 2012-13, with mean SCMR of 37.41 and 41.43 in respective irrigation levels. During summer 2013-14, moderate heritability (50.33 %) and low GAM (7.81 %) was recorded for this trait. In WW condition it ranged from 33.00 to 62.04 with mean SLA of 45.79 while in WS condition it ranged from 41.82 to 68.57 with mean SCMR of 45.79.

4.1.3 Variability for oil quality traits in RILs of TMV-2 x GM 6-1

4.1.3.1 Analysis of variance (ANOVA)

Analysis of variance for individual seasons of summer 2012-13 and 2013-14 (Table 28 and 29) indicated that genotypes included in the study differed significantly for all traits studied in each season. Irrigation level (well watered and water stress conditions) and Genotypes * irrigation level had significant effect on all the traits studied. Pooled ANOVA across the two seasons (Table 30) for oil quality traits indicated significant difference among genotypes, seasons, irrigation levels and also their interactions for most of the traits studied.

4.1.3.2 Mean, range and components of variation

Mean and range of oil quality traits for WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 are presented in the Table 31. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean are presented in the Table 32.

Total oil content recorded low PCV (3.74, 3.17), GCV (3.62, 3.02) GAM (7.20, 5.93 %) but high heritability (93.34 % and 90.97 %) during two seasons of summer 2012-13 and summer 2013-14, respectively. Total oil content ranged from 43.14 to 51.03 in WW condition and from 39.89 to 48.44 in WS condition during summer 2012-13, with mean of 47.19 per cent and 44.32 per cent in respective irrigation level. During summer 2013-14, it ranged from 43.47 to 50.73 in WW condition and from 40.12 to 50.73 in WS condition with mean of 47.18 per cent and 45.21 per cent respectively.

Table 28: Analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Source of Variation	df	Total Oil Content	Total Protein Content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Arachidic acid	Eicosenoic acid	Behenic acid	Lignoceric acid	Oleic/ Linoleic ratio	Total unsaturated fattyacid	Total saturated fattyacid	L/S ratio	U/S ratio	Calculated Iodine Value	Oleic Acid Desaturation
Replication	1	0.08	1.55 [*]	0.17	0.03	2.5	1.97	0.09 ^{**}	0.26 ^{**}	2.54 ^{**}	0.07 ^{**}	1.501 ^{**}	0.48	0.08	0.002	0.02	0.442	0.001
Genotypes	308	10.00 ^{**}	13.82 ^{**}	3.07 ^{**}	0.66 ^{**}	148.28 ^{**}	87.39 ^{**}	0.11 ^{**}	0.02 ^{**}	0.48 ^{**}	0.03 ^{**}	2.49 ^{**}	28.67 ^{**}	3.65 ^{**}	0.17 ^{**}	0.44 ^{**}	62.05 ^{**}	0.02 ^{**}
Irrigation Level	1	2535.92 ^{**}	1513.58 ^{**}	408.75 ^{**}	9.29 ^{**}	7434.04 ^{**}	3395.92 ^{**}	0.03 ^{**}	3.56 ^{**}	13.82 ^{**}	0.95 ^{**}	40.92 ^{**}	890.01 ^{**}	199.88 ^{**}	3.69 ^{**}	23.74 ^{**}	639.94 ^{**}	0.79 ^{**}
Genotypes * Irrigation Level	308	0.62 ^{**}	3.15 ^{**}	1.40 ^{**}	0.44 ^{**}	54.13 ^{**}	31.99 ^{**}	0.07 ^{**}	0.01 ^{**}	0.23 ^{**}	0.02 ^{**}	1.04 ^{**}	13.24 ^{**}	1.96 ^{**}	0.07 ^{**}	0.17 ^{**}	27.17 ^{**}	0.01 ^{**}
Error	617	0.19	0.36	0.05	0.01	1.73	1.28	0.001	0.001	0.01	0.001	0.12	0.21	0.05	0.003	0.01	0.95	0.002
Total	1235	4.8	5.64	1.47	0.29	57.36	33.16	0.05	0.01	0.2	0.01	0.98	11.28	1.59	0.06	0.17	23.25	0.01
General Mean		45.75	31.81	10.56	3.75	48.43	29.62	1.62	0.96	3.69	1.19	1.81	79.01	18.09	1.63	4.39	93.715	0.62
S.Em		0.221	0.301	0.114	0.048	0.656	0.566	0.017	0.013	0.048	0.013	0.171	0.226	0.111	0.027	0.037	0.486	0.007
CD 5%		0.61	0.84	0.32	0.13	1.82	1.57	0.05	0.04	0.13	0.04	0.48	0.64	0.31	0.08	0.1	1.913	0.03
C.V %		0.95	1.9	2.15	2.54	2.71	3.82	2.1	2.66	2.61	2.25	18.98	0.58	1.24	3.38	1.7	1.04	2.40

^{**} Significance at 1%, ^{*} Significance at 5%

Table 29: Analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Source of Variation	df	Total Oil Content	Total Protein Content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Arachidic acid	Eicosenoic acid	Behenic acid	Lignoceric acid	Oleic/ Linoleic ratio	Total unsaturated fattyacid	Total saturated fattyacid	L/S ratio	U/S ratio	Calculated Iodine Value	Oleic Acid Desaturation
Replication	1	0.02	0.2	0.19	0.03	3.13	3.98	0.09**	0.27**	2.53**	0.08**	1.79**	0.09	0.07	0.004*	0.02	2.32	0.001*
Genotypes	308	3.97**	7.19**	3.08**	0.27**	131.82**	89.73**	0.05**	0.01**	0.13**	0.02**	2.65**	7.35**	2.87**	0.17**	0.30**	46.70**	0.02**
Irrigation Level	1	1199.71**	21.58**	277.41**	2.98**	8114.81**	5126.57**	4.08**	4.92**	2.13**	1.89**	62.11**	428.53**	282.50**	5.99**	24.99**	2006.74**	1.04**
Genotypes * Irrigation Level	308	2.80**	7.29**	1.43**	0.25**	48.51**	32.72**	0.04**	0.01**	0.10**	0.02**	1.13**	4.81**	1.56**	0.07**	0.13**	20.13**	0.01**
Error	617	0.19	0.38	0.05	0.01	1.74	1.26	0.001	0.001	0.01	0.001	0.14	0.18	0.05	0.003	0.01	0.85	0.001
Total	1235	2.76	3.82	1.38	0.14	52.42	35.32	0.03	0.01	0.07	0.01	1.06	3.47	1.36	0.07	0.13	18.72	0.01
General Mean	1	46.19	33.3	10.66	3.91	48.52	29.54	1.69	0.97	3.84	1.2	1.83	79.03	18.44	1.59	4.31	93.66	0.62
S.Em		0.220	0.307	0.115	0.049	0.660	0.561	0.018	0.013	0.049	0.014	0.184	0.211	0.114	0.027	0.035	0.460	0.007
CD 5%	1	0.61	0.85	0.32	0.14	1.83	1.56	0.05	0.04	0.14	0.04	0.51	0.58	0.32	0.07	0.1	1.28	0.02
C.V %	1	0.95	1.85	2.16	2.52	2.72	3.8	2.08	2.67	2.57	2.25	20.15	0.53	1.23	3.35	1.65	0.98	2.4

** Significance at 1%, * Significance at 5%

Table 30: Pooled analysis of variance for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad

Source of Variation	df	Total Oil Content	Total Protein Content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Arachidic acid	Eicosenoic acid	Behenic acid	Lignoceric acid	Oleic/Linoleic ratio	Total unsaturated fattyacid	Total saturated fattyacid	L/S ratio	U/S ratio	Calculated Iodine Value	Oleic Acid Desaturation
Season	1	119.51**	1383.44**	6.17**	15.86**	4.76*	3.99*	3.24**	0.06*	15.01**	0.08**	0.29	0.18	77.27**	0.86*	4.62*	1.95	0.001
Irrigation Level	1	3612.05**	586.85**	679.82**	0.87**	15541.39**	8433.71**	1.72**	8.43**	2.55**	2.76**	101.92**	1276.84**	478.82**	9.54**	48.71**	2456.55**	1.82**
Season * Irrigation Level	1	123.58**	948.31**	6.34**	11.40**	7.46**	88.79**	2.39**	0.06**	13.4**	0.08**	1.10**	41.70**	3.56**	0.14**	0.01**	190.12**	0.01**
Genotype	308	10.84**	8.44**	5.99**	0.76**	276.32**	175.89**	0.13**	0.03**	0.45**	0.05**	5.14**	26.77**	6.25**	0.34**	0.71**	96.08**	0.03**
Season * Genotype	308	3.13**	12.57**	0.16**	0.16**	3.77**	1.22*	0.03**	0.001**	0.16**	0.002**	0.004	9.25**	0.27**	0.004**	0.03**	12.66**	0.001**
Irrigation Level* Genotype	308	1.83**	4.51**	2.76**	0.62**	101.00**	64.24**	0.10**	0.02**	0.25**	0.03**	2.16**	14.27**	3.22**	0.14**	0.29**	42.23**	0.01**
Season * Irrigation Level * Genotype	308	1.59**	5.93**	0.06	0.08**	1.63	0.48	0.02**	0.001**	0.08**	0.002**	0.01	3.78**	0.30**	0.003	0.01**	5.07**	0.001
Pooled Error	1234	0.19	0.37	0.05	0.01	1.74	1.27	0.001	0.001	0.01	0.001	0.13	0.19	0.05	0.003	0.01	0.90	0.001
General Mean		45.97	32.55	10.61	3.83	48.48	29.58	1.65	0.97	3.77	1.2	1.82	79.02	18.26	1.61	4.35	93.69	0.62
CD 5%		0.43	0.60	0.22	0.10	1.29	1.11	0.03	0.03	0.10	0.03	0.35	0.43	0.22	0.05	0.07	0.93	0.02
C.V %		0.95	1.87	2.15	2.53	2.72	3.81	2.09	2.66	2.59	2.25	19.58	0.56	1.23	3.36	1.67	1.01	2.40

** Significance at 1%, * Significance at 5%

Table 31: Mean and range oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	Mean of WW		Mean of WS		Range in WW Condition				Range in WS condition			
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13		S 2013-14		S 2012-13		S 2013-14	
Total oil content	47.19	47.18	44.32	45.21	43.14	- 51.03	43.47	- 50.73	39.89	- 48.44	40.12	- 53.78
Total Protein Content	30.7	33.43	32.91	33.17	24.96	- 38.72	28.65	- 40.56	28.17	- 42.22	24.63	- 42.84
Palmitic acid	11.14	11.14	9.99	10.2	6.97	- 16.3	6.9	- 16.59	6.43	- 12.5	6.49	- 12.69
Stearic acid	3.67	3.96	3.84	3.86	2.54	- 8.18	2.8	- 7.97	2.48	- 5.71	2.75	- 4.96
Oleic acid	45.97	45.96	50.87	51.08	31.28	- 75.31	31.97	- 73.39	37.41	- 79.51	38.89	- 77.78
Linoleic acid	31.28	31.58	27.96	27.5	6.62	- 43.19	6.73	- 43.47	7.44	- 39.56	6.36	- 37.99
Arachidic acid	1.61	1.75	1.62	1.63	1.02	- 3.18	1.19	- 3.1	1.15	- 2.29	1.14	- 2.15
Eicosenoic acid	0.91	0.91	1.02	1.03	0.43	- 1.2	0.45	- 1.17	0.65	- 1.25	0.65	- 1.21
Behenoic acid	3.58	3.89	3.79	3.8	2.57	- 5.09	3.01	- 4.8	2.54	- 5.07	3.18	- 4.64
Lignoceric acid	1.16	1.16	1.22	1.24	0.84	- 1.45	0.86	- 1.45	0.91	- 1.5	0.98	- 1.51
O/L ratio	1.62	1.6	1.99	2.05	0.74	- 12	0.74	- 11.5	1.01	- 10.03	1.02	- 11.61
Total unsaturated fatty acids	78.17	78.44	79.86	79.62	71.72	- 86.98	72.87	- 85.64	68.85	- 95.9	70.39	- 86.39
Total saturated fatty acids	18.49	18.92	17.68	17.96	13.71	- 29.19	14.5	- 29.18	13.4	- 20.11	14.37	- 20.25
L/S ratio	1.68	1.66	1.57	1.52	0.48	- 2.18	0.46	- 2.18	0.45	- 2.06	0.41	- 1.99
U/S ratio	4.26	4.17	4.53	4.45	2.62	- 6.35	2.67	- 5.87	3.46	- 6.92	3.53	- 6.01
Calculated Iodine Value	94.44	94.93	93	92.39	78.29	- 105.64	78.97	- 104.75	75.85	- 108.72	75.3	- 103.6
Oleic acid desaturation	0.59	0.59	0.64	0.65	0.43	- 0.92	0.42	- 0.92	0.5	- 0.91	0.51	- 0.92

Table 32: Genetic parameters for oil quality traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	PCV (%)		GCV (%)		h ² (Broad Sense)		GA		GAM	
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14
Total oil content	3.74	3.17	3.62	3.02	93.34	90.97	3.29	2.74	7.2	5.93
Total Protein Content	6.5	5.43	6.22	5.1	91.51	88.46	3.9	3.29	12.26	9.89
Palmitic acid	10.35	10.36	10.12	10.13	95.67	95.65	2.15	2.18	20.4	20.41
Stearic acid	12.78	9.3	12.52	8.95	96.05	92.65	0.95	0.7	25.28	17.76
Oleic acid	14.8	13.38	14.55	13.1	96.65	95.86	14.27	12.82	29.46	26.41
Linoleic acid	18.41	18.98	18.01	18.6	95.69	96	10.75	11.09	36.28	37.54
Arachidic acid	12.09	8.35	11.9	8.09	96.97	93.82	0.39	0.27	24.14	16.14
Eicosenoic acid	9.29	7.41	8.9	6.91	91.83	87	0.17	0.13	17.57	13.28
Behenoic acid	11.38	5.97	11.07	5.39	94.75	81.5	0.82	0.39	22.2	10.03
Lignoceric acid	8.81	7.21	8.51	6.85	93.45	90.27	0.2	0.16	16.96	13.41
O/L ratio	53.52	57.94	50.05	54.32	87.43	87.9	1.74	1.92	96.4	104.92
Total unsaturated fatty acids	4.97	1.99	4.94	1.92	98.67	92.82	7.98	3.01	10.1	3.81
Total saturated fatty acids	5.83	5.46	5.7	5.32	95.54	94.88	2.08	1.97	11.48	10.66
L/S ratio	15.62	15.94	15.25	15.58	95.33	95.59	0.5	0.5	30.68	31.38
U/S ratio	8.35	7.45	8.18	7.26	95.87	95.14	0.72	0.63	16.5	14.6
Calculated Iodine Value	5.74	4.71	5.65	4.61	96.74	95.65	10.72	8.7	11.44	9.29
Oleic acid desaturation	11.73	11.93	11.48	11.69	95.81	95.96	0.14	0.15	23.15	23.59

Similarly, protein content also exhibited high heritability (91.51 % and 88.46 %) but low PCV (6.50, 5.43), GCV (6.22, 5.10) and low to moderate GAM (12.26 % and 9.89 %) during summer 2012-13 and summer 2013-14, respectively. Total protein content ranged from 24.96 to 38.72 in WW condition and from 28.17 to 42.22 in WS condition during summer 2012-13, with mean of 32.91 per cent in WS condition which is higher than in WW condition (30.70 %). During summer 2013-14, it ranged from 28.65 to 40.56 in WW condition and from 24.63 to 42.84 in WS condition with mean of 33.43 per cent and 33.17 per cent, respectively.

During summer 2012-13, palmitic acid recorded moderate PCV (10.35), GCV (10.12) and high heritability (95.67 %) with high GAM (20.40 %). Range of palmitic acid in WW condition was from 6.97 to 16.30 and in WS condition from 6.43 to 12.50 with mean of 11.14 and 9.99 respectively during summer 2012-13. Similar to the previous season moderate GCV (10.36), PCV (10.13) and high heritability (95.65 %) with high GAM (20.41 %) was recorded for palmitic acid during summer 2013-14. Range of variation in WW (6.97-16.30, 6.90-16.59) was higher compared to WS conditions (6.43-12.50, 6.49-12.69) during both the seasons of summer 2012-13 and summer 2013-14 with mean of 11.14 per cent, 11.14 per cent and 9.99 per cent, 10.20 per cent respectively.

Stearic acid recorded low to moderate GCV (12.78, 9.30), PCV (12.52, 8.95) and high heritability (96.05 %, 92.65 %) with moderate to high genetic advance as per cent of mean (25.28 %, 17.76 %) during the two seasons of summer 2012-13 and 2013-14, respectively. During 2012-13, it ranged from 2.54 to 8.18 in WW condition and from 2.48 to 5.71 in WS condition with mean of 3.67 per cent and 3.84 per cent respectively. During summer 2013-14, the range for stearic acid was from 2.80 to 7.97 in WW condition with mean of 3.96 per cent and from 2.75 to 4.96 in WS conditions with mean of 3.86 per cent.

Moderate PCV (14.8, 13.38), GCV (14.55, 13.10) and high heritability (96.65 %, 95.86 %) along with high GAM (29.46 %, 26.41 %) was recorded for oleic acid during the summer 2012-13 and summer 2013-14 seasons respectively. Wide range of variation was exhibited during both the seasons in WW (31.28-75.31, 31.97-73.39) and WS (37.41-79.51, 38.89-77.78) conditions with mean 45.97 per cent, 45.96 per cent in

WW and 50.87 per cent, 51.08 per cent in WS conditions in the two seasons respectively.

Linoleic acid had moderate GCV (18.01, 18.60), PCV (18.41, 18.98) and high heritability (95.69 %, 96.00 %) with high genetic advance as per cent of mean (36.28, 37.54 %) during the two seasons of summer 2012-13 and summer 2013-14, respectively. During summer 2012-13, it ranged from 6.62 to 43.19 in WW condition and from 7.44 to 39.56 WS condition. During summer 2013-14, it ranged from 6.73 to 43.47 in WW condition and from 6.36 to 37.99 in WS conditions. Linoleic acid showed higher mean in WW condition (31.28 per cent, 31.58 %) compared to WS (27.96 per cent, 27.50 %) during both seasons, respectively.

Low to moderate PCV, GCV and high heritability with moderate to high GAM was recorded for the traits viz., arachidic acid, eicosenoic acid, behenoic acid, lignoceric acid during both the seasons.

During summer 2012-13, arachidic acid recorded a range of 1.02-3.18 in WW condition and 1.15-2.29 in WS condition with mean of 1.61 per cent and 1.62 per cent, respectively. Similar range of variation was recorded in the WW (1.19-3.10) and WS (1.14-2.15) during 2013-14, with mean of 1.75 per cent and 1.63 per cent in WW and WS conditions, respectively.

Similar range of variation was recorded for eicosenoic acid during the two seasons of summer 2012-13 and summer 2013-14 in WW condition in (0.43-1.20 and 0.45-1.17) and in WS condition (0.65-1.25 and 0.65-1.21). A mean of 0.91 per cent in WW condition during both seasons and mean of 1.02 per cent and 1.03 per cent in WS condition was recorded for eicosenoic acid during the two season respectively.

During 2012-13, range of behenoic acid in WW condition was from 2.57 to 5.09 per cent, and from 2.54-5.07 per cent in WS condition with mean of 3.58 per cent and 3.79 per cent respectively. During summer 2013-14, it ranged from 3.01 to 4.80 per cent in WW condition and from 3.18 to 4.64 per cent in WS condition with mean of 3.89 per cent and 3.80 per cent, respectively.

Lignoceric acid ranged from 0.84 to 1.45 in WW condition and from 0.91 to 1.50 in WS condition with mean of 1.16 per cent and 1.22 per cent respectively during

summer 2012-13. During summer 2013-14, it ranged from 0.86 to 1.45 in WW and from 0.98 to 1.51 in WS conditions with mean of 1.16 per cent and 1.24 per cent respectively.

O/L ratio had high PCV (53.52, 57.94), GCV (50.05, 54.32) high heritability (87.43 % and 87.90 %) along with high GAM (96.40 % and 104.92 %) during the two seasons of summer 2012-13 and summer 2013-14 respectively. It ranged from 0.74 to 12.00 in WW condition and from 1.01 to 10.03 in WS condition during summer 2012-13 with mean of 1.62 per cent and 1.99 per cent in respectively. During summer 2013-14, it from 0.74 to 11.50 in WW condition and from 1.02 to 11.61 in WS condition with mean of 1.60 per cent and 2.05 per cent, respectively.

Total unsaturated fatty acid had low PCV (4.97, 1.99), GCV (4.94, 1.92), high heritability (98.67 %, 92.82 %) along with low GAM (10.10 %, 3.81 %) during summer 2012-13 and summer 2013-14 respectively. During summer 2012-13, wide variation was recorded in WW (71.72-86.98) and WS (68.85-95.90) conditions with mean of 78.17 per cent and 79.86 per cent respectively. During summer 2013-14, it ranged from 72.87 to 85.64 in WW condition with mean of 78.44 per cent while in WS condition it ranged from 70.39 to 86.39 with mean of 79.62 per cent.

Low PCV, GCV and high heritability along with low to moderate heritability was recorded for the traits viz., total saturated fatty acid, U/S ratio and calculated iodine value. In contrast for the traits viz., L/S ratio and oleic acid desaturation moderate PCV, GCV and high heritability with high GAM was recorded during both the seasons

Total saturated fatty acid ranged from 13.71 to 29.19 in WW condition and from 13.40 to 20.11 in WS condition during summer 2012-13 with mean of 18.49 per cent and 17.68 per cent in respectively. Similarly during summer 2013-14 it ranged from 14.50 to 29.18 and from 14.37 to 20.25 in WW and WS conditions with mean of 18.92 per cent and 17.96 per cent, respectively.

Narrow range of variation was recorded for both L/S and U/S ratio in WW and WS conditions during both the seasons with mean L/S ratio of 1.68 per cent and 1.66 per cent in WW and 1.57 per cent and 1.52 per cent in WS conditions of summer 2012-13 and 2013-14 respectively. Mean of U/S ratio in WW condition was 4.26 per cent and

4.17 per cent while in WS condition mean of 4.53 per cent and 4.45 per cent was recorded.

During summer 2012-13, calculated iodine value ranged from 78.29 to 105.64 in WW condition and from 75.85 to 108.72 in WS condition with mean of 94.44 per cent and 93.00 per cent respectively. Similar range of variation was recorded in the WW (78.97-104.75) and WS (75.30-103.60) during 2013-14, with mean of 94.93 % and 92.39 % respectively.

During 2012-13, oleic acid desaturation ranged from 0.43 to 0.92 in WW condition, and from 0.50 to 0.91 in WS condition with mean of 0.59 per cent and 0.64 per cent respectively. During summer 2013-14, it ranged from 0.42 to 0.92 in WW condition and from 0.51 to 0.92 in WS condition with mean of 0.59 per cent and 0.65 per cent, respectively.

4.1.4 Variability for Foliar disease resistance traits in RILs of TMV-2 x GM 6-1

4.1.4.1 Analysis of variance (ANOVA)

Analysis of variance of foliar disease resistance traits for individual seasons of summer 2012-13 and 2013-14 (Table 33 and 34) indicated that genotypes included in the study differed significantly for all traits studied in each season. During summer 2012-13, Irrigation level (well watered and water stress conditions) and Genotypes * irrigation level had significant effect on most of the traits studied while in summer 2013-14, Genotypes * irrigation level had non-significant effect on most of the traits. Pooled ANOVA across the two seasons (Table 35) indicated significant difference among genotypes, irrigation levels and interaction effects such as season * irrigation level and irrigation level * genotype for most of the traits studied. Effect of seasons was significant only for rust score at 70 DAS. season * genotype and season * irrigation level * genotype interactions were significant for late leaf spot and rust scores at 70 DAS.

4.1.4.2 Mean, range and components of variation

Mean and range of foliar disease resistance traits for WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 are presented in the

Table 33: Analysis of variance for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Source of Variation	df	LLS70DAS	LLS80DAS	LLS90DAS	RUST70DAS	RUST80DAS	RUST90DAS
Replication	1	5.44**	4.19**	33.34**	0.94**	13.88**	17.96**
Genotypes	308	3.94**	4.46**	8.83**	1.83**	1.91**	5.32**
Irrigation Level	1	770.69**	497.3**	480.94**	457.53**	11.46**	233.31**
Genotypes * Irrigation Level	308	0.73**	0.46**	0.39**	0.65**	0.14	0.45**
Error	617	0.11	0.25	0.21	0.04	0.13	0.22
Total	1235	1.85	1.76	2.82	1.01	0.60	1.75
General Mean		2.82	4.82	6.36	2.32	4.08	5.59
S.Em		0.164	0.252	0.231	0.099	0.180	0.235
CD 5%		0.65	0.99	0.91	0.39	0.71	0.92
C.V %		11.63	10.45	7.26	8.52	8.80	8.42

** Significance at 1%, * Significance at 5%

LLS70DAS: Late Leaf Spot score at 70 days after sowing (DAS), LLS80DAS: Late Leaf Spot score at 80 DAS, LLS90DAS: Late Leaf Spot score at 90 DAS, RUST70DAS: Rust Score at 70 DAS, RUST80DAS: Rust Score at 80 DAS, RUST90DAS: Rust Score at 90 DAS

Table 34: Analysis of variance for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Source of Variation	df	LLS70DAS	LLS80DAS	LLS90DAS	RUST70DAS	RUST80DAS	RUST90DAS
Replication	1	25.63**	36.36**	9.97**	0.05	27.10**	0.08
Genotypes	308	2.87**	5.93**	10.50**	0.71**	1.44**	6.17**
Irrigation Level	1	2.72**	37.05**	127.52**	1.30**	5.85**	119.3**
Genotypes * Irrigation Level	308	0.04	0.22	0.16	0.03	0.05	0.19**
Error	617	0.14	0.46	0.14	0.04	0.12	0.11
Total	1235	0.82	1.82	2.84	0.21	0.46	1.74
General Mean		3.57	5.31	6.66	2.90	4.12	5.78
S.Em		0.184	0.338	0.184	0.099	0.175	0.166
CD 5%		0.72	1.33	0.72	0.39	0.69	0.65
C.V %		10.30	12.71	5.53	6.80	8.48	5.74

** Significance at 1%, * Significance at 5%

Table 35: Pooled analysis of variance for late leaf spot and rust disease scores in groundnut RILS of TMV-2 x GM 6-1 cross evaluation over both seasons of summer 2012-13 and 2013-14 at MARS, Dharwad

Source of Variation	df	LLS70DAS	LLS80DAS	LLS90DAS	RUST70DAS	RUST80DAS	RUST90DAS
Season	1	343.89	148.56	55.38	207.39*	1.01	22.72
Irrigation Level	1	432.51**	402.91**	551.87**	253.75**	16.84**	343.14**
Season * Irrigation Level	1	340.91**	131.43**	56.58**	205.07**	0.47	9.47**
Genotype	308	6.45**	10.19**	19.17**	2.22**	3.25**	11.38**
Season * Genotype	308	0.35**	0.20	0.15	0.32**	0.10	0.11
Irrigation Level * Genotype	308	0.41**	0.53**	0.47**	0.37**	0.11	0.57**
Season * Irrigation Level * Genotype	308	0.35**	0.15	0.08	0.32**	0.08	0.06
Pooled Error	1234	0.12	0.36	0.17	0.04	0.13	0.17
General Mean		3.20	5.07	6.51	2.61	4.10	5.69
CD 5%		0.34	0.59	0.41	0.19	0.35	0.40
C.V %		10.90	11.76	6.41	7.56	8.64	7.16

** Significance at 1%, * Significance at 5%

Table 36. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean are presented in the Table 37.

Moderate to high PCV, GCV and high heritability with high GAM was recorded for all the foliar disease resistance traits viz., late leaf spot at 70, 80 and 90 DAS and rust score at 70, 80 and 90 DAS during summer 2012-13. Similarly during summer 2013-14, moderate to high PCV, GCV and high heritability with moderate to high GAM was recorded for most of the traits studied.

Under WW condition LLS score at 70 DAS recorded wide range (2.03 - 5.00) and higher mean score (3.61) compared to range of 0.00-3.00 and mean score (2.00) under WS condition during summer 2012-13. Similarly during summer 2013-14, it ranged from 3.52 to 5.00 and from 2.00 to 4.50 with mean of 3.62 and 2.00 in WW and WS conditions respectively. It had high PCV (44.21 and 23.44), GCV (42.65 and 21.06), and heritability (93.08 % and 80.70 %) along with high GAM (84.77 and 38.97) during the two seasons respectively.

LLS score at 80 DAS ranged from 4.19 to 7.00 and from 2.00 to 5.50 with mean LLS score of 5.46 and 2.50 under WW and WS conditions respectively during summer 2012-13. Similarly during summer 2013-14 it ranged from 5.14 to 7.00 and from 2.50 to 6.50 with mean LLS score of 5.49 and 2.50 in WW and WS conditions, respectively. It had moderate to high PCV (18.99 and 22.25) and GCV (15.85 and 18.26) coupled with high heritability (69.70 % and 67.34 %) and high GAM (27.26 and 30.86) during the two seasons respectively.

Mean LLS score at 90 DAS under WW and WS conditions was 6.98 and 3 with range from 5.73 to 6.50 and from 6.33 to 8.50 during summer 2012-13 respectively. During summer 2013-14, it ranged from 3.00 to 8.50 in WW condition with mean LLS score of 6.98 and from 3.00 to 7.50 in WS conditions with mean LLS score of 3. Moderate to high PCV (19.75 and 22.48) and GCV (18.37 and 21.79) was recorded for LLS score at 90 DAS with high heritability (86.51 % and 93.95 %) and high GAM (35.21 % and 43.50 %) during the two seasons respectively.

Table 36: Mean and range for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation under WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	Mean of WW		Mean of WS		Range in WW condition				Range in WS condition							
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13		S 2013-14		S 2012-13		S 2013-14					
LLS70DAS	3.61	3.62	2	2	2.03	-	5	3.52	-	5	0	-	3	2	-	4.5
LLS80DAS	5.46	5.49	2.5	2.5	4.19	-	7	5.14	-	7	2	-	5.5	2.5	-	6.5
LLS90DAS	6.98	6.98	3	3	5.73	-	8.5	6.33	-	8.5	3	-	6.5	3	-	7.5
RUST70DAS	2.93	2.93	2	2	1.71	-	4	2.87	-	4	0	-	4	2	-	3.5
RUST80DAS	4.18	4.19	2.5	2.5	3.99	-	5.5	4.06	-	5.5	2	-	5	2.5	-	5.5
RUST90DAS	6.02	6.09	3	3	5.16	-	7	5.47	-	7.5	3	-	6	3	-	6.5

Table 37: Genetic parameters for late leaf spot and rust disease scores in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during the two seasons of summer 2012-13 and summer 2013-14 at MARS, Dharwad

Character	PCV (%)		GCV (%)		h ² (Broad Sense)		GA		GAM	
	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14	S 2012-13	S 2013-14
LLS70DAS	44.21	23.44	42.65	21.06	93.08	80.7	2.39	1.39	84.77	38.97
LLS80DAS	18.99	22.25	15.85	18.26	69.7	67.34	1.31	1.64	27.26	30.86
LLS90DAS	19.75	22.48	18.37	21.79	86.51	93.95	2.24	2.89	35.21	43.5
RUST70DAS	44.02	14.4	43.18	12.7	96.26	77.72	2.02	0.67	87.28	23.06
RUST80DAS	19.48	14.29	17.38	11.5	79.6	64.78	1.3	0.79	31.94	19.06
RUST90DAS	18.11	19.18	16.04	18.3	78.41	91.05	1.64	2.08	29.25	35.97

Rust score at 70 DAS ranged from 1.71 to 4.00 and from 0.00 to 4.00 with mean rust score of 2.93 and 2.00 under WW and WS conditions respectively during summer 2012-13 while in summer 2013-14, it ranged from 2.87 to 4.00 and from 2.00 to 3.50 with mean rust score of 2.93 and 2.00 under WW and WS conditions respectively. It had high PCV (44.02) and GCV (43.18) summer 2012-13 while moderate PCV (14.40) and GCV (12.70) during summer 2013-14. Heritability as high as 96.26 % and 77.72 % was recorded for this trait with high GAM (87.28 % and 23.06 %) during the two seasons, respectively.

During summer 2012-13, rust score at 80 DAS ranged from 3.99 to 5.50 and from 2.00 to 5.00 under WW and WS with mean rust score of 4.18 and 2.50 respectively. It had moderate PCV (19.48), GCV (17.38) and high heritability (79.60) accompanied with high GAM (31.94 %). During summer 2013-14, it ranged from 4.06 to 5.50 and from 2.50 to 5.50 under WW and WS conditions with mean rust score of 4.19 and 2.50 respectively. It had moderate PCV (14.29), GCV (11.50) and high heritability (64.78) accompanied with moderate GAM (19.06 %) during summer 2013-14.

Rust score at 90 DAS ranged from 5.16-7.00 and 3.00-6.00 with mean rust score of 6.02 and 3.00 under WW and WS conditions respectively, during summer 2012-13. Similar range of variation of 5.47-7.50 and 3.00-6.50 was recorded during summer 2013-14 with mean rust score of 6.09 and 3.00 in WW and WS conditions respectively. It had moderate PCV (18.11 and 19.18), GCV (16.04 and 18.30) and high heritability (78.41 % and 91.05 %) along with high GAM (29.25 % and 35.97 %) during the two seasons of summer 2012-13 and summer 2013-14.

4.1.5 Correlation between yield and yield components

Development of varieties with high yield under normal and water limited conditions depends on the efficiency of plant breeder and the association of trait under selection with the yield. In general, yield is a complex character and is multiplicative and product of many factors called yield components. To make effective selection for higher yield under different water regimes a thorough understanding of various characters contributing to yield, interrelationship among themselves and with yield is necessary. Improvement in yield can be brought about by effecting indirect selection for

yield related traits, whose heritability is high and show a strong association with yield. Hence, estimation of correlation coefficients are the best measures to understand the interrelationship between the various components and selection based on nature and degree of correlation will be more effective in increasing the yield gain under varied water regimes.

The phenotypic and genotypic correlations of different yield components with pod yield per plant along with their interrelationships under WW and WS conditions of two seasons of summer 2012-13 and summer 2013-14 have been determined and presented in Table 38 and 39.

4.1.5.1 Correlations analysis for pod yield and other traits

The pod yield per plant under WW condition during summer seasons of consecutive years had significant and positive correlation with number of secondary branches per plant (0.345**, 0.364** and 0.365**, 0.388**), number of pegs per plant (0.469**, 0.483** and 0.111**, 0.118**) number of mature pods per plant (0.547**, 0.565** and 0.312**, 0.329**), kernel yield per plant (0.998**, 0.998** and 0.994**, 0.994**) and sound mature kernel per cent (0.540**, 0.569** and 0.274**, 0.288**) while it had significant negative association with shelling per cent (-0.240**, 0.234** and -0.288**, -0.282**). During summer 2012-13 pod yield per plant had significant negative correlation with plant height (-0.176** and -0.210**) and non-significant association with days to maturity (0.076 and 0.080) and hundred seed weight (-0.026 and -0.046), in contrast it showed significant positive correlation with plant height (0.292** and 0.327**) and hundred seed weight (0.299** and 0.298**) and significant negative correlation with days to maturity (-0.158** and -0.175**).

The pod yield per plant under WS condition during the two summer seasons 2012-13 and 2013-14 showed significant and positive correlation with number of primary branches per plant (0.105**, 0.116** and 0.732**, 0.996**), number of secondary branches per plant (0.564**, 0.628** and 0.251**, 0.351**), number of pegs per plant (0.697**, 0.747** and 0.500**, 0.613**) number of mature pods per plant (0.640**, 0.694** and 0.848**, 0.967**), kernel yield per plant (0.995**, 0.996** and

Table 38: Estimates of phenotypic and genotypic correlation coefficients for pod yield and its component traits in WW block during the two seasons of summer 2012-13 and summer 2013-14

		DFF	DM	PH	NPBP	NSBP	NPPP	NMPP	NIPP	KYP	SP	SMK%	HSW	PYP
DFF	r_p	1	0.055	-0.058	-0.002	-0.083 [*]	0.043	-0.147 ^{**}	-0.037	-0.026	0.044	-0.064	0.016	-0.029
	r_g	1	0.039	-0.067	0.001	-0.087 [*]	0.050	-0.161 ^{**}	-0.034	-0.025	0.049	-0.067	0.020	-0.031
DM	r_p	0.838 ^{**}	1	0.023	-0.199 ^{**}	-0.024	-0.053	-0.082 [*]	0.085 [*]	-0.163 ^{**}	-0.008	-0.124 ^{**}	-0.067	-0.158 ^{**}
	r_g	0.854 ^{**}	1	0.050	-0.232 ^{**}	-0.031	-0.064	-0.092 [*]	0.098	-0.180 ^{**}	-0.013	-0.132 ^{**}	-0.077	-0.175 ^{**}
PH	r_p	0.133 ^{**}	0.116 ^{**}	1	-0.015	0.133 ^{**}	0.108 ^{**}	0.132 ^{**}	0.067	0.278 ^{**}	-0.177 ^{**}	0.024	-0.002	0.292 ^{**}
	r_g	0.158 ^{**}	0.151 ^{**}	1	-0.041	0.142 ^{**}	0.121 ^{**}	0.147 ^{**}	0.079	0.312 ^{**}	-0.201 ^{**}	0.031	-0.004	0.327 ^{**}
NPBP	r_p	-0.127 ^{**}	-0.161 ^{**}	-0.141 ^{**}	1	0.077 [*]	-0.016	0.055	-0.047	0.056	0.042	0.068	0.144 ^{**}	0.061
	r_g	-0.259 ^{**}	-0.278 ^{**}	-0.259 ^{**}	1	0.086 [*]	-0.016	0.066	-0.053	0.075	0.038	0.074	0.159 ^{**}	0.081 [*]
NSBP	r_p	0.061	0.062	0.006	-0.056	1	0.017	0.197 ^{**}	-0.049	0.367 ^{**}	-0.046	0.164 ^{**}	0.174 [*]	0.365 ^{**}
	r_g	0.069	0.067	0.002	-0.064	1	0.026	0.216 [*]	-0.058	0.389 ^{**}	-0.044	0.172 ^{**}	0.182 [*]	0.388 ^{**}
NPPP	r_p	0.114 ^{**}	0.112 ^{**}	-0.068	-0.01	0.520 ^{**}	1	0.253 ^{**}	0.004	0.117 ^{**}	-0.025	0.150 ^{**}	0.028	0.111 ^{**}
	r_g	0.120 ^{**}	0.118 ^{**}	-0.077	-0.015	0.537 ^{**}	1	0.265 ^{**}	0.008	0.124 ^{**}	-0.030	0.158 ^{**}	0.026	0.118 ^{**}
NMPP	r_p	0.058	0.085	-0.053	-0.035	0.527 ^{**}	0.762 ^{**}	1	-0.009	0.315 ^{**}	-0.090	0.601 ^{**}	0.133 ^{**}	0.312 ^{**}
	r_g	0.061	0.090	-0.062	-0.045	0.544 ^{**}	0.774 ^{**}	1	-0.013	0.331 ^{**}	-0.099	0.642 ^{**}	0.135 ^{**}	0.329 ^{**}
NIPP	r_p	0.044	0.01	0.143 ^{**}	-0.086	0.250 ^{**}	0.205 ^{**}	0.289 ^{**}	1	-0.065	-0.044	-0.731 ^{**}	-0.066	-0.063
	r_g	0.053	0.014	0.186 ^{**}	-0.154	0.277 ^{**}	0.224 ^{**}	0.318 ^{**}	1	-0.071	-0.060	-0.782 ^{**}	-0.074	-0.068
KYP	r_p	0.007	0.072	-0.190 ^{**}	0.071	0.336 ^{**}	0.453 ^{**}	0.527 ^{**}	0.022	1	-0.239 ^{**}	0.277 ^{**}	0.317 ^{**}	0.994 ^{**}
	r_g	0.007	0.077	-0.229 ^{**}	0.128 ^{**}	0.355 ^{**}	0.466 ^{**}	0.544 ^{**}	0.034	1	-0.234 ^{**}	0.292 ^{**}	0.317 ^{**}	0.994 ^{**}
SP	r_p	0.002	-0.051	-0.191 ^{**}	0.119 ^{**}	-0.207 ^{**}	-0.367 ^{**}	-0.411 ^{**}	-0.472 ^{**}	-0.184 ^{**}	1	-0.021	0.329 ^{**}	-0.288 ^{**}
	r_g	-0.002	-0.052	-0.259 ^{**}	0.242 ^{**}	-0.223 ^{**}	-0.385 ^{**}	-0.431 ^{**}	-0.491 ^{**}	-0.178 ^{**}	1	-0.030	0.352 ^{**}	-0.282 ^{**}
SMK%	r_p	0.069	0.109 ^{**}	-0.152 ^{**}	0.033	0.357 ^{**}	0.571 ^{**}	0.691 ^{**}	-0.325 ^{**}	0.537 ^{**}	-0.175 ^{**}	1	0.258 ^{**}	0.274 ^{**}
	r_g	0.081 ^{**}	0.124 ^{**}	-0.176 ^{**}	0.055	0.378 ^{**}	0.592 ^{**}	0.712 ^{**}	-0.347 ^{**}	0.549 ^{**}	-0.186 ^{**}	1	0.269 ^{**}	0.288 ^{**}
HSW	r_p	-0.018	0.027	-0.106 ^{**}	0.004	-0.205 ^{**}	-0.366 ^{**}	-0.454 ^{**}	-0.253 ^{**}	0.003	0.544 ^{**}	-0.326 ^{**}	1	0.299 ^{**}
	r_g	-0.017	0.032	-0.132 ^{**}	0.031	-0.220 ^{**}	-0.382 ^{**}	-0.474 ^{**}	-0.314 ^{**}	-0.016	0.574 ^{**}	-0.348 ^{**}	1	0.298 ^{**}
PYP	r_p	0.007	0.076	-0.176 ^{**}	0.061	0.345 ^{**}	0.469 ^{**}	0.547 ^{**}	0.050	0.998 ^{**}	-0.240 ^{**}	0.540 ^{**}	-0.026	1
	r_g	0.007	0.080 [*]	-0.210 ^{**}	0.111 [*]	0.364 [*]	0.483 ^{**}	0.565 ^{**}	0.063	0.998 ^{**}	-0.235 ^{**}	0.569 ^{**}	-0.046	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

Table 39: Estimates of phenotypic and genotypic correlation coefficients for pod yield and its component traits in WS block during the two seasons of summer 2012-13 and summer 2013-14

		DFF	DM	PH	NPBP	NSBP	NPPP	NMPP	NIPP	KYP	SP	SMK %	HSW	PYP
DFF	r_p	1	0.427	0.031	-0.467	-0.224	-0.364	-0.532	0.344	-0.613	-0.018	-0.543	-0.143	-0.625
	r_g	1	0.513	0.059	-0.607	-0.260	-0.397	-0.584	0.384	-0.797	-0.038	-0.599	-0.154	-0.813
DM	r_p	0.977	1	0.027	-0.426	-0.088	-0.262	-0.508	0.313	-0.565	0.011	-0.562	-0.203	-0.567
	r_g	0.998	1	0.026	-0.517	-0.101	-0.285	-0.565	0.354	-0.749	0.011	0.608	-0.222	-0.750
PH	r_p	0.078	0.060	1	0.023	-0.078	-0.143	-0.067	0.035	-0.053	0.094	-0.022	-0.053	-0.046
	r_g	0.106	0.100	1	0.097	-0.108	-0.223	-0.109	0.075	-0.092	0.376	-0.068	-0.074	-0.068
NPBP	r_p	-0.035	-0.037	-0.021	1	-0.023	0.312	0.628	-0.464	0.726	0.028	0.693	0.203	0.732
	r_g	-0.044	-0.019	-0.410	1	-0.006	0.357	0.752	-0.538	0.982	-0.278	0.785	0.244	0.996
NSBP	r_p	0.010	0.019	0.072	0.199	1	0.173	0.209	0.046	0.247	0.010	0.059	0.095	0.251
	r_g	0.015	0.021	0.130	0.327	1	0.187	0.227	0.049	0.342	-0.043	0.078	0.114	0.351
NPPP	r_p	-0.030	-0.025	0.104	0.149	0.744	1	0.680	-0.278	0.493	-0.009	0.436	0.154	0.500
	r_g	-0.039	-0.032	0.174	0.271	0.800	1	0.703	-0.291	0.604	-0.036	0.518	0.159	0.613
NMPP	r_p	-0.002	-0.003	0.087	0.148	0.716	0.865	1	-0.402	0.839	0.016	0.794	0.241	0.848
	r_g	0.004	0.001	0.130	0.290	0.788	0.902	1	-0.422	0.954	0.049	0.889	0.252	0.967
NIPP	r_p	-0.034	-0.023	-0.181	-0.027	-0.549	-0.659	-0.572	1	-0.479	-0.026	-0.685	-0.085	-0.481
	r_g	-0.022	-0.009	-0.263	-0.069	-0.619	-0.709	-0.624	1	-0.598	-0.010	0.769	-0.093	-0.601
KYP	r_p	-0.039	-0.054	0.065	0.103	0.597	0.735	0.680	-0.607	1	0.088	0.843	0.351	0.988
	r_g	-0.047	-0.058	-0.046	0.121	0.660	0.782	0.734	-0.658	1	0.068	0.978	0.413	0.988
SP	r_p	-0.014	-0.018	0.090	0.037	0.514	0.620	0.573	-0.730	0.717	1	-0.036	0.080	0.011
	r_g	-0.021	-0.019	0.178	0.115	0.611	0.696	0.668	-0.820	0.789	1	-0.065	0.160	-0.036
SMK%	r_p	0.012	0.001	0.123	0.106	0.706	0.820	0.824	-0.867	0.793	0.779	1	0.114	0.856
	r_g	0.015	0.014	0.141	0.128	0.723	0.821	0.830	-0.889	0.804	0.794	1	0.128	0.954
HSW	r_p	-0.022	-0.022	0.045	0.160	0.675	0.817	0.972	-0.394	0.690	0.496	0.724	1	0.336
	r_g	-0.015	-0.015	0.049	0.299	0.747	0.859	0.978	-0.468	0.738	0.590	0.780	1	0.394
PYP	r_p	-0.046	-0.060	0.053	0.105	0.564	0.697	0.640	-0.538	0.995	0.673	0.738	0.668	1
	r_g	-0.052	-0.063	-0.075	0.116	0.628	0.747	0.694	-0.597	0.996	0.755	0.751	0.713	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

0.988**, 0.988**), sound mature kernel per cent (0.738**, 0.751** and 0.856**, 0.954**) and hundred seed weight (0.668**, 0.713** and 0.336**, 0.394**) while it had significant negative association with number of immature pods per plant (-0.538**, -0.597** and -0.481**, -0.601**). During summer 2012-13 pod yield per plant showed significant positive correlation with shelling per cent (0.673** and 0.755**) and non-significant association with days to 50 per cent flowering (-0.046 and -0.052) and days to maturity (-0.060 and -0.063), in contrast it showed significant negative correlation with days to 50 per cent flowering (-0.625** and -0.813**), days to maturity (-0.567** and -0.750**) and non-significant association with shelling per cent (0.011 and -0.036) during summer 2013-14.

4.1.5.2 Interrelations among other traits

Days to 50 per cent flowering

In WW condition, days to 50 per cent flowering recorded significant positive correlation with days to maturity (0.838** and 0.854**), plant height (0.133** and 0.158**) and number of pegs per plant (0.114** and 0.120**) during summer 2012-13, in contrast it recorded non-significant association with the above traits during summer 2013-14. It recorded significant negative correlation with number of primary branches per plant (-0.127** and -0.259**) in the first season and with number of secondary branches per plant (-0.083* and -0.087*) and number of mature pods per plant (-0.147** and -0.161**) during the next season.

In WS condition it recorded significant positive correlation with days to maturity (0.977**, 0.998** and 0.427**, 0.513**) irrespective of the season. In contrast to the non-significant associations with other traits during the summer 2012-13, it recorded significant positive correlation with number of immature pods per plant (0.344** and 0.384**) and significant negative correlation with most of the traits except plant height and shelling per cent.

Days to maturity

Days to maturity recorded significant positive correlation with days to 50 per cent flowering (0.838** and 0.854**), plant height (0.116** and 0.151**), number of

pegs per plant (0.112** and 0.118**) and sound mature kernel per cent (0.109** and 0.124**) and significant negative correlation with number of primary branches per plant (-0.161** and -0.278**) in the WW condition during summer 2012-13. In WW condition of summer 2013-13, it recorded significant positive correlation with number of immature pods per plant (0.085* and 0.098*), while negative correlation with number of primary branches per plant (-0.199** and -0.232**), number of mature pods per plant (-0.082* and -0.092*), kernel yield per plant (-0.163** and -0.180**) and sound mature kernel per cent (-0.124** and -0.132**) in the WW condition during summer 2013-14.

In WS condition it has recorded significant positive correlation with days to 50 per cent flowering (0.977**, 0.998** and 0.427** and 0.513**) irrespective of the season. It has recorded significant negative correlation with most of the traits except plant height and shelling per cent during summer 2013-14, in contrast to the non-significant associations recorded with most of the traits during the summer 2012-13.

Plant Height

Plant height recorded significant positive correlation with days to 50 per cent flowering (0.133** and 0.158**), days to maturity (0.116** and 0.151**) and number of immature pods per plant (0.143** and 0.186**) while significant negative correlation with number of primary branches per plant (-0.141** and -0.259**), kernel yield per plant (-0.190** and -0.229**), shelling per cent (-0.191** and -0.259**), sound mature kernel per cent (-0.152** and -0.176**) and 100 seed weight (-0.106** and -0.132**) in the WW condition during summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with number of secondary branches per plant (0.133** and 0.142**), number of pegs per plant (0.108** and 0.121**), number of mature pods per plant (0.132** and 0.147**), and kernel yield per plant (0.278** and 0.312**), while negative correlation with shelling per cent (-0.177** and -0.201**).

