ANALYSIS OF TAXONOMIC, AGRONOMIC, PRODUCTIVITY AND NUTRITIONAL TRAITS, AND RESISTANCE TO FOLIAR DISEASES FOR THEIR ASSOCIATION WITH TE MARKERS IN GROUNDNUT

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CERTIFICATE

This is to certify that the thesis entitled "**ANALYSIS OF TAXONOMIC, AGRONOMIC, PRODUCTIVITY AND NUTRITIONAL TRAITS, AND RESISTANCE TO FOLIAR DISEASES FOR THEIR ASSOCIATION WITH TE MARKERS IN GROUNDNUT**" submitted by **Mr. HAKE ANIL ARJUN** for the degree of **DOCTOR OF PHILOSOPHY (AGRICULTURE)** in **MOLECULAR BIOLOGY AND BIOTECHNOLOGY** to the University of Agricultural Sciences, Dharwad is a record of research work done by him during the period of his study in this University under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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CONTENT

Sl. No.	Chapter Particulars	Page No.
	CERTIFICATE	iii
	ACKNOWLEDGEMENT	iv
	ABBREVIATIONS	viii
	LIST OF TABLE	ix
	LIST OF FIGURES	xi
	LIST OF PLATES	xii
	LIST OF APPENDICES	Xiii
1.	INTRODUCTION	1-3
2.	REVIEW OF LITERATURE	4-14
	2.1 Origin, domestication and botany of groundnut	4
	2.2 DNA markers in groundnut	5
	2.3 Mapping populations	9
	2.4 Trait mapping	13
3.	MATERIAL AND METHODS	14-38
	3.1 RIL mapping population	14
	3.2 Mutant population	16
	3.3 Experimental site	16
	3.4 Raising RIL and mutant populations	16
	3.5 Phenotyping of RIL and mutant populations	16
	3.6 Statistical analysis	28
	3.7 Genotyping with AhTE markers	32
	3.8 Double-digest restriction site-associated DNA sequencing (ddRAD-Seq)	35
	3.9 Marker-trait association analysis with RIL population	35
	3.10 Marker-trait association analysis with RIL population	36

4.	EXPERIMENTAL RESULTS	39-87
	4.1 Phenotypic and genotypic differences between TMV 2 and TMV 2-NLM	39
	4.2 Genetic mapping with the RILs of TMV 2 × TMV 2-NLM	41
	4.3 Selection of superior RILs	55
	4.4 Association studies using a mutant population	62
5.	DISCUSSION	88-97
	5.1 Mapping with RILs	90
	5.2 Association studies in the mutant population	93
6.	SUMMARY AND CONCLUSIONS	98-100
	REFERENCES	101-125
	APPENDICES	126-186

LIST OF ABBREVIATIONS

Particulars	Abbreviations
U	Unit
m	Meter/s
g	Gram/s
%	Per cent
min	Minute/s
s	Second/s
mha	Million Hectare/s
mt	Million tonne/s
bp	Base pair
µl	Microliter/s
mM	Millimolar
ml	Milliliter/s
^{0}C	Degree celsius
mg	Milligram/s
kg	Kilogram/s
$T_{10}E_1$	Tris (10 mM)-EDTA (1 mM)
pmol	Picomole/s
ng	Nanogram/s
cm	Centimeter/s
cM	Centi Morgan
r	Correlation coefficient
CV	Coefficient of variation
R^2	Phenotypic variance
Tm	Melting temperature
QTL	Quantitative trait locus/loci
RPM	Revolutions per minute
CTAB	Cetyl-trimethyl-ammonium bromide
AhTE	*Arachis hypogaea* transposable element
SSR	Simple sequence repeat
LG	Linkage group
CNV/s	Copy number variation/s
SNP	Single nucleotide polymorphism
DArT	Diversity arrays technology
RFLP	Restriction fragment length polymorphism
RAPD	Random amplified polymorphic DNA

LIST OF TABLES

Table No.	Title	Page No.
1.	Modified 9 point scale used for field screening of groundnut genotypes for resistance to rust disease	23
2.	Modified 9 point scale used for field screening of groundnut genotypes for resistance to late leaf spot disease	25
3.	PCR reaction mixture used for AhTE-PCR	34
4.	PCR profile for AhTE-PCR	34
5.	Distinguishing features of TMV 2 and TMV 2-NLM	40
6.	Single nucleotide polymorphism between TMV 2 and TMV 2-NLM	42
7.	Copy number variations between TMV 2 and TMV 2-NLM	43
8.	ANOVA for disease resistance, productivity, agronomic, nutritional and physiological traits among RILs of TMV 2 × TMV 2-NLM	45
9.	Mean, range and genetic variability components for agronomic, productivity, nutritional and disease resistance traits among the RILs of TMV 2 × TMV 2-NLM	47
10.	Frequency distribution of the RILs of TMV 2 × TMV 2-NLM for agronomic, disease resistance, physiological, productivity and nutritional traits	48
11.	Features of linkage map constructed using the RILs of TMV 2 × TMV 2-NLM	52
12.	Markers identified from single marker analysis for significant association with important agronomic, productivity and nutritional traits	53
13.	Details of major effect QTLs identified for important agronomic, productivity and nutritional traits in groundnut	56
14	Annotation of genes related to fatty acid metabolism	57
15a	Correlation coefficients for disease resistance, productivity, agronomic, taxonomic, physiological and nutritional traits in the RILs of TMV 2 × TMV 2-NLM	59
15b	Correlation coefficients for agronomic, taxonomic, productivity, physiological and nutritional, traits in the RILs of TMV 2 × TMV 2-NLM	60

16.	Performance of superior RILs from TMV 2 × TMV 2-NLM mapping population	61
17.	ANOVA for disease resistance, productivity, agronomic and nutritional traits in mutant population	63
18.	Mean, range and genetic variability components for agronomic, disease resistance, productivity and nutritional traits in mutant population	64
19.	Frequency distribution of genotypes in the mutant population for the disease resistance, agronomic, productivity and nutritional traits	65
20a.	Correlation coefficients for disease resistance, productivity, agronomic, taxonomic, and nutritional traits in the mutant population	67
20b.	Correlation coefficients for agronomic and nutritional traits in the mutant population	68
21.	Major allele frequency, gene diversity, heterozygosity and polymorphic information content of AhTE markers used in the mutant population	71
22.	Major allele frequency, gene diversity, heterozygosity, polymorphic information content and percent polymorphism in subgroups of mutant population	75
23.	Marker-trait associations identified for taxonomic, disease resistance, agronomic, nutritional and productivity traits	77
24.	Prediction and annotation of candidate genes for associated markers	81
25.	Co-segregation of AhTE markers with selected traits	85
26.	Performance of superior mutants from mutant population of groundnut	87

LIST OF FIGURES

Figure No.	Title	Page No.
1.	Branching pattern in groundnut	18
2.	Growth habit in groundnut	18
3.	Leaflet shapes in groundnut	20
4.	Modified 9 point scale used for field evaluation of rust in groundnut	22
5.	Modified 9 point scale used for field evaluation of late leaf spot in groundnut	24
6.	Copy number variation in TMV 2-NLM when compared to TMV 2	44
7.	Frequency distribution of RILs of TMV 2 × TMV 2-NLM	49
8.	QTL map for agronomic, productivity and nutritional traits	51
9.	Insertion of *AhMITE1* in the intronic region of the gene *Aradu.7N61X*	54
10.	Frequency distribution of genotypes in mutant population	66
11.	Population structure and diversity analysis of mutant population	74
12.	QQ plot showing marker-trait association	80

LIST OF PLATES

Plate No.	Title	Page No.
1.	Morphology of TMV 2 and TMV 2-NLM	15
2.	PCR amplification with AhTE0572 in a few RILs of TMV 2 × TMV 2-NLM	50
3.	PCR amplification with AhTE0233 among a few genotypes of mutant population	70