In WS condition it recorded significant positive correlation with days to 50 per cent flowering (0.078 and 0.106**), number of secondary branches per plant (0.072 and 0.130**), number of pegs per plant (0.104** and 0.174**), number of mature pods per plant (0.087* and 0.130**), shelling per cent (0.090* and 0.178**), sound mature kernel per cent (0.123** and 0.141**), while It recorded significant negative correlation

with number of immature pods per plant (-0.181** and -0.263**) during summer 2012-13. In contrast, plant height recorded significant negative correlation with number of secondary branches per plant (-0.078 and -0.108**) and number of pegs per plant (-0.143** and -0.223**) and significant positive correlation with shelling per cent (0.094* and 0.376**), during the summer 2013-14.

Number of primary branches per plant

In WW condition, number of primary branches per plant recorded significant positive correlation with shelling per cent (0.119** and 0.242**) and significant negative correlation with number of immature pods per plant (-0.086* and -0.154**) during summer 2012-13. During summer 2013-14, it recorded significant positive correlation with number of secondary branches per plant (0.077 and 0.086*) and 100 seed weight (0.144** and 0.159**) while significant negative correlation with days to maturity (-0.199 and -0.232**).

Irrespective of the season in WS condition, number of primary branches per plant recorded significant positive correlation with number of pegs per plant (0.149**, 0.271** and 0.312** and 0.357**), number of mature pods per plant (0.148**, 0.290** and 0.628**, 0.752**), kernel yield per plant (0.103**, 0.121** and 0.726**, 0.982**), sound mature kernel per cent (0.106**, 0.128** and 0.693**, 0.785**) and 100 seed weight (0.160**, 0.299** and 0.203**, 0.244**). During summer 2012-13, it recorded significant positive correlation with number of secondary branches per plant (0.199** and 0.327**). In contrast to the previous season it recorded significant negative correlation with days to 50 per cent flowering (-0.467** and -0.607**), days to maturity (-0.426** and -0.517**) and number of immature pods per plant (-0.464** and -0.538**).

Number of secondary branches per plant

Number of secondary branches per plant recorded significant positive correlation with number of pegs per plant (0.520** and 0.537**), number of mature pods per plant (0.527** and 0.554**), number of immature pods per plant (0.250** and 0.277**), kernel yield per plant (0.336** and 0.355**) and sound mature kernel per cent (0.357** and 0.378**) while significant negative correlation with shelling per cent

(-0.207** and -0.223**) and 100 seed weight (-0.205** and -0.220**) in the WW condition during summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with plant height (0.133** and 0.142**), number of primary branches per plant (0.077 and 0.086*), number of mature pods per plant (0.197** and 0.216**), kernel yield per plant (0.367** and 0.389**), sound mature kernel per cent (0.164** and 0.172**) and 100 seed weight (0.174** and 0.182**) while negative correlation with days to 50 per cent flowering (-0.083* and -0.087*).

In WS condition it recorded significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and significant negative correlation with number of immature pods per plant (-0.549** and -0.619**) during summer 2012-13. During the next season it showed significant positive correlation with number of pegs per plant (0.173** and 0.187**), number of mature pods per plant (0.209** and 0.227**), kernel yield per plant (0.247** and 0.342**) and 100 seed weight (0.095* and 0.114**) while It recorded significant negative correlation with days to 50 per cent flowering (-0.224** and -0.260**), days to maturity (-0.088* and -0.101**) and plant height (-0.078 and -0.108**).

Number of pegs per plant

Number of pegs per plant recorded significant positive correlation with days to 50 per cent flowering (0.114** and 0.120**), days to maturity (0.112** and 0.118**), number of secondary branches per plant (0.520** and 0.537**), number of mature pods per plant (0.762** and 0.774**), number of immature pods per plant (0.205** and 0.224**), kernel yield per plant (0.453** and 0.466**) and sound mature kernel per cent (0.571** and 0.592**) while significant negative correlation with shelling per cent (-0.367** and -0.385**) and 100 seed weight (-0.366** and -0.382**) in the WW condition during summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with plant height (0.108** and 0.121**), number of mature pods per plant (0.253** and 0.265**), kernel yield per plant (0.117** and 0.124**) and sound mature kernel per cent (0.150** and 0.158**).

In WS condition it recorded significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and significant negative

correlation with number of immature pods per plant (-0.659** and -0.709**) during summer 2012-13. During the summer 2013-14, it recorded significant positive correlation with number of primary branches per plant (0.312** and 0.357**), number of secondary branches per plant (0.173** and 0.187**), number of mature pods per plant (0.680** and 0.703**), kernel yield per plant (0.493** and 0.604**), sound mature kernel per cent (0.436** and 0.518**) and 100 seed weight (0.154** and 0.159**) while It recorded significant negative correlation with days to 50 per cent flowering (-0.364** and -0.397**), days to maturity (-0.262** and -0.285**), plant height (-0.143** and -0.223**) and number of immature pods per plant (-0.278** and -0.291**).

Number of mature pods per plant

In WW condition of summer 2012-13, number of mature pods per plant recorded significant positive correlation with days to maturity (0.085* and 0.090*), number of secondary branches per plant (0.527** and 0.544**), number of pegs per plant (0.762** and 0.774**), number of immature pods per plant (0.289** and 0.318**), kernel yield per plant (0.527** and 0.544**) and sound mature kernel per cent (0.691** and 0.712**) while significant negative correlation with shelling per cent (-0.411** and -0.431**) and 100 seed weight (-0.454** and -0.474**). In WW condition of summer 2013-14, it recorded significant positive correlation with plant height (0.132** and 0.147**), number of secondary branches per plant (0.197** and 0.216**), number of pegs per plant (0.253** and 0.265**), kernel yield per plant (0.315** and 0.331**), sound mature kernel per cent (0.601** and 0.642**) and 100 seed weight (0.133** and 0.135**) while significant negative correlation with days to 50 per cent flowering (-0.147** and -0.167**), days to maturity (-0.082* and -0.092*) and shelling per cent (-0.090* and -0.099*).

In WS condition it had significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and significant negative correlation with number of immature pods per plant (-0.572** and -0.624**) during summer 2012-13. During the summer 2013-14, it recorded significant positive correlation with number of primary branches per plant (0.628** and 0.752**), number of secondary branches per plant (0.209** and 0.227**), number of pegs per plant

(0.680** and 0.703**), kernel yield per plant (0.839** and 0.954**), sound mature kernel per cent (0.794** and 0.889**) and 100 seed weight (0.241** and 0.252**) while It recorded significant negative correlation with days to 50 per cent flowering (-0.532** and -0.584**) and days to maturity (-0.508** and -0.565**).

Number of immature pods per plant

In WW condition of summer 2012-13, number of immature pods per plant recorded significant positive correlation with plant height (0.143** and 0.186**), number of secondary branches per plant (0.250** and 0.277**), number of pegs per plant (0.205** and 0.224**) and number of mature pods per plant (0.289** and 0.318**) while significant negative correlation with number of primary branches per plant (-0.086* and -0.154**), shelling per cent (-0.472** and -0.491**), sound mature kernel per cent (-0.325** and -0.347**) and 100 seed weight (-0.253** and -0.314**). In WW condition of summer 2013-14, it recorded significant positive correlation with days to maturity (0.085* and 0.098*) and significant negative correlation with sound mature kernel per cent (-0.731** and -0.782**).

In WS condition it recorded significant negative correlations with most of the traits except days to 50 per cent flowering, days to maturity and number of primary branches per plant during summer 2012-13. Similarly during the summer 2013-14, it recorded significant negative correlation with most of the traits except plant height and significant negative correlation with days to 50 per cent flowering (0.344** and 0.384**) and days to maturity (0.313** and 0.354**).

Kernel yield per plant

Kernel yield per plant had significant positive correlation with number of secondary branches per plant (0.336** and 0.355**), number of pegs per plant (0.453** and 0.466**), number of mature pods per plant (0.527** and 0.544**) and sound mature kernel per cent (0.537** and 0.549**) while significant negative correlation with plant height (-0.190** and -0.229**) and shelling per cent (-0.184** and -0.178**) in WW condition of summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with plant height (0.278** and 0.312**), number of secondary branches per plant (0.367** and 0.389**), number of pegs per

plant (0.117** and 0.124**), number of mature pods per plant (0.315** and 0.331**), sound mature kernel per cent (0.277** and 0.292**) and 100 seed weight (0.317** and 0.317**) while significant negative correlation with days to maturity (-0.163** and -0.180**) and shelling per cent (-0.239** and -0.234**).

In WS condition it had significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and plant height and significant negative correlation with number of immature pods per plant (-0.607** and -0.658**) during summer 2012-13. Similarly during the summer 2013-14, it recorded significant negative correlation with most of the traits except plant height and significant positive correlation with days to 50 per cent flowering (-0.613** and -0.797**), days to maturity (-0.565** and -0.749**) and number of immature pods per plant (-0.479** and -0.598**).

Shelling per cent

In WW condition shelling per cent recorded significant negative correlation with most of the traits except days to 50 per cent flowering, days to maturity and significant positive correlation with number of primary branches per plant (0.119** and 0.242**) and 100 seed weight (0.544** and 0.574**) during summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with 100 seed weight (0.329** and 0.352**) while significant negative correlation with plant height (-0.177** and -0.201**), number of mature pods per plant (-0.090* and -0.099*) and kernel yield per plant (-0.239** and -0.234**).

In WS condition it had significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and number of primary branches per plant and significant negative correlation with number of immature pods per plant (-0.730** and -0.820**) during summer 2012-13. Similarly during the summer 2013-14, it recorded significant positive correlation with plant height (0.094* and 0.376**), kernel yield per plant (0.088* and 0.068) and 100 seed weight (0.080* and 0.160**).

Sound mature kernel per cent

Sound mature kernel per cent recorded significant positive correlation with days to maturity (0.109** and 0.124**), number of secondary branches per plant (0.357**

and 0.378**), number of pegs per plant (0.571** and 0.592**), number of mature pods per plant (0.691** and 0.712**) and kernel yield per plant (0.537** and 0.549**) while significant negative correlation with plant height (-0.152** and -0.176**), number of immature pods per plant (-0.325** and -0.347**), shelling per cent (-0.175** and -0.186**) and 100 seed weight (-0.326** and -0.348**) in WW condition of summer 2012-13. In WW condition of summer 2013-14, it recorded significant positive correlation with number of secondary branches per plant (0.164** and 0.172**), number of pegs per plant (0.150** and 0.158**), number of mature pods per plant (0.601** and 0.642**), kernel yield per plant (0.277** and 0.292**) and 100 seed weight (0.258** and 0.269**) while significant negative correlation with days to maturity (-0.124** and -0.132**), and number of immature pods per plant (-0.731** and -0.782**).

In WS condition it recorded significant positive correlation with most of the traits except days to 50 per cent flowering and days to maturity and significant negative correlation with number of immature pods per plant (-0.867** and -0.889**) during summer 2012-13. Similarly during the summer 2013-14, it recorded significant positive correlation with number of primary branches per plant (0.693** and 0.785**), number of pegs per plant (0.436** and 0.518**), number of mature pods per plant (0.794** and 0.889**), kernel yield per plant (0.843** and 0.978**) and 100 seed weight (0.144** and 0.128**) while significant negative correlation with days to 50 per cent flowering (-0.543** and -0.599**), days to maturity (-0.562** and -0.608**) and number of immature pods per plant (-0.685** and -0.769**).

Hundred seed weight

In WW condition of summer 2012-13, hundred seed weight recorded significant negative correlation with most of the traits except days to 50 per cent flowering, days to maturity, number of primary branches per and kernel yield per plant while significant positive correlation with shelling per cent (0.544** and 0.574**). In WW condition of summer 2013-14, it recorded significant positive correlation with number of primary branches per plant (0.144** and 0.159**), number of secondary branches per plant (0.174** and 0.182**), number of mature pods per plant (0.133** and 0.135**), kernel

yield per plant (0.317** and 0.317**), shelling per cent (0.329** and 0.352**) and sound mature kernel per cent (0.258** and 0.269**).

In WS condition it recorded significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and plant height and significant negative correlation with number of immature pods per plant (-0.394** and -0.468**) during summer 2012-13. During the summer 2013-14, it recorded significant positive correlation with most of the traits except plant height and significant negative correlation with days to 50 per cent flowering (-0.143** and -0.153**), days to maturity (-0.203** and -0.222**) and number of immature pods per plant (-0.085* and -0.093*).

4.1.6 Correlation analysis for physiological traits under WS condition

Phenotypic and genotypic correlation of pod yield with physiological traits along with their interrelationships under WS condition during the two seasons of summer 2012-13, summer 2013-14 and pooled across the two seasons were determined and are presented in Table 40 and 41.

4.1.6.1 Correlation between pod yield with physiological traits under WS condition

Pod yield under WS condition had significant positive correlation with drought tolerant index (0.621**, 0.656**, 0.491**, 0.600** and 0.507**), relative water content at 30 days of stress (0.674**, 0.861**, 0.496**, 0.672** and 0.549**), per cent reduction in RWC from 7 to 15 DAS (-0.033, -0.048; 0.245**, 0.465** and 0.072) and SPAD chlorophyll meter reading (0.670**, 0.842**, 0.331**, 0.576** and 0.443**) while it had significant negative association with relative water content at 15 DAS (0.004, -0.003; -0.301**, -0.394** and -0.073), per cent reduction in RWC from 15 to 30 DAS (-0.683**, -0.746**, -0.637**, -0.985** and -0.532**), per cent reduction in RWC from 7 to 30 DAS (-0.676**, -0.759**, -0.492**, -0.569** and -0.505**), specific leaf area at 15 DAS (-0.358**, -0.427**, -0.088*, -0.104** and -0.209**) and specific leaf area at 30 DAS (-0.718**, -0.954**, -0.440**, -0.804** and -0.593**) during summer 2012-13, summer 2013-14 and pooled across the two seasons, respectively.

Table 40: Estimates of phenotypic and genotypic correlation coefficients for physiological traits in WS block during the two seasons of summer 2012-13 and summer 2013-14

		DTI	RWCI	RWCII	RWCIII	PR RWC1	PR RWC2	PR RWC3	SLAI	SLAII	SLAIII	SCMR	PY WS
DTI	r_p	1	-0.018	-0.570**	0.562**	0.518***	-0.914**	-0.535**	-0.101**	-0.205**	-0.411**	0.295**	0.491**
	r_g	1	-0.021	-0.608**	0.644**	0.651**	-0.256**	-0.687**	-0.102**	-0.209**	-0.586**	0.429**	0.600**
RWCI	r_p	0.019	1	0.155**	0.074	0.403**	0.034	0.356**	-0.001	-0.066	-0.019	-0.046	-0.058
	r_g	0.021	1	0.184**	0.060	0.568**	0.045	0.487**	0.002	-0.080*	0.023	-0.127**	-0.066
RWCII	r_p	-0.003	0.100***	1	0.205**	-0.840**	0.512**	-0.125**	0.025	-0.071	-0.158**	0.091*	-0.301**
	r_g	-0.005	0.120**	1	0.255**	0.921**	0.689**	-0.568**	0.001	-0.081*	-0.262**	0.096*	-0.394**
RWCIII	r_p	0.773**	0.130**	0.221**	1	-0.149**	-0.731**	-0.904**	-0.125**	-0.332**	-0.753**	0.543**	0.496**
	r_g	0.918**	0.152**	0.288**	1	0.365**	-0.950**	-0.987**	-0.147**	-0.395**	-0.959**	0.867**	0.672**
PRRWC 1	r_p	0.019	0.692**	-0.641**	-0.059	1	-0.455**	0.311**	-0.004	0.030	0.135**	-0.112**	0.245**
	r_g	0.025	0.758**	-0.795**	-0.084*	1	-0.665**	0.546**	-0.056	0.056	0.254**	-0.264**	0.465**
PRRWC 2	r_p	-0.788**	-0.095*	0.146**	-0.932**	-0.178**	1	0.700**	0.111**	0.237**	0.549**	-0.409**	-0.637**
	r_g	-0.854**	-0.109**	0.215**	-0.987**	-0.225**	1	0.984**	0.249**	0.697**	0.589**	-0.698**	-0.985**
PRRWC 3	r_p	-0.747**	0.244**	-0.180**	-0.928**	0.320**	0.874**	1	0.116**	0.285**	0.697**	-0.531**	-0.492**
	r_g	-0.819**	0.302**	-0.222**	-0.986**	0.412**	0.913**	1	0.189**	0.365**	0.789**	-0.895**	-0.569**
SLAI	r_p	-0.050	-0.056	0.102**	-0.044	-0.106**	0.080*	0.025	1	0.055	0.044	-0.092*	-0.065
	r_g	-0.051	-0.049	0.121**	-0.054	-0.145**	0.150**	0.042	1	0.054	0.030	-0.134**	-0.081*
SLAII	r_p	-0.355**	-0.014	-0.002	-0.447**	-0.003	0.455**	0.433**	0.208**	1	-0.025	-0.045	-0.088**
	r_g	-0.400**	-0.014	-0.030	-0.621**	-0.012	0.758**	0.596**	0.230**	1	-0.092*	-0.098	-0.104**
SLAIII	r_p	-0.812**	-0.043	0.013	-0.880**	-0.044	0.897**	0.845**	0.103**	0.454**	1	-0.472**	-0.440**
	r_g	-0.901**	-0.065	-0.008	0.998**	-0.059	0.992**	0.948**	0.101**	0.528**	1	-0.998**	-0.804**
SCMR	r_p	0.825**	0.018	0.045	0.829**	-0.013	-0.826**	-0.802**	-0.052	-0.366**	-0.834**	1	0.331**
	r_g	0.810**	0.121**	0.237**	0.949**	-0.029	-0.901**	-0.896**	-0.123**	-0.865**	-0.995**	1	0.576**
PY WS	r_p	0.621**	-0.032	0.004	0.674**	-0.033	-0.683**	-0.676**	-0.005	-0.358**	-0.718**	0.670**	1
	r_g	0.656**	-0.027	-0.003	0.861**	-0.048	-0.746**	0.759**	-0.010	-0.427**	-0.954***	0.842**	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

Table 41: Pooled estimates of phenotypic correlation coefficients between pod yield and physiological traits in WS block over two seasons of summer 2012-13 and summer 2013-14

	DTI	RWCI	RWCII	RWCIII	PR RWC 1	PR RWC 2	PR RWC 3	SLAI	SLAII	SLAIII	SCMR	PY WS
DTI	1.000											
RWCI	0.059	1.000										
RWCII	-0.260**	0.117**	1.000									
RWCIII	0.638**	0.157**	0.216**	1.000								
PR RWC 1	0.264**	0.515**	-0.786**	-0.093*	1.000							
PR RWC 2	-0.750**	-0.082*	0.413**	-0.788**	-0.405**	1.000						
PR RWC 3	-0.569**	0.265**	-0.154**	-0.903**	0.305**	0.739**	1.000					
SLAI	-0.100**	-0.061	0.097*	-0.120**	-0.115**	0.170**	0.097*	1.000				
SLAII	-0.259**	-0.046	-0.027	-0.402**	0.004	0.345**	0.371**	0.128**	1.000			
SLAIII	-0.692**	-0.059	-0.109**	-0.794**	0.061	0.630**	0.718**	0.089*	0.225**	1.000		
SCMR	0.551**	0.007	0.096*	0.660**	-0.083*	-0.531**	-0.624**	-0.078*	-0.162**	-0.621**	1.000	
PY WS	0.507**	0.017	-0.073*	0.549**	0.072*	-0.532**	-0.505**	-0.064	-0.209**	-0.593**	0.443**	1.000

DTI: Drought Tolerance Index, PR RWC 1: Percent Reduction of RWC II from RWC I, PR RWC 2: Percent Reduction of RWC III from RWC II, PR RWC 3: Percent Reduction of RWC III from RWC I, PY WS: Pod yield under Water Stress

4.1.6.2 Interrelations among physiological traits

Drought Tolerant Index (DTI)

DTI for pod yield recorded significant positive correlation with relative water content at 30 DAS (0.773**, 0.918**, 0.562**, 0.644** and 0.638**), per cent reduction in RWC from 7 to 15 DAS (0.019, 0.025; 0.518**, 0.651** and 0.264**) and SPAD chlorophyll meter reading at 30 DAS (0.825**, 0.810**, 0.295**, 0.429** and 0.551**) while it showed significant negative correlation with relative water content at 15 DAS (-0.003, -0.005; -0.570**, -0.608** and -0.260**), per cent reduction in RWC from 15 to 30 DAS (-0.788**, -0.854**, -0.914**, -0.256** and -0.750**), per cent reduction in RWC from 7 to 30 DAS (-0.747**, -0.819**, -0.535**, -0.687** and -0.569**), specific leaf area at 7 DAS (-0.050, -0.051; -0.101**, -0.102** and -0.100**), specific leaf area at 15 DAS (-0.355**, -0.400**, -0.205** -0.209** and -0.259**), specific leaf area at 30 DAS (-0.812**, -0.901**, -0.411**, -0.586** and -0.692**) respectively during summer 2012-13, summer 2013-14 and pooled across the two seasons.

Relative Water Content at 7 DAS

During summer 2012-13, relative water content at 7 DAS recorded significant positive correlation with per cent reduction in RWC from 7 to 15 DAS (0.692** and 0.758**), per cent reduction in RWC from 15 to 30 DAS (0.244** and 0.302**). It recorded significant positive correlation with relative water content at 15 DAS (0.155**, 0.184** and 0.117**), relative water content at 30 DAS (0.074, 0.060 and 0.157**), per cent reduction in RWC from 7 to 15 DAS (0.403**, 0.568** and 0.515**) and per cent reduction in RWC from 7 to 30 DAS (0.356**, 0.487** and 0.265**) respectively during summer 2013-14 and pooled across the two seasons.

Relative Water Content at 15 DAS

Relative water content at 15 DAS recorded significant positive correlation with relative water content at 30 DAS (0.221**, 0.288**, 0.205**, 0.255** and 0.216**), per cent reduction in RWC from 15 to 30 DAS (0.146**, 0.215**, 0.512**, 0.689** and 0.413**), specific leaf area at 7 DAS (0.102**, 0.121**, 0.001, 0.025 and 0.097*) and SPAD chlorophyll meter reading at 30 DAS (0.045, 0.237**, 0.091*, 0.096* and

0.096*) while it recorded significant negative correlation with per cent reduction in RWC from 7 to 15 DAS (-0.641**, -0.795**, -0.840**, -0.921** and -0.786**) and per cent reduction in RWC from 7 to 30 DAS (-0.180**, -0.222**, -0.125**, -0.568** and -0.786**), and specific leaf area at 30 DAS (0.013, 0.008; -0.158**, -0.262** and -0.109**) during summer 2012-13, summer 2013-14 and pooled across the two seasons.

Relative Water Content at 30 DAS

Relative water content at 30 DAS recorded significant negative correlation with most of the traits and positive correlation with drought tolerance index (0.773**, 0.918**, 0.562**, 0.644** and 0.638**), relative water content at 15 DAS (0.221**, 0.288**, 0.205**, 0.255** and 0.216**) and SPAD chlorophyll meter reading at 30 DAS (0.829**, 0.949**, 0.543**, 0.867** and 0.660**) during both seasons and pooled across the two seasons.

Specific Leaf Area at 7 DAS

During summer 2012-13, specific leaf area at 7 DAS recorded significant positive correlation relative water content at 15 DAS (0.102** and 0.121**), specific leaf area at 15 DAS (0.208** and 0.230**) and specific leaf area at 30 DAS (0.103** and 0.101**) while significant negative correlation with per cent reduction in RWC from 7 to 15 DAS (-0.106** and -0.145**). Whereas, during summer 2013-14 and pooled across the two seasons It recorded significant positive correlation with per cent reduction in RWC from 15 to 30 DAS (0.111**, 0.249** and 0.170**) and per cent reduction in RWC from 7 to 30 DAS (0.116**, 0.189** and 0.097**) while it showed significant negative correlation with drought tolerant index (-0.101**, -0.102** and -0.100**), relative water content at 30 DAS (-0.125**, -0.147** and -0.120**) and SPAD chlorophyll meter reading at 30 DAS (-0.092*, -0.134** and -0.078) respectively, during summer 2013-14 and pooled across the two seasons.

Specific Leaf Area at 15 DAS

Specific leaf area at 15 DAS recorded significant positive correlation with per cent reduction in RWC from 15 to 30 DAS (0.455**, 0.758**, 0.237**, 0.697** and 0.345**) per cent reduction in RWC from 15 to 30 DAS (0.433**, 0.596**, 0.285**, 0.365** and 0.371**), specific leaf area at 7 DAS (0.208**, 0.230**, 0.055, 0.054 and

0.128**) and specific leaf area at 30 DAS (0.454**, 0.528**; -0.025, -0.092* and -0.225**) while it recorded significant negative correlation with drought tolerant index (-0.355**, -0.400**; -0.205**, -0.209** and -0.259**), relative water content at 15 DAS (-0.002, -0.030; -0.071, -0.081* and -0.027), relative water content at 30 DAS (-0.447**, -0.621**; -0.332**, -0.395** and -0.402**) and SPAD chlorophyll meter reading at 30 DAS (-0.366**, -0.865**; -0.045, -0.098* and -0.162**) during summer 2012-13, summer 2013-14 and pooled across the two seasons.

Specific Leaf Area at 30 DAS

During summer 2012-13, specific leaf area at 30 DAS recorded significant positive correlation with per cent reduction in RWC from 15 to 30 DAS (0.897** and 0.992**), per cent reduction in RWC from 7 to 30 DAS (0.845** and 0.948**), specific leaf area at 7 DAS (0.103** and 0.101**) and specific leaf area at 15 DAS (0.454** and 0.528**) while significant negative correlation with drought tolerant index (-0.812** and -0.901**), relative water content at 30 DAS (-0.880** and -0.998**) and SPAD chlorophyll meter reading at 30 DAS (-0.834** and -0.995**). Whereas, during summer 2013-14 and pooled across the two seasons it recorded significant positive correlation with per cent reduction in RWC from 7 to 15 DAS (0.135**, 0.254** and 0.061), per cent reduction in RWC from 15 to 30 DAS (0.549**, 0.589** and 0.630**) and per cent reduction in RWC from 7 to 30 DAS (0.697**, 0.789** and 0.718**) while it showed significant negative correlation with drought tolerant index (-0.411**, -0.586** and -0.692**), relative water content at 15 DAS (-0.158**, -0.262** and -0.109**), relative water content at 30 DAS (-0.753**, -0.959** and -0.794**) and SPAD chlorophyll meter reading at 30 DAS (-0.472**, -0.998** and -0.621**) respectively, during summer 2013-14 and pooled across the two seasons.

SPAD chlorophyll meter reading at 30 DAS

SPAD chlorophyll meter reading at 30 DAS recorded significant positive correlation with drought tolerant index (0.825**, 0.810**; 0.295**, 0.429** and 0.551**), relative water content at 15 DAS (0.045, 0.237**; 0.091*, 0.096* and 0.096*), relative water content at 30 DAS (0.829**, 0.849**; 0.543**, 0.867* and

0.660**) while it recorded significant negative correlation with per cent reduction in RWC from 7 to 15 DAS (-0.013, -0.029; -0.112**, -0.264** and -0.083*), per cent reduction in RWC from 15 to 30 DAS (-0.826**, -0.901**; -0.409**, -0.698** and -0.531**) per cent reduction in RWC from 15 to 30 DAS (-0.802**, -0.896**; -0.531**, -0.895** and -0.624**), specific leaf area at 7 DAS (-0.052, -0.123**; -0.092*, -0.134** and -0.078), specific leaf area at 15 DAS (-0.366**, -0.865**; -0.045, -0.098* and -0.162**) and specific leaf area at 30 DAS (-0.834**, -0.995**; -0.472**, -0.998** and -0.621**) during summer 2012-13, summer 2013-14 and pooled across the two seasons respectively.

4.1.7 Correlation analysis for oil quality traits

Phenotypic and genotypic correlations of different oil quality traits with oleic acid along with their interrelationships under WW and WS conditions of both the seasons were determined and are presented in Table 42 and 43.

4.1.7.1 Correlation between oleic acid and other oil quality traits

Oleic acid recorded significant positive correlation with total oil content (0.197**, 0.200**, 0.110**, 0.11**; 0.332**, 0.338** and -0.201**, -0.221**), eicosenoic acid (0.493**, 0.502**, 0.472**, 0.482**; 0.408**, 0.413** and 0.139**, 0.138**), lignoceric acid (0.554**, 0.568**, 0.535**, 0.550**; 0.415**, 0.518** and 0.143**, 0.143**), oleic/linoleic acid ratio (0.898**, 0.913**; 0.905**, 0.920**; 0.882**, 0.896** and 0.910**, 0.928**), total unsaturated fatty acid (0.774**, 0.778**; 0.842**, 0.849**; 0.663**, 0.666** and 0.653**, 0.653**), unsaturated/saturated fatty acid ratio (0.914**, 0.915**; 0.932**, 0.934**; 0.868**, 0.870** and 0.919**, 0.921**) and calculated iodine value (0.989**, 0.990**; 0.995**, 0.995; 0.943**, 0.942** and 0.990**, 0.991**) while significant negative correlation with palmitic acid (-0.869**, -0.871**; -0.904**, -0.907**; -0.697**, -0.696** and -0.935**, -0.940**) linoleic acid (-0.963**, -0.964**; -0.982**, -0.983**; -0.843**, -0.842** and -0.977**, -0.977**), behenic acid (-0.521**, -0.522**; -0.523**, -0.528**; -0.237**, -0.236** and -0.383**, -0.383**), total saturated fatty acid (-0.806**, -0.807**; -0.831**, -0.832**; -0.576**, -0.574** and -0.898**,

Table 42: Estimates of phenotypic and genotypic correlation coefficients for oil quality traits in WW block during the two seasons of summer 2012-13 and summer 2013-14

Characters		TOC	TPC	PAL	STE	LIN	ARA	ECO	BEH	LIG	O/L ratio	USFA	SFA	L/S ratio	U/S ratio	CIV	OAD	OLE
TOC	r_D	1	0.221	-0.078	-0.053	-0.109	-0.027	0.148	-0.005	0.217	0.078	0.094	-0.062	-0.107	0.083	-0.098	0.112	0.110
	r_g	1	0.223	-0.079	-0.054	-0.110	-0.024	0.150	-0.007	0.221	0.077	0.097	-0.061	-0.108	0.083	-0.099	0.113	0.111
TPC	r_D	-0.600	1	-0.323	-0.260	-0.358	0.024	0.433	-0.230	0.461	0.265	0.374	-0.303	-0.334	0.341	-0.292	0.373	0.379
	r_g	-0.670	1	-0.328	-0.271	-0.365	0.025	0.442	-0.238	0.474	0.274	0.385	-0.308	-0.341	0.348	-0.299	0.380	0.387
PAL	r_D	0.062	-0.018	1	0.303	0.901	-0.102	-0.434	0.291	-0.459	-0.847	-0.722	0.934	0.826	-0.938	0.830	-0.903	-0.904
	r_g	0.065	-0.016	1	0.318	0.905	-0.100	-0.444	0.294	-0.469	-0.865	-0.730	0.937	0.832	-0.942	0.838	-0.906	-0.907
STE	r_D	-0.424	0.583	0.290	1	0.235	0.441	-0.631	0.307	-0.522	-0.186	-0.345	0.574	0.101	-0.461	0.150	-0.259	-0.273
	r_g	-0.430	0.594	0.298	1	0.242	0.448	-0.642	0.317	-0.542	-0.182	-0.355	0.582	0.105	-0.467	0.155	-0.266	-0.279
LIN	r_D	-0.031	0.020	0.899	0.285	1	-0.088	-0.476	0.487	-0.514	-0.910	-0.725	0.815	0.981	-0.887	0.954	-0.995	-0.982
	r_g	-0.031	0.021	0.903	0.290	1	-0.087	-0.487	0.490	-0.529	-0.924	-0.739	0.817	0.981	-0.892	0.956	-0.995	-0.983
ARA	r_D	-0.434	0.556	0.067	0.781	0.113	1	-0.279	0.318	-0.089	0.095	-0.030	0.170	-0.162	-0.069	-0.124	0.071	0.065
	r_g	-0.437	0.563	0.072	0.789	0.118	1	-0.285	0.322	-0.096	0.098	-0.032	0.171	-0.161	-0.070	-0.124	0.070	0.063
ECO	r_D	0.248	-0.178	-0.376	-0.627	-0.445	-0.479	1	-0.215	0.884	0.361	0.398	-0.488	-0.427	0.461	-0.432	0.483	0.472
	r_g	0.251	-0.183	-0.383	-0.632	-0.454	-0.487	1	-0.230	0.890	0.379	0.408	-0.498	-0.438	0.472	-0.445	0.493	0.482
BEH	r_D	-0.459	0.630	0.274	0.759	0.428	0.727	-0.395	1	-0.129	-0.402	-0.518	0.390	0.468	-0.459	0.392	-0.513	-0.523
	r_g	-0.467	0.642	0.275	0.770	0.427	0.735	-0.407	1	-0.145	-0.415	-0.532	0.391	0.472	-0.465	0.394	-0.516	-0.528
LIG	r_D	0.304	-0.209	-0.398	-0.584	-0.481	-0.377	0.889	-0.380	1	0.401	0.511	-0.445	-0.478	0.493	-0.432	0.534	0.535
	r_g	0.309	-0.214	-0.405	-0.597	-0.495	-0.388	0.895	-0.395	1	0.425	0.526	-0.459	-0.493	0.508	-0.448	0.548	0.550
O/L ratio	r_D	0.083	-0.058	-0.835	-0.249	-0.903	-0.096	0.357	-0.368	0.396	1	0.700	-0.767	-0.912	0.864	-0.850	0.901	0.905
	r_g	0.083	-0.062	-0.853	-0.251	-0.918	-0.100	0.375	-0.376	0.419	1	0.721	-0.777	-0.925	0.875	-0.866	0.915	0.920
USFA	r_D	0.529	-0.307	-0.524	-0.508	-0.574	-0.375	0.479	-0.582	0.574	0.601	1	-0.708	-0.665	0.868	-0.485	0.787	0.842
	r_g	0.539	-0.314	-0.526	-0.517	-0.583	-0.383	0.489	-0.590	0.588	0.617	1	-0.715	-0.679	0.873	-0.508	0.797	0.849
SFA	r_D	-0.169	0.307	0.866	0.707	0.781	0.502	-0.510	0.614	-0.489	-0.724	-0.617	1	0.697	-0.949	0.726	-0.824	-0.831
	r_g	-0.169	0.313	0.966	0.713	0.782	0.507	-0.519	0.617	-0.501	-0.735	-0.622	1	0.701	-0.950	0.732	-0.826	-0.832
L/S ratio	r_D	0.041	-0.119	0.808	0.054	0.960	-0.078	-0.353	0.264	-0.394	-0.894	-0.477	0.589	1	-0.801	0.956	-0.969	-0.951
	r_g	0.043	-0.120	0.813	0.055	0.961	-0.076	-0.361	0.261	-0.406	-0.906	-0.486	0.591	1	-0.808	0.958	-0.970	-0.953
U/S ratio	r_D	0.298	-0.317	-0.850	-0.642	-0.835	-0.442	0.515	-0.646	0.556	0.822	0.813	-0.943	-0.683	1	-0.748	0.910	0.932
	r_g	0.301	-0.323	-0.851	-0.649	-0.839	-0.448	0.525	-0.651	0.570	0.832	0.815	-0.944	-0.687	1	-0.759	0.913	0.934
CIV	r_D	0.231	-0.132	0.814	0.086	0.910	-0.054	-0.292	0.218	-0.288	-0.780	-0.183	0.625	0.911	-0.591	1	-0.921	-0.880
	r_g	0.237	-0.134	0.822	0.087	0.911	-0.052	-0.301	0.216	-0.299	-0.794	-0.195	0.628	0.912	-0.598	1	-0.925	-0.886
OAD	r_D	0.111	-0.064	-0.890	-0.338	-0.991	-0.163	0.477	-0.481	0.527	0.897	0.677	-0.799	-0.938	0.878	-0.846	1	0.995
	r_g	0.112	-0.066	-0.892	-0.343	-0.991	-0.168	0.486	-0.481	0.540	0.913	0.683	-0.800	-0.938	0.880	-0.848	1	0.995
OLE	r_D	0.197	-0.116	-0.869	-0.383	-0.963	-0.207	0.493	-0.521	0.554	0.898	0.774	-0.806	-0.901	0.914	-0.764	0.989	1
	r_g	0.200	-0.118	-0.871	-0.389	-0.964	-0.212	0.502	-0.522	0.568	0.913	0.778	-0.807	-0.902	0.915	-0.768	0.990	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

Table 43: Estimates of phenotypic and genotypic correlation coefficients for oil quality traits in WS block during the two seasons of summer 2012-13 and summer 2013-14

Characters		TOC	TPC	PAL	STE	LIN	ARA	ECO	BEH	LIG	O/Lratio	USFA	SFA	L/Sratio	U/Sratio	CIV	OAD	OLE
TOC	r_p	1	0.122 ^{**}	0.160 ^{**}	-0.060	0.197 ^{**}	-0.144 ^{**}	-0.086 [*]	-0.022	0.060	-0.228 ^{**}	-0.135 ^{**}	0.133 ^{**}	0.217 ^{**}	-0.144 ^{**}	0.177 ^{**}	-0.198 ^{**}	-0.201 ^{**}
	r_g	1	0.149 ^{**}	0.176 ^{**}	-0.062	0.216 ^{**}	-0.158 ^{**}	-0.091 [*]	-0.019	0.065	-0.262 ^{**}	-0.146 ^{**}	0.148 ^{**}	0.238 ^{**}	-0.160 ^{**}	0.196 ^{**}	-0.218 ^{**}	-0.221 ^{**}
TPC	r_p	-0.654 ^{**}	1	0.043	-0.107 ^{**}	0.051	-0.116 ^{**}	0.127 ^{**}	0.092	0.212 ^{**}	-0.071	-0.119 ^{**}	0.019	0.060	-0.046	0.021	-0.060	-0.075
	r_g	-0.688 ^{**}	1	0.047	-0.112 [*]	0.055	-0.118 ^{**}	0.125 ^{**}	0.096	0.215 ^{**}	-0.077	-0.123 ^{**}	0.022	0.064	-0.049	0.024	-0.064	-0.079
PAL	r_p	0.199 ^{**}	-0.136 ^{**}	1	-0.158 ^{**}	0.924 ^{**}	-0.620 ^{**}	-0.105 ^{**}	0.258 ^{**}	-0.127 ^{**}	-0.840 ^{**}	-0.573 ^{**}	0.938 ^{**}	0.869 ^{**}	-0.924 ^{**}	0.850 ^{**}	-0.934 ^{**}	-0.935 ^{**}
	r_g	0.213 ^{**}	-0.142 ^{**}	1	-0.156 ^{**}	0.928 ^{**}	-0.624 ^{**}	-0.107 ^{**}	0.259 ^{**}	-0.130 ^{**}	-0.861 ^{**}	-0.576 ^{**}	0.938 ^{**}	0.876 ^{**}	-0.924 ^{**}	0.854 ^{**}	-0.938 ^{**}	-0.940 ^{**}
STE	r_p	-0.351 ^{**}	0.516 ^{**}	-0.201 ^{**}	1	-0.120 ^{**}	0.291 ^{**}	-0.370 ^{**}	0.163 ^{**}	-0.442 ^{**}	0.166 ^{**}	0.017	0.163 ^{**}	-0.213 ^{**}	-0.115 ^{**}	-0.128 ^{**}	0.116 ^{**}	0.112 ^{**}
	r_g	-0.363 ^{**}	0.539 ^{**}	-0.200 ^{**}	1	-0.121 ^{**}	0.291 ^{**}	-0.371 ^{**}	0.163 ^{**}	-0.443 ^{**}	0.168 ^{**}	0.017	0.166 ^{**}	-0.214 ^{**}	-0.117 ^{**}	-0.128 ^{**}	0.117 ^{**}	0.112 ^{**}
LIN	r_p	0.078	-0.091 [*]	0.907 ^{**}	-0.166 ^{**}	1	-0.484 ^{**}	-0.172 ^{**}	0.404 ^{**}	-0.132 ^{**}	-0.912 ^{**}	-0.477 ^{**}	0.882 ^{**}	0.985 ^{**}	-0.859 ^{**}	0.964 ^{**}	-0.997 ^{**}	-0.977 ^{**}
	r_g	0.089	-0.095 [*]	0.911 ^{**}	-0.167 ^{**}	1	-0.484 ^{**}	-0.172 ^{**}	0.404 ^{**}	-0.132 ^{**}	-0.930 ^{**}	-0.477 ^{**}	0.887 ^{**}	0.986 ^{**}	-0.861 ^{**}	0.964 ^{**}	-0.997 ^{**}	-0.977 ^{**}
ARA	r_p	-0.313 ^{**}	0.554 ^{**}	-0.493 ^{**}	0.621 ^{**}	-0.408 ^{**}	1	-0.258 ^{**}	0.032	-0.099	0.436 ^{**}	0.298 ^{**}	-0.465 ^{**}	-0.466 ^{**}	0.464 ^{**}	-0.446 ^{**}	0.491 ^{**}	0.493 ^{**}
	r_g	-0.328 ^{**}	0.580 ^{**}	-0.494 ^{**}	0.625 ^{**}	-0.407 ^{**}	1	-0.257 ^{**}	0.032	-0.098	0.446 ^{**}	0.298 ^{**}	-0.468 ^{**}	-0.466 ^{**}	0.466 ^{**}	-0.446 ^{**}	0.492 ^{**}	0.493 ^{**}
ECO	r_p	0.394 ^{**}	-0.210 ^{**}	0.010	-0.315 ^{**}	-0.155 ^{**}	-0.186 ^{**}	1	-0.015	0.695 ^{**}	0.091	0.002	-0.156 ^{**}	-0.157 ^{**}	0.107 ^{**}	-0.192 ^{**}	0.167 ^{**}	0.139 ^{**}
	r_g	0.410 ^{**}	-0.226 ^{**}	0.010	-0.315 ^{**}	-0.155 ^{**}	-0.185 ^{**}	1	-0.015	0.695 ^{**}	0.094	0.001	-0.158 ^{**}	-0.157 ^{**}	0.108 ^{**}	-0.192 ^{**}	0.167 ^{**}	0.138 ^{**}
BEH	r_p	-0.427 ^{**}	0.634 ^{**}	0.030	0.590 ^{**}	0.137 ^{**}	0.593 ^{**}	-0.191 ^{**}	1	0.207 ^{**}	-0.339 ^{**}	-0.140	0.364 ^{**}	0.387 ^{**}	-0.338 ^{**}	0.405 ^{**}	-0.398 ^{**}	-0.383 ^{**}
	r_g	-0.439 ^{**}	0.663 ^{**}	0.028	0.595 ^{**}	0.134 ^{**}	0.598 ^{**}	-0.192 ^{**}	1	0.207 ^{**}	-0.346 ^{**}	-0.140	0.365 ^{**}	0.388 ^{**}	-0.338 ^{**}	0.405 ^{**}	-0.398 ^{**}	-0.383 ^{**}
LIG	r_p	0.462 ^{**}	-0.224 ^{**}	-0.016	-0.403 ^{**}	-0.130 ^{**}	-0.140 ^{**}	0.808 ^{**}	-0.137 ^{**}	1	0.064	0.152 ^{**}	-0.179 ^{**}	-0.101	0.178 ^{**}	-0.101	0.142 ^{**}	0.143 ^{**}
	r_g	0.479 ^{**}	-0.240 ^{**}	-0.015	-0.404 ^{**}	-0.129 ^{**}	-0.141 ^{**}	0.809 ^{**}	-0.140 ^{**}	1	0.068	0.151 ^{**}	-0.183 ^{**}	-0.101	0.181 ^{**}	-0.101	0.142 ^{**}	0.143 ^{**}
O/L ratio	r_p	0.056	-0.017	-0.780 ^{**}	0.160 ^{**}	-0.904 ^{**}	0.349 ^{**}	0.207 ^{**}	-0.146 ^{**}	0.191 ^{**}	1	0.511 ^{**}	-0.791 ^{**}	-0.927 ^{**}	0.811 ^{**}	-0.856 ^{**}	0.911 ^{**}	0.910 ^{**}
	r_g	0.048	-0.017	-0.795 ^{**}	0.162 ^{**}	-0.917 ^{**}	0.354 ^{**}	0.216 ^{**}	-0.146 ^{**}	0.199 ^{**}	1	0.521 ^{**}	-0.812 ^{**}	-0.942 ^{**}	0.828 ^{**}	-0.872 ^{**}	0.929 ^{**}	0.928 ^{**}
USFA	r_p	0.720 ^{**}	-0.435 ^{**}	-0.016	-0.169 ^{**}	-0.157 ^{**}	-0.036	0.550 ^{**}	-0.246 ^{**}	0.592 ^{**}	0.361 ^{**}	1	-0.569 ^{**}	-0.430 ^{**}	0.742 ^{**}	-0.225 ^{**}	0.544 ^{**}	0.653 ^{**}
	r_g	0.741 ^{**}	-0.452 ^{**}	-0.012	-0.171 ^{**}	-0.156 ^{**}	-0.038	0.555 ^{**}	-0.247 ^{**}	0.596 ^{**}	0.369 ^{**}	1	-0.573 ^{**}	-0.430 ^{**}	0.743 ^{**}	-0.225 ^{**}	0.544 ^{**}	0.653 ^{**}
SFA	r_p	0.067	0.157 ^{**}	0.853 ^{**}	0.297 ^{**}	0.763 ^{**}	-0.072	-0.003	0.381 ^{**}	-0.059	-0.635 ^{**}	0.004	1	0.794 ^{**}	-0.970 ^{**}	0.805 ^{**}	-0.893 ^{**}	-0.898 ^{**}
	r_g	0.075	0.166 ^{**}	0.851 ^{**}	0.301 ^{**}	0.765 ^{**}	-0.068	-0.003	0.383 ^{**}	-0.059	-0.645 ^{**}	0.008	1	0.802 ^{**}	-0.971 ^{**}	0.809 ^{**}	-0.898 ^{**}	-0.902 ^{**}
L/S ratio	r_p	0.071	-0.162 ^{**}	0.818 ^{**}	-0.314 ^{**}	0.969 ^{**}	-0.480 ^{**}	-0.187 ^{**}	0.031	-0.139 ^{**}	-0.916 ^{**}	-0.211 ^{**}	0.586 ^{**}	1	-0.781 ^{**}	0.961 ^{**}	-0.977 ^{**}	-0.953 ^{**}
	r_g	0.082 ^{**}	-0.171 ^{**}	0.825 ^{**}	-0.317 ^{**}	0.970 ^{**}	-0.481 ^{**}	-0.188 ^{**}	0.027	-0.139 ^{**}	-0.928 ^{**}	-0.212 ^{**}	0.590 ^{**}	1	-0.784 ^{**}	0.962 ^{**}	-0.978 ^{**}	-0.954 ^{**}
U/S ratio	r_p	0.405 ^{**}	-0.393 ^{**}	-0.674 ^{**}	-0.328 ^{**}	-0.696 ^{**}	0.034	0.328 ^{**}	-0.451 ^{**}	0.409 ^{**}	0.739 ^{**}	0.624 ^{**}	-0.773 ^{**}	-0.599 ^{**}	1	-0.726 ^{**}	0.884 ^{**}	0.919 ^{**}
	r_g	0.416 ^{**}	-0.412 ^{**}	-0.669 ^{**}	-0.332 ^{**}	-0.697 ^{**}	0.030	0.334 ^{**}	-0.454 ^{**}	0.415 ^{**}	0.751 ^{**}	0.626 ^{**}	-0.770 ^{**}	-0.601 ^{**}	1	-0.728 ^{**}	0.887 ^{**}	0.921 ^{**}
CIV	r_p	0.523 ^{**}	-0.355 ^{**}	0.789 ^{**}	-0.252 ^{**}	0.783 ^{**}	-0.382 ^{**}	0.209 ^{**}	-0.035	0.259 ^{**}	-0.569 ^{**}	0.492 ^{**}	0.675 ^{**}	0.721 ^{**}	-0.220 ^{**}	1	-0.940 ^{**}	-0.885 ^{**}
	r_g	0.548 ^{**}	-0.370 ^{**}	0.793 ^{**}	-0.255 ^{**}	0.780 ^{**}	-0.382 ^{**}	0.215 ^{**}	-0.039	0.264 ^{**}	-0.572 ^{**}	0.497 ^{**}	0.678 ^{**}	0.717 ^{**}	-0.215 ^{**}	1	-0.940 ^{**}	-0.885 ^{**}
OAD	r_p	0.098 [*]	-0.016	-0.854 ^{**}	0.119 ^{**}	-0.972 ^{**}	0.379 ^{**}	0.274 ^{**}	-0.183 ^{**}	0.260 ^{**}	0.921 ^{**}	0.378 ^{**}	-0.712 ^{**}	-0.955 ^{**}	0.794 ^{**}	-0.618 ^{**}	1	0.990 ^{**}
	r_g	0.094 [*]	-0.017	-0.857 ^{**}	0.120 ^{**}	-0.971 ^{**}	0.378 ^{**}	0.276 ^{**}	-0.181 ^{**}	0.261 ^{**}	0.936 ^{**}	0.380 ^{**}	-0.713 ^{**}	-0.956 ^{**}	0.796 ^{**}	-0.613 ^{**}	1	0.991 ^{**}
OLE	r_p	0.332 ^{**}	-0.168 ^{**}	-0.697 ^{**}	0.036	-0.843 ^{**}	0.292 ^{**}	0.408 ^{**}	-0.237 ^{**}	0.415 ^{**}	0.882 ^{**}	0.663 ^{**}	-0.576 ^{**}	-0.849 ^{**}	0.868 ^{**}	-0.325 ^{**}	0.943 ^{**}	1
	r_g	0.338 ^{**}	-0.176 ^{**}	-0.696 ^{**}	0.036	-0.841 ^{**}	0.290 ^{**}	0.413 ^{**}	-0.236 ^{**}	0.418 ^{**}	0.896 ^{**}	0.666 ^{**}	-0.574 ^{**}	-0.849 ^{**}	0.870 ^{**}	-0.317 ^{**}	0.942 ^{**}	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

-0.902**), polyunsaturated/ saturated fatty acid ratio (-0.901**, -0.902**, -0.951**, -0.953**, -0.849**, -0.849** and -0.953**, -0.953**), and oleic acid desaturation ratio (-0.764**, -0.768**, -0.880**, -0.886**, -0.325**, -0.317** and -0.885**, -0.885**) in the WW condition of summer 2012-13, summer 2013-14 and in WS condition of summer 2012-13, summer 2013-14 respectively. In most of the above conditions among the two seasons oleic acid recorded significant positive correlation with arachidic acid and significant negative correlation with total protein content and stearic acid.

4.1.7.2 Correlations among other oil quality traits

Total Oil Content

In WW condition of consecutive seasons, total oleic acid recorded significant positive correlation with eicosenoic acid (0.248**, 0.257** and 0.148**, 0.150**), lignoceric acid (0.304**, 0.309** and 0.217**, 0.221**), oleic/linoleic acid ratio (0.083**, 0.529** and 0.078, 0.077), total unsaturated fatty acid (0.529**, 0.539** and 0.094, 0.097), unsaturated/saturated fatty acid ratio (0.298**, 0.301** and 0.083**, 0.083**) and oleic acid desaturation (0.111**, 0.112** and 0.112**, 0.113**), while oleic acid had contrast but significant associations during consecutive seasons with total protein content (-0.600**, -0.670** and 0.221**, 0.223**), palmitic acid (0.062, 0.06 and -0.078, -0.079*) and calculated iodine value (0.231**, 0.237** and -0.098*, -0.099*).

In the WS condition of summer 2012-13 and summer 2013-14, total oil content recorded significant positive correlation with palmitic acid (0.199**, 0.213** and 0.160**, 0.176**), linoleic acid (0.078, 0.089* and 0.197**, 0.216**), polyunsaturated/saturated fatty acid ratio (0.071, 0.082* and 0.217**, 0.238**) and calculated iodine value (0.523**, 0.548** and 0.177**, 0.196**) and significant negative correlation with arachidic acid (-0.313**, -0.328** and -0.144**, -0.158**) while total oil content had contrast but significant associations during respective seasons with total protein content (-0.654**, -0.688** and 0.122**, 0.149**), eicosenoic acid (0.394**, 0.410** and -0.086*, -0.091*), total unsaturated fatty acid (0.720**, 0.741** and -0.135**, -0.146**), and unsaturated/saturated fatty acid ratio (0.405**, 0.416** and -0.144**, -0.160**).

Total Protein Content

In WW condition of consecutive seasons, total protein content recorded contrast but significant associations with most of the traits except with polyunsaturated/saturated fatty acid ratio (-0.119**, -0.120** and -0.334**, -0.341**) and calculated iodine value (-0.132**, -0.134** and -0.292**, -0.299**).

In the WS condition of summer 2012-13, summer 2013-14, total protein content recorded contrast but significant associations with most of the traits except with behenic acid (0.634**, 0.663** and 0.092*, 0.096*) and total unsaturated fatty acid (-0.435**, -0.452** and -0.119**, -0.123**).

Palmitic acid

In WW condition during both the seasons, palmitic acid had significant positive correlation with stearic acid (0.290**, 0.298** and 0.303**, 0.318**), linoleic acid (0.899**, 0.903** and 0.901**, 0.905**), behenic acid (0.274**, 0.275** and 0.291**, 0.294**), total saturated fatty acid (0.866**, 0.966** and 0.934**, 0.937**), polyunsaturated to saturated fatty acid ratio (0.808**, 0.813** and 0.826**, 0.832**) and iodine value (0.814**, 0.822** and 0.830**, 0.838**) while it had significant negative correlation with eicosenoic (-0.376**, -0.383** and -0.434**, -0.444**), lignoceric acid (-0.398**, -0.405** and -0.459**, -0.469**), oleic acid to linoleic acid ratio (-0.835**, -0.853** and -0.847**, -0.865**), total unsaturated fattyacid (-0.524**, -0.526** and -0.722**, -0.730**), unsaturated to saturated fatty acid ratio (-0.850**, -0.851** and -0.938**, -0.942**) and oleic acid desaturation ratio (-0.890**, -0.892** and -0.903**, -0.906**).

In WS condition during both the seasons, palmitic acid had significant positive correlation with total oil content (0.199**, 0.213** and 0.160**, 0.176**), linoleic acid (0.907**, 0.911** and 0.924**, 0.928**), behenic acid (0.030, 0.028 and 0.258**, 0.259**), total saturated fatty acid (0.853**, 0.851** and 0.938**, 0.938**), polyunsaturated to saturated fatty acid ratio (0.818**, 0.825** and 0.869**, 0.876**) and iodine value (0.789**, 0.793** and 0.850**, 0.854**) while it had significant negative correlation with stearic acid (-0.201**, -0.200** and -0.158**, -0.156**), arachidic acid (-0.493**, -0.494** and -0.620**, -0.624**), lignoceric acid (-0.016,

-0.015 and -0.127**, -0.130**), oleic acid to linoleic acid ratio (-0.780**, -0.795** and -0.840**, -0.861**), total unsaturated fatty acid (-0.016, -0.012 and -0.573**, -0.576**), unsaturated to saturated fatty acid ratio (-0.674**, -0.669** and -0.924**, -0.924**) and oleic acid desaturation ratio (-0.854**, -0.859** and -0.934**, -0.938**).

Stearic acid

In WW condition during both the seasons, stearic acid had significant positive correlation with palmitic acid (0.290**, 0.298** and 0.303**, 0.318**), linoleic acid (0.285**, 0.290** and 0.235**, 0.242**), arachidic acid (0.781**, 0.789** and 0.441**, 0.448**), behenic acid (0.759**, 0.770** and 0.307**, 0.317**), total saturated fatty acid (0.707**, 0.713** and 0.574**, 0.582**), and iodine value (0.086**, 0.087** and 0.150**, 0.155**) while it had significant negative correlation with eicosenoic (-0.627**, -0.632** and -0.631**, -0.642**), lignoceric acid (-0.584**, -0.597** and -0.522**, -0.542**), oleic acid to linoleic acid ratio (-0.249**, -0.251** and -0.186**, -0.182**), total unsaturated fatty acid (-0.508**, -0.517** and -0.345**, -0.355**), unsaturated to saturated fatty acid ratio (-0.642**, -0.649** and -0.461**, -0.467**) and oleic acid desaturation ratio (-0.338**, -0.343** and -0.259**, -0.266**).

In WS condition during both the seasons, stearic acid had significant negative correlation with most of the traits except arachidic acid (0.621**, 0.625** and 0.291**, 0.291**), behenic acid (0.590**, 0.595** and 0.163**, 0.163**), oleic acid to linoleic acid ratio (0.160**, 0.162** and 0.166**, 0.168**), total saturated fatty acid (0.297**, 0.301** and 0.163**, 0.166**) and oleic acid desaturation ratio (0.119**, 0.120** and 0.116**, 0.117**).

Linoleic acid

In WW condition during both the seasons, linoleic acid had significant positive correlation with palmitic acid (0.899**, 0.903** and 0.901**, 0.905**), stearic acid (0.285**, 0.290** and 0.235**, 0.242**), behenic acid (0.428**, 0.427** and 0.487**, 0.490**), total saturated fatty acid (0.781**, 0.782** and 0.815**, 0.717**), polyunsaturated to saturated fatty acid ratio (0.960**, 0.961** and 0.981**, 0.981**) and iodine value (0.910**, 0.911** to 0.954**, 0.956**) while it had significant

negative correlation with eicosenoic (-0.445**, -0.454** and -0.476**, -0.487**), lignoceric acid (-0.481**, -0.495** and -0.514**, 0.529**), oleic acid to linoleic acid ratio (-0.903**, -0.918** and -0.910**, -0.924**), total unsaturated fatty acid (-0.574**, -0.583** and -0.725**, -0.739**), unsaturated to saturated fatty acid ratio (-0.835**, -0.839** and -0.887**, -0.892**) and oleic acid desaturation ratio (-0.991**, -0.991** and -0.995**, -0.995**).

In WS condition during both the seasons, linoleic acid had significant positive correlation with most of the traits except for the traits viz., total oil content (0.078, 0.089* and 0.197**, 0.216**), behenoic acid (0.137**, 0.134** and 0.404**, 0.404**), total saturated fatty acid (0.763**, 0.765** and 0.882**, 0.887**), polyunsaturated to saturated fatty acid ratio (0.969**, 0.970** and 0.985**, 0.986**) and iodine value (0.783**, 0.780** and 0.964**, 0.964**) for which significant and positive correlations were recorded during both seasons.

Arachidic acid

In WW condition of consecutive seasons, arachidic acid recorded significant negative association with most of the traits except with stearic acid (0.781**, 0.789** and 0.441**, 0.448**), behenoic acid (0.727**, 0.735** and 0.318**, 0.322**) and total saturated fatty acid (0.502**, 0.507** and 0.170**, 0.171**).

In the WS condition of summer 2012-13, summer 2013-14, arachidic acid recorded significant negative association with most of the traits except with stearic acid (0.621**, 0.625** and 0.291**, 0.291**), behenoic acid (0.593**, 0.598** and 0.032, 0.032), oleic acid to linoleic acid ratio (0.349**, 0.354** and 0.436**, 0.436**) and oleic acid desaturation ratio (0.379**, 0.378** and 0.491**, 0.492**).

Eicosenoic acid

In both the water regimes during both the seasons, eicosenoic acid recorded significant negative association with most of the traits except with lignoceric acid (0.889**, 0.895**; 0.884**, 0.890**; 0.808**, 0.809** and 0.695**, 0.695**), oleic/linoleic acid ratio (0.357**, 0.375**; 0.361**, 0.379**; 0.207**, 0.216** and 0.091*, 0.094*), total unsaturated fatty acid (0.479**, 0.489**; 0.398**, 0.408**; 0.550**, 0.555** and 0.002, 0.001), unsaturated/saturated fatty acid ratio (0.515**,

0.525**, 0.461**, 0.472**, 0.328**, 0.334** and 0.107**, 0.108**), oleic acid desaturation ratio (0.477**, 0.486**, 0.483**, 0.493**, 0.274**, 0.276** and 0.167**, 0.167**).

Behenoic acid

Behenoic acid recorded significant negative association with most of the traits except with total protein content (0.630**, 0.642**, -0.230**, -0.238**, 0.634**, 0.663** and 0.092*, 0.096*), palmitic acid (0.274**, 0.275**, 0.291**, 0.294**, 0.030, 0.028 and 0.258**, 0.259**), stearic acid (0.759**, 0.770**, 0.307**, 0.317**, 0.590**, 0.595** and 0.163**, 0.163**), linoleic acid (0.428**, 0.427**, 0.487**, 0.490**, 0.137**, 0.134** and 0.404**, 0.404**), arachidic acid (0.727**, 0.735**, 0.318**, 0.322**, 0.593**, 0.598** and 0.032, 0.032), total saturated fatty acid (0.614*, 0.617**, 0.390**, 0.391**, 0.381**, 0.383** and 0.364**, 0.365**), polyunsaturated/saturated fatty acid ratio (0.264**, 0.261**, 0.468**, 0.472**, 0.031, 0.027 and 0.387**, 0.388**), calculated iodine value (0.218**, 0.216**, 0.392**, 0.394**, -0.035, -0.039 and 0.405**, 0.405**) in both the water regimes during both the seasons.

Lignoceric acid

Lignoceric acid recorded significant negative association with most of the traits except with total oil content (0.304**, 0.309**, 0.217**, 0.221**, -0.427**, -0.479** and 0.060, 0.065), eicosenoic acid (0.889**, 0.895**, 0.884**, 0.890**, 0.808**, 0.809** and 0.695**, 0.695**), oleic to linoleic ratio (0.396**, 0.419**, 0.401**, 0.425**, 0.191**, 0.199** and 0.064, 0.068), total unsaturated fatty acid (0.574**, 0.588**, 0.511**, 0.526**, 0.592**, 0.596** and 0.152**, 0.151**), unsaturated/saturated fatty acid ratio (0.556**, 0.570**, 0.493**, 0.508**, 0.409**, 0.415** and 0.178**, 0.181**) and oleic acid desaturation ratio (0.527**, 0.540**, 0.534**, 0.548**, 0.260**, 0.261** and 0.142**, 0.142**) in both the water regimes during both the seasons

Oleic acid to linoleic acid ratio

Oleic acid to linoleic acid ratio recorded significant negative association with most of the traits except with the traits viz., total oil content (0.083*, 0.083*, 0.078,

0.077; 0.056, 0.048 and -0.228**, -0.026), eicosenoic acid (0.357**, 0.375**; 0.361**, 0.379**;
0.207**, 0.216** and 0.091*, 0.094*), lignoceric acid (0.396*, 0.419**; 0.401**, 0.425**;
0.191**, 0.199** and 0.064, 0.068), total unsaturated fatty acid (0.601**, 0.617**; 0.700**,
0.721, 0.361**, 0.369** and 0.511**, 0.521**), unsaturated/saturated fatty acid ratio (0.822**,
0.832**; 0.864**, 0.875**, 0.739**, 0.751** and 0.811**, 0.828**) and oleic acid desaturation
ratio (0.897**, 0.913**; 0.901**, 0.915**; 0.921**, 0.936** and 0.911**, 0.929**) for which
positive correlations were recorded in most of the conditions during both the seasons.

Total unsaturated fatty acid

Total saturated fatty acid recorded significant negative association with most of the
traits except with the traits viz., total oil content (0.529**, 0.539**; 0.094*, 0.097*; 0.720**,
0.741** and -0.135**, -0.146**), eicosenoic acid (0.479**, 0.489**; 0.398**, 0.408**; 0.550**,
0.555** and 0.002, 0.001), lignoceric acid (0.574**, 0.588**; 0.511**, 0.526**; 0.592**, 0.596**
and 0.152**, 0.152**), oleic to linoleic ratio (0.601**, 0.617**; 0.700**, 0.721**; 0.361**,
0.369** and 0.511**, 0.521**), unsaturated/saturated fatty acid ratio (0.813**, 0.815**;
0.868**, 0.873**; 0.624**, 0.626** and 0.742**, 0.743**) and oleic acid desaturation ratio
(0.677**, 0.683**; 0.787**, 0.797**; 0.378**, 0.380** and 0.544**, 0.544**) for which positive
correlations were recorded in most of the conditions during both the seasons.

Total saturated fatty acid

In contrast to the association had by total unsaturated fatty acid, total saturated fatty
acid recorded significant positive association with most of the traits except with the traits viz.,
total oil content (-0.169**, -0.169**; -0.062, -0.062; 0.067, 0.075 and 0.133**, 0.148**),
eicosenoic acid (-0.510**, -0.0519**; -0.488**, -0.498**; -0.003, -0.003 and -0.156**, -0.158**),
lignoceric acid (-0.489**, -0.501**; -0.445**, -0.459**; -0.059, -0.059 and -0.179**, -0.183**),
oleic to linoleic ratio (-0.724**, -0.734**; -0.767**, -0.777**; -0.635**, -0.645** and -0.791**, -
0.812**), total saturated fatty acid (-0.617**, -0.622**; -0.708**, 0.715**; 0.004, 0.008 and -
0.569**, -0.573**), unsaturated/saturated fatty acid ratio (-0.943**, - 0.944**; -0.949**,
-0.950**; -0.773**, -0.770** and -0.970**, -0.971**) and oleic acid desaturation ratio (-0.799**,
-0.800; -0.824**, -0.826**; -0.712**, -0.713** and -0.893**, -0.898**) for

which negative correlations were recorded in most of the conditions during both the seasons.

Polyunsaturated to saturated fatty acid ratio

Polyunsaturated to saturated fatty acid ratio recorded significant negative association with most of the traits except with the traits *viz.*, palmitic acid (0.808**, 0.813**, 0.826**, 0.832**, 0.818**, 0.825** and 0.869**, 0.876**), linoleic acid (0.960**, 0.961**, 0.981**, 0.981**, 0.969**, 0.970** and 0.985**, 0.986**), behenic acid (0.264**, 0.261**, 0.468**, 0.472**, 0.031, 0.027 and 0.387**, 0.388**), total saturated fatty acid (0.589**, 0.591**, 0.697**, 0.701**, 0.586**, 0.590** and 0.794**, 0.802**), calculated iodine value (0.911**, 0.912**, 0.956**, 0.958**, 0.721**, 0.717** and 0.961**, 0.962**) for which positive correlations were recorded in most of the conditions during both the seasons.

Unsaturated to saturated fatty acid ratio

Unsaturated to saturated fatty acid ratio recorded significant negative association with most of the traits except with the traits *viz.*, total oil content (0.298**, 0.301**, 0.083*, 0.083*, 0.405**, 0.416** and -0.144**, -0.160**), eicosenoic acid (0.515**, .0525**, 0.461**, 0.467**, 0.328**, 0.334** and 0.107**, 0.108**), lignoceric acid (0.556**, 0.570**, 0.493**, 0.508**, 0.409**, 0.415** and 0.178**, 0.181**), oleic/linoleic acid ratio (0.822**, 0.832**, 0.864**, 0.875**, 0.739**, 0.751** and 0.811**, 0.828**), total unsaturated fatty acid (0.813**, 0.815**, 0.868**, 0.873**, 0.624**, 0.626** and 0.742**, 0.743**) and oleic acid desaturation ratio (0.878**, 0.880**, 0.910**, 0.913**, 0.794**, 0.796** and 0.884**, 0.887**) for which positive correlations were recorded in most of the conditions during both the seasons.

Calculated iodine value

Iodine value recorded significant negative association with most of the traits except with the traits *viz.*, total oil content (0.231**, 0.237**, -0.098*, -0.099*, 0.523**, 0.548** and 0.177**, 0.196**), palmitic acid (0.814**, 0.822**, 0.830**, 0.838**, 0.789**, 0.783** and 0.850**, 0.854**), stearic acid (0.086*, 0.087*,

0.150**, 0.155**, -0.252**, -0.255** and -0.128**, -0.128**), linoleic acid (0.910**, 0.911**, 0.954**, 0.956**, 0.783**, 0.780** and 0.964**, 0.964**), behenic acid (0.218**, 0.216**, 0.392**, 0.394**, -0.035, -0.039 and 0.405**, 0.405**), total saturated fatty acid (0.625**, 0.628**, 0.726**, 0.732**, 0.675**, 0.678** and 0.805**, 0.809**) and polyunsaturated/saturated fatty acid ratio (0.911**, 0.912**, 0.956**, 0.958**, 0.721**, 0.717** and 0.961**, 0.962**) for which positive correlations were recorded in most of the conditions during both the seasons.

Oleic acid desaturation ratio

Oleic acid desaturation ratio recorded significant negative association with most of the traits except with the traits *viz.*, total oil content (0.111**, 0.112**, 0.112**, 0.113**, 0.098*, 0.094* and -0.198**, -0.218**), eicosenoic acid (0.477**, 0.486**, 0.483**, 0.493**, 0.274**, 0.276** and 0.167**, 0.167**), lignoceric acid (0.527**, 0.540**, 0.534**, 0.548**, 0.260**, 0.261** and 0.142**, 0.142**), oleic/linoleic acid ratio (0.897**, 0.913**, 0.901**, 0.915**, 0.921**, 0.936** and 0.911**, 0.929**), total unsaturated fatty acid (0.677**, 0.683**, 0.787**, 0.797**, 0.378**, 0.380** and 0.544**, 0.544**) and unsaturated/saturated fatty acid ratio (0.878**, 0.880**, 0.910**, 0.913**, 0.794**, 0.796** and 0.884**, 0.887**) for which positive correlations were recorded in most of the conditions during both the seasons.

4.1.8 Correlation analysis for foliar disease resistance traits

Phenotypic and genotypic correlations of different foliar disease resistance traits with pod yield WW and WS conditions along with their interrelationships under were determined and are presented in Table 44 and 45.

4.1.8.1 Correlation of foliar disease resistance traits with pod yield

Pod yield under WW and WS conditions during the consecutive seasons of summer 2012-13 and summer 2013-14 recorded significant negative correlations with late leaf spot score at 70 DAS (-0.036, -0.051; -0.093*, -0.127**, -0.252**, -0.119** and -0.288**, -0.364**), late leaf spot score at 80 DAS (-0.057, -0.062; -0.155**, -0.146**, -0.235**, -0.244** and -0.361**, -0.465**), late leaf spot score at 90 DAS

Table 44: Estimates of phenotypic and genotypic correlation coefficients for foliar disease resistance traits in WW block during the two seasons of summer 2012-13 and summer 2013-14

		LLS70DAS	LLS80DAS	LLS90DAS	RUST70DAS	RUST80DAS	RUST90DAS	PYP WW
LLS70DAS	r_p	1	0.849**	0.935**	0.932**	0.760**	0.900**	-0.252**
	r_g	1	0.837**	0.853**	0.924**	0.755**	0.820**	-0.119**
LLS80DAS	r_p	0.607**	1	0.873**	0.830**	0.958**	0.886**	-0.235**
	r_g	0.872**	1	0.903**	0.803**	0.975**	0.906**	-0.244**
LLS90DAS	r_p	0.665**	0.719**	1	0.852**	0.788**	0.975**	-0.313**
	r_g	0.848**	0.917**	1	0.914**	0.881**	0.998**	-0.314**
RUST70DAS	r_p	0.622**	0.715**	0.858**	1	0.713**	0.818**	-0.190**
	r_g	0.926**	0.841**	0.916**	1	0.733**	0.885	-0.207**
RUST80DAS	r_p	0.574**	0.865**	0.735**	0.705**	1	0.824**	-0.220**
	r_g	0.718**	0.916**	0.861**	0.748**	1	0.872**	-0.232**
RUST90DAS	r_p	0.658**	0.777**	0.908**	0.797**	0.817**	1	-0.319**
	r_g	0.763**	0.906*	0.988**	0.882**	0.859**	1	-0.337**
PYP WW	r_p	-0.036	-0.057	-0.109**	-0.041	-0.058	-0.104**	1
	r_g	-0.051	-0.062	-0.110**	-0.062	-0.072	-0.171**	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

Table 45: Estimates of phenotypic and genotypic correlation coefficients for foliar disease resistance traits in WS block during the two seasons of summer 2012-13 and summer 2013-14

		LLS70DAS	LLS80DAS	LLS90DAS	RUST70DAS	RUST80DAS	RUST90DAS	PYP WS
LLS70DAS	r_p	1	0.885**	0.871**	0.982**	0.798**	0.864**	-0.288**
	r_g	1	0.984**	0.929**	0.934**	0.886**	0.879**	-0.364**
LLS80DAS	r_p	0.710**	1	0.916**	0.850**	0.956**	0.928**	-0.361**
	r_g	0.800**	1	0.944**	0.938**	0.987**	0.920**	-0.465**
LLS90DAS	r_p	0.696**	0.859**	1	0.824**	0.848**	0.988**	-0.298**
	r_g	0.728**	0.994**	1	0.991**	0.940**	0.999**	-0.367**
RUST70DAS	r_p	0.720**	0.776**	0.757**	1	0.774**	0.812**	-0.255**
	r_g	0.863**	0.740**	0.719**	1	0.961**	0.991**	-0.378**
RUST80DAS	r_p	0.727**	0.898**	0.844**	0.808**	1	0.867**	-0.329**
	r_g	0.759**	0.982**	0.889**	0.666**	1	0.907**	-0.414**
RUST90DAS	r_p	0.718**	0.882**	0.982**	0.806**	0.877**	1	-0.328**
	r_g	0.684**	0.976**	0.986**	0.697**	0.819**	1	-0.364**
PYP WS	r_p	-0.093*	-0.155**	-0.108**	-0.068	-0.190**	-0.177**	1
	r_g	-0.127**	-0.146**	-0.181**	-0.099*	-0.185**	-0.123**	1

Below the diagonal - summer 2012-13; Above the diagonal - summer 2013-14

(-0.109**, -0.110**, -0.108**, -0.181**, -0.313**, -0.314** and -0.298**, -0.367**), rust score at 70 DAS (-0.041, -0.062; -0.068, 0.099*, -0.190**, -0.207** and -0.255**, -0.378**), rust score at 80 DAS (-0.058, -0.072 ; -0.190**, -0.185**, -0.220**, -0.232** and -0.329**, -0.414**), rust score at 90 DAS (-0.104**, -0.171**, -0.177**, -0.123**, -0.319**, -0.337** and -0.328**, -0.364**). Pod yield under WW and WS (0.197** and 0.298**) conditions had significant positive association among them during both the seasons

4.1.8.2 Interrelations among foliar disease resistance traits

Highly significant and positive correlations were recorded among late leaf spot score and rust scores at different stages. The range of correlations varied from 0.574 to 0.988, where the highest significant and positive correlations was recorded between late leaf spot score at 90 DAS and rust score at 90 DAS in both water regimes during the two consecutive seasons.

4.2 Phenotyping for root traits in RILs of TMV-2 x GM 6-1 during summer 2012-13 and summer 2013-14

4.2.1 Variability for root traits

4.2.1.1 Analysis of variance (ANOVA)

Analysis of variance of root traits for individual seasons of summer 2012-13 and 2013-14 was indicated in Table 46 and 47. During summer 2012-13 all the genotypes included in the study differed significantly for all traits studied in each season. Effects of entries, checks, varieties and the interaction effect checks * varieties were significant for most of the traits studied under both well watered and water stress conditions.

During summer 2013-14, all genotypes included in the study differed for all traits in each season. Irrigation level (well watered and water stress conditions) and Genotypes * irrigation level had significant effect on all the traits studied.

Table 46: Analysis of variance for root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Source of variation	Root length (WW)	Root length (WS)	Shoot length (WW)	Shoot length (WS)	Root/shoot ratio (WW)	Root/shoot ratio (WS)	Root dry weight (WW)	Root dry weight (WS)	Shoot dry weight (WW)	Shoot dry weight (WS)
Blocks	62.23**	49.10	1.31**	0.28	5.92**	16.25**	0.01	0.02	0.85	16.10**
Entries	93.44**	87.24**	8.19**	2.65**	5.03**	7.22**	0.01**	0.03**	1.48**	2.17**
Checks	76.20**	61.91**	7.56**	2.86**	6.09**	5.56**	0.01**	0.03**	0.86**	5.88**
Varieties	92.29**	84.57**	8.06**	2.63**	5.01**	7.08**	0.01**	0.02**	1.45**	2.08**
Checks * varieties	664.38**	1218.34**	55.26**	4.75**	9.32**	70.59**	0.06**	0.03**	17.30**	1.23**
Error	16.05	13.23	1.89	0.72	1.50	0.67	0.00	0.01	0.28	0.49
General mean	28.31	26.91	8.48	4.48	3.81	6.43	0.29	0.36	4.19	2.21
S.Ed	2.83	0.05	0.97	0.60	0.87	0.58	0.04	0.05	0.38	0.39
CD 5%	6.12	0.12	2.10	1.30	1.87	1.25	0.09	0.12	0.82	0.84
C.V %	10.00	14.68	11.46	13.37	22.70	8.99	14.02	14.68	9.05	19.21

** Significance at 1%, * Significance at 5%

Table 47: Analysis of variance for root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Source of Variation	df	Root Length	Shoot Length	Root/Shoot ratio	No of Nodules per Plant	Root Dry Weight	Shoot Dry Weight
Replication	1	20.15	17.46	0.24	3.11	0.01	4.2
Genotypes	308	185.06**	70.13**	1.80**	319.22**	0.11**	66.15**
Irrigation Level	1	58259.55**	12822.94**	566.50**	15267.26**	2.59**	1896.9**
Genotypes * Irrigation Level	308	153.77**	21.23**	0.95**	351.56**	0.02**	8.03**
Error	617	31.28	9.5	0.2	20.83	0.01	1.34
Total	1235	147.32	37.93	1.24	190.06	0.04	20.71
General Mean		48.87	23.11	2.35	35.42	0.45	10.18
S.Em		2.796	1.541	0.223	2.282	0.036	0.578
CD 5%		7.77	4.28	0.62	6.34	0.1	1.61
C.V %		11.45	13.34	18.98	12.89	16.05	11.36

** Significance at 1%, * Significance at 5%

4.2.1.2 Mean, range and components of variation

Mean and range of root traits for WW and WS conditions during the two seasons of summer 2012-13 and summer 2013-14 are presented in the Table 48. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean are presented in the Table 49.

Moderate to high PCV, GCV and high heritability coupled with high GAM was recorded by most of the root traits in both the irrigation levels of summer 2012-13 and summer 2013-14.

Root length ranged from 3.00 to 65.00 in WW condition and from 4.00 to 57.60 in WS condition during summer 2012-13, with mean of 28.31 cm and 26.91 cm in respective irrigation level. During summer 2013-14, it ranged from 15.00 to 82.00 in WW condition and from 20.50 to 89.00 was shown in WS condition with mean of 42.07 cm and 55.73 cm respectively.

During summer 2012-13, shoot length recorded narrow range in both WW (2.00-16.20) and WS (1.00-13.40) treatments compared wide range recorded during summer 2013-14 in WW (10.00-50.00) and WS (7.50-13.40) conditions respectively. Mean of shoot length was also higher in the summer 2013-14 in both WW (26.33 cm) and WS (19.89 cm) conditions compared to summer 2012-13 in the individual irrigation levels (8.48 cm and 4.48 cm) respectively.

Root/Shoot ratio ranged from 0.30 to 17.00 in WW condition and from 0.90-28.18 in WS condition with mean root to shoot ratio of 3.81 and 6.43 in respective irrigation levels of summer 2012-13. During summer 2013-14, in WW condition root to shoot ratio ranged from 0.00 to 4.60 and mean of 1.67 was recorded, while in WS condition it ranged from 0.98 to 9.09 and mean of 3.03 was recorded.

During summer 2012-13, shoot dry weight recorded narrow range in both WW (1.10-9.70) and WS (0.41-6.70) treatments with mean of 4.19 gm and 2.21 gm respectively, compared to wide range in WW (2.91-31.96) and WS (1.94-25.44) conditions during summer 2013-14 with mean of 11.42 gm and 8.94 gm, respectively.

Table 48: Mean, range and genetic parameters of root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2012-13 at MARS, Dharwad

Character	Mean	Range			GCV	PCV	h^2_{bs} (%)	GA	GAM
Root Length (WW)	28.31	3.00	-	65.00	21.97	26.13	70.69	10.77	38.05
Root Length (WS)	26.91	4.00	-	57.60	22.61	26.34	73.66	10.76	39.97
Shoot Length (WW)	8.48	2.00	-	16.20	20.93	26.47	62.54	2.89	34.10
Shoot Length (WS)	4.48	1.00	-	13.40	21.90	28.93	57.28	1.53	34.14
Root/Shoot ratio (WW)	3.81	0.30	-	17.00	34.85	47.38	54.10	2.01	52.80
Root/Shoot ratio (WS)	6.43	0.90	-	28.18	28.15	30.88	83.05	3.40	52.84
Root dry weight (WW)	0.29	0.00	-	0.70	20.49	28.51	51.65	0.09	30.33
Root dry weight (WS)	0.36	0.06	-	0.93	27.17	34.20	63.14	0.16	44.48
Shoot dry weight (WW)	4.19	1.10	-	9.70	18.55	22.45	68.30	1.32	31.58
Shoot dry weight (WS)	2.21	0.41	-	6.50	33.47	44.68	63.01	1.49	58.00

Table 49: Mean, range and genetic parameters root traits in groundnut RILs of TMV-2 x GM 6-1 cross evaluation during summer 2013-14 at MARS, Dharwad

Character	Mean of WW	Mean of WS	Range in WW treatment	Range in WS treatment	PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GAM
Root Length	42.07	55.73	15.00 - 82.00	20.50 - 89.00	22.63	19.52	74.42	16.95	34.69
Shoot Length	26.33	19.89	10.00 - 50.00	7.50 - 34.00	22.99	18.73	66.35	7.26	31.42
Root/Shoot ratio	1.67	3.03	0.00 - 4.60	0.98 - 9.09	47.29	43.32	83.89	1.92	81.73
Root Dry Weight	0.40	0.49	0.00 - 2.27	0.16 - 3.16	50.21	47.57	89.78	0.42	92.86
Shoot Dry Weight	11.42	8.94	2.91 - 31.16	1.94 - 25.44	40.46	38.83	92.12	7.82	76.78

Root dry weight ranged from 0.00 to 0.70 in WW condition and from 0.06 to 0.93 in WS condition with mean of 0.29 gm and 0.36 gm in respective irrigation levels of summer 2012-13. During summer 2013-14, in WW condition it ranged from 0.00 to 2.27 with mean of 0.40 gm and from 0.16 to 3.16 in WS condition with mean of 0.49 gm.

4.2.2 Correlation analysis of root traits under WS condition

The associations of root length with pod yield, physiological traits and other root traits along with their interrelationships under WS condition during the two seasons of summer 2012-13, summer 2013-14 and pooled across the two seasons have been determined and presented in Table 50, 51 and 52.

4.2.2.1 Correlation between root length, pod yield, physiological traits and other root traits under WS condition

Root length under WS condition showed significant positive correlation with drought tolerant index (0.337**, 0.074 and 0.192**), pod yield per plant (0.300**, 0.118** and 0.229**), root to shoot ratio (0.448**, 0.597** and 0.245**), number of nodules per plant (0.231**, 0.323** and 0.245**), root dry weight (0.074, 0.279** and 0.105**), relative water content at 15 DAS (0.028, 0.001 and 0.091*), relative water content at 30 DAS (0.415**, 0.138** and 0.289**) and SPAD chlorophyll meter reading (0.350**, 0.037 and 0.177**) while it had significant negative association with per cent reduction in RWC from 7 to 15 DAS (-0.025, 0.016 and -0.179**), per cent reduction in RWC from 15 to 30 DAS (-0.401**, -0.114** and -0.189**), per cent reduction in RWC from 7 to 30 DAS (-0.399**, -0.116** and -0.264**) and specific leaf area at 30 DAS (-0.369**, -0.180** and -0.331**) during summer 2012-13, summer 2013-14 and pooled across the two seasons, respectively.

4.2.2.2 Interrelations among root traits

Shoot Length

Shoot length recorded significant positive correlation with root dry weight (0.221**, 0.205** and 0.216**) and shoot dry weight (0.221**, 0.205** and 0.216**) while significant negative correlation with root to shoot ratio (-0.829**, -0.543** and

Table 50: Estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block during the two seasons of summer 2012-13 and summer 2013-14

	DTI	PYP	SL	RVS	NNPP	RDW	SDW	RWCi	RWCII	RWCIII	PR RWC 1	PR RWC 2	PR RWC 3	SLAI	SLAII	SLAIII	SCMR	RL
DTI	1.000																	
PYP	0.620**	1.000																
SL	0.152**	0.188**	1.000															
RVS	0.229**	0.200**	-0.572**	1.000														
NNPP	0.124**	0.200**	0.243**	0.044	1.000													
RDW	-0.008	0.030	0.380**	-0.233**	0.221**	1.000												
SDW	0.020	0.007	0.153**	0.112**	0.050	0.166**	1.000											
RWCi	0.022	-0.047	-0.057	0.046	0.025	-0.058	-0.008	1.000										
RWCII	-0.004	-0.006	0.031	-0.038	0.024	0.006	-0.009	0.092*	1.000									
RWCIII	0.762**	0.631**	0.157**	0.302**	0.176**	-0.025	0.048	0.141**	0.230**	1.000								
PRRWC 1	0.021	-0.028	-0.090	0.082	-0.023	-0.089*	0.004	0.665**	-0.614	-0.064	1.000							
PRRWC 2	-0.789**	-0.685**	-0.166**	-0.305**	-0.173**	-0.008	-0.041	-0.099	0.140**	-0.912**	-0.178**	1.000						
PRRWC 3	-0.747**	-0.675**	-0.196**	-0.257**	-0.174**	-0.051	-0.036	0.226**	-0.171**	-0.912**	0.320**	0.874**	1.000					
SLAI	-0.039	-0.012	-0.014	-0.056**	0.003	-0.085*	-0.020	-0.035	0.091	-0.031	-0.078*	0.066	0.024	1.000				
SLAII	-0.363**	-0.353**	-0.132**	-0.192**	-0.095*	0.003	-0.085*	-0.007	0.006	-0.442**	-0.006	0.460**	0.437**	0.244**	1.000			
SLAIII	-0.802**	-0.719**	-0.164**	-0.260**	-0.154**	0.013	-0.060	-0.025	0.024	-0.845**	-0.048	0.890**	0.836**	0.072	0.455**	1.000		
SCMR	0.820**	0.664**	0.183**	0.253**	0.169**	0.027	0.066	0.026	0.044	0.809**	-0.020	-0.819**	-0.799**	-0.035	-0.374**	-0.812**	1.000	
RL	0.337**	0.300**	0.210**	0.448**	0.231**	0.074*	0.184**	-0.018	0.028	0.415**	-0.025	-0.401**	-0.399**	-0.012	-0.243**	-0.369**	0.350**	1.000

Table 51: Estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block during summer 2013-14

	DTI for pod yield	POD Y/ plant	SL	R/S	NNPP	RDW	SDW	RWC I	RWC II	RWC III	PR RWC 1	PR RWC 2	PR RWC 3	SLA I	SLA II	SLA III	SCMR	RL
DTI for pod yield	1.000																	
POD Y/ plant	0.491**	1.000																
SL	-0.121**	-0.467**	1.000															
R/S	0.162**	0.437**	-0.778**	1.000														
NNPP	0.068	-0.119**	0.028	0.160**	1.000													
RDW	0.175**	0.135**	-0.030	0.192**	0.119**	1.000												
SDW	-0.051	-0.209**	0.529**	-0.390**	-0.079*	0.010	1.000											
RWC I	-0.018	-0.058	-0.080*	0.105**	0.028	0.021	-0.065	1.000										
RWC II	-0.570**	-0.301**	0.144**	-0.125**	-0.074*	-0.117**	0.041	0.155**	1.000									
RWC III	0.562**	0.496**	-0.088*	0.163**	-0.006	0.080*	-0.059	0.074*	0.205**	1.000								
PR RWC 1	0.518**	0.245**	-0.171**	0.165**	0.081*	0.120**	0.070*	0.403**	-0.840**	-0.149**	1.000							
PR RWC 2	-0.914**	-0.637**	0.174**	-0.223**	-0.046	-0.157**	0.081*	0.034	0.512**	-0.731**	-0.455**	1.000						
PR RWC 3	-0.535**	-0.492**	0.053	-0.113**	0.014	-0.064	0.033	0.355**	-0.125**	-0.904*	0.311**	0.700**	1.000					
SLA I	-0.101**	-0.065	0.057	-0.016**	0.042	-0.045	0.038	-0.001	0.000	-0.125**	-0.004	0.111**	0.116**	1.000				
SLA II	-0.205**	-0.088*	0.122**	-0.112**	-0.046	-0.059	0.048	-0.066	-0.071	-0.332**	0.030	0.237**	0.285**	0.055	1.000			
SLA III	-0.411**	-0.440**	0.096*	-0.184**	-0.021	-0.086*	0.068	-0.019	-0.158**	-0.753**	0.135**	0.549**	0.697**	0.044	-0.025	1.000		
SPAD SCMR	0.295**	0.331**	-0.096*	0.098*	-0.087	0.024	-0.011	-0.046	0.091	0.543**	-0.112**	-0.409**	-0.531**	0.092*	-0.045	-0.472**	1.000	
RL	0.074*	0.118**	-0.073*	0.597**	0.323	0.279	0.014	0.035	0.001	0.138**	0.016	-0.114**	-0.116**	-0.005	0.008	-0.180**	0.037	1

Table 52: Pooled estimates of phenotypic correlation coefficients between pod yield, physiological traits and root traits in WS block over two seasons of summer 2012-13 and 2013-14

	<i>DTI for pod yield</i>	<i>POD Y/ plant</i>	<i>SL</i>	<i>R/S</i>	<i>NNPP</i>	<i>RDW</i>	<i>SDW</i>	<i>RWC I</i>	<i>RWC II</i>	<i>RWC III</i>	<i>PR RWC 1</i>	<i>PR RWC 2</i>	<i>PR RWC 3</i>	<i>SLA I</i>	<i>SLA II</i>	<i>SLA III</i>	<i>SPAD SCMR</i>	<i>RL</i>
DTI for pod yield	1.000																	
POD Y/ plant	0.507**	1.000																
SL	-0.001	-0.268**	1.000															
R/S	0.164**	0.246**	-0.465**	1.000														
NNPP	0.082*	0.002	0.013	0.093*	1.000													
RDW	-0.032	0.016	0.164**	-0.208**	0.122**	1.000												
SDW	-0.022	-0.174**	0.488**	-0.119**	-0.069	0.045	1.000											
RWC I	0.060	0.002	0.020	0.000	0.045	0.009	-0.013	1.000										
RWC II	-0.259**	-0.071*	0.149**	-0.065	-0.041	0.111**	0.038	0.115**	1.000									
RWC III	0.645**	0.532**	0.005	0.157**	0.075*	0.016	-0.040	0.157**	0.206**	1.000								
PR RWC 1	0.263**	0.071*	-0.133**	0.067	0.041	-0.111**	-0.040	0.510**	-0.777**	-0.079*	1.000							
PR RWC 2	-0.750**	-0.532**	0.101**	-0.150**	-0.096*	0.035	0.074*	-0.075*	0.411**	-0.789**	-0.405**	1.000						
PR RWC 3	-0.570**	-0.506**	0.005	-0.118**	-0.059	-0.042	0.043	0.270**	-0.149**	-0.892**	0.305**	0.739**	1.000					
SLA I	-0.089*	-0.061	0.060	-0.027	-0.004	-0.087*	0.028	-0.045	0.089*	-0.117**	-0.091*	0.159**	0.100**	1.000				
SLA II	-0.262**	-0.208**	0.122**	-0.141**	-0.065	0.007	0.066	-0.035	-0.019	-0.392**	0.001	0.346**	0.370**	0.134**	1.000			
SLA III	-0.687**	-0.601**	0.006	-0.190**	-0.050	-0.002	0.040	-0.035	-0.101**	-0.773**	0.059	0.628**	0.714**	0.077*	0.222**	1.000		
SPAD SCMR	0.550**	0.441**	-0.033	0.113**	-0.018	0.002	0.015	-0.001	0.103**	0.656**	-0.091*	-0.526**	-0.625**	-0.067	-0.160**	-0.619**	1.000	
RL	0.192**	0.223**	-0.038	0.458**	0.245**	0.105**	-0.045	-0.002	0.091*	0.289**	-0.079*	-0.189**	-0.264**	-0.046	-0.025	-0.331**	0.177**	1.000

-0.660**) irrespective of the season and pooled across the two seasons. During summer 2012-13 shoot length recorded significant positive correlation with drought tolerance index (0.152**), pod yield per plant (0.188**) and number of nodules per plant (0.243**). In contrast, it recorded negative correlation with drought tolerance index (0.152**) and pod yield per plant (0.188**) during summer 2013-14.

Root to Shoot Ratio

Root to shoot ratio recorded significant positive correlation with drought tolerance index (0.229**, 0.162** and 0.164**) and pod yield per plant (0.200**, 0.135** and 0.246**) while significant negative correlation with shoot length (-0.572**, -0.778** and -0.465**) irrespective of the season and pooled across the two seasons. During summer 2012-13, root to shoot ratio recorded significant positive correlation with shoot dry weight (0.112**) and negative correlation with root dry weight (-0.233**). In contrast to the previous season, it recorded negative correlation with shoot dry weight (-0.390**) and positive correlation with root dry weight (0.192**) during summer 2013-14.

Number of Nodules per Plant

During both summer seasons and pooled across the two seasons number of nodules per plant significant positive correlation with drought tolerance index (0.124**, 0.068 and 0.082*) root to shoot ratio (0.044, 0.160** and 0.093*) and root dry weight (0.221**, 0.119** and 0.122**). During summer 2012-13 it recorded significant positive correlation with pod yield per plant (0.200**) In contrast, to the previous season it recorded negative correlation with pod yield per plant (-0.390**) and shoot dry weight (-0.079*) during summer 2013-14.

Root Dry Weight

During summer 2012-13, root dry weight recorded significant positive correlation with shoot length (0.380**), number of nodules per plant (0.221**) and shoot dry weight while significant negative correlation with root to shoot ratio (-0.233**). During summer 2013-14, root dry weight recorded significant positive correlation drought tolerance index (0.175**), pod yield per plant (0.135**), root to shoot ratio (0.192**) and number of nodules per plant (0.119**).

Shoot Dry Weight

During summer 2012-13, shoot dry weight recorded significant positive correlation with shoot length (0.153**), root to shoot ratio (0.112**) and root dry weight (0.166**). In contrast to the earlier season, root dry weight recorded significant negative correlation with most of the traits except shoot length (0.529**) during summer 2013-14.

4.3 Multilocation yield trials of selected lines during *Kharif* 2014-15

Pooled performance of selected recombinant inbred lines in multilocation yield trials at Annigeri and Bijapur during Kharif 2014-15 is given in Table 52. Among the selected lines 41, 50, 58 and 179 had high pod yield per hectare compared to the best parent GM 6-1 (2648.54 kg/ha).

4.4 Construction of Genetic linkage map

RIL populations are ideally considered for QTL mapping because of several advantages over F_2 population. The major advantage of RIL is as each line is 'true-breeding' or homozygous line that can be multiplied and reproduced without genetic change occurring there by allowing for genotyping and phenotyping of many traits under various environmental conditions to be performed on the same material (Simon *et al.*, 2008). Further, the RIL population undergo several rounds of meiosis before homozygosity is reached, the degree of recombination is higher compared to F_2 populations. Consequently, RIL populations show a higher resolution than maps generated from F_2 populations (Burr and Burr 1991). Seeds may be transferred between different laboratories for further linkage analysis and the addition of markers to existing maps ensuring that all collaborators examine identical material (Paterson 1991 and Young 1996). Therefore, RIL mapping population serves as 'eternal' resource for QTL mapping.

4.4.1 Parental polymorphism survey

A total of 430 SSR markers (both genomic and EST based) available in public domain and/or accessed from other sources/various collaborators were used to screen the polymorphism on the parental genotypes of the mapping populations TMV-2 x GM

Table 53: Pooled performance of selected recombinant inbred lines in multilocation yield trials at Annigeri and Bijapur during Kharif 2014-15

S.No	RIL No.	Pod Yield Per Plant (g) (Gm)	Pod Yield (Kg/Ha)	Plant Height (cm)	No Primary Branches /plant	No Secondary Branches/ plant	No. Mature Pods/ Plant	Rwc at 15 DAS	Rwc at 30 DAS	RWC at 45 DAS	SLA at 15 DAS	SLA at 30 DAS	SLA at 45 DAS	SCMR
1	1	4.29	1428.65	36.6	5.8	2.0	27.4	82.35	79.96	73.24	67.50	51.91	45.06	41.45
2	2	4.43	1478.06	32.0	6.0	2.3	16.1	84.78	79.20	74.55	64.97	55.12	44.14	41.78
3	26	7.63	2542.25	30.0	5.7	4.3	25.5	86.00	78.81	74.78	61.62	53.35	43.65	46.48
4	30	5.91	1972.20	34.6	5.7	4.9	31.0	86.21	79.93	76.70	63.11	52.10	44.37	37.93
5	41	9.73	3241.32	34.1	5.4	1.6	30.6	82.68	74.69	72.02	63.99	49.45	43.73	44.53
6	50	10.28	3425.53	21.3	5.7	3.2	32.4	82.43	76.91	73.53	64.70	53.09	45.52	44.45
7	53	8.02	2672.74	29.1	8.8	3.6	17.2	80.92	74.29	69.57	64.27	51.86	45.56	42.98
8	58	10.01	3334.94	29.6	6.0	6.5	34.4	85.71	78.38	70.43	64.10	50.26	45.32	38.05
9	102	6.91	2302.87	31.6	5.7	3.5	23.9	81.61	78.59	71.80	56.72	49.34	46.54	42.38
10	179	9.08	3024.43	27.6	6.0	3.9	26.1	84.23	77.29	72.55	66.15	51.92	46.10	43.78
11	181	8.99	2996.13	33.9	5.4	3.5	28.5	82.01	80.57	74.37	64.77	57.53	53.78	38.53
12	202	8.52	2839.86	25.8	5.0	2.3	18.0	82.57	77.17	66.56	64.47	58.30	46.68	44.75
13	265	7.07	2354.23	31.3	7.6	4.6	28.1	82.52	75.26	70.71	60.42	53.45	46.16	42.63
14	296	5.78	1925.06	35.0	6.3	3.6	31.8	82.55	74.36	66.56	56.61	52.59	44.48	45.70
15	TMV-2	7.73	2577.45	27.6	5.0	1.8	23.6	81.48	75.12	71.36	59.83	56.89	51.67	41.73
16	GM 6-1	7.95	2648.54	21.9	5.5	4.2	21.2	80.99	75.93	69.71	54.76	51.61	46.70	39.15
17	GPBD-4	8.00	2666.58	30.0	4.7	3.2	31.5	83.65	76.04	71.07	58.61	48.25	45.93	43.53
18	DH-86	5.54	1844.13	25.5	6.1	2.5	19.6	81.23	76.37	73.17	65.17	52.33	44.01	40.33
19	JL-24	6.11	2037.67	27.3	5.8	2.0	18.1	80.43	77.00	71.89	56.92	49.61	45.10	39.70
20	ICGV-91114	5.94	1978.56	30.8	7.3	2.7	14.1	81.74	76.39	68.59	65.59	59.32	46.76	43.55
21	G-2-52	8.05	2680.05	26.5	5.0	3.5	24.9	81.56	73.66	67.75	69.68	59.13	51.08	45.43
	CV	16.32	14.29	6.73	7.52	8.56	12.07	2.18	2.69	8.41	1.83	3.19	3.59	8.86
	CD 5%	1.89	559.72	4.8	1.4	1.0	3.6	2.96	2.41	3.12	1.86	2.06	2.31	3.29

6-1 and were subsequently used in the present study for construction of linkage map and further for identifying QTLs associated with drought related traits.