LIST OF APPENDICES

Appendix No.	Title	Page No.
I	Taxonomic, agronomic and productivity traits among TMV 2, TMV 2-NLM and their RILs	126
II	Mean performance of the RILs of TMV 2 × TMV 2-NLM for disease resistance, agronomic and physiological traits	137
III	Mean performance of the RILs of TMV 2 × TMV 2-NLM for productivity and nutritional traits	153
IV	AhTE markers used for genotyping the RILs of TMV 2 × TMV 2-NLM	169
V	Taxonomic, agronomic and productivity features of genotypes in the mutant population	172
VI	Mean performance of genotypes for disease resistance and agronomic traits in the mutant population	176
VII	Mean performance of genotypes for productivity and nutritional traits in the mutant population	181
VIII	AhTE primers used for genotyping the mutant population	186

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L. 2n=4x=40) is a major food, oilseed and fodder crop world-wide with a global production of 45.22 million tonnes from an area of 25.44 million hectares (FAOSTAT, 2016). Groundnut has high nutritive values in terms of protein (20–40 %), carbohydrate (10–20 %), vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium. Groundnut is generally used for confectionaries, oil production and extenders in meat product formulations, soups and desserts.

Groundnut productivity is mainly influenced by biotic and abiotic stresses (Janila *et al.*, 2016). Intermittent drought in about 70 per cent groundnut-growing area impacts adversely on yield and yield-related traits including quality of the produce due to reduced photosynthesis, N_2 fixation, and calcium uptake by developing pods. Salinity and heat stress are also limiting the productivity. Among the biotic stresses, the foliar diseases *viz.*, early leaf spot (ELS) (*Cercospora arachidicola*), late leaf spot (LLS) (*Phaeoisariopsis personata*) and rust (*Puccinia arachidis*) are widespread and economically important. Mottle virus, rosette virus, aphids, jassids, thrips and tomato spotted wilt virus (TSWV) also affect the production.

Several improved varieties have been developed with better phenotypes for these traits and these improved varieties alone have contributed to 30 per cent yield increase in India since 1967 (Reddy and Basu, 1989). Recently, molecular breeding is preferred over conventional breeding for the obvious advantages; not only for breeding improved varieties, but also for understanding the genetics of the traits (Bevan *et al.*, 2017). Interval mapping based on DNA markers is used to genetically localize QTLs in natural and experimental populations. These ideas led to the development of DNA markers, identification of polymorphisms, development of analytical methods for studying QTL and the chromosomal localization of numerous QTLs (Paterson, 1997). The development of new QTL mapping strategies and the successful identification of genes responsible for many simple mendelian traits have reinvigorated interest in QTLs (Nadeau and Frankel, 2000). Most of the traits being quantitative, the genomic regions (QTLs) have been mapped for the important traits of biotic and abiotic stresses in crop

plants. Also, the assays for gene products (RNA and protein) have identified candidate genes governing a few traits.

However, gene discovery for crop improvement is a huge task considering the complexity of the traits. It requires advanced tools and ideal genotypes. Use of ideal genotypes for dissecting the genes/markers for complex traits is very critical in reducing the background noise and identifying the candidate genomic regions or genes for the traits of interest. TMV 2, an elite variety known for its extreme adaptation over the last 40 years, and its EMS-derived mutant TMV 2-NLM (Prasad *et al.*, 1984), might help in reducing the background noise. TMV 2 and TMV 2-NLM differ for many taxonomic and productivity traits and drought tolerance. Thus, the RIL mapping population of TMV 2 × TMV 2-NLM (Pattanashetti, 2005) might allow identification of genomic regions/genes governing the complex traits.

Compared to QTL mapping, chemical or physical mutagenesis provides a powerful alternative to natural, polygenic variation for identifying functional pathways and complex genes. Mutagenesis would ultimately prove more effective because the prospects of gene identification are high and every gene affecting a trait is potentially a target (Nadeau and Frankel, 2000). Mutants have been used directly (Bolon *et al.*, 2011; Sikora *et al.*, 2012; Schneeberger, 2014) or indirectly by developing near isogenic lines (Zou *et al.*, 2005), F_2s and inbred lines (Liu *et al.*, 2007; Luo *et al.*, 2007) for gene discovery.