In summary, after screening a total of 430 SSR markers on the parental genotypes of the mapping population, 105 polymorphic markers were obtained out of which 71 markers were used for genotyping and linkage map construction (Plate 4).

4.4.2 Marker segregation

The genotypic data obtained for 71 SSR markers in 299 RILs was analyzed for marker segregation (Plate 5a and 5b). The expected frequency of homozygous TMV-2 alleles and GM 6-1 alleles in RIL population are 50 and 50 respectively.

4.4.3 Construction of linkage map

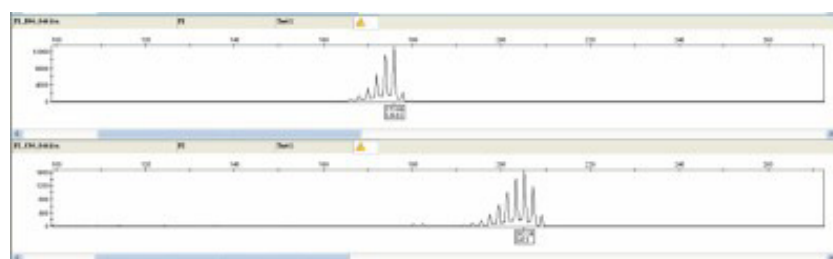
Linkage map was developed based on the marker data produced from the RILs of TMV-2 x GM 6-1. Out of 430 microsatellite markers used for screening the parents, 71 (15.67 %) were polymorphic (Appendices). Marker segregation data was used to construct the linkage map using QTL IciMapping v.4.0 (Wang *et al.* 2014) software (Plate 6). The chi-square (χ^2) test was employed to test segregation ratio for the markers. Due to less number of polymorphic markers, all the 71 markers were used for linkage map construction despite of the segregation distortion observed among the markers. Linkage groups were formed at a minimum LOD of 3.0 and a maximum distance of 50.0 cM. Sixty seven markers were mapped on 13 linkage groups. The linkage map covered 399.04 cM with an average marker distance of 5.96 cM. Four markers remained ungrouped. The number of markers mapped per linkage group ranged from 1 (LG-14, LG-15, LG16 and LG17) to ten (LG-5). The length of the linkage group varied from 3.82 cM (LG-07) to 109.85 cM (LG-13). The number of marker loci mapped on each linkage group along with the number of markers mapped, total length (cM) and average marker density (cM) was given in Table 54.

4.4.4 Phenotyping data analyses

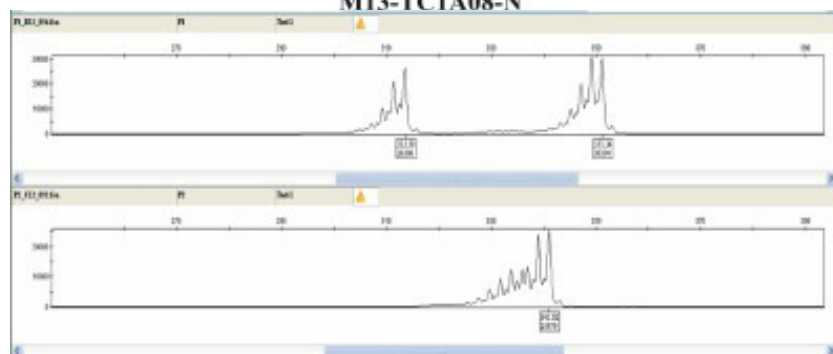
In order to identify quantitative trait loci (QTLs) for drought related traits in mapping populations, the phenotyping was done for drought tolerance traits for two seasons of summer 2012-13 and summer 2013-14 in the UAS, Dharwad. The



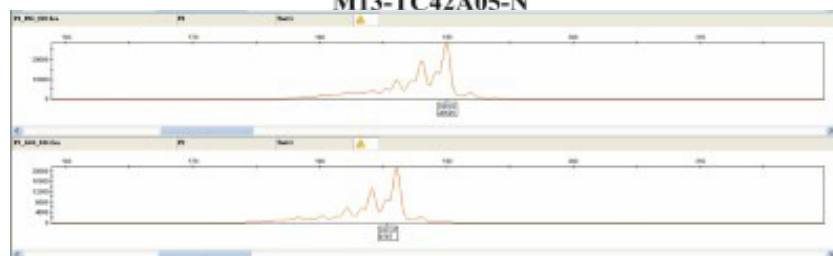
m13-AHGS0228-F



M13-TC1A08-N

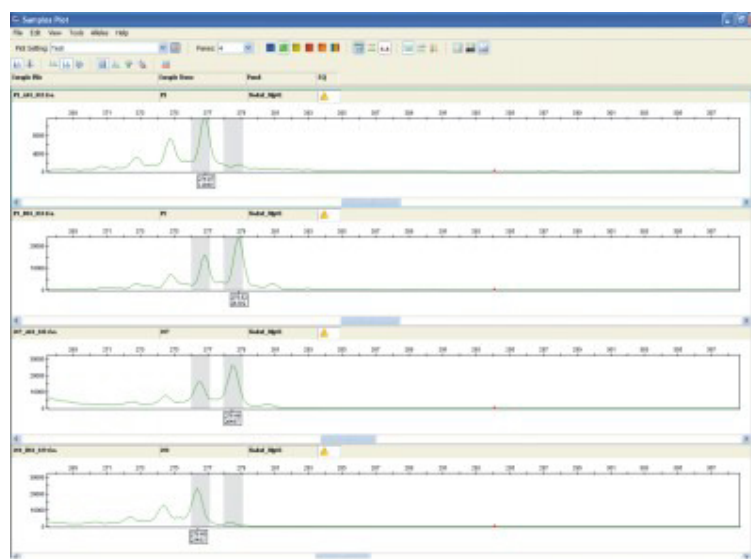


M13-TC42A05-N

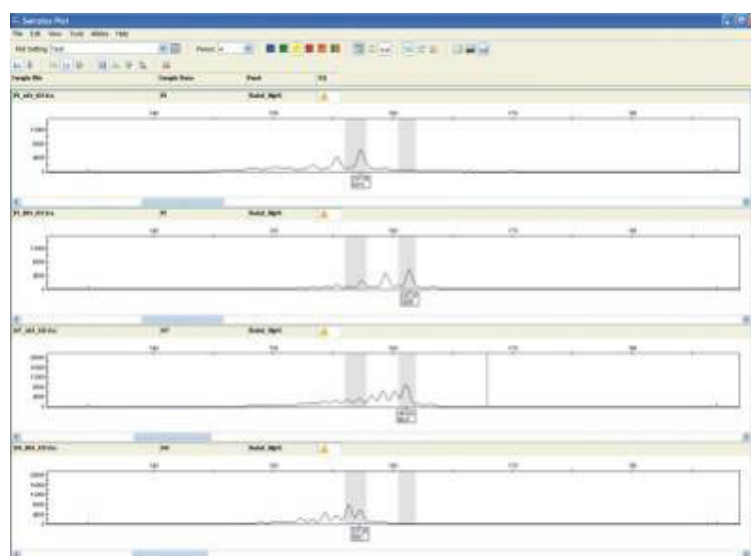


m13-AHGS2572-P

Plate 4: Parental polymorphism for some of the markers

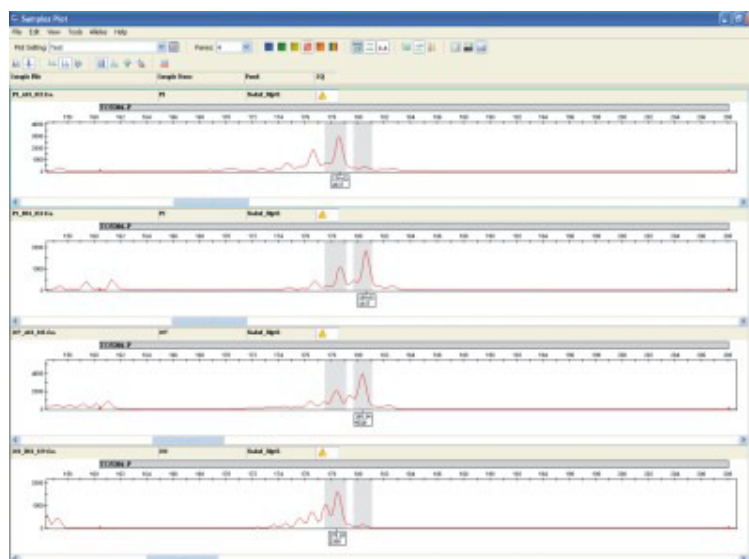


Seq15F12-V

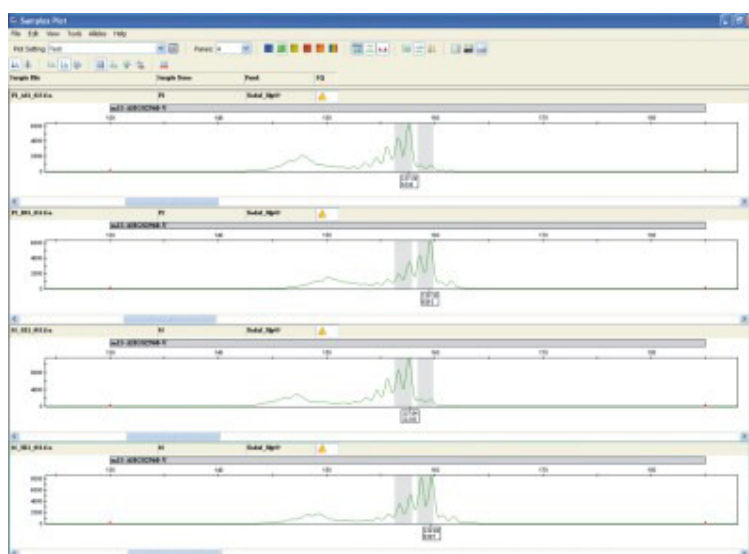


TC7C06-N

Plate 5a: Genotyping with markers Seq 15F12-V and TC7C06-NT in the RIL population on capillary electrophoresis ABI 3730 XL genetic analyzer



TC5D06-P



m13-AHGS2960-V

Plate 5b: Genotyping with markers TC 5D06-P and m13-AHGS2960-V in the RIL population on capillary electrophoresis ABI 3730 XL genetic analyzer

Table 54: General features of genetic map of groundnut (*Arachis hypogaea* L.) developed using SSR markers based on 299 RILs developed from the cross TMV-2 x GM 6-1

Sl. No.	Linkage Group	Number of markers mapped	Total length (cM)	Average marker density (cM)
1	LG-1	3	44.18	14.73
2	LG-2	6	20.64	3.44
3	LG-3	8	57.79	7.22
4	LG-4	6	21.48	3.58
5	LG-5	10	38.33	3.83
6	LG-6	5	7.21	1.44
7	LG-7	2	3.82	1.91
8	LG-8	6	32.44	5.41
9	LG-9	2	25.04	12.52
10	LG-10	5	16.24	3.25
11	LG-11	7	9.00	1.29
12	LG-12	4	13.02	3.26
13	LG-13	3	109.85	36.62
14	LG-14	1	0	0.00
15	LG-15	1	0	0.00
16	LG-16	1	0	0.00
17	LG-17	1	0	0.00
	Whole Genome	71	399.04	5.96

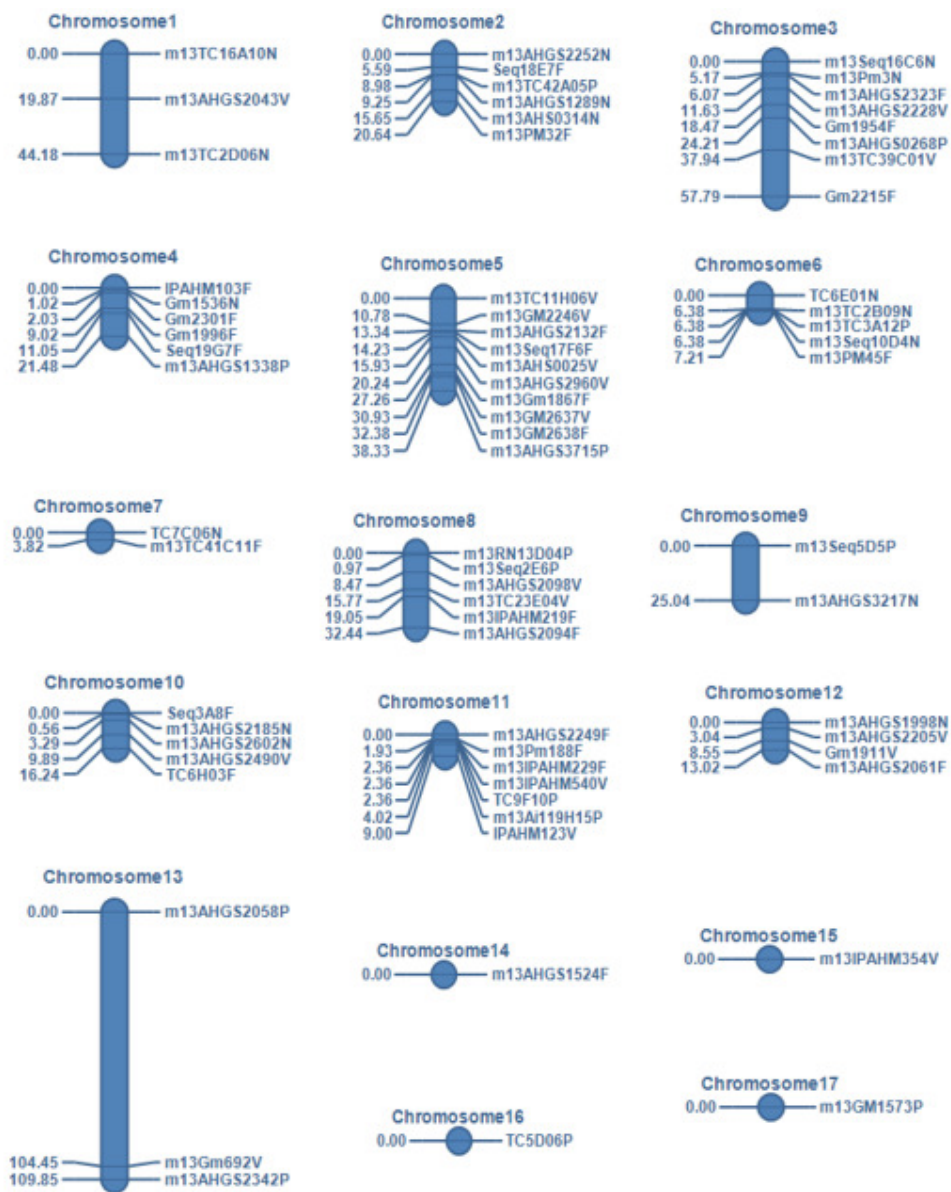


Plate 6: Genetic linkage map of TMV-2 x GM 6-1

phenotypic data was obtained for various quantitative, physiological and root traits related to drought tolerance. The phenotyping data of parents and RILs were subjected to analysis of variance (ANOVA). The results on ANOVA and genetic parameters were presented in the section 4.1-4.5.

4.5 QTL mapping for traits related to drought tolerance and quality traits

4.5.1 QTLs associated with quantitative, physiological and root traits

QTLs for quantitative, physiological and root traits were identified by integrating the genotyping and phenotyping data using the QTL IciMapping v.4.0 (Wang *et al.* 2014) software by following Inclusive composite interval mapping (ICIM) method. Results on QTLs identified for various traits are presented in Table 55 to 57. In present study totally 63 QTLs were identified for 23 different traits related to drought tolerance and 21 quality traits (oil quality and foliar disease resistance) recorded under two water regimes in two seasons in groundnut. The QTLs explaining more than 20% phenotypic variation were considered as major QTLs (Collard *et al.*, 2005). Among all traits, there were no QTLs have been identified for traits like, number of immature pods per plant, drought tolerance index, SPAD chlorophyll meter reading and root to shoot ratio.

4.5.1.1 Quantitative traits

Days to 50 per cent flowering

One QTLs namely, qDFFWS14-10-1 was identified for days to 50% flowering under WS condition on LG-10 and was derived from GM 6-1. This was flanked by the markers *viz.*, m13AHGS2602N and m13AHGS2490V and was identified with the LOD value of 3.90 with the phenotypic variation of 6.23 %.

Days to maturity

Totally four minor QTLs, namely qDMWW13-8-1, qDMWS13-8-1, qDMWW14-10-1 and qDMWS14-10-1 were identified for days to maturity on LG-8, LG-8, LG-10 and LG-10 respectively. All the QTLs were derived from GM 6-1 with an

Table 55: QTLs associated with quantitative traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
Days to 50 % flowering	qDFFWS14-10-1	10	4	m13AHGS2602N	m13AHGS2490V	3.901	6.2346	0.2505
Days to maturity	qDMWW13-8-1	8	32	m13IPAHM219F	m13AHGS2094F	3.7764	5.8666	0.2059
	qDMWS13-8-1	8	32	m13IPAHM219F	m13AHGS2094F	2.7697	4.2609	0.1207
	qDMWW14-10-1	10	1	m13AHGS2185N	m13AHGS2602N	2.9634	5.2769	0.1769
	qDMWS14-10-1	10	0	Seq3A8F	m13AHGS2185N	4.4995	6.7352	0.1871
Plant height	qPHWW13-10-1	10	8	m13AHGS2602N	m13AHGS2490V	11.9692	18.5341	2.2904
	qPHWS13-10-1	10	10	m13AHGS2490V	TC6H03F	8.5665	12.4675	1.7531
Number of primary branches per plant	qNPBPWW13-2-1	2	6	Seq18E7F	m13TC42A05P	5.6027	7.8251	-0.335
	qNPBPWW13-10-1	10	0	Seq3A8F	m13AHGS2185N	3.3411	4.3763	-0.2235
	qNPBPWS13-3-1	3	1	m13Seq16C6N	m13Pm3N	3.2492	5.2306	-0.2191
	qNPBPWW14-3-1	3	55	m13TC39C01V	Gm2215F	3.9629	30.2731	-1.2769
	qNPBPWS14-3-1	3	52	m13TC39C01V	Gm2215F	17.1345	59.758	-1.2492
	qNPBPWS14-8-1	8	12	m13AHGS2098V	m13TC23E04V	3.8242	7.1395	-0.3066
Number of secondary branches per plant	qNSBPWW14-3-1	3	55	m13TC39C01V	Gm2215F	46.0171	69.6507	-1.7157
	qNSBPWS14-3-1	3	55	m13TC39C01V	Gm2215F	20.9307	53.4284	-1.2048
	qNSBPWS14-4-1	5	4	m13TC11H06V	m13GM2246V	2.7901	7.4375	-0.2606
Number of pegs per plant	qNPPWS14-3-1	3	56	m13TC39C01V	Gm2215F	37.944	56.2842	-17.527
	qNPPWS14-5-1	5	17	m13AHS0025V	m13AHGS2960V	2.8875	4.8218	-2.1808
Number of mature pods per plant	qNMPPWS14-3-1	3	55	m13TC39C01V	Gm2215F	6.7719	29.9439	-6.4767
	qNMPPWS14-10-1	10	0	Seq3A8F	m13AHGS2185N	6.7311	9.8481	-1.7922

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Pod yield per plant	qPYPWW13-9-1	9	4	m13Seq5D5P	m13AHGS3217N	10.7084	20.5417	-1.4046
	qPYPWS13-10-1	10	0	Seq3A8F	m13AHGS2185N	5.5813	8.2373	-0.5375
	qPYPWW14-1-1	1	4	m13TC16A10N	m13AHGS2043V	3.4909	7.0805	1.0596
	qPYPWW14-2-1	2	0	m13AHGS2252N	Seq18E7F	3.3184	4.3088	-0.7338
	qPYPWW14-3-1	3	55	m13TC39C01V	Gm2215F	3.4125	20.6952	-3.0883
	qPYPWW14-10-1	10	0	Seq3A8F	m13AHGS2185N	5.7655	7.6304	-0.9089
	qPYPWS14-8-1	8	9	m13AHGS2098V	m13TC23E04V	9.4606	14.0826	-0.4557
Kernel yield per plant	qKYPWW13-9-1	9	4	m13Seq5D5P	m13AHGS3217N	11.4273	21.6863	-0.973
	qKYPWS13-10-1	10	0	Seq3A8F	m13AHGS2185N	5.0254	7.4482	-0.3371
	qKYPWW14-1-1	1	4	m13TC16A10N	m13AHGS2043V	3.2227	6.5283	0.698
	qKYPWW14-2-1	2	0	m13AHGS2252N	Seq18E7F	3.4499	4.4731	-0.5126
	qKYPWW14-3-1	3	55	m13TC39C01V	Gm2215F	4.1679	21.9403	-2.1762
	qKYPWW14-10-1	10	0	Seq3A8F	m13AHGS2185N	5.8559	7.7365	-0.6276
	qKYPWS14-10-1	10	1	m13AHGS2185N	m13AHGS2602N	9.8009	15.456	-0.2835
Shelling per cent	qSOTWW13-3-1	3	36	m13AHGS0268P	m13TC39C01V	3.4507	6.5561	-0.4907
	qSOTWS13-10-1	10	0	Seq3A8F	m13AHGS2185N	3.5739	5.3558	-2.5375
	qSOTWW14-1-1	1	7	m13TC16A10N	m13AHGS2043V	3.3631	10.0114	-0.6484
	qSOTWW14-3-1	3	57	m13TC39C01V	Gm2215F	12.4323	28.5793	-4.0354
SMK %	qSMKWS14-10-1	10	0	Seq3A8F	m13AHGS2185N	5.6868	8.3859	-5.8269
100 seed weight	qHSWWW13-10-1	10	1	m13AHGS2185N	m13AHGS2602N	2.6394	4.344	-1.3906
	qHSWWS14-3-1	3	53	m13TC39C01V	Gm2215F	7.9862	34.7998	-8.1957
	qHSWWS14-17-1	17	0	m13GM1573P	m13GM1573P	3.3799	4.6282	-1.8112

Table 56: QTLs associated with physiological traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
RWC	qRWC2WW13-3-1	3	37	m13AHGS0268P	m13TC39C01V	4.4761	7.2184	-0.852
	qRWC2WW13-16-1	16	0	TC5D06P	TC5D06P	5.2209	7.5461	0.7818
	qRWC2WS13-3-1	3	56	m13TC39C01V	Gm2215F	2.5855	18.9516	2.8519
	qRWC3WW13-3-1	3	34	m13AHGS0268P	m13TC39C01V	6.0201	11.92	-1.4621
	qRWC3WW13-5-1	5	0	m13TC11H06V	m13GM2246V	4.1589	5.8532	1.1596
	qRWC3WS14-1-1	1	0	m13TC16A10N	m13AHGS2043V	2.8573	4.3055	-1.0384
SLA	qSLA1WW13-13-1	13	53	m13AHGS2058P	m13Gm692V	12.063	73.8319	4.6307
	qSLA2WS14-13-1	13	49	m13AHGS2058P	m13Gm692V	6.0968	60.9007	4.0625
	qSLA3WW13-3-1	3	56	m13TC39C01V	Gm2215F	12.647	47.1683	3.3393

Table 57: QTLs associated with root traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
Root length	qRLWW14-3-1	3	56	m13TC39C01V	Gm2215F	3.1108	21.0927	-8.8039
Shoot length	qSLWW14-10-1	10	0	Seq3A8F	m13AHGS2185N	4.8343	7.1752	1.2619
	qSLWS14-3-1	3	21	Gm1954F	m13AHGS0268P	5.9502	10.3941	1.7871
Number of nodules per plant	qNNPPWW13-3-1	3	53	m13TC39C01V	Gm2215F	16.6312	56.7854	-19.8489
	qNNPPWS13-3-1	3	57	m13TC39C01V	Gm2215F	4.8639	21.0344	-16.3405
	qNNPPWW14-3-1	3	55	m13TC39C01V	Gm2215F	5.772	32.8305	-13.841
	qNNPPWW14-9-1	9	7	m13Seq5D5P	m13AHGS3217N	3.9844	10.0359	-3.729
	qNNPPWS14-8-1	8	32	m13IPAHM219F	m13AHGS2094F	2.5758	4.0976	2.9051
Root dry weight	qRDWWW13-3-1	3	57	m13TC39C01V	Gm2215F	3.2525	16.7867	-0.1608
	qRDWWW14-3-1	3	54	m13TC39C01V	Gm2215F	11.5246	54.3226	-5.8404
Shoot dry weight	qSDWWW14-3-1	3	57	m13TC39C01V	Gm2215F	14.5804	23.4534	-0.5363
	qSDWWW14-5-1	5	32	m13GM2637V	m13GM2638F	2.8306	4.3614	-0.029

additive effect of 0.206, 0.121, 0.177 and 0.187 respectively. Among these, common QTL was identified for days to maturity under WW (qDMWW13-8-1) and WS (qDMWS13-8-1) conditions which were mapped between the flanking markers m13IPAHM219F and m13AHGS2094F. Among all QTLs identified, qDMWS14-10-1 was identified with highest LOD value of 4.50 with highest phenotypic variation explanation of 6.74 %.

Plant height

Two major QTLs were detected for plant height under WW and WS conditions viz; qPHWW13-10-1 and qPHWS13-10-1 on LG-10. QTL qPHWW13-10-1, expressed 18.53 PVE% with a LOD value of 11.96 and derived from parent GM 6-1. Whereas another QTL qPHWW13-10-1 expressed a PVE% of 12.47 with a LOD value of 8.53 and derived from the same parent.

Number of primary branches per plant

Six QTLs were detected for this trait on 2, 3, 8 and 10 chromosomes which were derived from the parent TMV-2. Among these two major QTLs were detected, among which qNPBPWS14-3-1 was detected with high LOD (17.35) and phenotypic variation explained (59.76 %), whereas qNPBPWW14-3-1 showed a PVE % of 30.27 and LOD of 3.96.

Number of secondary branches per plant

Totally three QTLs, namely qNSBPWW14-3-1, qNSBPWS14-3-1 and qNSBPWS14-4-1 were identified for this trait on LG-3 and LG-5 respectively. All the QTLs were derived from TMV-2 with an additive effect, among which, two major QTLs were identified for this trait under WW (qNSBPWW13-8-1) and WS (qNSBPWS13-8-1) conditions which were mapped at a common position between the flanking markers m13TC39C01V and Gm2215F with high LOD (46.01 and 20.93) and phenotypic variation explained (69.65 % and 53.43 %) respectively.

Number of pegs per plant

Among the two QTLs detected for this trait a major QTL namely, qNPPWS14-3-1 derived from TMV-2 was present on LG-3 with a LOD value of 37.94 and

phenotypic variation explained was 56.28. This marker was at terminal position and tagged between markers m13TC39C01V and Gm2215F.

Number of mature pods per plant

Two QTLs were detected on two chromosomes (3 and 10), which were derived from TMV-2. A major QTL namely, qNMPPWS14-3-1 with a LOD value of 6.77 and phenotypic variation explained was 29.94 was tagged between markers m13TC39C01V and Gm2215F.

Pod yield per plant

Among seven QTLs, five QTLs were detected for pod yield per plant under WW condition on LG 1, 3, 9 and 10 and two QTLs were detected for pod yield per plant under WS condition on LG-8 and 10. All QTLs were derived from the parent TMV-2. In WW condition a major QTL namely, qPYPWW14-3-1 explained highest phenotypic variation (20.67) with a LOD value of 3.41 and was flanked by two markers m13TC39C01V and Gm2215F at a position of 55cM on LG-3. Similarly in WS condition a major QTL qPYPWW14-3-1 was detected which explained phenotypic variation (14.08) with a LOD value of 9.46 and was flanked by two markers m13AHGS2098V and m13TC23E04V at a position of 9cM on LG-8.

Kernel yield per plant

For kernel yield per plant, seven QTLs among which five QTLs were detected under WW condition on LG 1, 2, 3, 9 and 10 and two QTLs were detected for pod yield per plant under WS condition on LG-10. QTL qKYPWW14-1-1 was derived from the parent GM 6-1 and the remaining QTLs were derived from the parent TMV-2. In WW condition a major QTL namely, qKYPWW14-3-1 explained highest phenotypic variation (21.94) with a LOD value of 4.16 and was flanked by two markers m13TC39C01V and Gm2215F at a position of 55cM on LG-3. Similarly in WS condition a major QTL qKYPWW14-10-1 was detected which explained phenotypic variation (15.47) with a LOD value of 9.40 and was flanked by two markers m13AHGS2185N and m13AHGS2602N at a position of 1cM on LG-10. Two QTLs qKYPWS13-10-1 (summer 2012-13) and qKYPWS14-10-1 (summer 2013-14) were

mapped at a common position on LG-10 between the flanking markers Seq3A8F and m13AHGS2185N.

Shelling per cent

Totally four QTLs, namely qSOTWW13-3-1, qSOTWS13-10-1, qSOTWW14-1-1 and qSOTWW14-3-1 were identified for this trait on LG-1, 3 and 10. All the QTLs were derived from TMV-2 among which, two major QTLs were identified for this trait under WW condition. QTL qSOTWW14-3-1 was positioned between the flanking markers m13TC39C01V and Gm2215F with highest LOD (12.43) and phenotypic variation of 28.58 %.

Sound mature kernel per cent

Only one minor QTL qSMK-10-1 was identified for this trait on LG-10. This QTL derived from TMV-2 and explained 8.39 phenotypic variation with a LOD value of 5.69 and this QTL was flanked by markers Seq3A8F and m13AHGS2185N.

100 seed weight

Among the three QTLs, one for WW and two for WS condition were mapped on LG-10, 3 and 17 respectively and were derived from TMV-2. A major QTL namely, qHSWWS14-3-1 with a LOD value of 7.99 and phenotypic variation explained was 34.80 was tagged between markers m13TC39C01V and Gm2215F at a position of 53 cM on LG-3.

4.5.1.2 Physiological traits

Relative water content

Six QTLs were identified for Relative water content at two stages on chromosomes 1, 3, 5 and 16. No QTL was identified for RWC at 7 days after stress. Among the QTLs for RWC at 15 days after stress two minor QTLs were detected for WW condition (qRWC2WW13-3-1 and qRWC2WW13-16-1) and one major QTL for WS condition (qRWC2WS13-3-1). qRWC2WS13-3-1 present on chromosome 3 at a position 56 cM flanked by markers m13TC39C01V and Gm2215F explained highest phenotypic variation (18.95) with LOD value of 2.59 and was derived from GM 6-1.

Similarly among the QTLs for RWC at 30 days after stress, one major and one minor QTLs were detected for WW condition (qRWC3WW13-3-1 and qRWC3WW13-5-1) and one minor QTL for WS condition (qRWC3WS14-1-1). QTL qRWC3WW13-3-1 was derived from the parent TMV-2 and was present on chromosome 3 at a position 34 cM flanked by markers m13AHGS0268P and m13TC39C01V explained highest phenotypic variation (11.92) with LOD value of 6.02.

Specific Leaf Area

Three major QTLs namely, qSLA1WW13-13-1, qSLA2WS14-13-1 and qSLA3WW13-3-1 were identified for SLA at respective stages which explained highest phenotypic variance (73.83, 60.90 and 47.17) and LOD value of 12.06, 6.10 and 12.65 respectively. Favorable alleles for all the three QTLs were derived from GM 6-1. qSLA1WW13-13-1, qSLA2WS14-13-1 and qSLA3WW13-3-1 were flanked by the markers viz., m13AHGS2058P and m13Gm692V; m13AHGS2058P and m13Gm692V; m13TC39C01V and Gm2215F on LG-13, 13 and 3 respectively.

4.5.1.3 Root traits

Root length

Only one QTL qRLWW14-3-1 was identified for this trait on LG-3. This QTL derived from TMV-2 explained 21.09 phenotypic variation with highest LOD value of 3.11 and this QTL was flanked by markers m13TC39C01V and Gm2215F at a position of 56 cM.

Shoot length

Among the two QTLs detected for this trait a major QTL namely, qSLWS13-3-1 derived from GM-6-1 was present on LG-3 with a LOD value of 5.95 and phenotypic variation explained was 10.39 and was tagged between markers Gm1954F and m13AHGS0268P

Number of nodules per plant

For number of nodules per plant, five QTLs among which three major QTLs were detected under WW condition on LG 3 and 9 and two QTLs were detected for this

trait under WS condition on LG-10. QTL qNNPPWS14-8-1 was derived from the parent GM 6-1 and the remaining QTLs were derived from the parent TMV-2. In WW condition QTL qNNPPWW13-3-1 explained highest phenotypic variation (56.79) with a LOD value of 16.63 and was flanked by two markers m13TC39C01V and Gm2215F at a position of 53 cM on LG-3. Similarly in WS condition a major QTL qNNPPWS13-3-1 was detected which explained phenotypic variation (21.03) with a LOD value of 4.86 and was flanked by two markers m13TC39C01V and Gm2215F at a position of 57 cM on LG-3. Three QTLs qNNPPWW13-3-1 (summer 2012-13), qNNPPWS13-3-1 (summer 2012-13) and qNNPPWW14-3-1 (summer 2013-14) were mapped on LG-3 between the flanking markers m13TC39C01V and Gm2215F.

Root Dry Weight

Two QTLs were detected on LG-3, which were derived from TMV-2. A major QTL namely, qRDWWW14-3-1 with a LOD value of 11.52 and phenotypic variation explained was 54.32 was tagged between markers m13TC39C01V and Gm2215F.

Shoot Dry Weight

Two QTLs were detected on two LG-3 and 5, which were derived from TMV-2. A major QTL namely, qSDWWW14-3-1 with a LOD value of 14.58 and phenotypic variation explained was 23.45 was tagged between markers m13TC39C01V and Gm2215F.

4.5.2 Oil quality traits and foliar disease resistance

In addition to the QTLs for the traits related to drought tolerance, QTLs for quality traits such as oil quality and foliar disease resistance traits were also identified as the parents used for developing the mapping population were widely varied for those traits especially for oleic acid, LLS and rust disease resistance. They were listed in the Table 58 and 59 along with the position in the linkage group, flanking markers, LOD value, PVE explained and additive effect.

Table 58: QTLs associated with oil quality traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
Total oil content	qTOCWW13-5-1	5	24	m13AHGS2960V	m13Gm1867F	3.9074	7.0288	-0.4556
	qTOCWW14-5-1	5	22	m13AHGS2960V	m13Gm1867F	3.1744	5.5171	-0.2971
	qTOCWS14-17-1	17	0	m13GM1573P	m13GM1573P	4.3625	6.4959	0.3475
Total protein content	qTPCWW14-3-1	3	5	m13Seq16C6N	m13Pm3N	9.0045	10.6009	-0.732
	qTPCWW14-13-1	13	108	m13Gm692V	m13AHGS2342P	7.6127	10.0688	-0.7541
	qTPCWS13-3-1	3	57	m13TC39C01V	Gm2215F	5.2319	18.7842	-3.1544
Palmitic acid	qPALWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	8.1273	11.7655	0.3748
	qPALWW14-8-1	8	19	m13TC23E04V	m13IPAHM219F	8.9274	12.918	0.4183
	qPALWS13-2-1	2	17	m13AHS0314N	m13PM32F	5.0619	7.8866	0.3258
	qPALWS13-9-1	9	11	m13Seq5D5P	m13AHGS3217N	4.4998	11.4761	0.3596
	qPALWS14-9-1	9	7	m13Seq5D5P	m13AHGS3217N	6.263	12.7497	0.3847
	qPALWS14-10-1	10	4	m13AHGS2602N	m13AHGS2490V	6.4749	8.6356	0.3438
Stearic acid	qSTEW13-10-1	10	3	m13AHGS2185N	m13AHGS2602N	6.6934	9.092	0.1681
	qSTEW13-13-1	13	108	m13Gm692V	m13AHGS2342P	5.4866	8.265	0.1758
	qSTEW14-2-1	2	0	m13AHGS2252N	Seq18E7F	10.5819	13.4032	-0.1192
	qSTEW14-2-2	2	20	m13AHS0314N	m13PM32F	6.242	8.0051	0.0906
	qSTEW14-13-1	13	109	m13Gm692V	m13AHGS2342P	12.8554	18.2037	0.1505
Oleic acid	qOLEWW13-5-1	5	25	m13AHGS2960V	m13Gm1867F	13.8667	25.3185	-3.8662
	qOLEWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	12.6599	19.876	-3.431
	qOLEWS13-1-1	1	13	m13TC16A10N	m13AHGS2043V	9.8543	31.0249	-4.4972
	qOLEWS13-9-1	9	5	m13Seq5D5P	m13AHGS3217N	4.9055	8.6905	-2.0973
	qOLEWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	11.0443	38.7212	-4.5937
	qOLEWS14	9	8	m13Seq5D5P	m13AHGS3217N	4.2774	9.2164	-1.9554
Linoleic acid	qLINWW13	11	9	m13Ai119H15P	IPAHM123V	11.0904	15.702	2.406
	qLINWW14	11	8	m13Ai119H15P	IPAHM123V	11.2832	17.816	2.578
	qLINWS13-1-1	1	14	m13TC16A10N	m13AHGS2043V	11.2249	33.3804	3.4811

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	qLINWS13-1-2	1	26	m13AHGS2043V	m13TC2D06N	11.6449	30.3039	3.118
	qLINWS13-3-1	3	54	m13TC39C01V	Gm2215F	11.8027	39.4962	5.9954
	qLINWS13-4-1	4	20	Seq19G7F	m13AHGS1338P	3.6766	5.8756	1.7053
	qLINWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.6529	41.0935	4.0426
	qLINWS14-1-2	1	25	m13AHGS2043V	m13TC2D06N	10.3039	28.0909	3.131
	qLINWS14-9-1	9	9	m13Seq5D5P	m13AHGS3217N	4.9526	10.9894	1.8398
Arachidic acid	qARAWW13-2-1	2	9	m13TC42A05P	m13AHGS1289N	7.7245	11.226	0.0797
	qARAWW14-2-1	2	10	m13AHGS1289N	m13AHS0314N	11.0227	16.0816	0.0699
	qARAWW14-5-1	5	37	m13GM2638F	m13AHGS3715P	6.9493	10.8074	-0.0538
	qARAWW14-8-1	8	31	m13IPAHM219F	m13AHGS2094F	5.6444	8.6581	-0.0469
	qARAWS13-9-1	9	0	m13Seq5D5P	m13AHGS3217N	5.7204	8.4331	-0.057
	qARAWS14-9-1	9	0	m13Seq5D5P	m13AHGS3217N	11.5825	16.3379	-0.0569
Ecosenoic acid	qECOWW13-3-1	3	23	Gm1954F	m13AHGS0268P	8.0199	10.5198	-0.0311
	qECOWW13-13-1	13	109	m13Gm692V	m13AHGS2342P	10.2308	12.9697	-0.0353
	qECOWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	8.4283	10.7444	-0.03
	qECOWW14-13-1	13	109	m13Gm692V	m13AHGS2342P	7.3869	9.1989	-0.0291
	qECOWS13-8-1	8	19	m13TC23E04V	m13IPAHM219F	10.5138	15.0516	-0.0398
	qECOWS14-10-1	10	0	Seq3A8F	m13AHGS2185N	3.8318	5.122	0.0152
	qECOWS14-11-8	11	8	m13Ai119H15P	IPAHM123V	15.1487	24.2424	-0.0365
Behenoic acid	qBEHWW13-3-1	3	5	m13Seq16C6N	m13Pm3N	4.9441	6.3009	0.1184
	qBEHWW13-5-1	5	22	m13AHGS2960V	m13Gm1867F	5.3837	7.636	0.1326
	qBEHWW14-2-1	2	9	m13TC42A05P	m13AHGS1289N	4.339	5.7697	0.0712
	qBEHWW14-4-1	4	9	Gm2301F	Gm1996F	6.5786	8.8972	0.0874
	qBEHWW14-9-1	9	0	m13Seq5D5P	m13AHGS3217N	6.3115	8.5015	-0.0774
	qBEHWS13-5-1	5	30	m13Gm1867F	m13GM2637V	4.8585	8.0141	0.1257
	qBEHWS14-4-1	4	14	Seq19G7F	m13AHGS1338P	11.694	21.1961	0.1169
Lignoceric acid	qLIGWW13-5-1	5	28	m13Gm1867F	m13GM2637V	9.5328	12.2915	-0.0412
	qLIGWW13-13-1	13	109	m13Gm692V	m13AHGS2342P	4.7123	6.1262	-0.0311
	qLIGWW14-5-1	5	29	m13Gm1867F	m13GM2637V	8.334	11.1575	-0.0386
	qLIGWW14-13-2	13	109	m13Gm692V	m13AHGS2342P	5.2614	6.9184	-0.0324

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	qLIGWS13-8-1	8	19	m13TC23E04V	m13IPAHM219F	3.6788	5.5373	-0.0287
	qLIGWS14-13-1	13	4	m13AHGS2058P	m13Gm692V	2.629	5.6733	0.0207
O/L ratio	qOLRWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	6.3703	9.3455	-0.3184
	qOLRWW14-11-1	11	9	m13Ai119H15P	IPAHM123V	6.4503	9.4572	-0.3097
	qOLRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.8319	34.4039	-0.6456
	qOLRWS13-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.6724	22.7805	-0.4856
	qOLRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.107	32.4316	-0.6871
	qOLRWS14-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.1185	21.3013	-0.5156
	qOLRWS14-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.1185	21.3013	-0.5156
Total unsaturated fatty acid	qUWW13-5-1	5	26	m13AHGS2960V	m13Gm1867F	15.3481	23.4384	-1.224
	qUWW14-2-1	2	0	m13AHGS2252N	Seq18E7F	8.3957	10.2756	0.6612
	qUWW14-5-1	5	25	m13AHGS2960V	m13Gm1867F	8.7835	12.8897	-0.7489
	qUWW14-11-1	11	9	m13Ai119H15P	IPAHM123V	10.3802	12.912	-0.7552
	qUWS13-10-1	10	0	Seq3A8F	m13AHGS2185N	4.2332	6.3107	-0.977
	qUWS14-10-1	10	3	m13AHGS2185N	m13AHGS2602N	3.5707	5.9412	-0.3713
Total saturated fatty acid	qSWW13-11-1	11	8	m13Ai119H15P	IPAHM123V	13.3609	20.7842	0.6003
	qSWW14-2-1	2	0	m13AHGS2252N	Seq18E7F	8.3759	10.7607	-0.3441
	qSWW14-5-1	5	25	m13AHGS2960V	m13Gm1867F	6.9536	10.8962	0.3507
	qSWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	9.2037	13.6557	0.3988
	qSWS13-10-1	10	4	m13AHGS2602N	m13AHGS2490V	9.1249	13.7727	0.389
	qSWS14-3-1	3	24	Gm1954F	m13AHGS0268P	3.5701	4.472	0.2311
	qSWS14-10-1	10	3	m13AHGS2185N	m13AHGS2602N	8.2733	11.7138	0.3512
	qSWS14-10-1	10	3	m13AHGS2185N	m13AHGS2602N	8.2733	11.7138	0.3512
L/S ratio	qLSRWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	7.4998	10.909	0.0853
	qLSRWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	10.4784	16.6909	0.1066
	qLSRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	9.9018	35.8286	0.1745
	qLSRWS13-3-1	9	7	m13Seq5D5P	m13AHGS3217N	3.6955	7.6153	0.0695
	qLSRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.8211	38.7244	0.1801
	qLSRWS14-9-1	9	7	m13Seq5D5P	m13AHGS3217N	4.1961	8.4171	0.0728
U/S ratio	qUSRWW13-5-1	5	25	m13AHGS2960V	m13Gm1867F	15.2476	28.1939	-0.2326
	qUSRWW14-2-1	2	0	m13AHGS2252N	Seq18E7F	8.3247	10.5393	0.1157
	qUSRWW14-5-1	5	25	m13AHGS2960V	m13Gm1867F	7.3664	11.8217	-0.124

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	qUSRWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	9.8378	14.7341	-0.1406
	qUSRWS13-10-1	10	3	m13AHGS2185N	m13AHGS2602N	13.3444	20.5126	-0.1676
	qUSRWS14-10-1	10	3	m13AHGS2185N	m13AHGS2602N	12.4037	19.6841	-0.1456
CIV	qCIVWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	6.0743	8.9318	1.3129
	qCIVWW14-11-1	11	9	m13Ai119H15P	IPAHM123V	7.701	11.1851	1.385
	qCIVWS13-2-1	2	16	m13AHS0314N	m13PM32F	5.8237	8.986	1.7382
	qCIVWS14-4-1	4	21	Seq19G7F	m13AHGS1338P	2.7492	3.4126	1.06
	qCIVWS14-9-1	9	10	m13Seq5D5P	m13AHGS3217N	3.6447	7.5783	1.1786
	qCIVWS14-11-1	11	1	m13AHGS2249F	m13Pm188F	9.0344	11.0778	1.7158
OAD	qOADWW13-11-1	11	8	m13Ai119H15P	IPAHM123V	12.0123	18.8814	-0.0371
	qOADWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	12.2046	19.1358	-0.0371
	qOADWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.3521	40.799	-0.0522
	qOADWS13-1-2	1	25	m13AHGS2043V	m13TC2D06N	10.0831	27.4804	-0.0401
	qOADWS13-9-1	9	9	m13Seq5D5P	m13AHGS3217N	4.7213	10.6439	-0.0235
	qOADWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.2952	41.1846	-0.0536
	qOADWS14-9-1	9	9	m13Seq5D5P	m13AHGS3217N	4.771	10.7315	-0.0241

Table 59: QTLs associated with foliar disease resistance traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
LLS Score at 70 DAS	qLLS70WW13-2-1	2	0	m13AHGS2252N	Seq18E7F	14.705	12.8932	-0.35
	qLLS70WW13-3-1	3	57	m13TC39C01V	Gm2215F	3.9677	7.9845	-0.9372
	qLLS70WW13-4-1	4	14	Seq19G7F	m13AHGS1338P	22.5228	27.7764	0.559
	qLLS70WW13-7-1	7	1	TC7C06N	m13TC41C11F	12.2529	11.5455	0.3562
	qLLS70WW13-13-2	13	108	m13Gm692V	m13AHGS2342P	13.6252	14.0964	0.4015
	qLLS70WW14-2-1	2	0	m13AHGS2252N	Seq18E7F	14.705	12.8932	-0.35
	qLLS70WW14-3-1	3	57	m13TC39C01V	Gm2215F	3.9677	7.9845	-0.9372
	qLLS70WW14-4-1	4	14	Seq19G7F	m13AHGS1338P	22.5228	27.7764	0.559
	qLLS70WW14-7-1	7	1	TC7C06N	m13TC41C11F	12.2529	11.5455	0.3562
	qLLS70WW14-13-1	13	108	m13Gm692V	m13AHGS2342P	13.6252	14.0964	0.4015
	qLLS70WS13-5-1	5	24	m13AHGS2960V	m13Gm1867F	23.185	51.4753	0.9665
	qLLS70WS13-5-2	5	29	m13Gm1867F	m13GM2637V	19.0417	19.6613	0.5924
	qLLS70WS13-12-1	12	2	m13AHGS1998N	m13AHGS2205V	13.6622	13.3877	0.5123
	qLLS70WS14-2-1	2	0	m13AHGS2252N	Seq18E7F	8.2691	6.2223	-0.2129
	qLLS70WS14-3-1	3	56	m13TC39C01V	Gm2215F	4.1945	8.8561	-0.6343
	qLLS70WS14-4-1	4	15	Seq19G7F	m13AHGS1338P	16.0706	21.5445	0.4339
	qLLS70WS14-6-1	6	6	TC6E01N	m13TC2B09N	9.2425	7.4562	0.2544
	qLLS70WS14-10-1	10	7	m13AHGS2602N	m13AHGS2490V	6.0369	5.3725	0.2015
	qLLS70WS14-13-1	13	108	m13Gm692V	m13AHGS2342P	10.7081	10.1022	0.2969
LLS score at 80 DAS	qLLS80WW13-3-1	3	57	m13TC39C01V	Gm2215F	5.0844	6.3095	-1.3309
	qLLS80WW13-4-1	4	7	Gm2301F	Gm1996F	19.487	16.9999	0.6042
	qLLS80WW13-6-1	6	6	TC6E01N	m13TC2B09N	9.2337	5.8142	0.372

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	qLLS80WW13-10-1	10	0	Seq3A8F	m13AHGS2185N	3.8547	2.1924	-0.1951
	qLLS80WW13-10-2	10	7	m13AHGS2602N	m13AHGS2490V	9.101	6.6046	0.3699
	qLLS80WW13-13-1	13	109	m13Gm692V	m13AHGS2342P	9.8814	6.7264	0.396
	qLLS80WW14-4-1	4	7	Gm2301F	Gm1996F	17.4351	14.7677	0.5906
	qLLS80WW14-6-1	6	6	TC6E01N	m13TC2B09N	12.9515	9.3145	0.4926
	qLLS80WW14-8-1	8	0	m13RN13D04P	m13Seq2E6P	10.1982	6.7504	0.3753
	qLLS80WS13-3-1	3	56	m13TC39C01V	Gm2215F	2.6126	6.3612	-0.5665
	qLLS80WS13-4-1	4	5	Gm2301F	Gm1996F	6.2285	4.8342	0.2082
	qLLS80WS13-6-1	6	6	TC6E01N	m13TC2B09N	24.5502	19.0095	0.4298
	qLLS80WS13-8-1	8	32	m13IPAHM219F	m13AHGS2094F	8.5097	5.5504	-0.2045
	qLLS80WS13-10-1	10	8	m13AHGS2602N	m13AHGS2490V	6.4328	4.555	0.1961
	qLLS80WS13-13-1	13	109	m13Gm692V	m13AHGS2342P	10.0409	6.9499	0.2564
	qLLS80WS14-3-1	3	57	m13TC39C01V	Gm2215F	6.0596	6.6222	-1.1823
	qLLS80WS14-4-1	4	10	Gm1996F	Seq19G7F	29.8664	25.5542	0.6174
	qLLS80WS14-4-2	4	14	Seq19G7F	m13AHGS1338P	43.5372	34.2892	0.7274
	qLLS80WS14-10-1	10	7	m13AHGS2602N	m13AHGS2490V	12.4022	14.8272	0.4597
	qLLS80WS14-10-2	10	13	m13AHGS2490V	TC6H03F	12.1945	14.5952	0.4565
	qLLS80WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	12.1876	14.3371	0.4822
LLS score at 90 DAS	qLLS90WW13-3-1	3	56	m13TC39C01V	Gm2215F	5.4051	9.378	-1.3875
	qLLS90WW13-6-1	6	4	TC6E01N	m13TC2B09N	35.484	41.6331	1.5481
	qLLS90WW13-10-1	10	13	m13AHGS2490V	TC6H03F	5.7161	4.5816	0.4232
	qLLS90WW13-13-1	13	107	m13Gm692V	m13AHGS2342P	38.8059	39.3538	1.5077
	qLLS90WW14-3-1	3	56	m13TC39C01V	Gm2215F	5.1332	8.3231	-1.3662
	qLLS90WW14-6-1	6	4	TC6E01N	m13TC2B09N	30.1672	38.4985	1.49
	qLLS90WW14-10-1	10	13	m13AHGS2490V	TC6H03F	6.8211	5.6266	0.4717
	qLLS90WW14-13-2	13	107	m13Gm692V	m13AHGS2342P	38.2057	38.9583	1.5063

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	qLLS90WS13-3-1	3	56	m13TC39C01V	Gm2215F	4.8082	10.6829	-0.9972
	qLLS90WS13-6-1	6	4	TC6E01N	m13TC2B09N	26.4251	38.952	0.9881
	qLLS90WS13-10-1	10	7	m13AHGS2602N	m13AHGS2490V	4.8562	4.059	0.269
	qLLS90WS13-13-2	13	107	m13Gm692V	m13AHGS2342P	29.7087	38.6361	1.0254
	qLLS90WS14-3-1	3	55	m13TC39C01V	Gm2215F	5.3446	10.3087	-1.03
	qLLS90WS14-6-1	6	4	TC6E01N	m13TC2B09N	30.9342	41.2403	1.2792
	qLLS90WS14-10-1	10	13	m13AHGS2490V	TC6H03F	6.8511	5.8697	0.4006
	qLLS90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	32.4002	37.7005	1.2353
RUST score at 70 DAS	qRUST70WW13-3-1	3	52	m13TC39C01V	Gm2215F	11.7421	26.3975	-0.3606
	qRUST70WW13-6-1	6	6	TC6E01N	m13TC2B09N	18.5791	18.0241	0.2324
	qRUST70WW13-13-1	13	109	m13Gm692V	m13AHGS2342P	16.542	16.0028	0.2164
	qRUST70WW14-3-1	3	52	m13TC39C01V	Gm2215F	11.7421	26.3975	-0.3606
	qRUST70WW14-6-1	6	6	TC6E01N	m13TC2B09N	18.5791	18.0241	0.2324
	qRUST70WW14-13-1	13	109	m13Gm692V	m13AHGS2342P	16.542	16.0028	0.2164
	qRUST70WS13-3-1	3	56	m13TC39C01V	Gm2215F	2.6466	11.7675	-0.9104
	qRUST70WS13-8-1	8	23	m13IPAHM219F	m13AHGS2094F	27.8722	63.2788	0.947
	qRUST70WS13-10-1	10	5	m13AHGS2602N	m13AHGS2490V	5.4814	6.412	0.2778
	qRUST70WS14-3-1	3	52	m13TC39C01V	Gm2215F	6.0948	17.1283	-0.2532
	qRUST70WS14-6-1	6	6	TC6E01N	m13TC2B09N	9.9586	8.1262	0.1308
	qRUST70WS14-7-1	7	0	TC7C06N	m13TC41C11F	6.4619	4.8117	0.1012
	qRUST70WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	15.5487	17.2741	0.1942
RUST score at 80 DAS	qRUST80WW13-6-1	6	6	TC6E01N	m13TC2B09N	11.807	9.9736	0.2474
	qRUST80WW13-10-1	10	6	m13AHGS2602N	m13AHGS2490V	10.6668	9.5203	0.2242
	qRUST80WW13-13-1	13	108	m13Gm692V	m13AHGS2342P	6.2103	5.4693	0.1814
	qRUST80WW14-6-1	6	6	TC6E01N	m13TC2B09N	12.3303	10.2687	0.2505
	qRUST80WW14-10-1	10	5	m13AHGS2602N	m13AHGS2490V	10.4483	8.9579	0.2166

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	qRUST80WW14-13-1	13	108	m13Gm692V	m13AHGS2342P	6.715	5.8316	0.1868
	qRUST80WS13-6-1	6	6	TC6E01N	m13TC2B09N	22.1786	22.3728	0.4151
	qRUST80WS13-10-1	10	6	m13AHGS2602N	m13AHGS2490V	11.1365	11.1294	0.2716
	qRUST80WS14-3-1	3	57	m13TC39C01V	Gm2215F	3.7318	7.3905	-0.5184
	qRUST80WS14-6-1	6	6	TC6E01N	m13TC2B09N	14.9598	12.0318	0.2131
	qRUST80WS14-10-1	10	8	m13AHGS2602N	m13AHGS2490V	7.6754	6.1916	0.1424
	qRUST80WS14-13-1	13	109	m13Gm692V	m13AHGS2342P	12.3416	10.4292	0.1965
RUST score at 90 DAS	qRUST90WW13-2-1	2	1	m13AHGS2252N	Seq18E7F	9.4904	6.8133	0.3925
	qRUST90WW13-3-1	3	56	m13TC39C01V	Gm2215F	3.7678	7.3887	-0.9727
	qRUST90WW13-6-1	6	6	TC6E01N	m13TC2B09N	9.6641	6.2337	0.4087
	qRUST90WW13-10-1	10	6	m13AHGS2602N	m13AHGS2490V	9.9216	8.8473	0.4569
	qRUST90WW13-13-1	13	107	m13Gm692V	m13AHGS2342P	13.8716	24.3895	0.8932
	qRUST90WW14-3-1	3	56	m13TC39C01V	Gm2215F	4.2732	7.1718	-1.0041
	qRUST90WW14-4-1	4	15	Seq19G7F	m13AHGS1338P	15.2854	22.0308	0.8283
	qRUST90WW14-5-1	5	20	m13AHS0025V	m13AHGS2960V	6.8132	4.2004	0.3264
	qRUST90WW14-6-1	6	6	TC6E01N	m13TC2B09N	6.5122	4.1129	0.3355
	qRUST90WW14-13-1	13	107	m13Gm692V	m13AHGS2342P	26.1699	32.843	1.09
	qRUST90WS13-3-1	3	54	m13TC39C01V	Gm2215F	6.4851	14.7451	-0.678
	qRUST90WS13-4-1	4	4	Gm2301F	Gm1996F	7.5048	7.5226	0.3009
	qRUST90WS13-5-1	5	32	m13GM2637V	m13GM2638F	9.172	7.2671	-0.2775
	qRUST90WS13-6-1	6	4	TC6E01N	m13TC2B09N	35.833	51.643	0.9155
	qRUST90WS13-13-1	13	107	m13Gm692V	m13AHGS2342P	30.9987	43.8737	0.8675
	qRUST90WS14-3-1	3	54	m13TC39C01V	Gm2215F	5.584	12.2532	-0.7096
	qRUST90WS14-4-1	4	4	Gm2301F	Gm1996F	6.7676	6.1094	0.3073
	qRUST90WS14-6-1	6	4	TC6E01N	m13TC2B09N	28.7839	40.078	0.938
	qRUST90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	44.5729	42.8251	0.9754

4.5.2.1 QTLs associated with oil quality Traits

Three minor QTLs were identified for total oil content on LG-5 and 17. Except the QTL, qTOCWS14, remaining were derived from TMV-2.

Totally three QTLs were identified for total protein content on LG-3 and LG-13. All the QTLs were derived from TMV-2. Among these, a major QTL namely qTPCWS13 was mapped between the flanking markers m13TC39C01V and Gm2215F with a LOD value of 5.23 and with a highest phenotypic variation explanation of 18.78%.

Six and five minor QTLs were detected for palmitic and stearic acid, respectively among which most of the QTLs were derived from GM 6-1.

Six QTLs were detected for oleic acid on 1, 5, 9 and 11 chromosomes which were derived from the parent TMV-2. Among these three were major QTLs, among which qOLEWS14 was detected with high LOD (11.04) and phenotypic variation explained (38.72 %).

Totally nine QTLs, were identified for linoleic acid on LG-1, 3, 4, 9 and 11 respectively. All the QTLs were derived from GM 6-1. Among the five major QTLs identified, QTL qLINWS14 was mapped between the flanking markers m13TC16A10N and m13AHGS2043V with high LOD (12.65) and highest phenotypic variation explained (41.09 %).

Totally, six, seven, seven and six QTLs were detected for arachidic acid, eicosenoic acid, behenoic acid and lignoceric acid, respectively. Among them, QTL for behenoic acid namely, qBEHWS14-4-1 derived from GM 6-1 was present on LG-4 with a LOD value of 11.69 and phenotypic variation explained was 21.19. This marker was tagged between markers Seq19G7F and m13AHGS1338P.

Six QTLs were detected on two linkage groups (1 and 11) for O/L ratio, which were derived from TMV-2. Two major QTLs (qOLRWS13 and qOLRWS14) were detected for this trait under water stress situation and were mapped at same position on LG-1 between the markers m13TC16A10N and m13AHGS2043V with high LOD value (10.83 and 10.10) and highest phenotypic variation explained (34.40 % and 32.43 %).

Among six and seven minor QTLs, detected for total unsaturated and total saturated fatty acids, most of the QTLs for unsaturated fatty acids were derived from TMV-2 while most of the QTLs for saturated fatty acids were derived from GM 6-1.

Totally, six QTLs were detected among which two were the major QTLs for each of the trait viz., U/S and L/S ratio. All the QTLs for L/S ratio were derived from GM 6-1 while for U/S ratio were derived from TMV-2. QTL for L/S ratio namely, qLSRWS14-1-1 explained highest phenotypic variation (38.72) with a LOD value of 9.90 and was flanked by two markers m13TC16A10N and m13AHGS2043V at a position of 12 cM on LG-1. Similarly, for U/S ratio QTL namely, qUSRWW13-5-1 was flanked between the markers m13AHGS2960V and m13Gm1867F at a position of 25 cM on LG-5 with a LOD value of 15.25 and PVE % of 28.19.

Totally, six and seven QTLs were detected for the traits CIV and OAD, respectively. Most of the QTLs for CIV were minor QTLs and were derived from the parent GM 6-1 while the QTLs for OAD were derived from TMV-2. Among the three major QTLs detected for the OAD, one of the major QTL, qOADWS14-1-1 explained highest phenotypic variation (41.18) with a LOD value of 12.29 and was flanked by two markers m13TC16A10N and m13AHGS2043V at a position of 12 cM on LG-1.

4.5.2.2 QTLs associated with foliar disease resistance traits

Among the foliar disease resistance traits, LLS score and rust scores at 80 and 90 DAS were found to be most important compared to the LLS and rust scores at 70 DAS depending upon the severity of infection at crop growth stage. Several major and minor QTLs were detected for those traits under both WW and WS conditions.

Totally 21 QTLs were detected for LLS score at 80 DAS among which two major QTLs were detected on LG-4. Both of them were detected for WS situation and were derived from GM 6-1. QTL qLLS80WS14-4-2 explained highest phenotypic variation (34.28) with the highest LOD value of 43.53 and was flanked by two markers Seq19G7F and m13AHGS1338P at a position of 14 cM on LG-4.

Similarly, 16 QTLs were detected for LLS score at 90 DAS and among which all the eight major QTLs were derived from the resistant parent GM 6-1. QTLs namely, qLLS90WW13-6-1 and qLLS90WS14-6-1 were identified for WW and WS conditions

at same position of 4 cM on the LG-6 with highest PVE % (41.63 and 41.24) and high LOD value (35.48 and 30.93).

For rust score at 80 DAS 13 QTLs were derived among which one of the major QTL namely, qRUST70WS13-8-1 was detected on LG-8 at a position of 23 cM between the flanking markers m13IPAHM219F and m13AHGS2094F with a high LOD value of 27.87 and highest PVE % of 63.28.

Similarly, 19 QTLs were detected for rust score at 90 DAS and among which all the seven major QTLs were derived from the resistant parent GM 6-1. QTL namely, qRUST90WS13-6-1 was identified for WS1 conditions at a position of 4 cM on the LG-6 with highest PVE % (51.64) and high LOD value (35.83).

5. DISCUSSION

Groundnut is usually grown under low input conditions particularly in developing countries. Productivity of the crop is restricted primarily by two types of stresses: (i) abiotic and (ii) biotic. Among the abiotic stresses, drought is the most important constraint challenging global groundnut production. Improvement of drought tolerance is being attempted on limited scale through breeding programmes as breeding for enhanced tolerance has been difficult due to the

- (i) Genetic complexity of the trait,
- (ii) High genotype by environment interactions,
- (iii) Lack of precise phenotypic evaluation strategies at the field level, and
- (iv) Differences in duration and severity of drought in many locations.

Thus, the improvement of key traits, especially drought tolerance, has become a key challenge for conventional breeding approaches that rely on selection for yield under stressed environments. The difficulties of controlling the level of water stress under natural conditions and genotype by environment interactions for yield makes direct selection difficult. Therefore, approaches that combine genomics with breeding and physiology, termed genomics-assisted breeding (Varshney *et al.*, 2005), provide strategies for improving component traits of drought tolerance.

The results oriented in this direction on genotyping and phenotyping of the RILs for quantitative, physiological, root, oil quality and foliar disease resistance traits under two water regimes over two seasons from the study are discussed under the following subheadings.

- 5.1 Mean performance for quantitative, physiological, root, oil quality and foliar disease resistance traits
- 5.2 Genetic variability for quantitative, physiological, root, oil quality and foliar disease resistance traits
- 5.3 Correlation analysis for quantitative, physiological, root, oil quality and foliar disease resistance traits

5.4 Construction of genetic linkage map

5.5 QTL mapping for traits related to drought tolerance and quality traits

5.1 Mean performance of the RILs for quantitative, physiological, root, oil quality and foliar disease resistance traits

Trait specific breeding is a cumbersome process when one may not end up with expected output unless the genotypes used in the programme are consistent in the phenotypic expression. It is important to trace the genotypes having the desired trait for such purpose. Recombinant inbred lines (RILs) provide an opportunity for selection, since the combinations among the different traits adds to the variability. Identified RILs performing better for a trait under specific conditions can be used as a reservoir in the crop improvement programmes aimed towards trait specific breeding. Variation observed during 15 and 30 DAS in WS condition of field evaluation is indicated in Plate 7 and 8.

In this context, an attempt was made in the present study to generate the information on mean performance of the RILs for various traits and identify superior RILs that are stable across the seasons for each trait. RILs were evaluated in two water regimes during two seasons of summer 2012-13 and summer 2013-14 at UAS, Dharwad to understand the effect of water regime and season on quantitative, physiological, root and quality traits. Frequency distribution for all the traits indicated the normal distribution in the population (Appendix VII to IX). Critical analysis of the means of the RILs indicated the consistent performance in the oil quality and foliar disease resistance traits under each water regime of two seasons. Whereas a slight variation in some of the quantitative, physiological and root traits can be attributed to the slight variation in the time of occurrence, intensity and duration of drought stress during the crop growth period of the two seasons and also indicates the complex nature of drought tolerance mechanism in the crop. However, to exploit the genotypic differences, RILs showing



Plate 7: Variation observed among the genotypes at 15 days after water stress with in WS condition of field evaluation

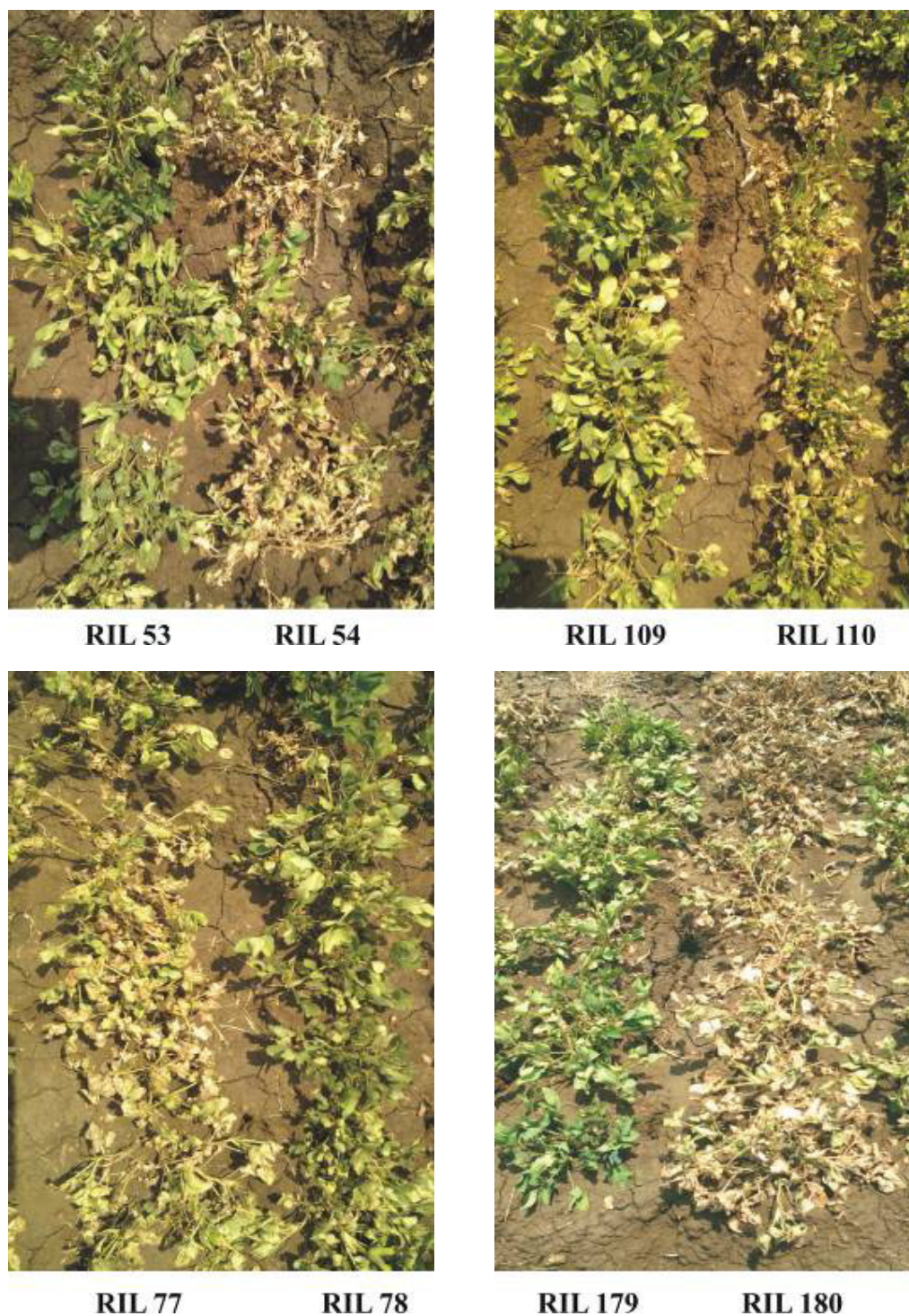


Plate 8: Variation observed among the genotypes at 30 days after water stress with in WS condition of field evaluation

better and consistent performance over the seasons for each of the trait were identified and can be used in future breeding programmes.

5.1.1 Quantitative traits

Seasonal variation was highly significant for the traits *viz.*, days to 50 per cent flowering and days to maturity as indicated through mean and range for these traits in consecutive seasons. This variation could be due to different dates of sowing in the two seasons. Similar results of effect of sowing dates on phenology in groundnut were in clear agreement with the reports of Ntare *et al.* (1998).

Effect of irrigation level was more significant than the effect of season on expression of the traits *viz.*, number of pegs per plant, number of mature pods per plant, pod yield per plant, kernel yield per plant, shelling per cent, sound mature kernel per cent and hundred seed weight which is indicated through decrease in the mean and range for these traits under WS condition compared to WW condition in both the seasons. The number of mature pods per plant was low under WS condition due to increases in soil resistance caused by prolonged drought while reduction in pod yield under water stress is primarily due to the decreased duration of the pod development phase. These results were in agreement with the reports of effect of water stress on yield and agronomic characters by Vorasoot *et al.* (2003).

Superior RILs for quantitative traits pooled across the both the seasons under WS condition are as given below.

Under WS condition RILs 58, 200, 184, 26, 40, 50, 53, 54, 57 and 94 were early in flowering compared to best parent GM 6-1 (29.5 days). Similarly, RILs 26, 2, 16, 24, 58, 71, 200, 269, 275 and 278 were early to mature compared to best parent GM 6-1 (102 days). RILs 64, 88, 59, 62, 178, 183, 53, 63, 176 and 49 had short plant type compared to the best parent GM 6-1 (20.25 cm). Similarly, RILs 41, 47, 190, 259, 254, 162, 14, 70, 137 and 262 for number of secondary branches per plant; RILs 201, 216, 58, 63, 75, 269, 72, 202, 11 and 197 for mature pods per plant; RILs 266, 158, 69, 126, 129, 255, 212, 114, 152 and 156 for shelling per cent; RILs 280, 194, 65, 199, 99, 72, 201, 176, 108 and 215 for SMKper cent; RILs 26, 14, 119, 35, 7, 33, 2, 47, 201 and 3 for hundred seed weight were superior to the parent GM 6-1. RILs *viz.*, 7, 289, 202, 70,

101, 50, 265, 261, 58 and 26 were superior for both pod yield per plant and kernel yield per plant compared to drought tolerant parent GM 6-1 (5.10 gm and 3.11 gm) respectively.

5.1.2 Physiological traits

In general relative water content (RWC) of leaves was higher in the initial stages of leaf development and declined as the dry matter accumulates and leaf matures. RWC of the RILs under WS condition was lower compared to the RWC under WW condition as indicated through mean for this trait at different stages of stress. These results were in conformity with the reports of Jain *et al.* 1997. Water stress also decreased the SLA but increased SCMR (Songsri *et al.*, 2009).

RWC, SLA and SCMR are very important drought tolerant attributes and in general genotypes which can maintain higher RWC and SCMR and lower SLA were considered to have higher water saving capacity (Songsri *et al.* 2008). For RWC at 15 days after stress (DAS) RILs 69, 8, 128, 59, 254, 119, 162, 187, 149 and 7; for RWC at 30 DAS, RILs 254, 35, 195, 7, 188, 206, 69, 88, 217 and 47; for SLA at 15 DAS, RILs 92, 57, 246, 206, 231, 217, 76, 38, 45 and 72; for SLA at 30 DAS, RILs 35, 201, 213, 206, 7, 47, 11, 196, 149 and 198 while for SCMR, RILs 7, 61, 206, 254, 72, 202, 198, 5, 195 and 35 were superior than the drought tolerant parent GM 6-1. Among all the genotypes RIL-7 could maintain higher RWC and SPAD and SLA at later stages of the stress period and also recorded highest pod yield under stress compared to other genotypes.

5.1.3 Root traits

Root growth of groundnut is influenced by soil moisture (Jongrunklang *et al.*, 2011). Irrigation level had significant effect on most of the root traits under both seasons. Water stress stimulates the growth of roots into deeper soil even though vegetative growth appears to stop as indicated through increase in the mean of root to shoot ratio under water stress condition.

Superior RILs for root traits under water stress condition are RILs 101, 194, 91, 83, 46, 40, 147, 13, 27 and 47; RILs 197, 256, 298, 268, 147, 148, 244, 145, 243 and 189 while RILs 22, 76, 14, 11, 13, 5, 98, 4, 33, 6 were superior to parent GM 6-1(48.3

cm, 6.5 and 0.4 gm respectively) with higher root length, root to shoot ratio and root dry weight, respectively.

5.1.4 Oil quality traits

Fatty acid profiles of oil from groundnut can vary with growing seasons (Norden *et al.*, 1987) and water stress can also change the fatty acid profile (Dwivedi *et al.*, 1996). Abiotic stress-induced changes in the fatty acid composition of plant membrane lipids mainly occur through the regulated activities of fatty acid desaturases. Effect of water stress was positive and increased the mean of traits viz., oleic acid, oleic to linoleic acid ratio, eicosenoic acid, lignoceric acid total unsaturated fatty acids, unsaturated to saturated fatty acid ratio and oleic acid desaturation while effect was negative on the traits viz., palmitic acid, linoleic acid, total saturated fatty acids, linoleic to saturated fatty acid ratio and calculated iodine value during both the seasons. In contrast the effect of water stress was different in two seasons for the traits viz., total protein content, stearic acid, arachidic acid and behenoic acid as indicated by the highly significant effect of season on these traits compared to other sources of variation. In contrast to the above results Hashim *et al.* (1993), reported an increase in palmitic and linoleic acids and a decrease in stearic, oleic and eicosenoic acids when florunner groundnut was stressed for 30 days at maturation. These differences between the two studies could be ascribed to the larger number of genotypes in the present study and stage of water stress.

5.1.5 Foliar disease resistance traits

Rust and late leaf spot (LLS) are the two most widely distributed and economically important foliar diseases of groundnut causing severe damage to the crop (Mc Donald *et al.*, 1985 and Kokalis-Burette *et al.*, 1997). They are commonly present wherever groundnut is grown but their incidence and severity vary between localities and seasons. Each disease alone is capable of causing substantial yield loss but when they occur together losses are further increased. These foliar diseases besides reducing the yield also have an adverse influence on seed quality and grade characteristics, deteriorate the quality of plant biomass and thus render the fodder unsuitable as animal feed. So it is necessary to identify the lines which show resistant reaction against the infection at all the stages.

RILs 38, 39, 40, 41, 42, 43, 44, 45, 46 and 47 recorded lower LLS and rust scores compared to susceptible parent TMV-2 across the seasons and under both water regimes.

5.1.6 Superior RILs for pod yield under WS condition

Superior RILs for pod yield per plant under WS condition (Fig. 5) compared to the parent TMV-2 (3.6 gm) are listed in the Table 60 along with other important yield component traits, physiological and root traits. Among these, RILs 7, 289, 202, 70, 101 and 50 had significantly higher pod yield under WS condition compared to the drought tolerant parent, GM 6-1 (5.1 gm). These RILs also had significant superiority over GM 6-1 for traits *viz.*, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant and kernel yield per plant. These RILs can be used drought tolerance source for their use in further breeding programmes.

RILs 289, 50, 265, 26, 2, 44, 296, 53, 259 and 179 had superior for pod yield under both WW and WS conditions over both seasons. Drought tolerant and drought susceptible RILs identified across two seasons along with comparison of their drought tolerance index (DTI) for pod yield and DTI for other important attributes which exhibited significant positive correlations with pod yield under stress are furnished in Table 61 (Fig. 6; Plate 9 and 10). DTI of more than 1 for any trait indicates increased or higher performance, while less than 1 indicates decreased or lower performance under WS condition compared to WW condition. Field view of comparison of drought tolerant and susceptible RILs at 30 days after stress during summer 2012-13 is indicated in Plate 11.

In general DTI for most of the traits was less than one indicating the drought stress resulted in reduction in performance of genotype under WS compared to the WW condition; however some of the drought tolerant lines had showed DTI of more than one for some of the traits. DTI for most of the traits was higher for drought tolerant RILs as indicated by means and range for drought tolerant and susceptible RILs compared to the drought susceptible RILs except DTI for SLA indicating the reduction of performance was more prominent in the susceptible RILs compared to the tolerant RILs. Higher DTI for drought tolerant RILs compared to the susceptible RILs was more prominent for some of the traits *viz.*, number of secondary branches per plant, number

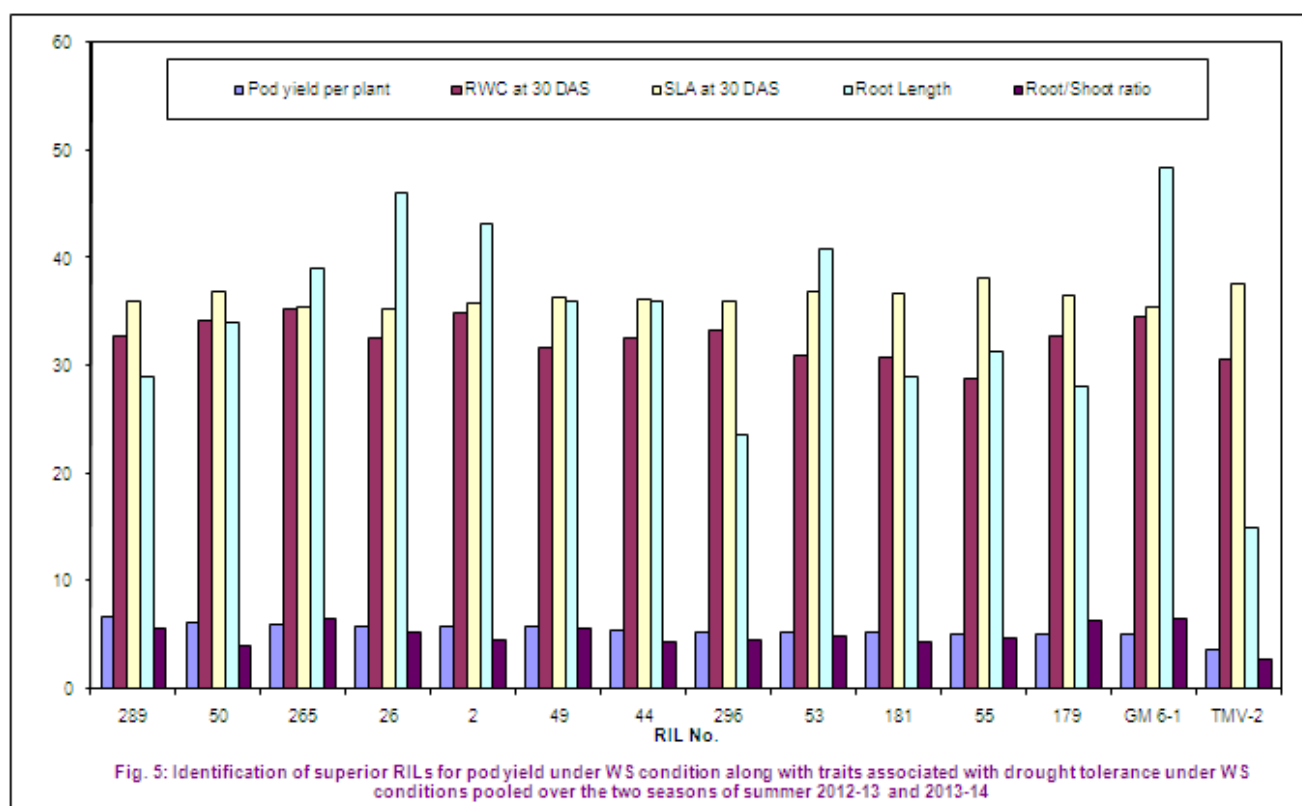


Table 60: Superior RILs for pod yield under WS condition along with its component traits, physiological and root traits under WW and WS conditions pooled over the two seasons of summer 2012-13 and 2013-14

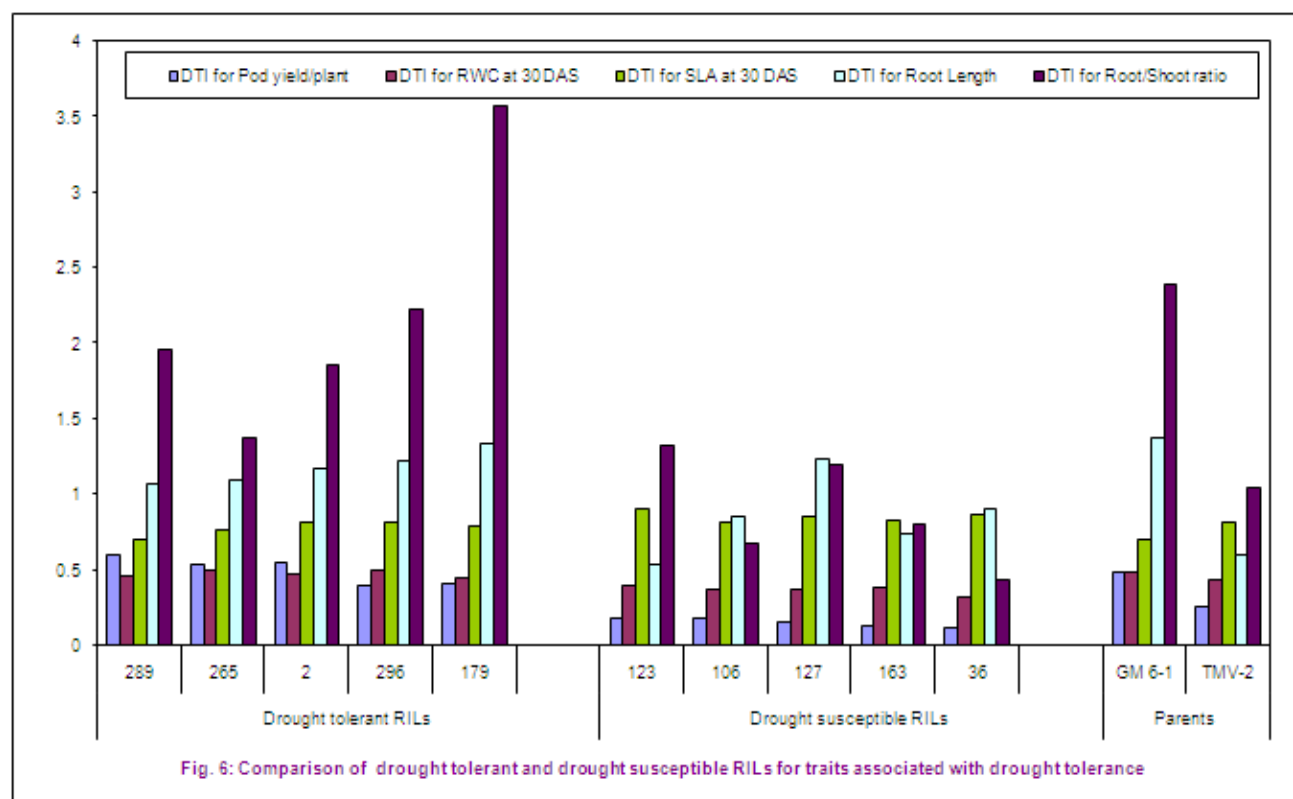
Genotype	Pod yield per plant		Days to 50% flowering		Days to maturity		Plant height		No of primary branches/ plant		No secondary branches/ plant		Number of pegs/ plant		Number of mature pods/ plant		Kernel yield per plant		Shelling per cent	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
7	8.2	6.8	32.0	30.3	103.0	102.8	29.4	24.0	5.7	5.7	1.9	3.7	16.6	26.0	13.3	16.1	5.5	4.1	67.6	60.8
289	11.2	6.6	31.5	28.8	102.5	101.8	30.8	24.8	6.2	6.2	4.3	2.9	24.2	20.9	23.8	16.9	7.7	4.0	68.7	60.6
202	9.4	6.5	30.5	28.5	102.5	102.0	25.8	17.1	5.0	4.1	2.3	4.1	7.4	33.4	18.0	20.0	6.3	3.9	67.5	60.4
70	9.6	6.2	31.5	30.0	103.5	102.5	27.0	18.3	6.5	5.0	2.5	4.5	10.2	20.9	12.7	15.4	6.8	3.8	70.3	59.6
101	9.4	6.1	31.5	30.0	103.5	102.5	31.3	19.0	6.0	5.2	4.5	2.5	13.9	18.7	15.8	13.2	6.5	3.7	69.8	59.8
50	11.1	6.1	31.3	28.5	102.5	102.0	21.3	19.5	5.7	5.4	3.2	4.4	20.7	22.4	18.4	15.4	7.8	3.6	70.5	59.0
265	11.8	6.0	31.0	29.5	103.0	102.0	31.3	20.0	7.6	6.5	4.6	2.7	24.9	15.6	28.1	14.1	7.9	3.7	67.1	61.2
261	8.6	5.9	31.3	29.5	103.3	102.0	36.5	28.5	5.8	5.5	2.3	2.2	30.0	16.4	25.5	14.2	5.9	3.6	68.4	62.5
58	9.8	5.9	31.5	28.0	102.3	101.5	29.6	20.8	6.0	5.9	6.5	2.6	22.0	31.4	14.4	23.8	6.9	3.5	70.6	59.9
26	14.6	5.8	30.0	28.5	102.0	101.0	30.0	23.4	5.7	6.5	4.3	2.8	16.3	14.9	25.5	12.0	9.9	3.5	67.7	61.1
194	5.9	5.8	30.8	28.5	102.8	102.0	31.8	21.3	4.7	5.6	2.0	4.0	9.3	25.0	14.7	18.4	3.9	3.5	67.1	60.2
2	10.5	5.8	31.5	29.8	102.0	101.5	32.0	21.8	6.0	7.3	2.3	3.8	34.5	19.9	16.1	16.8	7.1	3.4	68.2	59.9
49	15.3	5.7	31.0	29.0	103.0	102.0	28.1	15.3	6.1	6.3	3.7	2.4	33.7	16.0	26.0	15.1	10.7	3.3	69.6	58.5
215	8.0	5.5	31.5	30.0	103.5	102.8	37.8	19.3	5.9	6.4	2.2	2.9	7.9	21.3	12.7	13.8	5.4	3.3	67.5	60.5
284	9.1	5.5	31.5	30.5	103.5	102.5	27.3	20.0	6.0	5.7	2.8	3.4	8.6	23.4	12.5	16.0	6.2	3.4	68.4	62.7
44	10.6	5.4	31.0	29.8	103.0	102.3	21.3	22.3	6.8	5.6	2.2	3.1	11.1	13.7	13.7	12.8	7.5	3.3	70.8	62.4
199	7.6	5.4	31.0	28.8	103.0	102.3	29.0	16.9	5.8	6.0	2.9	4.0	6.3	23.4	14.2	14.1	5.2	3.2	68.2	59.8
296	13.5	5.3	31.3	29.5	104.0	102.0	35.0	18.3	6.3	5.2	3.6	2.7	40.1	20.9	31.8	10.0	9.1	3.5	67.6	58.5
27	9.2	5.3	32.0	30.0	103.0	102.8	29.1	22.3	6.3	6.1	1.5	2.5	10.3	15.2	11.4	15.7	6.3	3.3	69.2	62.5
53	15.7	5.3	31.5	28.5	102.5	102.0	29.1	14.5	8.8	5.3	3.6	3.3	20.7	14.9	17.2	12.9	11.0	3.1	69.7	58.9
259	10.6	5.2	31.3	29.5	103.3	102.0	32.0	26.3	5.5	5.8	4.3	5.0	32.6	21.4	20.9	16.5	7.4	3.3	69.9	62.3
83	9.6	5.2	31.5	29.3	103.5	102.3	34.3	19.8	5.4	5.0	2.3	3.9	28.9	36.9	17.0	15.9	6.5	3.1	68.3	59.8
181	12.9	5.2	31.3	29.5	103.3	102.0	33.9	19.5	5.4	6.2	3.5	2.7	20.8	17.7	28.5	17.3	8.6	3.1	67.2	58.7
197	5.5	5.2	31.5	29.3	102.5	102.3	34.6	25.5	6.2	5.7	5.1	3.1	16.9	36.2	15.4	19.2	3.7	3.1	67.0	59.9
55	18.0	5.1	31.0	29.5	103.0	102.3	39.1	17.5	6.4	5.1	8.4	1.8	43.5	13.9	37.3	8.2	12.5	3.0	69.4	59.7
72	7.5	5.1	31.0	29.0	103.0	102.0	26.3	19.8	6.6	6.1	4.8	4.0	13.3	24.4	17.2	20.1	5.4	3.1	71.2	61.3
179	13.0	5.1	31.0	29.5	103.0	102.0	27.6	17.8	6.0	5.2	3.9	2.9	26.0	17.8	26.1	13.1	8.7	3.0	67.0	59.6
GM 6-1	10.3	5.1	31.3	29.5	102.8	102.0	25.8	20.3	7.3	5.6	2.8	2.5	40.4	17.7	15.0	11.9	7.0	3.1	68.5	61.8
TMV-2	13.6	3.6	31.5	30.3	103.5	102.8	27.6	19.3	5.0	4.3	1.8	2.0	35.2	6.9	23.6	6.8	11.0	2.4	68.0	52.9
CD at 5 %	0.96		0.37		0.93		2.66		0.62		0.96		0.36		4.17		0.56		1.94	

Cont..

Genotype	SMK %		100 seed weight		RWC at 15 DAS		RWC at 30 DAS		SLA 15 DAS		SLA 30 ADS		SCMR		Root Length		R/S ratio		Root Dry weight	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
7	67.6	65.1	34.2	34.8	79.6	66.1	69.8	37.3	50.6	48.6	41.6	34.6	39.9	52.9	40.3	46.8	2.5	6.1	0.2	0.2
289	82.4	67.0	43.8	25.7	76.1	58.2	70.7	32.8	55.8	48.9	51.3	35.9	42.5	48.1	27.0	29.0	2.8	5.6	0.3	0.3
202	81.1	66.1	31.9	27.8	77.2	61.6	66.6	35.5	58.3	45.8	46.7	35.2	44.8	51.4	29.0	26.0	2.5	5.8	0.3	0.5
70	61.3	59.8	36.8	30.7	74.8	62.6	72.9	34.4	53.2	47.2	45.2	36.6	41.5	48.7	27.1	34.3	2.2	5.7	0.3	0.4
101	81.5	59.0	36.1	27.6	77.3	61.5	72.3	34.9	48.3	44.6	45.4	35.6	36.1	48.9	32.8	58.9	2.0	7.7	0.3	0.5
50	78.9	59.7	40.4	22.1	76.9	59.9	73.5	34.1	53.1	45.9	45.5	36.8	44.5	49.7	35.8	34.0	2.9	4.0	0.4	0.4
265	86.4	70.0	35.9	18.5	75.3	64.4	70.7	35.2	53.5	45.5	46.2	35.5	42.6	49.0	35.3	39.0	4.7	6.5	0.3	0.2
261	88.4	69.9	38.3	23.1	78.4	59.1	72.2	34.7	60.1	49.0	46.8	35.4	42.0	47.5	35.0	29.0	4.7	7.3	0.4	0.4
58	69.6	64.6	39.5	24.3	78.4	55.8	70.4	32.3	50.3	47.6	45.3	36.3	38.1	45.7	44.8	27.1	2.8	3.3	0.6	0.5
26	83.8	54.9	38.8	39.4	78.8	62.8	74.8	32.6	53.4	49.8	43.7	35.3	46.5	45.8	30.0	46.0	1.9	5.3	0.2	0.3
194	61.7	75.8	27.8	25.0	76.5	54.5	67.9	33.4	55.0	46.6	49.3	35.4	43.3	49.2	41.0	57.6	5.1	4.3	0.4	0.7
2	73.7	64.0	42.8	32.8	79.2	61.2	74.5	34.8	55.1	42.0	44.1	35.8	41.8	48.9	36.8	43.1	2.4	4.5	0.4	0.5
49	81.4	58.3	32.1	29.4	77.5	60.0	76.2	31.7	51.2	48.8	42.8	36.4	37.0	49.2	39.5	36.0	4.1	5.5	0.5	0.6
215	83.4	70.4	29.1	23.1	72.0	58.2	69.9	34.8	64.7	47.4	47.8	35.8	40.5	49.4	18.0	36.0	3.0	10.0	0.3	0.3
284	56.3	60.7	36.9	26.0	75.4	61.8	72.3	32.4	54.7	51.3	44.3	35.5	37.4	48.9	14.1	32.0	2.0	9.4	0.1	0.3
44	61.4	59.8	40.0	20.5	77.1	61.6	75.8	32.6	55.1	46.7	45.6	36.1	41.6	44.9	35.0	35.9	2.2	4.3	0.3	0.5
199	52.7	74.0	41.9	20.4	75.8	59.1	69.4	34.1	52.1	45.3	45.9	35.3	42.8	47.1	17.6	32.4	2.9	5.0	0.2	0.2
296	81.5	61.3	30.2	19.5	74.4	64.8	66.6	33.3	52.6	46.5	44.5	35.9	45.7	47.4	19.3	23.5	2.0	4.5	0.3	0.5
27	67.4	66.0	42.3	31.5	79.5	61.1	73.5	34.1	49.6	46.5	46.5	35.7	42.0	47.3	48.3	52.5	3.4	5.3	0.3	0.6
53	75.3	56.4	39.8	18.9	74.3	60.5	69.6	31.0	51.9	47.2	45.6	36.9	43.0	46.6	36.5	40.8	3.7	4.8	0.4	0.6
259	74.2	68.2	30.4	26.5	78.6	64.6	68.6	33.7	56.3	51.2	47.8	35.1	42.1	50.0	27.0	30.5	2.7	7.6	0.2	0.3
83	71.7	68.2	31.3	22.0	75.4	61.5	69.3	34.8	53.9	44.3	44.7	35.9	40.1	49.6	36.5	54.8	2.1	8.4	0.4	0.7
181	80.6	68.0	40.7	19.0	80.6	59.7	74.4	30.7	57.5	48.1	53.8	36.7	38.5	50.0	34.5	29.0	6.5	4.4	0.2	0.2
197	51.8	63.0	27.3	30.3	78.8	55.5	71.6	32.4	55.1	42.7	45.2	35.8	44.6	47.8	32.0	33.0	4.9	16.5	0.3	0.1
55	87.1	57.8	31.0	14.8	76.3	59.5	74.8	28.7	53.0	43.5	45.0	38.1	38.9	44.6	35.8	31.3	2.9	4.7	0.3	0.2
72	68.3	72.8	42.3	28.3	74.0	62.0	67.6	35.6	54.3	41.9	44.4	35.1	40.3	51.4	27.3	37.0	2.1	4.5	0.4	0.4
179	92.6	61.0	32.5	17.7	77.3	64.4	72.5	32.8	51.9	45.0	46.1	36.5	43.8	47.2	21.0	28.0	1.8	6.3	0.3	0.5
GM 6-1	71.7	70.3	38.7	24.8	76.9	58.8	72.1	34.5	54.9	50.4	50.2	35.4	42.5	47.8	34.9	48.3	2.7	6.5	0.3	0.4
TMV-2	75.4	32.8	35.2	20.6	75.1	63.5	71.4	30.6	56.9	46.5	51.7	37.6	41.7	44.8	25.0	15.0	2.8	2.7	0.3	0.2
CD at 5 %	9.55		2.46		3.04		3.54		1.57		1.45		3.05		7.77		0.62		0.1	

Table 61: Comparison of DTI for pod yield and DTI for other important attributes among drought tolerant and drought susceptible RILs identified across the seasons

RIL No.	PH	NPBP	NSBP	NPPP	NMPP	PYP	KYP	SP	SMK	HSW	R3	S2	S3	RL	R/S	NNPP	RDW
Drought tolerant RILs																	
289	0.80	1.00	0.66	0.86	0.71	0.60	0.52	0.88	0.81	0.59	0.46	0.88	0.70	1.07	1.96	1.00	1.12
50	0.92	0.94	1.39	1.08	0.84	0.56	0.46	0.84	0.76	0.55	0.46	0.86	0.81	0.95	1.36	0.74	0.97
265	0.64	0.87	0.59	0.62	0.50	0.53	0.46	0.91	0.81	0.52	0.50	0.85	0.77	1.10	1.38	0.45	0.64
26	0.78	1.14	0.65	0.92	0.47	0.39	0.35	0.90	0.66	1.02	0.44	0.93	0.81	1.53	2.76	1.02	1.22
2	0.68	1.21	1.65	0.58	1.04	0.55	0.48	0.88	0.87	0.76	0.47	0.76	0.81	1.17	1.86	0.96	1.27
44	1.05	0.82	1.39	1.23	0.94	0.49	0.44	0.88	0.97	0.51	0.43	0.85	0.79	1.03	1.95	0.94	1.66
296	0.52	0.83	0.75	0.52	0.31	0.39	0.38	0.86	0.75	0.65	0.50	0.89	0.81	1.22	2.22	0.31	1.65
53	0.50	0.61	0.91	0.72	0.75	0.36	0.28	0.84	0.75	0.48	0.44	0.91	0.81	1.12	1.30	0.75	1.56
259	0.82	1.05	1.16	0.66	0.79	0.75	0.44	0.89	0.92	0.87	0.49	0.91	0.73	1.13	2.85	1.00	1.39
179	0.64	0.88	0.74	0.69	0.50	0.41	0.35	0.89	0.66	0.54	0.45	0.87	0.79	1.33	3.57	2.09	2.09
Mean	0.74	0.93	0.99	0.79	0.68	0.50	0.42	0.88	0.80	0.65	0.46	0.87	0.78	1.17	2.12	0.93	1.36
Min	0.50	0.61	0.59	0.52	0.31	0.36	0.28	0.84	0.66	0.48	0.43	0.76	0.70	0.95	1.30	0.31	0.64
Max	1.05	1.21	1.65	1.23	1.04	0.75	0.52	0.91	0.97	1.02	0.50	0.93	0.81	1.53	3.57	2.09	2.09
Drought susceptible RILs																	
123	0.60	0.70	0.44	0.10	0.35	0.18	0.17	0.84	0.46	0.79	0.39	1.04	0.90	0.54	1.32	0.53	0.38
106	0.61	0.80	0.86	0.21	0.43	0.18	0.13	0.69	0.45	0.60	0.37	0.98	0.81	0.85	0.68	0.19	0.93
223	0.83	1.08	0.32	0.51	0.41	0.16	0.15	0.88	0.46	0.29	0.35	0.85	0.86	1.04	2.20	0.44	0.79
225	0.75	1.03	0.36	0.34	0.12	0.16	0.12	0.84	0.31	0.30	0.38	1.06	0.84	1.90	1.20	2.16	1.90
127	0.60	0.66	0.49	0.18	0.29	0.16	0.13	0.75	0.34	0.45	0.37	0.96	0.85	1.24	1.20	1.24	1.19
185	0.63	0.87	0.30	0.13	0.21	0.15	0.11	0.55	0.35	0.87	0.43	0.94	0.80	0.56	1.39	0.98	0.80
59	0.51	0.81	0.52	0.24	0.32	0.15	0.11	0.55	0.55	0.49	0.39	0.96	0.87	0.87	1.54	0.61	0.84
163	0.65	0.95	0.26	0.15	0.07	0.13	0.07	0.57	0.19	0.44	0.38	0.95	0.83	0.74	0.80	0.79	1.40
36	0.74	0.89	0.46	0.64	0.36	0.12	0.09	0.66	0.15	0.85	0.32	0.96	0.87	0.91	0.44	0.71	1.10
274	0.74	0.90	0.57	0.21	0.22	0.09	0.06	0.63	0.29	0.32	0.36	0.84	0.81	1.33	5.79	0.21	1.71
Mean	0.67	0.87	0.46	0.27	0.28	0.15	0.11	0.69	0.35	0.54	0.37	0.95	0.84	1.00	1.66	0.79	1.10
Min	0.51	0.66	0.26	0.10	0.07	0.09	0.06	0.55	0.15	0.29	0.32	0.84	0.80	0.54	0.44	0.19	0.38
Max	0.83	1.08	0.86	0.64	0.43	0.18	0.17	0.88	0.55	0.87	0.43	1.06	0.90	1.90	5.79	2.16	1.90
Checks																	
GPBD-4	0.73	1.28	0.66	0.63	0.41	0.39	0.34	0.87	0.73	0.52	0.46	1.02	0.77	0.97	1.14	1.21	1.22
GM 6-1	0.79	0.77	0.89	1.70	0.79	0.49	0.44	0.90	0.98	0.64	0.48	0.92	0.70	1.38	2.39	0.82	1.32
JL-24	0.81	0.86	1.11	1.03	0.69	0.41	0.37	0.87	0.76	0.69	0.48	0.85	0.80	0.83	1.53	0.86	0.93
G2-52	0.83	1.01	0.51	0.50	0.38	0.39	0.33	0.86	0.68	0.52	0.50	0.71	0.71	0.69	0.93	0.76	1.30
DH-86	0.48	0.84	0.83	0.81	0.79	0.41	0.35	0.87	0.89	0.68	0.41	0.84	0.83	1.23	1.19	0.59	1.44
TMV-2	0.50	0.97	0.30	0.48	0.27	0.26	0.27	0.82	0.49	0.54	0.43	0.92	0.81	0.60	1.04	1.01	0.91





RIL 101

WW condition



WS condition



WW condition



WS condition

Plate 9: Comparison of drought tolerant (RIL 101) and drought susceptible (RIL 59) RILs for pod yield under WW and WS conditions of field evaluation

**JL-24****GPBD-5****GM 6-1****GPBD-4**

Plate 10: Comparison of checks for pod yield under WW and WS conditions of field evaluation



RIL 57

RIL 58

RIL 59

Plate 11: Comparison of drought tolerant and drought susceptible lines during field evaluation of summer 2012-13

of pegs per plant, number of mature pods per plant, pod yield per plant, kernel yield per plant and sound mature kernel percent.