Thus, an association panel of independent mutants, and a RIL population of TMV 2 × TMV 2-NLM offer an advantage of reducing the background noise while detecting the marker-trait associations. Use of *Arachis hypogaea* transposable element (AhTE) marker system (Bhat *et al.*, 2008; Gowda *et al.*, 2010; Shirasawa *et al.*, 2012a) which detects the polymorphism for *Arachis hypogaea* miniature inverted-repeat transposable element (*AhMITE1*) insertion, might help in identifying the genomic regions and genes governing the taxonomic, agronomic, productivity and nutritional traits, and resistance to late leaf spot and rust in groundnut. With this background, the following objectives were set for this study.

1. To phenotype the mutant population and RIL population (TMV 2 × TMV 2-NLM) for taxonomic, agronomic, productivity and nutritional traits, and resistance to late leaf spot and rust.

2. To genotype the mutants and RILs using the transposon-specific markers.

3. To identify association of markers with taxonomic, agronomic, productivity and nutritional traits, and resistance to late leaf spot and rust.

4. To characterize the genomic region at marker loci confirmed for trait association to identify the candidate gene.

2. REVIEW OF LITERATURE

2.1 Origin, domestication and botany of groundnut

Cultivated groundnut (*Arachis hypogaea* L.) has evolved from a hybridization between A genome diploid donor (*Arachis duranensis*) and B genome diploid donor (*Arachis ipaensis*), followed by chromosome doubling (Husted, 1936; Kochert *et al.*, 1991; Halward *et al.*, 1992; Kochert *et al.*, 1996; Cuc *et al.*, 2008; Moretzsohn *et al.*, 2013). Subsequent domestication of the allotetraploid has resulted in the origin of two subspecies which differ for several morphological traits. The subspecies *hypogaea* is characterized by alternate branching, absence of flowers on main axis, long duration (120-160 days) and presence of seed dormancy, while subspecies *fastigiata* is marked by sequential branching, presence of flowers on main axis, short duration (85-130 days) and lack of seed dormancy. Morphological differences also exist within each subspecies, on which they are subdivided into botanical varieties. Subspecies *hypogaea* is subdivided into var. *hypogaea* (Virginia bunch/runner) and var. *hirsuta* (Peruvian runner), while the subspecies *fastigiata* is classified into var. *fastigiata* (Valencia), var. *vulgaris* (Spanish bunch), var. *aequatoriana* and var. *peruviana* (Krapovickas, 1969, 1973).

Cultivated groundnut has a genome size of 2.7 Gb, while the A and B genome donors have 1.25 Gb and 1.56 Gb, respectively (Samoluk *et al.*, 2015). The two progenitors of groundnut have been sequenced (Bertioli *et al.*, 2016; Chen *et al.*, 2016), but the closely related subgenomes and complex polyploid nature make assembling the chromosomal pseudomolecules very challenging in cultivated groundnut. Comparison of A and B genome sequences has revealed several interesting and useful features. A and B genomes were similar to the A and B subgenomes of cultivated groundnut (Bertioli *et al.*, 2016). The A genome chromosomes were distinctly less similar to *A. hypogaea* sequences than the B genome chromosomes. Genetic recombinations between the A and B subgenomes of *A. hypogaea* were more frequent in regions of the homeologous chromosome pairs that were collinear. Genome-wide methylation per cytosine content was similar for *A. duranensis* and *A. ipaensis*, with 73 and 75 per cent methylation at CG sites, 57 and 60 per cent methylation at CHG sites (where H is an A, T or C), and 8 and 6 per cent methylation at CHH sites, respectively (Bertioli *et al.*,

2016). These genomic features would help in developing better tools for molecular breeding and crop improvement apart from advancing the knowledge on the evolution of cultivated groundnut from the very recent polyploidization event.