Lower values of DTI for SLA in the drought tolerant RILs indicates important phenomenon of leaf thickening which can maintain higher RWC and could form the basis for the differences in drought tolerance (Nautiyal *et al.*, 2002).

Superiority of these RILs was also evident from the higher DTI values in the root length and root to shoot ratio. Faster rate of root growth alone had a negative effect on yield as a result of rapid use of soil water indicating the importance slower shoot growth as depicted through root to shoot ratio, provides water saving ability during vegetative stages and makes water available during pod filling. These results were in conformity with the reports of Sinclair *et al.* (2010) in soybean, Zaman-Allah *et al.* (2011a) in chick pea and Ratnakumar *et al.* (2009) in groundnut.

Utilization of DTI to identify drought tolerant genotypes was suggested by Nautiyal *et al.* (2002) in groundnut. Superior RILs for DTI across the two seasons compared to the drought tolerant parent GM 6-1 (0.49) along with other component traits under WW and WS conditions are given in Table 62 and Fig. 7. These RILs had least reduction in the pod yield under WS condition compared to WW condition. Superiority of these RILs for DTI (pod yield) is also evident from least reduction in most of the component traits, while some of the genotypes had even superior performance compared to the WW condition. Use of drought tolerance indices in selection of drought tolerant genotypes was also reported earlier by Arunachalam *et al.* (2013).

5.1.6 Superior RILs for root traits

Superior RILs for root length under water stress condition are given in Table 63; Fig. 8 and Plate 12. Drought stress induced root activity in both drought tolerant and drought susceptible RILs to acquire more water at deeper layers of the soil as indicated by DTI of more than one for root length, root to shoot ratio and root dry weight can be better resolved by categorization of the genotypes into distinct groups. Based on the response of increased root length and its effect on pod yield and physiological traits in these genotypes, these RILs were categorized into responsive and non-responsive

Table 62: Superior RILs for DTI (pod yield) along with other component traits under WW and WS conditions pooled over the two seasons

Genotype	PYP		DTI	NPBP		DTI	NSBP		DTI	NPPP		DTI	NMPP		DTI	KYP		DTI
	WW	WS		WW	WS		WW	WS		WW	WS		WW	WS		WW	WS	
194	5.86	5.77	0.98	4.73	5.59	1.18	1.95	4.00	2.05	9.33	25.00	2.68	14.68	18.40	1.25	3.93	3.47	0.88
197	5.51	5.18	0.94	6.16	5.69	0.92	5.06	3.10	0.61	16.85	36.15	2.15	15.35	19.15	1.25	3.70	3.12	0.84
7	8.16	6.78	0.83	5.70	5.73	1.01	1.90	3.73	1.96	16.58	26.04	1.57	13.33	16.13	1.21	5.52	4.13	0.75
199	7.61	5.36	0.70	5.77	6.04	1.05	2.87	3.98	1.39	6.25	23.40	3.74	14.23	14.08	0.99	5.19	3.25	0.63
172	2.98	2.07	0.70	6.47	4.82	0.74	2.30	3.05	1.33	5.83	14.40	2.47	9.38	9.00	0.96	2.18	1.21	0.55
215	7.98	5.53	0.69	5.87	6.44	1.10	2.21	2.90	1.32	7.88	21.25	2.70	12.68	13.78	1.09	5.39	3.35	0.62
202	9.40	6.45	0.69	4.95	4.10	0.83	2.25	4.09	1.82	7.43	33.40	4.50	18.00	20.00	1.11	6.34	3.91	0.62
261	8.59	5.88	0.69	5.78	5.54	0.96	2.30	2.15	0.93	29.95	16.35	0.55	25.50	14.15	0.55	5.86	3.65	0.62
72	7.53	5.11	0.68	6.56	6.05	0.92	4.79	3.99	0.83	13.28	24.35	1.83	17.15	20.08	1.17	5.36	3.14	0.59
101	9.36	6.13	0.65	5.96	5.23	0.88	4.50	2.50	0.56	13.90	18.65	1.34	15.75	13.20	0.84	6.54	3.71	0.57
GM 6-1	10.29	5.06	0.49	7.26	5.57	0.77	2.80	2.50	0.89	40.38	17.65	1.70	15.03	11.85	0.79	7.04	3.11	0.44
TMV-2	13.60	3.55	0.26	5.02	4.26	0.85	1.80	1.98	1.10	35.18	6.88	0.20	23.60	6.80	0.29	11.05	2.40	0.22
CD 5 %	0.96			0.93			0.56			2.66			1.94			0.62		

Genotype	SP		DTI	SMK %		DTI	HSW		DTI	RWC 15 DAS		DTI	RWC 30 DAS		DTI	SLA 15 DAS		DTI
	WW	WS		WW	WS		WW	WS		WW	WS		WW	WS		WW	WS	
194	67.09	60.21	0.90	61.68	75.85	1.23	27.79	24.98	0.90	76.54	54.46	0.71	67.85	33.45	0.49	55.00	46.56	0.85
197	67.00	59.93	0.89	51.78	62.99	1.22	27.32	30.26	1.11	78.78	55.55	0.71	71.56	32.40	0.45	55.07	42.65	0.77
7	67.59	60.81	0.90	67.65	65.14	0.96	34.19	34.85	1.02	79.58	66.12	0.83	69.81	37.31	0.53	50.63	48.64	0.96
199	68.23	59.83	0.88	52.67	73.97	1.40	41.95	20.35	0.49	75.78	59.14	0.78	69.36	34.12	0.49	52.05	45.25	0.87
172	74.98	55.65	0.74	69.76	42.19	0.60	40.76	20.49	0.50	76.63	58.19	0.76	73.87	34.35	0.47	54.36	44.89	0.83
215	67.50	60.51	0.90	83.44	70.36	0.84	29.08	23.14	0.80	72.04	58.22	0.81	69.93	34.82	0.50	64.74	47.35	0.73
202	67.47	60.44	0.90	81.05	66.13	0.82	31.92	27.84	0.87	77.17	61.58	0.80	66.56	35.49	0.53	58.30	45.79	0.79
261	68.35	62.46	0.91	88.39	69.93	0.79	38.32	23.07	0.60	78.44	59.11	0.75	72.24	34.67	0.48	60.09	48.99	0.82
72	71.16	61.28	0.86	68.32	72.83	1.07	42.34	28.33	0.67	74.01	62.05	0.84	67.65	35.63	0.53	54.33	41.95	0.77
101	69.82	59.76	0.86	81.46	58.95	0.72	36.07	27.57	0.76	77.28	61.47	0.80	72.28	34.91	0.48	48.31	44.56	0.92
GM 6-1	68.48	61.77	0.90	71.65	70.27	0.98	38.74	24.78	0.64	76.91	58.84	0.76	72.05	34.54	0.48	54.89	50.37	0.92
TMV-2	67.98	52.91	0.78	75.39	32.78	0.43	35.25	20.63	0.59	75.12	63.48	0.85	71.36	30.60	0.43	56.89	46.52	0.82
CD 5 %	4.52			9.55			2.46			3.035			3.536			1.57		

Cont..

Genotype	SLA 30 DAS		DTI	SCMR		DTI	Root Length		DTI	Shoot Length		DTI	Root Dry Weight		DTI
	WW	WS		WW	WS		WW	WS		WW	WS		WW	WS	
194	45.15	36.60	0.81	41.50	48.65	1.17	40.25	46.75	1.16	2.48	6.14	2.48	0.23	0.18	0.77
197	41.61	34.58	0.83	39.88	52.85	1.33	27.00	29.00	1.07	2.84	5.58	1.96	0.27	0.30	1.12
7	46.68	35.20	0.75	44.75	51.35	1.15	29.00	26.00	0.90	2.52	5.78	2.29	0.34	0.47	1.37
199	43.65	35.33	0.81	46.48	45.75	0.98	27.10	34.25	1.26	2.15	5.70	2.65	0.26	0.37	1.45
172	46.79	35.36	0.76	41.98	47.45	1.13	32.75	58.85	1.80	2.00	7.73	3.86	0.31	0.47	1.55
215	42.78	36.42	0.85	36.95	49.23	1.33	35.75	34.00	0.95	2.91	3.97	1.36	0.42	0.41	0.97
202	47.76	35.84	0.75	40.48	49.40	1.22	35.30	39.00	1.10	4.71	6.50	1.38	0.32	0.20	0.64
261	44.32	35.50	0.80	37.40	48.93	1.31	35.00	29.00	0.83	4.67	7.25	1.55	0.37	0.36	0.99
72	46.16	35.52	0.77	42.63	48.95	1.15	44.75	27.13	0.61	2.84	3.27	1.15	0.55	0.54	0.98
101	46.46	35.68	0.77	41.98	47.33	1.13	30.00	46.00	1.53	1.91	5.28	2.76	0.24	0.29	1.22
GM 6-1	50.24	35.39	0.70	42.45	47.83	1.13	34.90	48.25	1.38	2.72	6.51	2.39	0.32	0.42	1.32
TMV-2	51.67	37.64	0.73	41.73	44.83	1.07	25.00	15.00	0.60	2.76	2.68	0.97	0.27	0.22	0.82
CD 5 %	1.45			3.05			7.77			0.62			0.10		

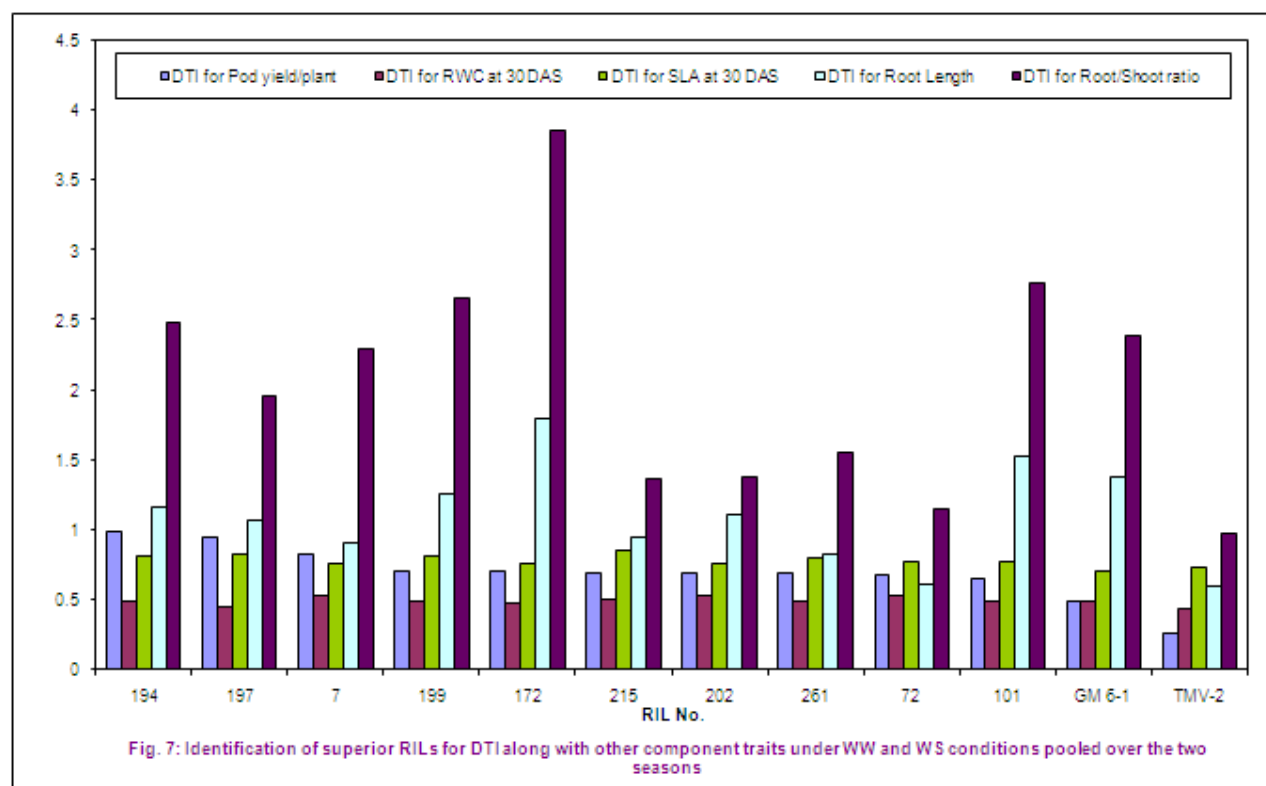


Table 63: Superior RILs for increased root length under WS condition

RIL No	Root Length		Pod yield/plant		RWC 15 DAS		RWC 30 DAS		SLA 15 DAS		SLA 30 DAS		SCMR		R/S ratio		Root dry weight	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
101	32.75	58.85	9.36	6.13	77.28	61.47	72.28	34.91	48.31	44.56	45.44	35.59	36.13	48.93	2.00	7.73	0.31	0.47
194	41.00	57.60	5.86	5.77	76.54	54.46	67.85	33.45	55.00	46.56	49.34	35.38	43.30	49.23	5.13	4.30	0.38	0.73
83	36.50	54.75	9.58	5.23	75.37	61.47	69.34	34.81	53.85	44.32	44.69	35.93	40.10	49.55	2.11	8.36	0.42	0.72
27	48.25	52.50	9.16	5.31	79.46	61.07	73.50	34.13	49.59	46.48	46.46	35.68	41.98	47.33	3.44	5.31	0.30	0.63
7	40.25	46.75	8.16	6.78	79.58	66.12	69.81	37.31	50.63	48.64	41.61	34.58	39.88	52.85	2.48	6.14	0.23	0.18
26	30.00	46.00	14.59	5.77	78.81	62.83	74.78	32.60	53.35	49.81	43.65	35.33	46.48	45.75	1.91	5.28	0.24	0.29
2	36.75	43.13	10.46	5.75	79.20	61.22	74.55	34.80	55.12	41.97	44.14	35.84	41.78	48.88	2.40	4.46	0.40	0.50
53	36.50	40.75	15.73	5.26	74.29	60.47	69.57	30.95	51.86	47.24	45.56	36.86	42.98	46.58	3.67	4.77	0.36	0.57
265	35.30	39.00	11.80	5.98	75.26	64.45	70.71	35.17	53.45	45.46	46.16	35.52	42.63	48.95	4.71	6.50	0.32	0.20
72	27.25	37.00	7.53	5.11	74.01	62.05	67.65	35.63	54.33	41.95	44.36	35.08	40.25	51.35	2.09	4.51	0.41	0.44
215	18.00	36.00	7.98	5.53	72.04	58.22	69.93	34.82	64.74	47.35	47.76	35.84	40.48	49.40	3.00	10.00	0.26	0.30
70	27.10	34.25	9.61	6.20	74.85	62.59	72.90	34.44	53.18	47.23	45.15	36.60	41.50	48.65	2.15	5.70	0.26	0.37
Mean	34.14	45.55	9.98	5.73	76.39	61.37	71.07	34.42	53.62	45.96	45.36	35.68	41.45	48.95	2.92	6.09	0.32	0.45
Min	18.00	34.25	5.86	5.11	72.04	54.46	67.65	30.95	48.31	41.95	41.61	34.58	36.13	45.75	1.91	4.30	0.23	0.18
Max	48.25	58.85	15.73	6.78	79.58	66.12	74.78	37.31	64.74	49.81	49.34	36.86	46.48	52.85	5.13	10.00	0.42	0.73
Parents																		
GM 6-1	34.90	48.25	10.29	5.06	76.91	58.84	72.05	34.54	54.89	50.37	50.24	35.39	42.45	47.83	2.72	6.51	0.32	0.42
TMV-2	25.00	15.00	13.60	3.55	75.12	63.48	71.36	30.60	56.89	46.52	51.67	37.64	41.73	44.83	2.76	2.68	0.27	0.22
CD at 5%	7.77		0.96		3.035		3.536		1.57		1.447		3.048		0.62		0.1	

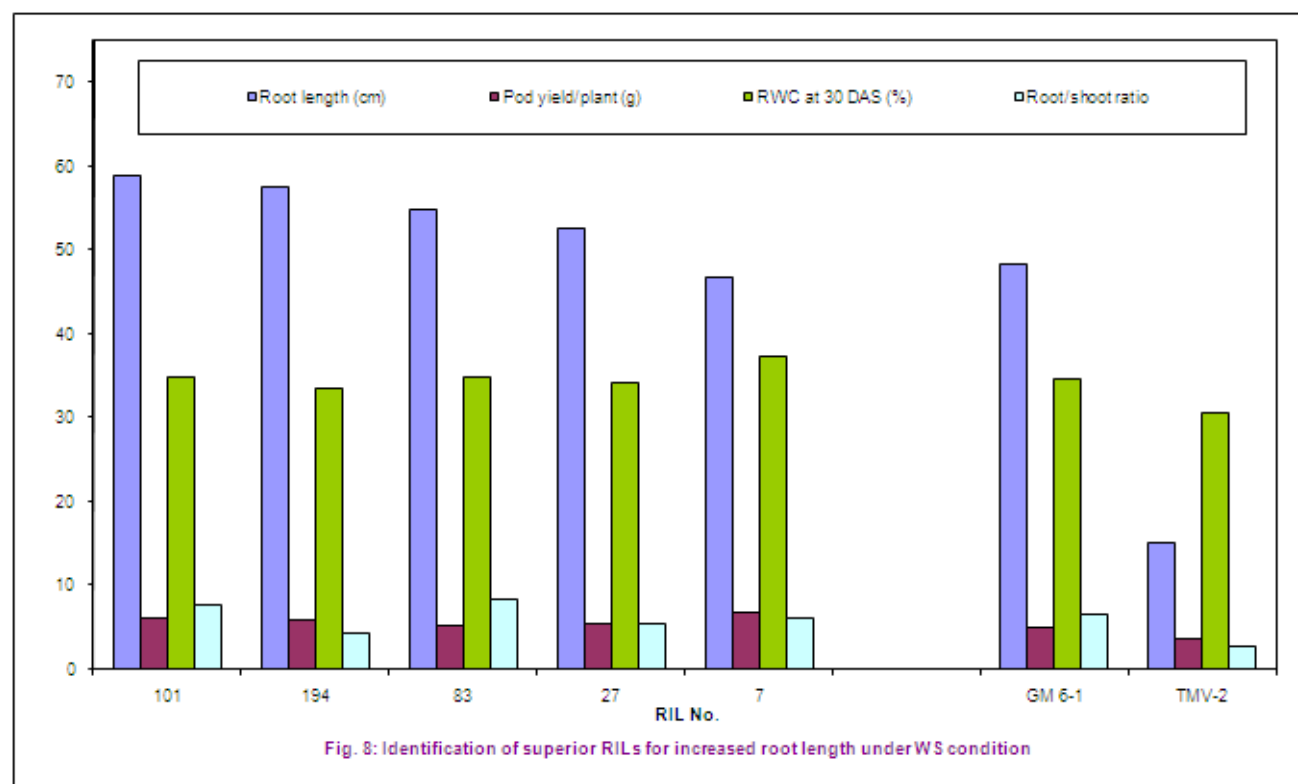




Plate 12: Superior RILs for higher root length under WS condition of raised bed evaluation

groups. Categorization groundnut genotypes into three groups, e.g. increasing, decreasing and non-responsive groups based on root dry weight and root length density and their response to pod yield under drought condition was reported earlier by Jongrunklang *et al.* (2011).

RILs in the responsive group had superior pod yield and physiological traits (higher RWC and lower SLA) exhibiting a potential mechanism of drought avoidance mediated by stomatal closure (Gilbert *et al.*, 2011) and/or deeper root systems (Songsri *et al.*, 2009). Eventhough, some of the RILs in the non-responsive group had higher root growth but lack of balance between the increase in water uptake by deeper roots and the reduction in water loss by stomatal control resulted in reduction in the pod yield in these genotypes. Similar findings were reported earlier by Songsri *et al.* (2008).

5.1.7 Superior lines identified from multilocation yield trials during *kharif* 2014-15

Among the selected lines for multilocation yield trials, RILs 41, 50, 58 and 179 were superior for pod yield (kg/ha) in both the seasons. These RILs also had superior performance for yield components such as number of mature pods per plant and physiological traits such as RWC at 15, 30 and 45 days after sowing and SCMR compared to the best parent GM 6-1. Eventhough the selected regions for MLT had low rainfall in the previous years, because of higher rainfall recorded during the crop growth season of *kharif* 2014-15 sufficient water stress was not imposed. Hence further evaluation of the selected lines is necessary to identify superior drought tolerant lines.

5.2 Genetic variability for quantitative, physiological, root, oil quality and foliar disease resistance traits

Since the effectiveness of the selection depends on the extent of genetic variability present for different characters, it is essential to study the variability with reference to genetic parameters like genotypic coefficient of variability, heritability and genetic advance. In the present study, an attempt has been made to partition the total variability into genetic and non-genetic and their magnitude for different groups has been compared by computing genotypic and phenotypic coefficient of variation. Other genetic parameters *viz.*, heritability in broad sense and genetic advance were also calculated and the results obtained are discussed as below.

5.2.1 Quantitative traits

5.2.1.1 Genotypic (GCV) and phenotypic (PCV) coefficients of variation

Phenotypic co-efficient of variation was of higher in magnitude than the genotypic co-efficient of variation for all the characters indicating the influence of environment in expression of the traits. Similar kind of observation was also reported by Korat *et al.* (2009) and Savaliya *et al.* (2009).

During both the seasons days to 50 per cent flowering and days to maturity recorded low GCV and PCV among the RILs evaluated indicating the lack of variability for these traits since the parents of the RILs developed also had less variation for these traits. This is in accordance with the reports of Venkateshmurthy (2005), Vishnuvardhan *et al.* (2012), Zaman *et al.* (2011) and Rao *et al.* (2012).

During summer 2012-13, number of primary branches per plant had moderate PCV but low GCV. In contrast, moderate GCV but high PCV were recorded by this trait during summer 2013-14. Seasonal variation in the variability of this trait is probably due to high season and G x E interaction effects. This is in accordance with the reports of John *et al.* (2011).

High PCV, GCV and wide range of variation were recorded by most of the quantitative traits *viz.*, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, sound mature kernel per cent and hundred seed weight in both the irrigation levels and both seasons, indicating wide range of variability for these characters in the population and scope for selection for these traits. Similar to these results, high PCV and GCV reported for number of secondary branches per plant by Dixit *et al.* (1970), Raman and Sree Rangaswamy (1970), Lakshmaiah (1978), Mahalakshmi *et al.* (2005) and Korat *et al.* (2009) were in accordance with the findings of the present study and for hundred seed weight by Suryanarayana Reddy *et al.* (2001), Venkataramana *et al.* (2001) and Thaware *et al.* (2008).

Moderate PCV and GCV for plant height while moderate to high PCV and GCV for pod yield per plant and kernel yield per plant were recorded during both the seasons indicating the wide variability for these traits in the population. Similarly, Vasanthi *et*

al. (2004), John *et al.* (2004) and Ravikumar (2005), Zaman *et al.* (2011), Rao *et al.* (2012) and Sudha *et al.* (2012) revealed high GCV and PCV for pod yield per plant. Reports of high GCV and PCV for kernel yield per plant by Venkataravana (2001), Kumar (2004), Kumar and Rajamani (2004), John *et al.* (2004), Golakia *et al.* (2005) and John *et al.* (2005) were in accordance with the present findings.

Shelling per cent had low to moderate GCV and PCV in both seasons of summer 2012-13 and summer 2013-14 indicating less response to selection. The results were in accordance with the reports of Korat *et al.* (2009), Azharudheen (2010), John *et al.* (2011), Thakur *et al.* (2011), Zaman *et al.* (2011), Jonah *et al.* (2012) and Rao *et al.* (2012).

5.2.1.2 Heritability and genetic advance as per cent of mean

Heritability was high for the traits viz., days to 50 per cent flowering, days to maturity, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, sound mature kernel per cent and hundred seed weight during both seasons. Similar results of high heritability for these traits were reported by Venkateshmurthy (2005), Vishnuvardhan *et al.* (2012), Rao *et al.* (2010) for days to 50 per cent flowering; Vishnuvardhan *et al.* (2012) and Makhan *et al.* (2003) for days to maturity; John *et al.* (2007), John *et al.* (2011), Sudha *et al.* (2012) for number of secondary branches per plant.

Low heritability was recorded for primary branches per plant during summer 2012-13 whereas, high heritability was recorded by this trait during summer 2013-14 which could be due to more influence of environment on this trait. High heritability for this trait were reported by Channaayya (2009), Korat *et al.* (2009) and Sudha *et al.* (2012).

Moderate to high heritability was estimated for plant height, pod yield per plant, kernel yield per plant and shelling per cent. Similar results of high heritability for these traits were reported by John *et al.* (2007), Kavera (2008) and Rao *et al.* (2010) whereas, moderate heritability for pod yield per plant and shelling per cent were reported by Vishnuvardhan *et al.* (2012).

As heritability in broad sense includes both additive and epistatic gene effects, it will be reliable only if accompanied by high genetic advance.

Low genetic advance as per cent of mean was recorded for days to 50 per cent flowering and days to maturity during the two seasons since the genetic variability is low for this trait. High heritability along with low genetic advance for these traits indicates the greater role of non-additive genetic variance like epistatic and dominant interaction factors controlling the inheritance of these traits. This is in accordance with the findings of Channayya (2009), John *et al.* (2011) and Vishnuvardhan *et al.* (2012).

During summer 2012-13, number of primary branches per plant recorded low genetic advance as per cent of mean. In contrast, high GAM was recorded by this trait during summer 2013-14. Similar kind of results of low GAM for this trait were reported by Channayya (2009), John *et al.* (2011), Thakur *et al.* (2011) and Vishnuvardhan *et al.* (2012), while high GAM for this trait was reported by Jatti *et al.* (2008), Thaware *et al.* (2008), Raut *et al.* (2010) and Rao *et al.* (2012).

High GAM was recorded by most of the quantitative traits in both the seasons *viz.*, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, sound mature kernel per cent and hundred seed weight. High genetic advance coupled with high heritability estimates for these traits suggested the importance of additive genetic variance and improvement of these characters could be made by simple phenotypic selection. These results are in conformity with the observations made by Reddy *et al.* (1987a) for secondary branches per plant; Vaddoria and Patel (1990), Reddy and Gupta (1992) for mature pods per plant; Apte *et al.* (2008), Jatti *et al.* (2008), John *et al.* (2008), Thaware *et al.* (2008), Savaliya *et al.* (2009) and Rao *et al.* (2012) for hundred seed weight.

Moderate to high GAM was recorded for plant height, pod yield per plant, kernel yield per plant and shelling per cent in both seasons which was in accordance with the findings of Venkateshmurthy (2005) and John *et al.* (2006) for plant height; Raut *et al.* (2010), Rao *et al.* (2012) for pod yield and kernel yield per plant. Moderate to high heritability and GAM for these traits indicates the substantial contribution of additive genetic variance in the expression of these characters. It is proven fact that additive gene effects are more amenable for external environmental variations than non-

additive gene action. Hence multi locational evaluation is required to judge the real potentiality of the genotype.

5.2.2 Physiological traits

Efficient utilization of the physiological traits for improving drought resistance in a breeding program requires an understanding of the inheritance and genetic relationships of the traits that are available for selection. Series of experiment were conducted to estimate the heritability of physiological traits related to drought resistance under different drought conditions (Cruickshank *et al.*, 2004; Hubick *et al.*, 1988; Ntare and Williams, 1998a, 1998b; Nigam *et al.*, 2005; Puangbut *et al.*, 2011; Songsri *et al.*, 2008).

Low PCV and GCV were recorded by all the physiological traits measured at all stages during both the seasons indicated low genetic variation in the population and difference between PCV and GCV for this traits indicated prevalence of environment on these traits during both the seasons. In contrast to these results, significant genotypic variation for the traits related to drought tolerance was reported in numerous reports depending upon the material used for their study by Vorasoot *et al.*, 2003 (four groundnut cultivars), Ndunguru *et al.*, 1995 (36 cultivars); Jongrunklang *et al.*, 2008 (80 germplasm lines) and Painawadee *et al.*, 2009 (four groundnut genotypes in a pot experiment).

RWC at seven days after stress recorded moderate to high heritability and low GAM during two seasons respectively. Moderate heritability and low GAM was observed for RWC at 15 DAS during consecutive seasons while moderate to high heritability and moderate GAM was estimated for RWC at 30 DAS. This indicated that selection for the drought tolerance based on RWC could be affective only ay later stages of stress compared to the early stages. Similar kind of results of high heritability and moderate GAM was reported for RWC by Painwadee *et al.* (2009).

High heritability and moderate to high GAM were observed during consecutive seasons for SLA at 7 DAS indicated that selection for this trait could be affective in the early stages. The results were in accordance with the reports of high heritability and

high GAM for SLW by Songsri *et al.*, 2008, Wunna *et al.*, 2009, Boontang *et al.*, 2010, Nandini *et al.*, 2011, Puangbut *et al.*, 2011, Girdthai *et al.*, 2012 and Savitha (2012).

Moderate heritability along with low GAM were estimated during summer 2012-13, for SLA at 15 DAS while during summer 2013-14, high heritability and moderate GAM were observed for this trait indicating the influence of environment in the expression of SLA at this stage. The results were in accordance with the reports of moderate $h^2(b)$ and low GAM by John *et al.* (2011) and Savitha (2012)

Low to moderate heritability and low GAM were recorded for SLA at 30 DAS and SPAD chlorophyll meter reading during both the seasons. Similar kind of results of low heritability and low GAM were reported by John *et al.* (2011). These results were in accordance with the reports of Painawadee *et al.*, 2009 for SLA. In contrast to the above results moderate heritability and moderate GAM was reported for SCMR by Nandini *et al.* (2011), moderate to high heritability and moderate to high GAM by Savitha (2012) and high heritability and high GAM by Upadhyaya (2005) and Songsri *et al.* (2008).

Differential heritability and GAM estimates for physiological traits by several reports are because of varied stages and duration of drought stress imposition. The mechanisms of physiological responses to early season drought might be different from those for long duration drought, which have been reported previously (Songsri *et al.*, 2008).

Cruickshank *et al.* (2004) reported that broadsense heritability of drought tolerance traits were varied among groundnut crosses, traits and stages depending on levels of genetic variation for the trait and stage of imposition of drought stress.

5.2.3 Root traits

High PCV, GCV and high heritability in broadsense along with high GAM were estimated for most of the root traits recorded in the present study indicating the wide variability, prevalence of additive genetic variance and high scope for selection of these traits. Hence the genetic improvement of these traits would be possible through simple selection.

Significant genetic variation was reported by Serraj *et al.* (2003) among the RIL population of chickpea derived from a cross ICC 4958 x Annigeri for root length density, root dry weight and shoot dry weight at 35 days after sowing. They also observed high heritability ($h^2=0.49$) for shoot dry weight compared to moderate heritability for root dry weight and root length density at the same stage. These reports were in accordance with the results of the present investigation.

In contrast to the above results, Ren *et al.* (2006) revealed low heritability estimates for most of the root traits. Similarly low heritability estimates for root length and root dry weight were reported by Painawadee *et al.* (2009) and these reports were in contrast with the present study.

5.2.4 Oil quality traits

5.2.4.1 Genotypic (GCV) and phenotypic (PCV) coefficients of variation

Low PCV and GCV were recorded for oil content, protein content, total unsaturated fattyacid, total saturated fattyacid, U/S ratio and calculated iodine value for both seasons while low to moderate GCV and PCV were exhibited by stearic acid, arachidic acid, ecosenoic acid, behenoic acid and lignoceric acid in all the seasons. Low variation in the population for these traits could be due to the less variation for these traits in the parents used for development of the RILs. These results are in conformity with the observation made by Venkateshmurthy (2005), Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat *et al.*, 2009 and Azharudheen (2010) for total oil content; Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen *et al.*, 2010 and John *et al.*, 2011 for total protein content; Channayya (2009) and Sarvamangala (2009) for total saturated fattyacid; Kavera (2008), Channayya (2009), Sarvamangala (2009) and Azharudheen (2010) for U/S ratio; Kavera (2008) and Sarvamangala (2009) for calculated iodine value.

Palmitic acid, oleic acid, linoleic acid, L/S ratio and oleic acid desaturation had moderate GCV and PCV in both the seasons while high PCV and GCV were recorded for O/L ratio during the two seasons indicating wide variability for these traits since the parents had wide variation for these traits. These results are in conformity with the

observation made by Kavera (2008) for oleic acid; Kavera (2008) and Channayya (2009) for linoleic acid.

5.2.4.2 Heritability and genetic advance as per cent of mean

High heritability was recorded for most of the oil quality traits viz., total oil content, total protein content, palmitic acid, stearic acid, oleic acid, linoleic acid, arachidic acid, eicosenoic acid, behenic acid, lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid, total saturated fatty acid, polyunsaturated/saturated fatty acid ratio, unsaturated/saturated fatty acid ratio, calculated iodine value and oleic acid desaturation ratio.

Moderate to high GAM was estimated for the traits viz., stearic acid, arachidic acid, eicosenoic acid, behenic acid, lignoceric acid, oleic acid, linoleic acid O/L ratio, L/S ratio and oleic acid desaturation acid during both the seasons indicating less influence of environment and wider scope for selection of these traits.

These results were in accordance with the reports of Korat *et al.* (2009), Venkataramana *et al.* (2001), Kavera (2008), Channayya (2009) and Sarvamangala (2009) for total oil content; Chiow and Wynne (1983), Kavera (2008), Channayya (2009), Sarvamangala (2009), and Azharudheen (2010) for protein content; Kavera (2008), Channayya (2009) and Sarvamangala (2009) for palmitic acid; Kavera (2008) for stearic acid; Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010) and Singkham *et al.* (2010) for oleic acid; Kavera (2008), Channayya (2009), Sarvamangala (2009), Azharudheen (2010) and Singkham *et al.* (2010) for linoleic acid; Channayya (2009) for arachidic acid and behenic acid; Kavera (2008) for eicosenoic acid and lignoceric acid; Kavera (2008) for O/L ratio and U/S ratio; Channayya (2009) and Sarvamangala (2009) for CIV value.

Low GAM was estimated for total oil content, palmitic acid and total unsaturated fatty acid while low to moderate was recorded for the traits viz., protein content, total saturated fatty acid, U/S ratio and calculated iodine value. It indicates that expression of traits is influenced by environment restricting the scope of selection. Similar reports were given by Kavera (2008), Sarvamangala (2009) and Azharudheen

(2010) for total oil content, total protein content and palmitic acid; Channayya (2009) and Sarvamangala (2009) for SFA; Sarvamangala (2009) for U/S ratio and CIV.

5.2.5 Foliar disease resistance

Moderate to high GCV and PCV estimates were recorded for rust and LLS scores at 70, 80 and 90 DAS during both the seasons. Similar kind of results were reported by Khedikar (2008) and Vishnuvardhan *et al.* (2012).

High heritability was recorded for LLS and rust scores at all stages and during both the seasons. Similar results were reported by Khedikar (2008) and Vishnuvardhan *et al.* (2012). Sandhu and Khehra (1977) also observed similar kind of high heritability estimates for late leaf spot severity, whereas Anderson *et al.* (1991) reported moderate to high heritability estimates for late leaf spot scores and for defoliation.

High genetic advance as per cent of mean was observed for LLS and rust scores at all the stages. These results were in accordance with the reports of Venkataravana *et al.* (2008), Venkataravana and Injethi (2008), Giri *et al.* (2009), Sawargaonkar *et al.* (2010), Vishnuvardhan *et al.* (2012).

Results on genetic variability for foliar disease resistance traits indicated wide variability for these traits since the parents are widely varied for their disease resistance reaction. High heritability coupled with high GAM indicates that these characters are under the influence of additive gene action and prediction of high genetic advance supports better improvement for these traits.

5.3 Association studies

The phenotype of the plant is the result of interaction of large number of traits. Hence the final yield is the sum total of several component traits. Drought stress is the result of numerous climatic, edaphic, and agronomic factors that are further confounded frequently by major variations in their timing, duration, and intensity. The combinations of morphological, physiological, and phenological traits required for optimal adaptation to drought stress varies with each local environment. To breed for the drought tolerance it is very important to know which of the characters have contributed towards the higher pod yield under water stress situations as well as normal conditions. Therefore, it is

important to know direction and extent of interrelationship between and among pod yield, quantitative, physiological traits and other contributory characters towards the improved drought tolerance such as root traits.

Oil stability and nutritional quality are both dependent on the relative proportions of the saturated and unsaturated fatty acids that constitute the oil. Oxidative rancidity increases with increased levels of polyunsaturated fatty acids. Oxidation of the carbon double bonds of the fatty acids produces acids, aldehydes, ketones and other hydrocarbons that cause unpleasant odour and flavours commonly associated with rancidity, thus limiting the storage quality of the oil (Moore and Knauft, 1989). Vegetable oils with increased levels of monounsaturated oleic acid in combination with reduced levels of the polyunsaturated linoleic acid show a higher oxidative stability as well as lower oxidative products (McVetty and Scarth, 2002). Monounsaturated oleic acid is significantly more stable for oxidation (rancidity) than polyunsaturated linoleic acid. It can be heated to a higher temperature without smoking and has advantages like reduced cooking time, less oil is absorbed and less food impurities enter the oil (Miller *et al.*, 1987). Before formulating suitable strategies to breed varieties for better quality, understanding the relationship among oil quality traits is of paramount importance. All the fatty acids are synthesized in the biosynthetic pathway through modification such as elongation and desaturation. Hence alteration in biosynthetic steps influences the whole fatty acid profile and determines the relationships among different fatty acids. These correlations may reflect genetic linkage of various enzymes involved in the conversion (Andersen *et al.*, 1998).

5.3.1 Correlation analysis for yield and yield components

Effect of water stress on yield and yield components varies depending on the intensity and duration of stress period. Contribution of yield components towards the yield in WW condition may be sometimes reverse the results of the case against water deficit but such associations provides a better way for improving the performance under stress conditions (Vorasoort *et al.*, 2003). Existence of seasonal variation of association between the yield and yield components with in WW and WS conditions gives an idea of identification of continuous and stable relationships (Turner *et al.*, 2007) with in each water regime. In the present study, an attempt has been made to know the stable

associations with in each water regime and also changed associations across the water regime as discussed as below.

The results on phenotypic and genotypic correlations between yield and its components in the present investigation indicate that genotypic correlation coefficients were higher than phenotypic values indicating that strong intrinsic association are reduced at phenotypic level due to environmental effects. Higher genotypic correlation coefficients compared to phenotypic correlation coefficients have been reported by Nadaf and Habib (1989).

Pod yield per plant

The pod yield per plant under WW condition during summer seasons of consecutive years showed significant and positive correlation with number of secondary branches per plant, number of pegs per plant, number of mature pods per, kernel yield per plant and sound mature kernel per cent.

In general in most of the genotypes, mean pod yield per plant was reduced under the WS conditions compared to the WW conditions. These results were similar to previous finding that pod yield were reduced when groundnut was subjected to terminal drought (Boontang *et al.*, 2010; Girdthai *et al.*, 2010) and the reduction also varies among groundnut genotypes (Harris *et al.*, 1988).

Significant positive correlation was also recorded between the pod yield per plant under WW and pod yield per plant WS condition (0.197 and 0.298) of the two seasons respectively. Similar to the above findings, Boontang *et al.* (2010) also reported that for pod yield of groundnut, high potential under well watered conditions had significant contribution to maintaining high pod yield under drought.

The pod yield per plant under WS condition during the two summer seasons of 2012-13 and 2013-14 had significant and positive correlation with number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, kernel yield per plant, sound mature kernel per cent and hundred seed weight. These correlations indicated that it is possible to derive the

superior recombinants considering the combination of above traits under WW and WS conditions, respectively.

Under WS condition, negative association of number of immature pods per plant, days to 50 per cent flowering and days to maturity with pod yield was observed. It indicates that, the genotypes which have taken less days for flowering can escape the water scarcity during the peg initiation and peg penetration, the stages which are critical for the irrigation timing in groundnut. Those genotypes which are early to flower will also mature early and can escape the end of season drought and yields better with more mature pods per plant and less immature pods per plant.

Significant negative correlation of days to 50 per cent flowering with pod yield was reported by Mathews *et al.* (2001) and Giri *et al.* (2009); and days to maturity with pod yield by Giri *et al.* (2009) were in accordance with the results of the present study.

Significant positive correlation between number of mature pods per plant and pod yield was reported earlier by Venkataravana *et al.* (2000), Venkateswarlu *et al.* (2007), Sharma and Gupta (2008) and Raut *et al.* (2010b). Azad and Hamid (2000), Sah *et al.* (2000), Dashora and Nagda (2002), Sumathi and Muralidharan (2007), Giri *et al.* (2009) and Awatade *et al.* (2010) reported positive correlation between kernel weight per plant and pod yield.

Similarly, significant positive correlation between hundred seed weight and pod yield was reported earlier by John *et al.* (2007), Kavera (2008), Channayya (2009), Sarvamangala (2009), Korat *et al.* (2010) and Rao *et al.* (2012)

Significant negative correlation of pod yield per plant with shelling out-turn was reported earlier by Sah *et al.* (2000), Sumathi and Muralidharan (2007) and Giri *et al.* (2009).

Correlations among other traits

In WW condition, days to 50 per cent flowering had significant positive correlation with days to maturity and plant height. It recorded significant negative correlation with number of primary branches per plant and number of secondary

branches per plant. Similarly, days to maturity recorded significant positive correlation with plant height, number of pegs per plant, immature pods per plant and shelling per cent and significant negative correlation with number of primary branches per plant.

It indicated that the genotypes which are early to flower and mature were short statured and have more number of primary and secondary branches per plant. Plant height recorded significant positive correlation with days to 50 per cent flowering, days to maturity which were similar to the finding of Sunday and Omolayo (2013).

Number of primary branches per plant recorded significant positive correlation with number of secondary branches per plant, hundred seed weight and it had significant negative correlation with number of immature pods per plant during summer 2013-14. Channayya (2009) reported similar kind of association of primary branches per plant with number of secondary branches but in contrast he reported negative association of number of secondary branches per plant with hundred seed weight.

Number of secondary branches per plant recorded significant positive correlation with number of pegs per plant, number of mature pods per plant, kernel yield per plant and sound mature kernel per cent while significant negative correlation with shelling per cent.

Number of pegs per plant recorded significant positive correlation with days to 50 per cent flowering, days to maturity, plant height, number of immature pods per plant, number of secondary branches per plant, number of mature pods per plant, kernel yield per plant, sound mature kernel per cent and hundred seed weight. It indicated that in WW condition long statured, late flowering and late maturing genotypes were desirable with more number of pegs per plant.

Number of mature pods per plant had significant positive correlation with number of pegs per plant, number of immature pods per plant, kernel yield per plant and sound mature kernel per cent. Number of immature pods per plant recorded significant negative correlation with shelling per cent and sound mature kernel per cent.

Number of mature pods per plant, kernel yield per plant sound mature kernel per cent and hundred seed weight recorded significant positive correlation with number of secondary branches per plant, number of pegs per plant negative correlation with plant

height days to maturity and shelling per cent. Shelling per cent recorded significant positive correlation with hundred seed weight during both the seasons and negative correlations with most of the traits.

In the WS condition, days to 50 per cent flowering and days to maturity had significant negative correlation with most of the traits.

Days to maturity recorded significant positive correlation with days to 50 per cent flowering, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, shelling per cent, sound mature kernel per cent while It recorded significant negative correlation with number of immature pods per plant.

Irrespective of the season in WS condition, number of primary branches per plant recorded significant positive correlation with number of pegs per plant, number of mature pods per plant, kernel yield per plant, sound mature kernel per cent and hundred seed weight. Uddin *et al.* (1995) reported significant positive association of number of primary branches per plant with kernel weight and is in conformity with findings of the present study under water stress conditions. Similar kind of association was also reported with kernel yield per plant by Kavera (2008) and with hundred seed weight by Channayya (2009). Contrary to this, Antony *et al.* (2000) observed negative correlation of plant height with number of primary branches per plant.

Number of secondary branches per plant recorded significant positive correlation with most of the traits except days to 50 per cent flowering, days to maturity and significant negative correlation with number of immature pods per plant during summer. This is indicative of importance of this trait for improving the pod yield under WS conditions.

In contrast number of pegs per plant recorded significant negative correlation with days to 50 per cent flowering, days to maturity, plant height and number of immature pods per plant in WS condition. In contrast to the WW condition, early flowering, early maturing and short statured genotypes are desirable for more number of pegs per plant under WS conditions

Number of mature pods per plant, kernel yield per plant sound mature kernel per cent and hundred seed weight recorded significant positive correlation with most of the

traits significant negative correlation with days to 50 per cent flowering, days to maturity and number of immature pods per plant during both the seasons. Number of immature pods per plant recorded significant negative correlations with most of the traits except days to 50 per cent flowering, days to maturity. The reports of positive significant association of number of mature pods per plant with kernel yield per plant by Ursal *et al.* (1995), Jayalakshmi *et al.* (2000) and Venkataravana (2000) were in accordance with the findings of the present study

Shelling per cent recorded significant positive correlation with kernel yield per plant and hundred seed weight in both the seasons at genotypic level.

5.3.3 Physiological traits

Drought related reduction in growth and yield of plants could be ascribed to stomatal closure in response to low soil moisture, which decreased the intake of CO₂ and, as a result photosynthesis is decreased (Cornic, 2000; Flexas *et al.*, 2004).

Pod yield under stress was positively and significantly correlated with the DTI, RWC and SCMR while significant negative correlation was observed with SLA. Low SLA genotypes were expected to have greater photosynthetic capacity per unit leaf area (Nageswara Rao *et al.*, 1995). SCMR was positively and significantly correlated with chlorophyll content (Akkasaeng *et al.*, 2003) and chlorophyll density (Arunyanark *et al.*, 2008). Similarly, findings of Nageswara Rao *et al.* (1995) that high SCMR genotypes had greater photosynthetic capacity further strengthened the results of the present study of using high SCMR or low SLA as a selection criterion for enhancing pod yield under drought in groundnut. Similarly, Puangbut *et al.* (2011) also reported that SCMR had moderate correlation with pod yield indicating the possibility of selection for this trait to improve yield.

In general DTI for the pod yield was correlated with pod yield under stress and also with the RWC, SCMR while negatively correlated with SLA at later stages of the crop growth period these results were in conformity with the findings of Jongrunklang *et al.* (2011).

RWC was positively correlated with the SCMR and recorded significant negative correlations at most of the stages. Similar to the present results Painwadee *et al.* (2009)

also observed negative correlation between drought resistance traits such as RWC and SLA; SCMR with SLA.

Reports of significant negative correlation of SLA with SCMR by Girdthai *et al.* (2012) were in conformity with the results of the present study. These results are also similar to the reports of Nageswara Rao *et al.* (2001) and Upadhyaya (2005), but in contrast, Hamidou *et al.* (2011) in their study involving reference collection of groundnut reported no significant relationship between yield under WS and SCMR, or specific leaf area (SLA).