2.2 DNA markers in groundnut

Large number of molecular markers like restriction fragment length polymorphism (RFLP) (Halward *et al.*, 1993), random amplified polymorphic DNA (RAPD) (Halward *et al.*, 1991), amplified fragment length polymorphism (AFLP) (Herselman, 2003) and Diversity Array Technology (DArT) markers (Kilian, 2008) have been developed and used in groundnut genetic studies. In some cases, the markers developed for other systems were transferred to groundnut (He *et al.*, 2006; Mace *et al.*, 2008; Savadi *et al.*, 2012).

2.2.1 Simple sequence repeat (SSR) markers

SSR markers have been very popular in groundnut. A large number of microsatellite markers were developed from SSR-enriched genomic libraries, expressed sequence tags (ESTs), and by "data-mining" sequences available in GenBank (Hopkins *et al.*, 1999; Palmieri *et al.*, 2002; He *et al.*, 2003; Ferguson *et al.*, 2004; Moretzsohn *et al.*, 2004; Moretzsohn *et al.*, 2005; Palmieri *et al.*, 2005; Hong *et al.*, 2008). Highly informative genic and genomic SSR markers facilitating molecular breeding in cultivated groundnut have been reviewed (Pandey *et al.*, 2012). Recently, 16,435 genome survey sequences SSRs (GSS-SSRs) and 40,199 expressed sequence tag SSRs (EST-SSRs) were identified in *A. hypogaea* and its wild relative species using the publicly available sequence data (Huang *et al.*, 2016). For the first time, single-locus SSRs were developed through *in silico* genomic survey of *A. hypogaea* (Zhou *et al.*, 2016a) for better application in genetic and breeding studies in groundnut. Recently, Peng *et al.* (2016) reported the development of SSR markers from NCBI EST dataset and in-house RNA-Seq dataset. From these two datasets, 6,455 novel SSRs were identified, and 89.2 per cent of them were amplified. These resources will be of great use in the groundnut improvement programmes. Properties of microsatellites like co-

dominant and multi-allelic nature, high polymorphism with cross species made them most preferable markers for groundnut breeding.

2.2.2 Single nucleotide polymorphism (SNP) markers

SNP markers are increasingly being used for various genome-wide studies. SNPs have been detected from diploids as well as cultivated tetraploid groundnut (Alves *et al.,* 2008; Nagy *et al.,* 2012; Khera *et al.,* 2013; Chopra *et al.,* 2015; Gupta *et al.,* 2015; Peng *et al.,* 2016). SNPs were used for the first time for the construction of linkage map in cultivated groundnut by Zhou *et al.* (2014). A 60 K SNP chip was developed by ICRISAT in collaboration with University of Georgia, USA using Affymetrix SNP platform which will boost genetics and breeding applications (Janila *et al.*, 2016). Recently, Shirasawa *et al.* (2016c) identified SNPs from the whole genome re-sequencing in cultivated groundnut. SNPs are marker of choice due to wide distribution throughout the genome, accuracy and rapidness in genotyping (Zhou *et al.*, 2014).

2.2.3 Transposable element (TE) markers

TE markers detect the polymorphism for transposable elements at a given locus. TEs are generally classified as class I and class II elements based on their mode of transposition. Class I elements transpose through an RNA intermediate, while class II elements transpose through DNA. Class I elements involve the replicative mode (copy and paste) of transposition of retrotransposons, where their copy number can increase. On the contrary, class II TEs are usually present in a low copy number, probably due to their “cut and paste” mechanism of transposition.