5.3.4 Root traits

Root length was positively correlated with pod yield under stress and also DTI. Similar to the results of the present study, Jongrunklang *et al.* (2014) also reported significant positive correlations between drought tolerance index (DTI) for pod yield and root length at deeper soil layer. Reports of Rucker *et al.* (1995) demonstrating positive correlation of large root systems with pod yield of groundnut grown under drought in field trials was in conformity with the present study.

In this study, earlier maturing genotypes had greater yield than later maturing genotype under WS condition. This result indicate that early root distribution is completed helping to maintain better partitioning into the seed at the later growth stage under drought conditions leading to better yield (Kashiwagi *et al.*, 2006). Similar to these reports, Ketring and Reid (1993) also found that groundnut was able to establish deep and laterally spreading root system fairly early during the life cycle and provide adaptation to the drought conditions later in the growing season.

Positive correlation among root characters such as root length and root dry weight was also reported by Painwadee *et al.* (2009). In contrast to the results, Sasmal (2008) observed significant negative correlation of root length with root dry weight. This could be due to the fact that rice is grown under water flooded conditions.

A strong correlation between root dry weight and shoot dry weight was observed in the present study which is in accordance with the reports of correlation among those traits grown under greenhouse (Ketring 1984) and field conditions (Wright *et al.* 1994).

Significant positive correlation of root length was observed with RWC at 30 DAS and SCMR at 30DAS while significant negative correlation with SLA at 15 and 30 DAS in the present study. But in contrast to these results Painwadee *et al.*, 2009 reported that physiological and root traits were not correlated which may be due to the different stages of measurement of physiological traits (70 DAS), and root traits where root traits were evaluated at the time of harvest. But in our study, correlations were observed between those physiological traits and root traits which are measured at similar stages (75 days after sowing)

5.3.5 Oil quality traits

The results on phenotypic and genotypic correlations between oil quality traits indicated that, genotypic correlation coefficients were higher than phenotypic values indicating that strong intrinsic associations at genotypic level are reduced at phenotypic level due to environmental effects.

Correlation of oil quality attributes with oleic acid

In both WW and WS oleic acid had significant positive correlation with total oil content, eicosenoic acid, lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid, unsaturated/saturated fatty acid ratio and calculated iodine value. Oleic acid was found to be positively and significantly correlated with stearic acid, arachidic acid, eicosenoic, lignoceric acid, oleic acid to linoleic acid ratio, unsaturated to saturated fatty acid ratio and oleic acid desaturation. The result of such positive associations are in total agreement with earlier reports of Sarvamagla (2009) for eicosenoic acid; Sarvamagla (2009) and Channayya (2009) for lignoceric acid; Asibuo *et al.* (2008); Kavera (2008), Channayya (2009) and Sarvamangala (2009) for oleic acid to linoleic acid ratio; Kavera (2008) and Sarvamangala (2009) for unsaturated to saturated fatty acid ratio. Positive correlation of eicosenoic acid with oleic acid is due to the synthesis of eicosenoic acid from oleic acid requires only the addition of a two carbon moiety via acetyl coenzyme A (Andersen *et al.*, 1998).

Irrespective of water regime oleic acid was found to be significantly negatively correlated with palmitic acid, linoleic acid, behenic acid, total saturated fatty acids, total

long chain saturated fatty acid, polyunsaturated to saturated fatty acid ratio and iodine value. Similar results were reported by Mercer *et al.* (1990) for linoleic acid in groundnut. The inverse relationship between oleic acid with palmitic acid and linoleic acid was also the inverse relationship between oleic acid with palmitic acid was also evident from various earlier studies of Andersen *et al.* (1998), Bovi (1983) and Sekhon *et al.* (1980).

The strong negative correlation between oleic acid and linoleic acid results from the fact that the chief acyl desaturation of oleic acid leads to linoleic acid accumulation in the oil. The negative relationship between palmitic acid and oleic acid was likely due to an increased rate of palmitic acid elongation to stearic acid with rapid desaturation to oleic acid via delta-9 desaturase (Groff *et al.*, 1996). From these correlations it can be concluded that breeding for increased oleic acid normally results in reduced palmitic acid and linoleic acid. This indicates that, it is possible to reduce these fatty acids that are undesirable and increase the desirable oleic acid, the major determinant factor of oil quality (Wilson, 2004) irrespective of the water regime. These findings are in conformity with Andersen and Gorbet (2002) and Sarvamangala (2009) with palmitic acid, Asibuo *et al.* (2008) and Singkham *et al.* (2010) with linoleic acid; Channayya (2009) with behenic acid and total saturated fatty acid; and with iodine value by Andersen *et al.* (1998) and Kavera (2008).

Correlations among other oil quality traits

Total Oil Content

In WW condition of consecutive seasons, oleic acid had significant positive correlation with eicosenoic acid, lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid, unsaturated/saturated fatty acid ratio and oleic acid desaturation while oleic acid exhibited contrast but significant associations during consecutive seasons with total protein content, palmitic acid and calculated iodine value. Similar results were reported by Sarvamangala (2009) with eicosenoic acid and lignoceric acid; Dwivedi *et al.* (1990) and Sarvamangala *et al.* (2010) with protein content.

In WS condition, oil content had significant positive correlation with palmitic acid, linoleic acid, polyunsaturated/saturated fatty acid ratio and calculated iodine value and significant negative correlation with arachidic acid, while total oil content exhibited contrast but significant associations during respective seasons with total protein content, eicosenoic acid, total unsaturated fatty acid, and unsaturated/saturated fatty acid ratio. Such contrast associations with in WW and WS conditions could be due to significant G x E interaction effects.

Total Protein Content

In WW condition of consecutive seasons, protein content had significant negative associations with most of the traits except with polyunsaturated/saturated fatty acid ratio and calculated iodine value.

In the WS condition, total protein content showed significant positive association with behenic acid and total unsaturated fatty acid. Contrast associations between the two water regimes may be due to highly significant effect of season on this trait.

Palmitic acid

In WW condition during both the seasons, palmitic acid had significant positive correlation with stearic acid, linoleic acid, behenic acid, total saturated fatty acid, polyunsaturated to saturated fatty acid ratio and iodine value while it had significant negative correlation with eicosenoic, lignoceric acid, oleic acid to linoleic acid ratio, total unsaturated fatty acid, unsaturated to saturated fatty acid ratio and oleic acid desaturation ratio. Similar kind of associations were reported by Lukenge *et al.* (2007), Kavera (2008), Channayya (2009), Sarvamangala (2009) and Gangadhar (2014).

In WS condition during both the seasons, palmitic acid recorded significant positive correlation with total oil content, linoleic acid, behenic acid, total saturated fatty acid, polyunsaturated to saturated fatty acid ratio and iodine value while it recorded significant negative correlation with stearic acid, arachidic acid, lignoceric acid, oleic acid to linoleic acid ratio, total unsaturated fatty acid, unsaturated to saturated fatty acid ratio and oleic acid desaturation ratio.

Stearic acid

In WW condition during both the seasons, stearic acid had significant positive correlation with palmitic acid, linoleic acid, arachidic acid, behenoic acid, total saturated fatty acid, and iodine value while it had significant negative correlation with eicosenoic, lignoceric acid, oleic acid to linoleic acid ratio, total unsaturated fatty acid, unsaturated to saturated fatty acid ratio and oleic acid desaturation ratio. Similar kind of positive association were reported by Channayya (2009) with lignoceric acid; in contrast to the above results, positive association was reported by Lukenge *et al.* (2007) with oleic acid; and with oleic acid to linoleic acid ratio by Kavera (2008).

In WS condition during both the seasons, stearic acid had significant negative correlation with most of the traits except arachidic acid, behenoic acid, oleic acid to linoleic acid ratio, total saturated fatty acid and oleic acid desaturation ratio. Similar kind of positive association was reported by Channayya (2009) with behenic acid. Contrast associations of stearic acid with other traits between the two water regimes could be due to highly significant effect of season on this trait.

Linoleic acid

In WW condition during both the seasons, linoleic acid recorded significant positive correlation with palmitic acid, stearic acid, behenoic acid, total saturated fatty acid, polyunsaturated to saturated fatty acid ratio and iodine value. These findings are in conformity with Channayya (2009) with behenic acid and total saturated fatty acid; Kavera (2008) with polyunsaturated to saturated fatty acid ratio and iodine value. While it had significant negative correlation with eicosenoic, lignoceric acid, oleic acid to linoleic acid ratio, total unsaturated fatty acid, unsaturated to saturated fatty acid ratio and oleic acid desaturation ratio. These results are in agreement with the findings of Kavera (2008) and Channayya (2009) with arachidic acid, lignoceric acid, eicosenoic and oleic acid to linoleic acid ratio.

In WS condition during both the seasons, linoleic acid had significant negative correlation with most of the traits and significant and positive correlations with the traits *viz.*, total oil content, behenoic acid, total saturated fatty acid, polyunsaturated to saturated fatty acid ratio and iodine value.

Arachidic acid

In WW condition of consecutive seasons, arachidic acid had significant negative association with most of the traits except with stearic acid, behenoic acid and total saturated fatty acid. Similar results of negative association of arachidic acid with polyunsaturated to saturated fatty acid ratio, unsaturated to saturated fatty acid ratio and iodine value were reported by Kavera (2008) and Channayya (2009) for unsaturated to saturated fatty acid ratio.

In the WS condition of summer 2012-13 and summer 2013-14, arachidic acid had significant negative association with most of the traits except with stearic acid, behenoic acid, oleic acid to linoleic acid ratio and oleic acid desaturation ratio. Similar results of positive association of arachidic acid with lignoceric acid were reported by Kavera (2008) and Channayya (2009) with oleic acid to linoleic acid ratio.

Eicosenoic acid

In both the water regimes during both the seasons, eicosenoic acid had significant negative association with most of the traits except with lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid, unsaturated/saturated fatty acid ratio and oleic acid desaturation ratio. This trend of association was also observed by Kavera (2008) and Channayya (2009) with oleic acid to linoleic acid ratio and unsaturated to saturated fatty acid ratio; with lignoceric acid by Kavera (2008) and Hammond *et al.* (1976).

Negative association of eicosenoic acid are in line with the reports of Kavera (2008) for polyunsaturated to saturated fatty acid ratio and iodine value; Channayya (2009) for total saturated fatty acid.

Behenoic acid

Behenoic acid had significant negative association with most of the traits studied except with total protein content, palmitic acid, stearic acid, linoleic acid, arachidic acid, total saturated fatty acid, polyunsaturated/saturated fatty acid ratio, calculated iodine value in both the water regimes during both the seasons. Similar positive associations observed by Channayya (2009) with total saturated fatty acid and Kavera (2009) with

polyunsaturated to saturated fatty acid ratio. Such negative associations of behenoic acid are in line with the reports of Channayya (2009) with oleic acid to linoleic acid; Kavera (2009) and Channayya (2009) with unsaturated to saturated fatty acid ratio.

Lignoceric acid

Lignoceric acid had significant negative association with most of the traits except with total oil content, eicosenoic acid, oleic to linoleic ratio, total unsaturated fatty acid, unsaturated/saturated fatty acid ratio and oleic acid desaturation ratio in both the water regimes during both the seasons. Similar kind of positive association were reported by Channayya (2009) with eicosenoic acid and oleic acid to linoleic acid ratio, while similar kind of association were reported by Kavera (2008) and Channayya (2009) with stearic acid, oleic acid, linoleic acid and Kavera (2008) with unsaturated to saturated fatty acid ratio.

Oleic acid to linoleic acid ratio

Oleic acid to linoleic acid ratio had significant negative association with most of the traits except with the traits viz., total oil content, eicosenoic acid, lignoceric acid, total unsaturated fatty acid, unsaturated/saturated fatty acid ratio and oleic acid desaturation ratio for which positive correlations were observed in most of the conditions during both the seasons. Similar positive and significant correlations were previously reported by Channayya (2009) with oleic acid, eicosenoic acid and unsaturated to saturated fatty acid ratio whereas, significant negative correlations were previously reported by Mercer *et al.* (1990) with polyunsaturated to saturated fatty acid ratio and iodine value.

Total unsaturated fatty acid

Total unsaturated fatty acid had significant negative association with most of the traits except with the traits viz., total oil content, eicosenoic acid, lignoceric acid, oleic to linoleic ratio, unsaturated/saturated fatty acid ratio and oleic acid desaturation ratio for which positive correlations were observed in most of the environments of two seasons.

Total saturated fatty acid

In contrast to the association had by total unsaturated fatty acid, total saturated fatty acid had significant positive association with most of the traits except with the traits *viz.*, total oil content, eicosenoic acid, lignoceric acid, oleic to linoleic ratio, total saturated fatty acid, unsaturated/saturated fatty acid ratio and oleic acid desaturation ratio for which negative correlations were observed in most of the conditions during both the seasons. These are in conformity with reports of positive association of total saturated fatty acids by Channayya (2009) with palmitic acid, linoleic acid and behenic acid and by Channayya (2009) with negative association of total saturated fatty acid with oleic acid, eicosenoic acid and unsaturated to saturated fatty acid ratio.

Polyunsaturated to saturated fatty acid ratio

Polyunsaturated to saturated fatty acid ratio had significant negative association with most of the traits except with the traits *viz.*, palmitic acid, linoleic acid, behenic acid, total saturated fatty acid, calculated iodine value for which positive correlations were observed in most of the environments of two seasons.

Unsaturated to saturated fatty acid ratio

Unsaturated to saturated fatty acid ratio had significant negative association with most of the traits except with the traits *viz.*, total oil content, eicosenoic acid, lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid and oleic acid desaturation ratio for which positive correlations were observed in most of the environments of two seasons. These findings are in clear agreement with the results reported by Channayya (2009) with oleic acid and oleic acid to linoleic acid ratio

Calculated Iodine value

Iodine value had significant negative association with most of the traits except with the traits *viz.*, total oil content, palmitic acid, stearic acid, linoleic acid, behenic acid, total saturated fatty acid and polyunsaturated/saturated fatty acid ratio for which positive correlations were observed in most of the environments of two seasons.

Oleic acid desaturation ratio

Oleic acid desaturation ratio had significant negative association with most of the traits except with the traits viz., total oil content, eicosenoic acid, lignoceric acid, oleic/linoleic acid ratio, total unsaturated fatty acid and unsaturated/saturated fatty acid ratio for which positive correlations were observed in of the environments of two seasons.

5.3.6 Correlation between foliar disease resistance traits

Pod yield under WW and WS conditions in both the seasons had significant negative correlations with late leaf spot score and rust scores at all the stages. Pod yield was significantly and negatively associated with reaction to rust and late leaf spot diseases as expected since these foliar diseases reduce the photosynthetic activity of the plant.

Highly significant and positive correlations were observed among late leaf spot score and rust scores at different stages. Indicating the resistance or susceptible reaction of the plants at these stages of growth was almost similar and thus direct selection would be effective.

Significant negative correlation of pod yield per plant with late leaf spot severity by Parameshwarappa *et al.* (2008) and John *et al.* (2005) were in accordance with the results of the present study.

5.4 Construction of genetic linkage map

Recently, a few genetic maps based on RIL populations have been developed in cultivated groundnut (Varshney *et al.*, 2009a; Hong *et al.*, 2010; Khedikar *et al.*, 2010; Ravi *et al.*, 2011 and Sarvamangla *et al.*, 2011) and only one population namely TAG 24 × ICGV 86031 has been used for developing the genetic map and QTL analysis for drought tolerance traits. While, Gauthami (2012) used two RIL populations namely ICGS 76 × CSMG 84-1 and ICGS 44 × ICGS 76 segregating for drought tolerance together with the genetic map of TAG 24 × ICGV 86031 developed from the earlier

studies (Ravi *et al.*, 2011) for constructing a dense consensus map for drought tolerance traits. In the present study a new mapping population of TMV-2 x GM 6-1, segregating for several traits such as quantitative, physiological, root traits which are related to drought tolerance and other quality parameters was used for the construction of genetic linkage map. The stringent mapping parameters adopted for individual map construction resulted in 17 linkage groups.

As a result of collaborative efforts made in last five years worldwide, nearly 4, 000 SSRs were developed by the groundnut community. The parental genotypes of mapping population TMV-2 x GM 6-1 were screened with a total of 430 SSR markers. However, low level of polymorphism was observed (23.95 %). This may be attributed mainly to a narrow genetic diversity in the cultivated groundnut gene pool (Young *et al.*, 1996; Varshney *et al.*, 2009; Hong *et al.*, 2010; Ravi *et al.*, 2011 and Sarvamangla *et al.*, 2011).

Availability of a high density genetic map in a crop species is must to initiate genetical and molecular breeding activities. The newly developed map consists of 71 SSR markers distributed over 17 linkage groups. Fourteen out of 17 linkage groups possessed more than one marker. LG-5 was the highest dense linkage group with 10 markers followed by LG-3 and LG-11 with 8 and 7 markers. LG-7 and LG-9 were very small with only two markers in each linkage groups (Plate 6 and Table 54). LG-14, 15, 16 and 17 had only one marker mapped on each of the linkage group. These small linkage groups could be artificial and additional genetic markers are needed to improve the linkage analysis. The observed total map distance of the newly developed map (399.04 cM) was less than the expected genome length of groundnut genome (2800 Mb/1C) representing the requirement for saturation of the linkage map with more number of SSR markers.

As groundnut is tetraploid crop species, 3 markers (Seq18E7-F, m13-AHGS2132-F and m13-GM2638-F) amplified more than one polymorphic locus. Amplification of more than one locus may be due to the polyploidy nature of the crop and has been reported in earlier studies (Hopkins *et al.*, 1999; Krishna *et al.*, 2004; Kottapalli *et al.*, 2007; Varshney *et al.*, 2009a; 2009b; Ravi *et al.*, 2011 and Hong *et al.*, 2010).

5.5 Identification of QTLs for various traits

To identify QTLs for drought tolerance, an extensive study was done in TAG 24 × ICGV 86031. Varshney *et al.* (2009a) and Ravi *et al.* (2011) identified several M-QTLs and a large number of E-QTLs for drought tolerance related traits in different seasons. Similarly Gauthami *et al.* (2012) also reported several M-QTLs and a large number of E-QTLs for drought tolerance related traits in their consensus map developed from the two new mapping populations ICGS 76 × CSMG 84-1 and ICGS 44 × ICGS 76 along with mapping population TAG 24 × ICGV 86031. Since the QTLs identified in all the previous studies on drought tolerance in groundnut revealed large number of QTLs with low phenotypic variance was imperative of complex nature of drought tolerance and its component traits, it is necessary to confirm these in new mapping populations and identify the new QTLs if any. In this context, QTL analysis for drought tolerance related traits was undertaken in the present study on the new mapping population of TMV-2 × GM 6-1.

In general, alleles with low to high additive effects were identified for majority of the traits under study. However, alleles with low to medium additive effects were detected in the earlier study using TAG 24 × ICGV 86031 (Ravi *et al.*, 2011). The combination of these favorable alleles derived from both the tolerant (positive additive effect) and the susceptible (negative effect) parents may confer more tolerance to drought (Gauthami *et al.*, 2012). Alleles that improve the trait being derived from parents agronomically inferior have also been identified for several plant species (Xiao *et al.*, 1998; Frary *et al.*, 2004 and Yoon *et al.*, 2006). Since QTLs with low to high phenotypic variation were detected in contrast with earlier study (Ravi *et al.*, 2011), there is a need for identification of stable QTLs over seasons. Stable QTLs which are identified in two or more environments of the two water regimes across the two seasons were given in the Table 64.

A considerable number of QTLs were identified in the present study for drought related traits with low to high phenotypic variation for different yield and drought component traits suggesting that drought tolerance is governed by a large number of main effect QTLs and epistatic QTLs. In the present study a total 233 QTLs were identified for 40 traits on 17 linkage groups among which 62 were major QTLs while

Table 64: Stable QTLs identified for various traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WW and WS conditions during summer 2012-13 and summer 2013-14

	Trait	Name of the QTL	Linkage group	Position (cM)	Left marker	Right marker	LOD	PVE%	Additive effect
1	Days to maturity	qDMWW13-8-1	8	32	m13IPAHM219F	m13AHGS2094F	3.7764	5.8666	0.2059
		qDMWS13-8-1	8	32	m13IPAHM219F	m13AHGS2094F	2.7697	4.2609	0.1207
2	Number of primary branches per plant	qNPBPWW14-3-1	3	55	m13TC39C01V	Gm2215F	3.9629	30.2731	-1.2769
		qNPBPWS14-3-1	3	52	m13TC39C01V	Gm2215F	17.1345	59.758	-1.2492
3	Number of secondary branches per plant	qNSBPWW14-3-1	3	55	m13TC39C01V	Gm2215F	46.0171	69.6507	-1.7157
		qNSBPWS14-3-1	3	55	m13TC39C01V	Gm2215F	20.9307	53.4284	-1.2048
4	RWC	qRWC2WW13-3-1	3	37	m13AHGS0268P	m13TC39C01V	4.4761	7.2184	-0.852
		qRWC3WW13-3-1	3	34	m13AHGS0268P	m13TC39C01V	6.0201	11.92	-1.4621
5	Number of nodules per plant	qNNPPWW13-3-1	3	53	m13TC39C01V	Gm2215F	16.6312	56.7854	-19.8489
		qNNPPWS13-3-1	3	57	m13TC39C01V	Gm2215F	4.8639	21.0344	-16.3405
		qNNPPWW14-3-1	3	55	m13TC39C01V	Gm2215F	5.772	32.8305	-13.841
6	Root dry weight	qRDWWW13-3-1	3	57	m13TC39C01V	Gm2215F	3.2525	16.7867	-0.1608
		qRDWWW14-3-1	3	54	m13TC39C01V	Gm2215F	11.5246	54.3226	-5.8404
7	Total oil content	qTOCWW13-5-1	5	24	m13AHGS2960V	m13Gm1867F	3.9074	7.0288	-0.4556
		qTOCWW14-5-1	5	22	m13AHGS2960V	m13Gm1867F	3.1744	5.5171	-0.2971
8	Palmitic acid	qPALWS13-9-1	9	11	m13Seq5D5P	m13AHGS3217N	4.4998	11.4761	0.3596
		qPALWS14-9-1	9	7	m13Seq5D5P	m13AHGS3217N	6.263	12.7497	0.3847
9	Stearic acid	qSTEW13-13-1	13	108	m13Gm692V	m13AHGS2342P	5.4866	8.265	0.1758
		qSTEW14-13-1	13	109	m13Gm692V	m13AHGS2342P	12.8554	18.2037	0.1505
10	Oleic acid	qOLEWS13-9-1	9	5	m13Seq5D5P	m13AHGS3217N	9.8543	31.0249	-4.4972
		qOLEWS14-9-1	9	8	m13Seq5D5P	m13AHGS3217N	4.9055	8.6905	-2.0973

Contd...

11	Oleic acid	qOLEWS13-1-1	1	13	m13TC16A10N	m13AHGS2043V	11.0443	38.7212	-4.5937
		qOLEWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	4.2774	9.2164	-1.9554
12	Linoleic acid	qLINWW13	11	9	m13Ai119H15P	IPAHM123V	11.0904	15.702	2.406
		qLINWW14	11	8	m13Ai119H15P	IPAHM123V	11.2832	17.816	2.578
13	Linoleic acid	qLINWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.6529	41.0935	4.0426
		qLINWS13-1-1	1	14	m13TC16A10N	m13AHGS2043V	11.2249	33.3804	3.4811
14	Linoleic acid	qLINWS14-1-2	1	25	m13AHGS2043V	m13TC2D06N	10.3039	28.0909	3.131
		qLINWS13-1-2	1	26	m13AHGS2043V	m13TC2D06N	11.6449	30.3039	3.118
15	Arachidic acid	qARAWS13-9-1	9	0	m13Seq5D5P	m13AHGS3217N	5.7204	8.4331	-0.057
		qARAWS14-9-1	9	0	m13Seq5D5P	m13AHGS3217N	11.5825	16.3379	-0.0569
16	Ecosenoic acid	qECOWW13-13-1	13	109	m13Gm692V	m13AHGS2342P	10.2308	12.9697	-0.0353
		qECOWW14-13-1	13	109	m13Gm692V	m13AHGS2342P	7.3869	9.1989	-0.0291
17	Lignoceric acid	qLIGWW13-5-1	5	28	m13Gm1867F	m13GM2637V	9.5328	12.2915	-0.0412
		qLIGWW14-5-1	5	29	m13Gm1867F	m13GM2637V	8.334	11.1575	-0.0386
18	Lignoceric acid	qLIGWW13-13-1	13	109	m13Gm692V	m13AHGS2342P	4.7123	6.1262	-0.0311
		qLIGWW14-13-2	13	109	m13Gm692V	m13AHGS2342P	5.2614	6.9184	-0.0324
19	O/L ratio	qOLRWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	6.3703	9.3455	-0.3184
		qOLRWW14-11-1	11	9	m13Ai119H15P	IPAHM123V	6.4503	9.4572	-0.3097
20	O/L ratio	qOLRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.8319	34.4039	-0.6456
		qOLRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.107	32.4316	-0.6871
21	O/L ratio	qOLRWS13-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.6724	22.7805	-0.4856
		qOLRWS14-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.1185	21.3013	-0.5156
22	Total unsaturated fatty acid	qUWW13-5-1	5	26	m13AHGS2960V	m13Gm1867F	15.3481	23.4384	-1.224
		qUWW14-5-1	5	25	m13AHGS2960V	m13Gm1867F	8.7835	12.8897	-0.7489
23	Total saturated fatty acid	qSWW13-11-1	11	8	m13Ai119H15P	IPAHM123V	13.3609	20.7842	0.6003
		qSWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	9.2037	13.6557	0.3988

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24	L/S ratio	qLSRWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	7.4998	10.909	0.0853
		qLSRWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	10.4784	16.6909	0.1066
25	L/S ratio	qLSRWS13-3-1	9	7	m13Seq5D5P	m13AHGS3217N	3.6955	7.6153	0.0695
		qLSRWS14-9-1	9	7	m13Seq5D5P	m13AHGS3217N	4.1961	8.4171	0.0728
26	L/S ratio	qLSRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	9.9018	35.8286	0.1745
		qLSRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.8211	38.7244	0.1801
27	U/S ratio	qUSRWW13-5-1	5	25	m13AHGS2960V	m13Gm1867F	15.2476	28.1939	-0.2326
		qUSRWW14-5-1	5	25	m13AHGS2960V	m13Gm1867F	7.3664	11.8217	-0.124
28	U/S ratio	qUSRWS13-10-1	10	3	m13AHGS2185N	m13AHGS2602N	13.3444	20.5126	-0.1676
		qUSRWS14-10-1	10	3	m13AHGS2185N	m13AHGS2602N	12.4037	19.6841	-0.1456
29	CIV	qCIVWW13-11-1	11	9	m13Ai119H15P	IPAHM123V	6.0743	8.9318	1.3129
		qCIVWW14-11-1	11	9	m13Ai119H15P	IPAHM123V	7.701	11.1851	1.385
30	OAD	qOADWW13-11-1	11	8	m13Ai119H15P	IPAHM123V	12.0123	18.8814	-0.0371
		qOADWW14-11-1	11	8	m13Ai119H15P	IPAHM123V	12.2046	19.1358	-0.0371
31	OAD	qOADWS13-9-1	9	9	m13Seq5D5P	m13AHGS3217N	4.7213	10.6439	-0.0235
		qOADWS14-9-1	9	9	m13Seq5D5P	m13AHGS3217N	4.771	10.7315	-0.0241
32	OAD	qOADWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.3521	40.799	-0.0522
		qOADWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.2952	41.1846	-0.0536
33	LLS score	qLLS80WW13-6-1	6	6	TC6E01N	m13TC2B09N	9.2337	5.8142	0.372
		qLLS80WW14-6-1	6	6	TC6E01N	m13TC2B09N	12.9515	9.3145	0.4926
		qLLS80WS13-6-1	6	6	TC6E01N	m13TC2B09N	24.5502	19.0095	0.4298
		qLLS90WW13-6-1	6	4	TC6E01N	m13TC2B09N	35.484	41.6331	1.5481
		qLLS90WW14-6-1	6	4	TC6E01N	m13TC2B09N	30.1672	38.4985	1.49
		qLLS90WS13-6-1	6	4	TC6E01N	m13TC2B09N	26.4251	38.952	0.9881
		qLLS90WS14-6-1	6	4	TC6E01N	m13TC2B09N	30.9342	41.2403	1.2792

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34	LLS score	qLLS80WW13-13-1	13	109	m13Gm692V	m13AHGS2342P	9.8814	6.7264	0.396
		qLLS80WS13-13-1	13	109	m13Gm692V	m13AHGS2342P	10.0409	6.9499	0.2564
		qLLS80WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	12.1876	14.3371	0.4822
		qLLS90WW13-13-1	13	107	m13Gm692V	m13AHGS2342P	38.8059	39.3538	1.5077
		qLLS90WW14-13-2	13	107	m13Gm692V	m13AHGS2342P	38.2057	38.9583	1.5063
		qLLS90WS13-13-2	13	107	m13Gm692V	m13AHGS2342P	29.7087	38.6361	1.0254
		35qLLS90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	32.4002	37.7005	1.2353
35	LLS score	qL36LS80WW13-3-1	3	57	m13TC39C01V	Gm2215F	5.0844	6.3095	-1.3309
		qLLS80WS13-3-1	3	56	m13TC39C01V	Gm2215F	2.6126	6.3612	-0.5665
		qLLS80WS14-3-1	3	57	m13TC39C01V	Gm2215F	6.0596	6.6222	-1.1823
		qLLS90WW13-3-1	3	56	m13TC39C01V	Gm2215F	5.4051	9.378	-1.3875
		qLLS90WW14-3-1	3	56	m13TC39C01V	Gm2215F	5.1332	8.3231	-1.3662
		qLLS90WS13-3-1	3	56	m13TC39C01V	Gm2215F	4.8082	10.6829	-0.9972
		qLLS90WS14-3-1	3	55	m13TC39C01V	Gm2215F	5.3446	10.3087	-1.03
36	LLS score	qLLS80WW13-4-1	4	7	Gm2301F	Gm1996F	19.487	16.9999	0.6042
		qLLS80WW14-4-1	4	7	Gm2301F	Gm1996F	17.4351	14.7677	0.5906
		qLLS80WS13-4-1	4	5	Gm2301F	Gm1996F	6.2285	4.8342	0.2082
37	LLS score	qLLS80WW13-10-2	10	7	m13AHGS2602N	m13AHGS2490V	9.101	6.6046	0.3699
		qLLS80WS13-10-1	10	8	m13AHGS2602N	m13AHGS2490V	6.4328	4.555	0.1961
		qLLS80WS14-10-1	10	7	m13AHGS2602N	m13AHGS2490V	12.4022	14.8272	0.4597
38	LLS score	qLLS90WW13-10-1	10	13	m13AHGS2490V	TC6H03F	5.7161	4.5816	0.4232
		qLLS90WW14-10-1	10	13	m13AHGS2490V	TC6H03F	6.8211	5.6266	0.4717
		qLLS90WS14-10-1	10	13	m13AHGS2490V	TC6H03F	6.8511	5.8697	0.4006
39	RUST score	qRUST80WW13-6-1	6	6	TC6E01N	m13TC2B09N	11.807	9.9736	0.2474
		qRUST80WW14-6-1	6	6	TC6E01N	m13TC2B09N	12.3303	10.2687	0.2505
		qRUST80WS13-6-1	6	6	TC6E01N	m13TC2B09N	22.1786	22.3728	0.4151

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		qRUST80WS14-6-1	6	6	TC6E01N	m13TC2B09N	14.9598	12.0318	0.2131
		qRUST90WW13-6-1	6	6	TC6E01N	m13TC2B09N	9.6641	6.2337	0.4087
		qRUST90WW14-6-1	6	6	TC6E01N	m13TC2B09N	6.5122	4.1129	0.3355
		qRUST90WS13-6-1	6	4	TC6E01N	m13TC2B09N	35.833	51.643	0.9155
		qRUST90WS14-6-1	6	4	TC6E01N	m13TC2B09N	28.7839	40.078	0.938
40	RUST score	qRUST80WW13-13-1	13	108	m13Gm692V	m13AHGS2342P	6.2103	5.4693	0.1814
		qRUST80WW14-13-1	13	108	m13Gm692V	m13AHGS2342P	6.715	5.8316	0.1868
		qRUST80WS14-13-1	13	109	m13Gm692V	m13AHGS2342P	12.3416	10.4292	0.1965
		qRUST90WW13-13-1	13	107	m13Gm692V	m13AHGS2342P	13.8716	24.3895	0.8932
		qRUST90WW14-13-1	13	107	m13Gm692V	m13AHGS2342P	26.1699	32.843	1.09
		qRUST90WS13-13-1	13	107	m13Gm692V	m13AHGS2342P	30.9987	43.8737	0.8675
		qRUST90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	44.5729	42.8251	0.9754
41	RUST score	qRUST90WW13-3-1	3	56	m13TC39C01V	Gm2215F	3.7678	7.3887	-0.9727
		qRUST90WW14-3-1	3	56	m13TC39C01V	Gm2215F	4.2732	7.1718	-1.0041
		qRUST90WS13-3-1	3	54	m13TC39C01V	Gm2215F	6.4851	14.7451	-0.678
		qRUST90WS14-3-1	3	54	m13TC39C01V	Gm2215F	5.584	12.2532	-0.7096
42	RUST score	qRUST90WS13-4-1	4	4	Gm2301F	Gm1996F	7.5048	7.5226	0.3009
		qRUST90WS14-4-1	4	4	Gm2301F	Gm1996F	6.7676	6.1094	0.3073
43	RUST score	qRUST80WW13-10-1	10	6	m13AHGS2602N	m13AHGS2490V	10.6668	9.5203	0.2242
		qRUST80WW14-10-1	10	5	m13AHGS2602N	m13AHGS2490V	10.4483	8.9579	0.2166
		qRUST80WS13-10-1	10	6	m13AHGS2602N	m13AHGS2490V	11.1365	11.1294	0.2716
		qRUST80WS14-10-1	10	8	m13AHGS2602N	m13AHGS2490V	7.6754	6.1916	0.1424

remaining 171 were minor QTLs. Among a total of 42 QTLs identified for quantitative traits 12 were major QTLs and 30 were minor QTLs. Similarly, three among nine QTLs for physiological traits, six out of 12 QTLs for root traits, 23 out of 102 and 25 out of 68 for foliar disease resistance traits were found to be major QTLs.

Major QTLs identified in water stress conditions are given in the Table 65 among which, QTLs for oleic acid, linoleic acid, oleic to linoleic ratio, linoleic to saturated fatty acid ratio, oleic acid desaturation, late leaf spot and rust scores were stably expressed in WS condition across the seasons. These stable QTLs should be validated in the other material and can be used in further breeding programmes for improving the quality of groundnut under water limited conditions. Other QTLs which are specific in each season have to be validated in different WS conditions for dissecting the stable QTLs in all water limiting situations.

Some of the genomic regions had QTLs mapped for various traits. Such regions between the markers which are common for various traits identified in the present study are given in Table 66. Understanding of relation between those traits can be useful for harnessing such QTLs (Gautami *et al.*, 2012).

The m13TC39C01V-Gm2215F (52-57cM) region on LG-3 (57.79 cM) harbored 19 QTLs for 14 different traits under two water regimes of two summer seasons. QTLs identified for traits include eight yield and yield component traits, two physiological traits and four root traits. Interestingly, four out of these 14 different traits *viz.*, number of primary branches per plant, number of secondary branches per plant, number of nodules per plant and root dry weight were stable across two or more conditions out of the two water regimes and seasons. Under water stress conditions, genotypes favoring dense plant canopy (lower plant height but with more number of primary and secondary branches per plant), higher root growth and lower leaf thickness, it is expected to have greater photosynthetic capacity per unit leaf area (Nageswara Rao *et al.*, 1995) and they can maintain water status and are likely to achieve higher yields under intermittent drought stress in that field experiment. As mentioned above, a recent finding indicated that lines having lower plant stature could be better adapted to intermittent stress conditions (Ratnakumar and Vadez 2011) by limiting the effect of stress on

Table 65: Major QTLs identified for various traits in the mapping population of a cross TMV-2 x GM 6-1 in groundnut under WS condition during summer 2012-13 and summer 2013-14

S.No	Trait	Name of the QTL	LG	Position (cM)	Left marker	Right marker	LOD	PVE%	AE
1	Number of primary branches per plant	qNPBPWS14-3-1	3	52	m13TC39C01V	Gm2215F	17.13	59.76	-1.25
2	Number of secondary branches per plant	qNSBPWS14-3-1	3	55	m13TC39C01V	Gm2215F	20.93	53.43	-1.20
3	Number of pegs per plant	qNPPWS14-3-1	3	56	m13TC39C01V	Gm2215F	37.94	56.28	-17.53
4	Number of mature pods per plant	qNMPPWS14-3-1	3	55	m13TC39C01V	Gm2215F	6.77	29.94	-6.48
5	100 seed weight	qHSWWS14-3-1	3	53	m13TC39C01V	Gm2215F	7.99	34.80	-8.20
6	SLA	qSLA2WS14-13-1	13	49	m13AHGS2058P	m13Gm692V	6.10	60.90	4.06
7	Number of nodules per plant	qNNPPWS13-3-1	3	57	m13TC39C01V	Gm2215F	4.86	21.03	-16.34
8	Oleic acid	qOLEWS13-1-1	1	13	m13TC16A10N	m13AHGS2043V	9.85	31.02	-4.50
		qOLEWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	11.04	38.72	-4.59
9	Linoleic acid	qLINWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.65	41.09	4.04
		qLINWS13-1-1	1	14	m13TC16A10N	m13AHGS2043V	11.22	33.38	3.48
		qLINWS14-1-2	1	25	m13AHGS2043V	m13TC2D06N	10.30	28.09	3.13
		qLINWS13-1-2	1	26	m13AHGS2043V	m13TC2D06N	11.64	30.30	3.12
		qLINWS13-3-1	3	54	m13TC39C01V	Gm2215F	11.80	39.50	6.00
10	Ecosenoic acid	qECOWS14-11-8	11	8	m13Ai119H15P	IPAHM123V	15.15	24.24	-0.04
11	Behenoic acid	qBEHWS14-4-1	4	14	Seq19G7F	m13AHGS1338P	11.69	21.20	0.12
12	O/L ratio	qOLRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.83	34.40	-0.65
		qOLRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.11	32.43	-0.69
		qOLRWS13-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.67	22.78	-0.49
		qOLRWS14-1-2	1	23	m13AHGS2043V	m13TC2D06N	9.12	21.30	-0.52
13	Total unsaturated fatty acid	qUWW13-5-1	5	26	m13AHGS2960V	m13Gm1867F	15.35	23.44	-1.22

14	L/S ratio	qLSRWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	9.90	35.83	0.17
		qLSRWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	10.82	38.72	0.18
15	U/S ratio	qUSRWW13-5-1	5	25	m13AHGS2960V	m13Gm1867F	15.25	28.19	-0.23
16	OAD	qOADWS13-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.35	40.80	-0.05
		qOADWS14-1-1	1	12	m13TC16A10N	m13AHGS2043V	12.30	41.18	-0.05
		qOADWS13-1-2	1	25	m13AHGS2043V	m13TC2D06N	10.08	27.48	-0.04
17	LLS score	qLLS90WS13-6-1	6	4	TC6E01N	m13TC2B09N	26.43	38.95	0.99
		qLLS90WS14-6-1	6	4	TC6E01N	m13TC2B09N	30.93	41.24	1.28
		qLLS80WS14-4-1	4	10	Gm1996F	Seq19G7F	29.87	25.55	0.62
		qLLS80WS14-4-2	4	14	Seq19G7F	m13AHGS1338P	43.54	34.29	0.73
		qLLS90WS13-13-2	13	107	m13Gm692V	m13AHGS2342P	29.71	38.64	1.03
		qLLS90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	32.40	37.70	1.24
18	RUST score	qRUST90WS13-6-1	6	4	TC6E01N	m13TC2B09N	35.83	51.64	0.92
		qRUST90WS14-6-1	6	4	TC6E01N	m13TC2B09N	28.78	40.08	0.94
		qRUST80WS13-6-1	6	6	TC6E01N	m13TC2B09N	22.18	22.37	0.42
		qRUST90WS13-13-1	13	107	m13Gm692V	m13AHGS2342P	31.00	43.87	0.87
		qRUST90WS14-13-1	13	107	m13Gm692V	m13AHGS2342P	44.57	42.83	0.98

Table 66: Important QTL regions mapped for various traits at common positions

Trait	Name of the QTL	Linkage group	Position (cM)	LOD	PVE%	Additive effect
m13TC16A10N-m13TC16A10N region on the LG-1						
Pod yield per plant	qPYPWW14-1-1	1	4	3.491	7.081	1.060
Kernel yield per plant	qKYPWW14-1-1	1	4	3.223	6.528	0.698
Shelling per cent	qSOTWW14-1-1	1	7	3.363	10.011	-0.648
RWC	qRWC3WS14-1-1	1	0	2.857	4.306	-1.038
Oleic acid	qOLEWS13-1-1	1	13	9.854	31.025	-4.497
	qOLEWS14-1-1	1	12	11.044	38.721	-4.594
Linoleic acid	qLINWS13-1-1	1	14	11.225	33.380	3.481
	qLINWS14-1-1	1	12	12.653	41.094	4.043
O/L ratio	qOLRWS13-1-1	1	12	10.832	34.404	-0.646
	qOLRWS14-1-1	1	12	10.107	32.432	-0.687
L/S ratio	qLSRWS13-1-1	1	12	9.902	35.829	0.175
	qLSRWS14-1-1	1	12	10.821	38.724	0.180
OAD	qOADWS13-1-1	1	12	12.352	40.799	-0.052
	qOADWS14-1-1	1	12	12.295	41.185	-0.054
m13AHGS2043V-m13TC2D06N region on the LG-1						
Linoleic acid	qLINWS13-1-2	1	26	11.645	30.304	3.118
	qLINWS14-1-2	1	25	10.304	28.091	3.131
O/L ratio	qOLRWS13-1-2	1	23	9.672	22.781	-0.486
	qOLRWS14-1-2	1	23	9.119	21.301	-0.516
OAD	qOADWS13-1-2	1	25	10.083	27.480	-0.040
m13TC39C01V-Gm2215F region on the LG-3						
Number of primary branches per plant	qNPBPWW14-3-1	3	55	3.963	30.273	-1.277
	qNPBPWS14-3-1	3	52	17.135	59.758	-1.249
Number of secondary branches per plant	qNSBPWW14-3-1	3	55	46.017	69.651	-1.716
	qNSBPWS14-3-1	3	55	20.931	53.428	-1.205
Number of pegs per plant	qNPPWS14-3-1	3	56	37.944	56.284	-17.527
Number of mature pods per plant	qNMPPWS14-3-1	3	55	6.772	29.944	-6.477
Pod yield per plant	qPYPWW14-3-1	3	55	3.413	20.695	-3.088
Kernel yield per plant	qKYPWW14-3-1	3	55	4.168	21.940	-2.176
Shelling per cent	qSOTWW14-3-1	3	57	12.432	28.579	-4.035
100 seed weight	qHSWWS14-3-1	3	53	7.986	34.800	-8.196
RWC	qRWC2WS13-3-1	3	56	2.586	18.952	2.852
SLA	qSLA3WW13-3-1	3	56	12.647	47.168	3.339
Root length	qRLWW14-3-1	3	56	3.111	21.093	-8.804
Number of nodules per plant	qNNPPWW13-3-1	3	53	16.631	56.785	-19.849

	qNNPPWS13-3-1	3	57	4.864	21.034	-16.341
	qNNPPWW14-3-1	3	55	5.772	32.831	-13.841
Root dry weight	qRDWWW13-3-1	3	57	3.253	16.787	-0.161
	qRDWWW14-3-1	3	54	11.525	54.323	-5.840
Shoot dry weight	qSDWWW14-3-1	3	57	14.580	23.453	-0.536
Total protein content	qTPCWS13-3-1	3	57	5.232	18.784	-3.154
Linoleic acid	qLINWS13-3-1	3	54	11.803	39.496	5.995
LLS score	qLLS80WW13-3-1	3	57	5.084	6.310	-1.331
	qLLS80WS13-3-1	3	56	2.613	6.361	-0.567
	qLLS80WS14-3-1	3	57	6.060	6.622	-1.182
	qLLS90WW13-3-1	3	56	5.405	9.378	-1.388
	qLLS90WW14-3-1	3	56	5.133	8.323	-1.366
	qLLS90WS13-3-1	3	56	4.808	10.683	-0.997
	qLLS90WS14-3-1	3	55	5.345	10.309	-1.030
RUST score	qRUST80WS14-3-1	3	57	3.732	7.391	-0.518
	qRUST90WW13-3-1	3	56	3.768	7.389	-0.973
	qRUST90WW14-3-1	3	56	4.273	7.172	-1.004
	qRUST90WS13-3-1	3	54	6.485	14.745	-0.678
	qRUST90WS14-3-1	3	54	5.584	12.253	-0.710
m13AHGS2960V-m13Gm1867F region on the LG-5						
Total oil content	qTOCWW13-5-1	5	24	3.907	7.029	-0.456
	qTOCWW14-5-1	5	22	3.174	5.517	-0.297
Oleic acid	qOLEWW13-5-1	5	25	13.867	25.319	-3.866
Behenoic acid	qBEHWW13-5-1	5	22	5.384	7.636	0.133
Total unsaturated fatty acid	qUWW13-5-1	5	26	15.348	23.438	-1.224
	qUWW14-5-1	5	25	8.784	12.890	-0.749
Total saturated fatty acid	qSWW14-5-1	5	25	6.954	10.896	0.351
U/S ratio	qUSRWW13-5-1	5	25	15.248	28.194	-0.233
	qUSRWW14-5-1	5	25	7.366	11.822	-0.124
TC6E01N-m13TC2B09N region on the LG-6						
LLS score	qLLS80WW13-6-1	6	6	9.234	5.814	0.372
	qLLS80WW14-6-1	6	6	12.952	9.315	0.493
	qLLS80WS13-6-1	6	6	24.550	19.010	0.430
	qLLS90WW13-6-1	6	4	35.484	41.633	1.548
	qLLS90WW14-6-1	6	4	30.167	38.499	1.490
	qLLS90WS13-6-1	6	4	26.425	38.952	0.988
	qLLS90WS14-6-1	6	4	30.934	41.240	1.279
RUST score	qRUST80WW13-6-1	6	6	11.807	9.974	0.247
	qRUST80WW14-6-1	6	6	12.330	10.269	0.251
	qRUST80WS13-6-1	6	6	22.179	22.373	0.415
	qRUST80WS14-6-1	6	6	14.960	12.032	0.213

	qRUST90WW13-6-1	6	6	9.664	6.234	0.409
	qRUST90WW14-6-1	6	6	6.512	4.113	0.336
	qRUST90WS13-6-1	6	4	35.833	51.643	0.916
	qRUST90WS14-6-1	6	4	28.784	40.078	0.938
m13Seq5D5P-m13AHGS3217N region on the LG-9						
Pod yield per plant	qPYPWW13-9-1	9	4	10.708	20.542	-1.405
Kernel yield per plant	qKYPWW13-9-1	9	4	11.427	21.686	-0.973
Number of nodules per plant	qNNPPWW14-9-1	9	7	3.984	10.036	-3.729
Palmitic acid	qPALWS13-9-1	9	11	4.500	11.476	0.360
	qPALWS14-9-1	9	7	6.263	12.750	0.385
Oleic acid	qOLEWS13-9-1	9	5	4.906	8.691	-2.097
	qOLEWS14	9	8	4.277	9.216	-1.955
Linoleic acid	qLINWS14-9-1	9	9	4.953	10.989	1.840
Arachidic acid	qARAWS13-9-1	9	0	5.720	8.433	-0.057
	qARAWS14-9-1	9	0	11.583	16.338	-0.057
Behenoic acid	qBEHWW14-9-1	9	0	6.312	8.502	-0.077
L/S ratio	qLSRWS13-3-1	9	7	3.696	7.615	0.070
	qLSRWS14-9-1	9	7	4.196	8.417	0.073
CIV	qCIVWS14-9-1	9	10	3.645	7.578	1.179
OAD	qOADWS13-9-1	9	9	4.721	10.644	-0.024
	qOADWS14-9-1	9	9	4.771	10.732	-0.024
Seq3A8F-m13AHGS2185N region on the LG-10						
Days to maturity	qDMWS14-10-1	10	0	4.500	6.735	0.187
Number of primary branches per plant	qNPBPWW13-10-1	10	0	3.341	4.376	-0.224
Number of mature pods per plant	qNMPPWS14-10-1	10	0	6.731	9.848	-1.792
Pod yield per plant	qPYPWS13-10-1	10	0	5.581	8.237	-0.538
	qPYPWW14-10-1	10	0	5.766	7.630	-0.909
Kernel yield per plant	qKYPWS13-10-1	10	0	5.025	7.448	-0.337
	qKYPWW14-10-1	10	0	5.856	7.737	-0.628
Shelling per cent	qSOTWS13-10-1	10	0	3.574	5.356	-2.538
SMK %	qSMKWS14-10-1	10	0	5.687	8.386	-5.827
Shoot length	qSLWW14-10-1	10	0	4.834	7.175	1.262
Ecosenoic acid	qECOWS14-10-1	10	0	3.832	5.122	0.015
Total unsaturated fatty acid	qUWS13-10-1	10	0	4.233	6.311	-0.977
LLS score at 80 DAS	qLLS80WW13-10-1	10	0	3.855	2.192	-0.195
m13AHGS2602N-m13AHGS2490V region on the LG-10						
Days to 50 % flowering	qDFFWS14-10-1	10	4	3.901	6.235	0.251
Plant height	qPHWW13-10-1	10	8	11.969	18.534	2.290
Palmitic acid	qPALWS14-10-1	10	4	6.475	8.636	0.344

Total saturated fatty acid	qSWS13-10-1	10	4	9.125	13.773	0.389
LLS score	qLLS80WW13-10-2	10	7	9.101	6.605	0.370
	qLLS80WS13-10-1	10	8	6.433	4.555	0.196
	qLLS80WS14-10-1	10	7	12.402	14.827	0.460
	qLLS90WS13-10-1	10	7	4.856	4.059	0.269
RUST score	qRUST80WW13-10-1	10	6	10.667	9.520	0.224
	qRUST80WW14-10-1	10	5	10.448	8.958	0.217
	qRUST80WS13-10-1	10	6	11.137	11.129	0.272
	qRUST80WS14-10-1	10	8	7.675	6.192	0.142
	qRUST90WW13-10-1	10	6	9.922	8.847	0.457
m13AHGS2490V-TC6H03F region on the LG-10						
LLS score	qLLS80WS14-10-2	10	13	12.195	14.595	0.457
	qLLS90WW13-10-1	10	13	5.716	4.582	0.423
	qLLS90WW14-10-1	10	13	6.821	5.627	0.472
	qLLS90WS14-10-1	10	13	6.851	5.870	0.401
m13Ai119H15P-IPAHM123V region on the LG-11						
Palmitic acid	qPALWW13-11-1	11	9	8.127	11.766	0.375
Oleic acid	qOLEWW14-11-1	11	8	12.660	19.876	-3.431
Linoleic acid	qLINWW13	11	9	11.090	15.702	2.406
	qLINWW14	11	8	11.283	17.816	2.578
Ecosenoic acid	qECOWW14-11-1	11	8	8.428	10.744	-0.030
	qECOWS14-11-8	11	8	15.149	24.242	-0.037
O/L ratio	qOLRWW13-11-1	11	9	6.370	9.346	-0.318
	qOLRWW14-11-1	11	9	6.450	9.457	-0.310
Total unsaturated fatty acid	qUWW14-11-1	11	9	10.380	12.912	-0.755
Total saturated fatty acid	qSWW13-11-1	11	8	13.361	20.784	0.600
	qSWW14-11-1	11	8	9.204	13.656	0.399
L/S ratio	qLSRWW13-11-1	11	9	7.500	10.909	0.085
	qLSRWW14-11-1	11	8	10.478	16.691	0.107
U/S ratio	qUSRWW14-11-1	11	8	9.838	14.734	-0.141
CIV	qCIVWW13-11-1	11	9	6.074	8.932	1.313
	qCIVWW14-11-1	11	9	7.701	11.185	1.385
OAD	qOADWW13-11-1	11	8	12.012	18.881	-0.037
	qOADWW14-11-1	11	8	12.205	19.136	-0.037
m13Gm692V-m13AHGS2342P region on the LG-13						
LLS score	qLLS80WW13-13-1	13	109	9.881	6.726	0.396
	qLLS80WS13-13-1	13	109	10.041	6.950	0.256
	qLLS80WS14-13-1	13	107	12.188	14.337	0.482
	qLLS90WW13-13-1	13	107	38.806	39.354	1.508
	qLLS90WW14-13-2	13	107	38.206	38.958	1.506

	qLLS90WS13-13-2	13	107	29.709	38.636	1.025
	qLLS90WS14-13-1	13	107	32.400	37.701	1.235
RUST score	qRUST80WW13-13-1	13	108	6.210	5.469	0.181
	qRUST80WW14-13-1	13	108	6.715	5.832	0.187
	qRUST80WS14-13-1	13	109	12.342	10.429	0.197
	qRUST90WW13-13-1	13	107	13.872	24.390	0.893
	qRUST90WW14-13-1	13	107	26.170	32.843	1.090
	qRUST90WS13-13-1	13	107	30.999	43.874	0.868
	qRUST90WS14-13-1	13	107	44.573	42.825	0.975

reproduction, thereby the link with the HI. LOD peak for various traits on LG-3 between m13TC39C01V-Gm2215-F region is given in the Plate 13.

Another region between Seq3A8F and m13AHGS2185N on LG-10 harbored QTLs for most of the yield and yield components such as number of primary branches per plant, pod yield per plant, kernel yield per plant, shelling per cent, sound mature kernel per cent and hundred seed weight.

Five clusters were harboring QTLs related to oil quality traits on LG-1, 5, 9, 11 and 13. Among these a major cluster on LG-11 was particularly important since all the QTLs which it harbors were oil quality attributes and also LG-1 which harbors stable QTLs for oleic acid and O/L ratio which are very important in determining the quality of oil in groundnut.

Four clusters were harboring QTLs related to foliar disease resistance on LG-3, 6, 10 and 13. Among these two major clusters on LG-6 and 10 were alone harboring major QTLs for most of foliar disease resistance traits. Similar to the above results, Khedikar *et al.* (2010) and Sujay *et al.* (2011) also reported QTLs for LLS and rust on LG 6 and 10.

Such clusters can be considered as hotspot genomic regions for further study and utilization in improving crop productivity through introgression of these genomic regions. Further studies are required to dissect these regions to identify tightly linked markers for the QTLs with high phenotypic variation as well as for the introgression either in the same genetic background for the improvement of crop productivity under water stressed conditions.

For the complex traits such as drought tolerance and yield which are controlled by several genes, many QTLs with moderate to high phenotypic variance are reported and those QTLs which are stable across the most of the conditions can be tackled through modern breeding approaches such as marker-assisted recurrent selection (MARS) or genomic selection (GS) (Ribaut and Ragot 2007; Bernardo 2008 and Varshney and Dubey 2009). Since, majority of the components of drought, root and yield are correlated, clustering of QTLs controlling these different components at specific genomic region has much significance and of practical use for crop

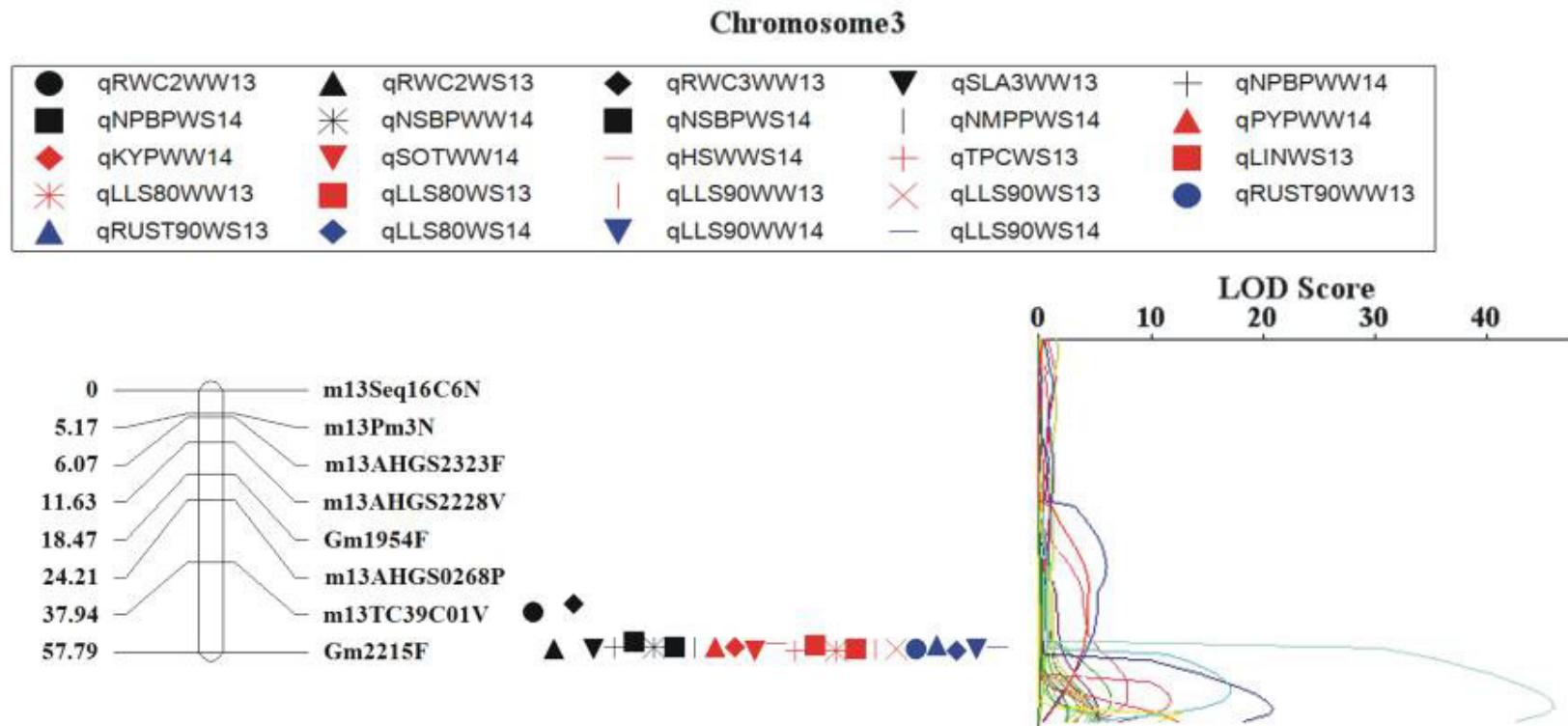


Plate 13: LOD peak for various traits on LG-3 between m13TC39C01V-Gm2215-F in TMV-2 x GM 6-1 mapping population of groundnut

improvement for these traits. Therefore, such key genomic regions, containing QTLs for aforementioned traits may be harnessed through marker-assisted selection (MAS) approach to enhance drought tolerance in the elite cultivars/varieties.

Future line of work

1. A number of recombinant inbred lines were observed to be significantly superior for individual characters compared to the best parent and also checks which could be valuable material for trait specific breeding.
2. Superior drought tolerant RILs having higher pod yield under intermittent drought stress conditions without yield penalty under normal conditions identified in the present study by using a combination of characters viz., quantitative, physiological and root traits in both the seasons may be further evaluated preferably over locations, seasons and in larger plot size to confirm their superiority and stability.
3. Superior recombinant inbred lines identified with desirable fatty acid profile need to be further tested for their agronomic performance in large scale trials over locations and seasons.
4. High oleate lines identified are to be evaluated under large scale yield trials in different locations for their stability in yield and oleic acid content.
5. QTL region between the markers m13TC39C01V-Gm2215F has to be validated for drought tolerance attributes, across locations and seasons and has to be fine mapped for use in map based cloning or subjected to functional genomics approach to identify candidate genes.
6. All the major QTLs which are stable across seasons have to be validated and used for stacking through marker-assisted backcrossing (MABC).
7. Linkage map needs to be saturated with more markers, including SNP and DArT for further QTL detection.

6. SUMMARY AND CONCLUSIONS

The present investigation was conducted during the two seasons of summer 2012-13 and summer 2013-14 at the Main Agricultural Research Station, University of Agricultural Sciences, Dharwad to study the extent of genetic variability, association and also to identify the QTLs for quantitative characters, physiological traits, root traits, oil quality traits and foliar disease resistance traits in groundnut

A total of 299 RILs derived from the cross TMV-2 X GM 6-1 in F_8 generation were evaluated along with two parents and eight checks. A factorial experiment was planned in a randomized complete block design (RCBD) with two replications during both the seasons where the two water regimes of Well Watered (WW) and Water Stress (WS) conditions are assigned as Factor A, while the genotypes (2 parents + 299 RILS + 8 checks) were considered as Factor B. Phenotyping of RILS along with parents and checks for root traits during summer 2012-13 was carried out in raised beds under well watered as well as water stress conditions where all the entries (2 parents + 299 RILS + 14 checks) were laid out in an augmented design with two blocks. A total of 13 quantitative characters, four physiological traits, five root traits, 17 oil quality traits and six foliar disease resistance traits were assessed and the data recorded were analyzed with appropriate statistical methods.

Parental screening was done using 430 SSR markers and polymorphic markers were used for genotyping of RIL population at ICRISAT, Hyderabad. Phenotyping and genotyping data generated on the RIL population was used to identify QTLs traits. The findings of the present study are summarized below.

6.1 The salient findings of the phenotyping

1. The analysis of variance revealed the prevalence of highly significant differences among the genotypes for most of the traits studied.
2. In general, phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect of all the characters studied, and also both GCV and PCV were more parallel for oil quality traits compared to all the other traits indicating less influence of environment on oil quality traits. Moderate

to high PCV, GCV and wide range of variation was recorded by most of the quantitative traits *viz.*, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, kernel yield per plant, sound mature kernel per cent and 100 seed weight in both the irrigation levels in each season. On the other hand days to 50 per cent flowering, days to maturity, and plant height recorded low to moderate GCV and PCV during both the seasons, indicating presence of considerable variability in the segregating populations.

3. Heritability in broad sense and genetic advance as per cent mean were moderate to high for the traits *viz.*, secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, kernel yield per plant, shelling per cent, sound mature kernel per cent and 100 seed weight during both seasons, indicating the simple selection scheme would be effective for these traits to bring genetic improvement in desired direction.
4. Low PCV, GCV and low to moderate were recorded by all the physiological traits, while moderate to high $h^2(b)$ was observed for RWC at all stages and SLA at 7 days after stress while, low heritability was observed for SLA at later stages of stress and SCMR.
5. High PCV, GCV and high heritability in broadsense along with high GAM was noticed for most of the root traits.
6. Moderate GCV and PCV for palmitic acid, oleic acid, linoleic acid, L/S ratio and oleic acid desaturation for the two consecutive seasons. High heritability coupled with moderate to high GAM was recorded for most of the oil quality traits *viz.*, oleic acid, linoleic acid, O/L ratio, stearic acid, arachidic acid, eicosenoic acid, behenoic acid, lignoceric acid, L/S ratio and oleic acid desaturation during both the seasons.
7. High PCV, GCV and high heritability in broadsense along with high GAM was noticed for all the foliar disease resistance traits during both the seasons of summer 2012-13 and summer 2013-14.

8. The pod yield per plant under WS condition during the two summer seasons 2012-13 and 2013-14 showed significant and positive correlation with number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, kernel yield per plant, sound mature kernel per cent and hundred seed weight. These correlations indicated that it is possible to derive the superior segregants considering the combination of above traits respectively under WW and WS conditions.
9. In the present investigation reduction in performance of genotype under moisture stress compared to the irrigated was noticed. Early maturity and reduction in yield as well as other yield component traits was observed under WS condition. On the contrary, higher SLA, SCMR values in most of the genotypes and root length in some of the genotypes was observed under WS condition compared to WW condition.
10. Correlation analysis indicated significant positive association of oleic acid with stearic acid, arachidic acid, eicosenoic acid, lignoceric acid, oleic acid to linoleic acid ratio, unsaturated to saturated fatty acid ratio and oleic acid desaturation ratio and negative association with linoleic acid, palmitic acid, behenic acid, total saturated fatty acids, polyunsaturated to saturated fatty acid ratio, iodine value and palmitic acid to stearic acid ratio. Similarly, pod yield per plant was associated negatively rust and late leaf spot scores at all the stages.
11. Superior segregants have been identified for pod yield per plant under WS condition compared to the drought tolerant parent GM 6-1 and were on par with the checks for the pod yield under WW condition viz., 2, 26, 27, 40, 43, 45, 49, 50, 53, 70, 179, 181, 212, 215, 261, 265 and 296.
12. The detailed analysis of phenotypic data showed lower incidence of tolerance towards the female parent in the mapping population; however, all traits showed continuous distribution indicating their polygenic nature.

6.2 Screening for parental polymorphisms using SSR markers and genotyping of the respective mapping populations

The parental genotypes of the recombinant inbred line (RIL) mapping populations (TMV-2 x GM 6-1) were screened with 430 SSR markers available in public domain and from various collaborators. In total 71 markers were found polymorphic between the parents and genotyping data was generated in the RIL population for these markers.

6.3 Construction of genetic linkage map using polymorphic microsatellite markers

Features of the map TMV-2 x GM 6-1:

Total number of markers mapped	: 71
Number of marker loci per linkage group	: 2 to 10
Total map distance	: 399.04 cM
Average map distance per linkage group	: 5.96 cM

6.4 Salient features of the QTL mapping

Genotyping data for the RIL mapping population was analyzed together with phenotyping data on quantitative, physiological, root and quality traits respectively for identification of QTLs using software QTL IciMapping v.4.0 and following inclusive composite interval mapping method.

A considerable number of QTLs were identified in the present study for different yield and drought component traits with low to high phenotypic variation suggesting that drought tolerance is governed by a large number of main effect QTLs and epistatic QTLs. In the present study a total 233 QTLs were identified for 40 traits on 17 linkage groups among which 62 were major QTLs while remaining 171 were minor QTLs. Among a total of 42 QTLs identified for quantitative traits 12 were major QTLs and 30 were minor QTLs. Similarly, three among nine QTLs for physiological

traits, six out of 12 QTLs for root traits, 23 out of 102 and 25 out of 68 for foliar disease resistance traits were found to be major QTLs.

The m13TC39C01V-Gm2215F (52-57cM) region on LG-3 (57.79 cM) harbored 19 QTLs for 14 different traits under two water regimes of two summer seasons. QTLs identified for traits include eight yield and yield component traits, two physiological traits and four root traits. Interestingly, four out of these 14 different traits *viz.*, number of primary branches per plant, number of secondary branches per plant, number of nodules per plant and root dry weight were stable across two or more conditions out of the two water regimes and seasons.

Another region between Seq3A8F and m13AHGS2185N on LG-10 harbored QTLs for most of the yield and yield components such as number of primary branches per plant, pod yield per plant, kernel yield per plant, shelling per cent, SMK % and 100 seed weight.

Five clusters were harboring QTLs related to oil quality traits on LG-1, 5, 9, 11 and 13. Among these a major cluster on LG-11 was particularly important since all the QTLs which it harbors were oil quality attributes and also LG-1 which harbors stable QTLs for oleic acid and O/L ratio which are very important in determining the quality of oil in groundnut.

Four clusters were harboring QTLs related to foliar disease resistance on LG-3, 6, 10 and 13. Among these two major clusters on LG-6 and 10 were alone harboring major QTLs for most of foliar disease resistance traits.

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Appendix I: Meteorological data during the crop growth periods of field and raised bed evaluation during summer 2012-13

Date	Average temperature	Vapour Pressure	Humidity (%)	Rainfall (mm)
15/02/2013	22.60	14.95	63.00	0.00
16/02/2013	21.70	16.25	75.00	0.00
17/02/2013	20.15	10.75	51.50	2.20
18/02/2013	22.40	9.05	39.50	0.00
19/02/2013	24.20	12.10	46.50	0.00
20/02/2013	25.55	10.35	44.50	0.00
21/02/2013	24.20	10.70	41.50	0.00
22/02/2013	24.05	15.40	57.00	0.00
23/02/2013	23.90	14.90	53.00	0.00
24/02/2013	25.55	14.90	52.00	0.00
25/02/2013	24.60	17.10	50.50	0.00
26/02/2013	26.75	15.25	65.50	0.00
27/02/2013	26.65	15.45	58.00	0.00
28/02/2013	25.15	17.10	55.50	0.00
01/03/2013	23.60	14.40	56.00	0.00
02/03/2013	22.80	10.90	45.00	0.00
03/03/2013	24.15	6.90	29.00	0.00
04/03/2013	24.30	8.20	31.50	0.00
05/03/2013	24.05	9.35	36.00	0.00
06/03/2013	23.80	9.85	42.00	0.00
07/03/2013	22.95	12.05	49.50	0.00
08/03/2013	25.40	11.25	45.00	0.00
09/03/2013	25.05	14.20	52.00	0.00
10/03/2013	23.95	16.30	66.00	0.00
11/03/2013	25.10	12.05	53.00	0.00
12/03/2013	26.20	13.25	55.50	0.00
13/03/2013	24.70	11.75	49.00	0.00
14/03/2013	25.80	12.10	50.00	0.00
15/03/2013	26.35	10.40	42.50	0.00
16/03/2013	27.05	13.65	55.50	0.00
17/03/2013	27.20	13.80	66.00	42.00
18/03/2013	27.95	14.00	58.00	0.00
19/03/2013	27.20	13.50	59.00	0.00
20/03/2013	27.85	11.35	47.50	0.00
21/03/2013	28.75	9.10	37.50	0.00
22/03/2013	28.15	8.20	32.50	0.00
23/03/2013	27.80	12.75	51.00	0.00
24/03/2013	28.85	12.70	56.50	0.00
25/03/2013	27.20	13.40	47.50	0.00
26/03/2013	28.50	14.00	57.50	0.00
27/03/2013	28.40	14.25	59.00	0.00
28/03/2013	27.90	14.15	53.00	0.00
29/03/2013	29.05	13.55	48.00	0.00
30/03/2013	29.65	12.10	40.50	0.00
31/03/2013	29.70	10.90	40.50	0.00
01/04/2013	28.90	13.45	53.50	0.00
02/04/2013	28.40	15.25	60.50	0.00
03/04/2013	29.75	12.95	46.00	0.00
04/04/2013	29.95	10.50	39.00	0.00
05/04/2013	29.05	9.20	33.00	0.00
06/04/2013	29.55	12.15	51.00	0.00
07/04/2013	29.55	8.05	29.00	0.00

08/04/2013	28.60	5.75	19.50	0.00
09/04/2013	28.80	9.15	30.50	0.00
10/04/2013	26.75	14.00	52.50	0.00
11/04/2013	28.90	15.90	61.00	0.00
12/04/2013	27.60	13.35	51.00	0.00
13/04/2013	28.15	16.70	62.50	0.00
14/04/2013	28.60	14.90	55.50	0.00
15/04/2013	29.20	15.05	58.00	0.00
16/04/2013	28.00	15.55	62.00	0.00
17/04/2013	28.35	13.65	54.00	0.00
18/04/2013	27.80	14.55	63.00	0.00
19/04/2013	27.25	10.75	49.00	0.00
20/04/2013	27.10	10.55	45.00	0.00
21/04/2013	28.05	11.75	51.50	0.00
22/04/2013	29.45	13.30	53.00	0.00
23/04/2013	29.10	14.10	55.50	0.00
24/04/2013	30.70	13.30	49.50	0.00
25/04/2013	29.90	14.20	54.50	0.00
26/04/2013	30.15	16.25	63.50	10.00
27/04/2013	29.75	14.60	52.50	0.00
28/04/2013	28.45	13.50	56.00	0.00
29/04/2013	28.90	16.35	61.00	0.00
30/04/2013	28.05	15.15	51.00	0.00
01/05/2013	29.25	16.20	57.50	2.80
02/05/2013	29.15	17.50	61.50	0.40
03/05/2013	28.00	14.85	56.00	1.80
04/05/2013	26.80	14.20	54.00	0.00
05/05/2013	28.80	13.85	50.00	0.00
06/05/2013	27.95	15.55	56.00	0.00
07/05/2013	29.35	14.80	54.50	0.00
08/05/2013	27.20	16.25	60.00	0.00
09/05/2013	24.75	15.80	63.00	22.40
10/05/2013	25.65	16.30	59.50	0.00
11/05/2013	26.25	16.30	60.00	0.00
12/05/2013	26.65	13.50	53.50	0.00
13/05/2013	26.60	7.80	27.50	0.00
14/05/2013	27.20	17.00	62.50	0.00
15/05/2013	27.10	16.25	60.50	0.20
16/05/2013	27.00	18.05	72.50	0.00
17/05/2013	27.65	16.70	62.00	0.00
18/05/2013	28.75	16.10	59.00	0.00
19/05/2013	29.00	14.95	54.50	0.00
20/05/2013	27.60	17.60	60.50	0.00
21/05/2013	26.20	16.80	69.50	15.80
22/05/2013	26.40	17.75	66.50	0.00
23/05/2013	26.55	16.90	64.50	0.00
24/05/2013	27.65	17.15	65.50	0.00
25/05/2013	27.65	15.85	58.50	0.00
average	27.05	13.57	52.57	97.60
max	30.70	18.05	75.00	42.00
min	20.15	5.75	19.50	0.00

Appendix II: Meteorological data during the crop growth periods of field and raised bed evaluation during summer 2013-14

Date	Average temperature	Vapour Pressure	Humidity (%)	Rainfall (mm)
02/01/2014	19.85	10.55	59.50	0.00
03/01/2014	19.45	9.05	52.50	0.00
04/01/2014	20.90	11.40	60.50	0.00
05/01/2014	21.55	10.10	49.00	0.00
06/01/2014	21.95	11.35	58.50	0.00
07/01/2014	22.45	9.85	49.50	0.00
08/01/2014	21.90	8.55	45.00	0.00
09/01/2014	22.75	9.90	50.50	0.00
10/01/2014	22.20	10.55	50.00	0.00
11/01/2014	22.40	11.05	53.50	0.00
12/01/2014	22.35	12.00	54.50	0.00
13/01/2014	23.00	11.20	56.50	0.00
14/01/2014	21.85	10.60	52.00	0.00
15/01/2014	22.15	11.40	51.50	0.00
16/01/2014	23.15	12.90	57.00	0.00
17/01/2014	23.65	13.60	66.00	0.00
18/01/2014	23.40	13.05	61.50	0.00
19/01/2014	23.20	11.90	59.50	0.00
20/01/2014	23.10	11.90	57.00	0.00
21/01/2014	22.60	11.00	52.00	0.00
22/01/2014	22.00	10.75	51.50	0.00
23/01/2014	24.05	11.10	56.00	0.00
24/01/2014	22.00	10.80	50.50	0.00
25/01/2014	22.45	9.30	47.50	0.00
26/01/2014	22.55	9.40	49.50	0.00
27/01/2014	22.10	9.05	49.00	0.00
28/01/2014	20.75	10.20	53.50	0.00
29/01/2014	21.45	10.25	50.50	0.00
30/01/2014	21.55	10.20	52.00	0.00
31/01/2014	21.30	9.15	46.00	0.00
01/02/2014	21.10	9.40	47.50	0.00
02/02/2014	21.90	10.25	50.50	0.00
03/02/2014	23.45	9.95	49.00	0.00
04/02/2014	22.55	8.60	39.00	0.00
05/02/2014	23.50	8.15	36.00	0.00
06/02/2014	24.05	8.00	36.00	0.00
07/02/2014	24.50	7.60	35.50	0.00
08/02/2014	24.20	9.10	37.00	0.00
09/02/2014	23.90	6.65	27.00	0.00
10/02/2014	24.10	6.20	27.00	0.00
11/02/2014	22.80	5.50	27.00	0.00
12/02/2014	23.30	7.15	33.50	0.00
13/02/2014	23.55	13.15	65.50	0.00
14/02/2014	21.20	11.75	58.00	0.00
15/02/2014	22.60	8.30	37.00	0.00
16/02/2014	21.70	10.10	52.50	0.00
17/02/2014	20.15	7.20	37.50	0.00
18/02/2014	22.40	7.55	36.50	0.00
19/02/2014	24.20	9.15	40.50	0.00
20/02/2014	25.55	12.95	54.50	0.00
21/02/2014	24.20	12.10	54.00	0.00
22/02/2014	24.05	12.40	61.50	0.00
23/02/2014	23.90	11.35	51.50	0.00
24/02/2014	25.55	7.00	32.00	0.00
25/02/2014	24.60	12.05	50.00	0.00
26/02/2014	26.75	14.10	60.00	0.00
27/02/2014	26.65	14.75	66.00	0.00
28/02/2014	25.15	11.80	49.50	0.00
01/03/2014	23.60	10.45	51.50	0.00
02/03/2014	22.80	6.80	29.00	0.00

03/03/2014	24.15	9.50	44.00	0.00
04/03/2014	24.30	11.45	55.00	0.00
05/03/2014	24.05	10.95	48.50	0.00
06/03/2014	23.80	10.20	44.00	0.00
07/03/2014	22.95	11.20	49.50	0.00
08/03/2014	25.40	13.10	56.50	0.00
09/03/2014	25.05	14.35	68.00	10.20
10/03/2014	23.95	13.05	54.00	0.00
11/03/2014	25.10	13.20	53.00	0.00
12/03/2014	26.20	11.15	45.50	1.20
13/03/2014	24.70	9.40	40.50	0.00
14/03/2014	25.80	8.10	30.00	0.00
15/03/2014	26.35	7.75	29.50	0.00
16/03/2014	27.05	7.95	29.50	0.00
17/03/2014	27.20	8.55	30.00	0.00
18/03/2014	27.95	9.00	32.50	0.00
19/03/2014	27.20	7.90	31.50	0.00
20/03/2014	27.85	11.65	53.00	0.00
21/03/2014	28.75	12.90	54.00	0.00
22/03/2014	28.15	7.45	28.00	0.00
23/03/2014	27.80	8.40	27.00	0.00
24/03/2014	28.85	10.55	40.50	0.00
25/03/2014	27.20	10.60	43.00	0.00
26/03/2014	28.50	9.30	35.50	0.00
27/03/2014	28.40	9.25	36.00	0.00
28/03/2014	27.90	12.45	54.00	0.00
29/03/2014	29.05	8.40	30.00	0.00
30/03/2014	29.65	9.35	30.50	0.00
31/03/2014	29.70	16.40	57.50	0.00
01/04/2014	28.90	12.90	53.00	0.00
02/04/2014	28.40	9.90	37.00	0.00
03/04/2014	29.75	11.85	42.00	0.00
04/04/2014	29.95	12.15	42.00	1.20
05/04/2014	29.05	14.55	54.50	0.00
06/04/2014	29.55	14.95	56.00	0.00
07/04/2014	29.55	14.15	52.00	0.00
08/04/2014	28.60	13.45	53.50	0.00
09/04/2014	28.80	14.10	55.50	0.00
10/04/2014	26.75	10.70	42.00	0.00
11/04/2014	28.90	11.15	44.00	0.00
12/04/2014	27.60	8.40	33.00	0.00
13/04/2014	28.15	7.90	30.50	0.00
14/04/2014	28.60	8.45	33.00	0.00
15/04/2014	29.20	10.05	33.50	0.00
16/04/2014	28.00	12.35	46.50	25.40
17/04/2014	28.35	15.15	58.50	0.00
18/04/2014	27.80	15.20	58.50	0.00
19/04/2014	27.25	14.85	59.50	10.80
20/04/2014	27.10	12.50	44.00	0.00
21/04/2014	28.05	9.60	34.50	0.00
22/04/2014	29.45	13.15	46.00	0.00
23/04/2014	29.10	13.30	49.00	0.00
24/04/2014	30.70	16.20	58.00	0.00
25/04/2014	29.90	15.60	60.00	0.00
26/04/2014	30.15	16.75	61.50	0.00
27/04/2014	29.75	15.75	58.00	0.00
28/04/2014	28.45	16.25	53.50	0.60
29/04/2014	28.90	17.80	68.50	0.00
30/04/2014	28.05	13.85	54.00	6.90
01/05/2014	29.25	14.15	49.50	0.00
02/05/2014	29.15	15.95	59.00	4.20
03/05/2014	28.00	15.85	61.50	47.40
04/05/2014	26.80	14.65	50.50	0.20
average	25.54	11.16	47.35	108.10
max	30.70	17.80	68.50	47.40
min	20.15	5.50	27.00	0.00

Appendix III: List of polymorphic SSR primers between the parents TMV-2 x GM 6-1 in groundnut

S.No	Marker	Dye	P1		P2	
			Allele 1	Allele 2	Allele 1	Allele 2
1	TC5D06-P	R	178		180	
2	TC7C06-N	Y	157		161	
3	m13-TC11H06-V	G	217		215	
4	m13-TC42A05-P	R	211		223	
5	TC6E01-N	Y	164		162	
6	Gm1954-F	B	137		139	
7	IPAHM123-V	G	127		129	
8	m13-Seq10D4-N	Y	220		214	
9	m13-TC3A12-P	R	214		222	
10	Gm1911-V	G	130		128	
11	Gm1996-F	B	123		157	
12	TC9F10-P	R	256		246	129
13	IPAHM103-F	B	129		124	166
14	m13-GM2246-V	G	163		163	
15	m13-TC16A10-N	Y	260		270	
16	Gm1536-N	Y	484		477	
17	Gm2301-F	B	137		128	
18	m13-AHGS2228-V	G	200		191	
19	m13-AHGS2252-N	Y	208		204	
20	m13-GM2637-V	G	166		172	
21	Seq19G7-F	B	152		148	
22	m13-IPAHM540-V	G	157		159	232
23	m13-Pm3-N	Y	207	221	217	
24	m13-Seq5D5-P	R	263		292	
25	Seq3A8-F	B	154		148	
26	m13-AHGS2960-V	G	157		159	
27	TC6H03-F	B	233		223	
28	Gm2215-F	B	287		289	
29	Seq18E7-F	B	323	341	314	337
30	m13-AHGS2132-F	B	152	159	154	163
31	M13ahgs2098v2	G	165		167	
32	m13AHGS2185N2	G	211		207	
33	m13-AHS0025-V	G	162		145	162
34	m13-GM1573-P	R	283		283	287
35	m13-TC2B09-N	Y	211		219	
36	m13-AHGS1524-F	B	150		152	
37	m13-AHGS2602-N	Y	210		214	
38	m13-AHGS2323-F	B	175		177	
39	m13-AHGS3715-P	R	282		284	
40	m13-TC2D06-N	Y	213		215	
41	m13-IPAHM229-F	B	143		145	

42	m13-Seq2E6-P	R	288		284	
43	m13-TC41C11-F	B	145	147	141	
44	m13-AHGS2061-F	B	157		159	
45	m13-AHGS2058-P	R	294		291	
46	m13-AHGS2094-F	B	134		138	
47	m13-AHGS2490-V	G	183		185	
48	m13-AHGS1338-P	R	294		328	
49	m13-AHGS2043-V	G	188		184	
50	m13-Seq17F6-F	B	141		135	
51	m13-IPAHM219-F	B	133		135	
52	m13-TC23E04-V	G	198		202	
53	m13-AHGS1289-N	Y	245		257	
54	m13-AHGS2249-F	B	126		172	
55	m13-AHGS2342-P	R	309		307	
56	m13-Seq16C6-N	Y	251		248	
57	m13-GM2638-F	B	123	135	123	142
58	m13-TC39C01-V	G	201		199	
59	m13-AHGS3217-N	Y	253		277	
60	m13-Ai119H15-P	R	343		336	
61	m13-Gm1867-F	B	125		119	
62	m13-Gm692-V	G	204		197	
63	m13-AHS0314-N	Y	260		257	
64	m13-PM32-F	B	119	123	119	
65	m13-RN13D04-P	R	415	432	415	
66	m13-AHGS1998-N	Y	260		264	
67	m13-IPAHM354-V	G	201		199	
68	m13-Pm188-F	B	117	119	119	
69	m13-AHGS2205-V	G	205		203	
70	m13-PM45-F	B	119		121	
71	m13AHGS0268P	R	275		275	279

Appendix IV: Meteorological data at Aniigeri during *kharif* 2014-15

Standard Meteorological week	Air Temperature (°C)		Rainfall (mm)	Rainy days	Relative Humidity (%)
	Max.	Min.			
23Jul–29 Jul	28.7	20.4	31.2	3	75.1
30Jul–05 Aug	27.1	21.4	35.8	1	75.7
06Aug–12 Aug	27.3	20.7	5.4	1	77.6
13Aug–19 Aug	29.5	21.9	20.4	1	81.7
20Aug–26 Aug	31.1	22.3	106.8	5	80.4
27Aug–02 Sep	30	21	38.8	5	78.3
03 Sep – 09 Sep	28.8	19.6	13.6	2	70.9
10 Sep – 16 Sep	29.9	20.7	15.6	1	74
17 Sep – 23 Sep	29.6	21.5	51.5	2	77.1
24 Sep – 30 Sep	30.4	22.4	42.8	2	77.9
01 Oct – 07 Oct	30.6	25.7	111.2	3	75.4
08 Oct – 14 Oct	30.9	22.3	4.4	1	76.7
15 Oct – 21 Oct	31.1	22	0	0	75.4
22 Oct – 28 Oct	27.9	19.1	12.8	1	77.1
29 Oct – 04 Nov	27.9	18.7	0	0	81.7

Appendix V: Meteorological data at Bijapur during *kharif* 2014-15

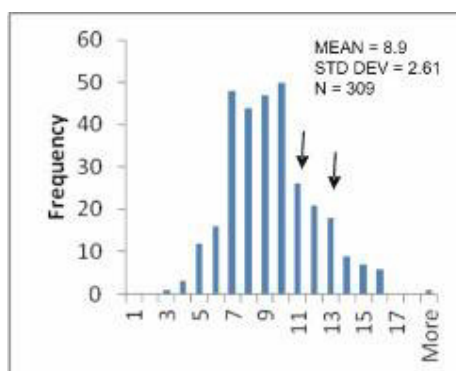
Standard Meteorological week	Air Temperature (°C)		Rainfall (mm)	Rainy days	Relative Humidity (%)
	Max.	Min.			
23Jul–29 Jul	29.1	21.3	44.6	3	90.6
30Jul–05 Aug	29	21.9	3	0	87
06Aug–12 Aug	30.3	21.3	1.4	0	88
13Aug–19 Aug	31.4	20.8	40.2	1	88
20Aug–26 Aug	31.9	21.8	48.7	3	90.4
27Aug–02 Sep	26.6	20.9	155.2	4	92.6
03 Sep – 09 Sep	29.2	21	19.7	1	88.7
10 Sep – 16 Sep	31.1	20.8	0	0	87.9
17 Sep – 23 Sep	30.4	20.9	39.5	3	90.7
24 Sep – 30 Sep	32.9	21.8	0	0	83.1
01 Oct – 07 Oct	34.2	21	10.6	1	80.3
08 Oct – 14 Oct	32.9	20.8	13.8	1	82.1
15 Oct – 21 Oct	33.1	19.9	0	0	86.3
22 Oct – 28 Oct	28.7	19	40.9	2	88.9
29 Oct – 04 Nov	30.1	14.7	0	0	80.6

Appendix VI: Mean air temperature and Rainfall at Bijapur and Annigeri from the years 2011-2014

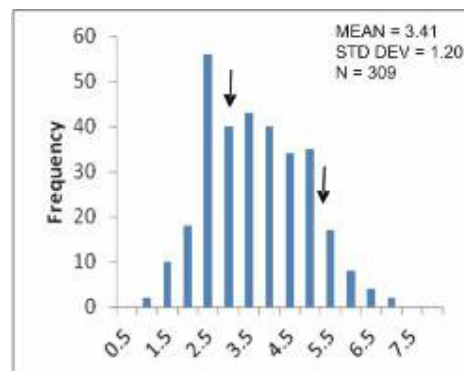
YEAR	Bijapur		
	Air Temperature (°C)		Rainfall (cm)
	Max.	Min.	
2011	32.78	19.13	550.40
2012	33.13	19.49	525.50
2013	32.43	19.38	771.60
2014	32.38	19.36	736.80

YEAR	Annigeri		
	Air Temperature (°C)		Rainfall (cm)
	Max.	Min.	
2011	31.31	19.52	644.70
2012	31.94	20.35	546.40
2013	31.85	21.79	624.80
2014	36.30	21.50	814.90

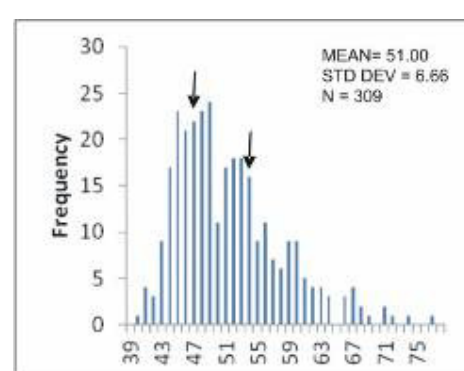
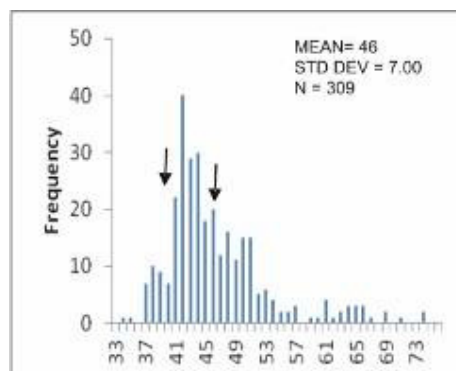
Appendix VII :Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for pod yield and oleic acid under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14



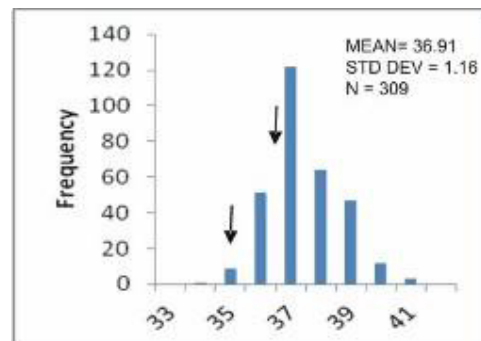
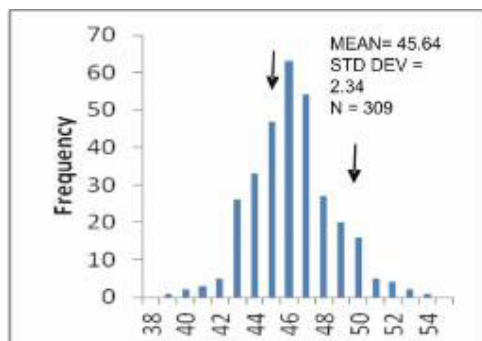
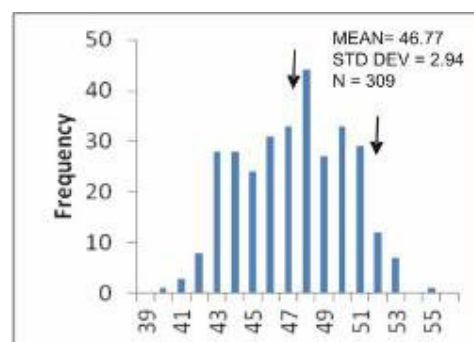
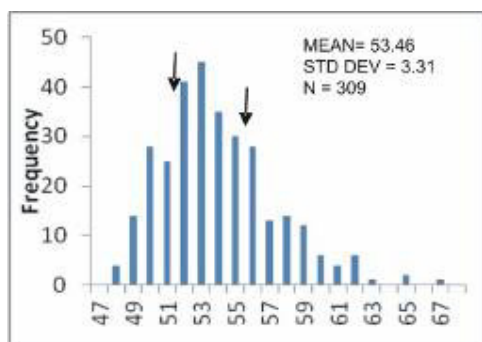
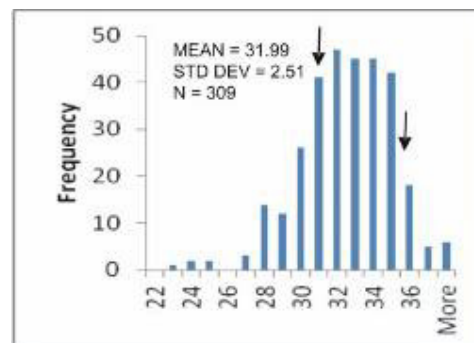
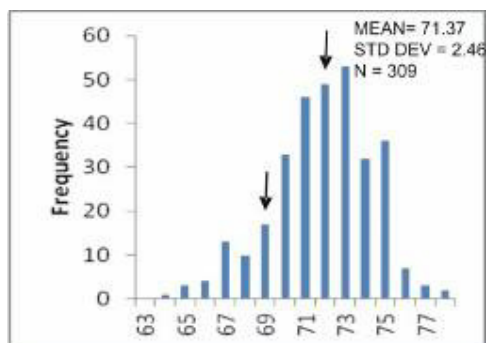
WW Condition

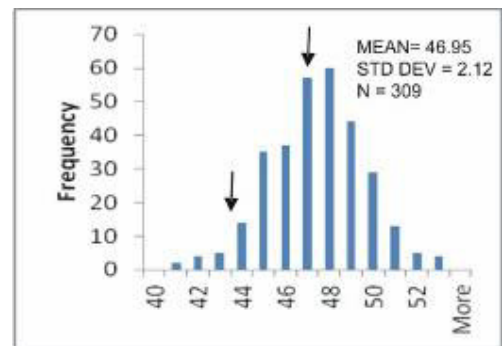
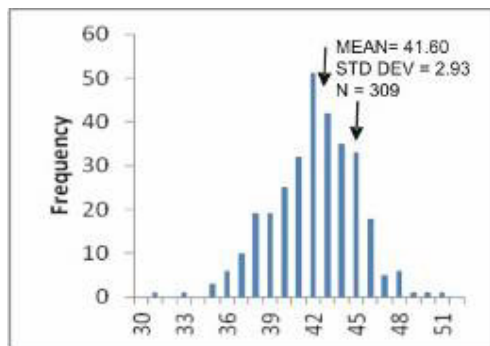


WS Condition

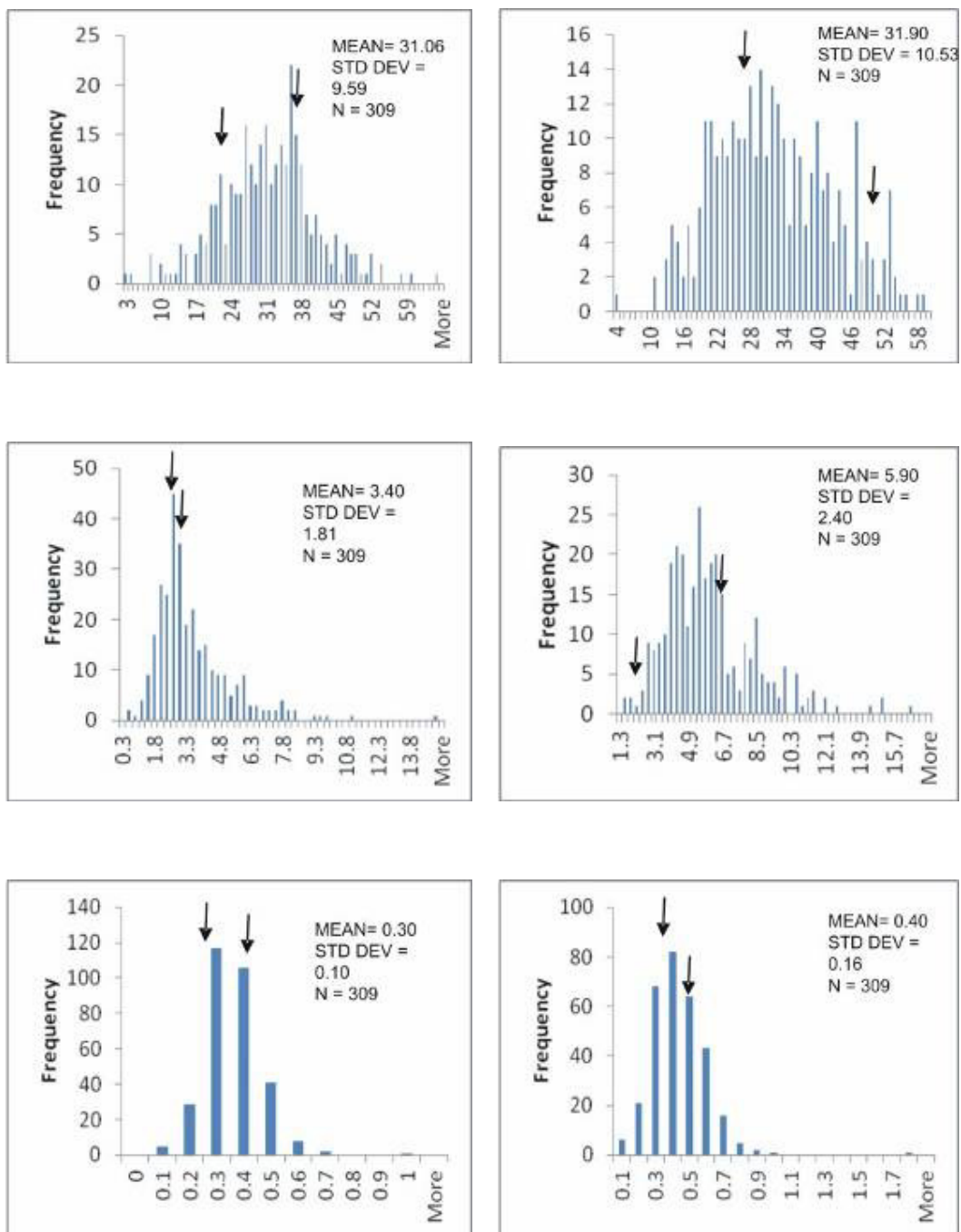


Appendix VII : Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for important physiological traits under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14





Appendix IX : Frequency distribution of mapping population developed from the cross TMV-2 x GM 6-1 for root traits under WW and WS conditions pooled across the two seasons of summer 2012-13 and summer 2013-14



GENETIC ANALYSIS OF DROUGHT TOLERANCE IN GROUNDNUT (*Arachis hypogaea* L.)

SRIVALLI POTHULA

2015

Dr. H. L. NADAF
Major Advisor

ABSTRACT

An investigation on genetic analysis of drought tolerance in recombinant inbred lines (RILs) of groundnut was undertaken during summer 2012-13 and summer 2013-14 at MARS, UAS, Dharwad.

Significant genetic variation was observed in RILs studied as evidenced by wider range and moderate to high PCV and GCV for most of the quantitative, root, oil quality and foliar disease resistance traits studied. High heritability and genetic advance as per cent of mean were recorded for all root traits and foliar disease resistance traits studied and for most of the quantitative traits and oil quality traits.

Correlation analysis during the two seasons indicated that high RWC at 30 days after stress, low SLA at 30 days after stress and high SPAD chlorophyll meter reading, increased root length and increased root to shoot ratio have contributed for high Drought Tolerance Index and for maintenance pod yield under stress condition. The superior RILs identified for pod yield per plant under WS condition were 2, 26, 27, 40, 43, 45, 49, 50, 53, 70, 179, 181, 212, 215, 261, 265 and 296.

Linkage mapping with 71 SSR markers resulted in map of 399.04cM with 13 linkage groups and 5.96cM inter-marker distance. Among 233 QTLs identified through Inclusive composite interval QTL mapping, 12 QTLs for quantitative traits, three for physiological traits, six for root traits, 23 for oil quality traits and 25 for foliar disease resistance traits were found to be major QTLs. The m13TC39C01V-Gm2215F (52-57cM) region on LG-3 (57.79 cM) harbored 19 QTLs for 14 different traits of which four traits viz., number of primary branches per plant, number of secondary branches per plant, number of nodules per plant and root dry weight were stable across two or more conditions out of the two water regimes and seasons.