Retrotransposons are the most widespread class of eukaryotic TE (Finnegan, 1989). They can be divided into two principal groups, the long terminal repeat (LTR) and the non-LTR retrotransposons. LTR retrotransposons are transcribed from one LTR of an integrated element to produce a nearly full-length RNA copy containing a single copy of the LTR split between its two ends (the LTR provides both the start site and polyadenylation signal for the element). This RNA is then reverse-transcribed into an extrachromosomal cDNA, reconstituting the full-length element that is ultimately integrated back into the genome. Immediately internal to the LTRs are the priming sites

for reverse transcription. The large central part of the retrotransposon encodes the structural components of a virus-like particle into which the RNA is inserted, together with reverse transcriptase and integrase enzymes (Finnegan, 1989; Kalendar, 2011).

Transposase enzyme recognises the short terminal inverted-repeat (TIR) sequences, and mediates the transposition of class II elements. The presence of certain conserved motives within transposases, as well as sequence and length similarities in the TIRs and in the target site duplications generated upon insertion, allow to classify eukaryotic class II transposons in 7 different superfamilies (Feschotte *et al.*, 2002b). Internal deletions within the coding sequences of transposons can generate defective elements that are no longer able to transpose autonomously, but can be transactivated by active transposases expressed by related elements.

Miniature inverted-repeat transposable elements (MITEs) are highly represented in plant genomes. MITE structure resembles to that of defective class II transposons in the absence of the coding capacity and the presence of TIRs. However, the high copy number and the sequence and size conservation of each MITE subfamily suggest that MITEs can be highly amplified from a limited number of progenitors, which is a characteristic of class I elements. For these reasons, MITEs remained long time unclassified. Recently, however, a direct link between a MITE family and a potential autonomous element was found, suggesting that MITEs are a particular type of defective class II transposon. The example of transposase-encoding element related to a MITE family was found in Arabidopsis, where an element closely related to the Emigrant family of MITEs was found to encode a pogo-like transposase (Feschotte and Mouchès, 2000). Since then, transposase-encoding elements related to most MITE families have been found in plants and other organisms (Le *et al.*, 2000; Yu *et al.*, 2000; Turcotte *et al.*, 2001; Zhang *et al.*, 2001; Feschotte and Wessler, 2002; Feschotte *et al.*, 2002b; Turcotte and Bureau, 2002), and it has been proposed that MITEs are a particular type of defective class II elements mobilised by transposases encoded by their related autonomous elements (Feschotte *et al.*, 2002a). Nevertheless, the mechanism by which these elements are amplified remains unknown.

Renaturation kinetic studies have estimated 64 per cent repetitive content in the genome of cultivated groundnut. Transposable elements constituted 61.7 and 68.5 per

cent of the *A. duranensis* and *A. ipaensis* genomes, respectively (Dhillon *et al.*, 1980). Most transposon families were shared by the two genomes; for abundant families, macroscale positioning in the two genomes was similar, though, such positions differed for others because of transposon activity and the divergence of the two genomes. Overall, long terminal repeat (LTR) retro-transposons comprised more than half of each genome. In contrast, DNA transposons constituted about 10 per cent (Bertioli *et al.*, 2016; Chen *et al.*, 2016), of which MITEs were highly represented (Shirasawa *et al.*, 2012a).

2.2.4 Retro-transposon markers

Abundance and ability to transpose make retro-transposons a potential genomic feature for marker development. PCR-based techniques like IRAP (inter-retrotransposon amplified polymorphism) and REMAP (retrotransposon-microsatellite amplified polymorphism) that detect retrotransposon integration events in the genome have been developed (Kalendar *et al.*, 1999). Retro-transposon markers were also developed in groundnut (Nielen *et al.*, 2009).

2.2.5 DNA TE markers

Induced mutation study in groundnut identified a MITE (subsequently called *AhMITE1*), and demonstrated its role in the functional disruption of the fatty-acid desaturase-encoding gene *AhFAD2B* resulting into high oleic acid mutations (Patel *et al.*, 2004). Development of AhTE (*Arachis hypogaea* TE) marker based on *AhMITE1* was proposed (Bhat *et al.*, 2008), and that marker showed strong association with LLS resistance (Gowda *et al.*, 2010) and a possible role in the mutation and evolution of botanical types of groundnut (Gowda *et al.*, 2011). Later, Shirasawa *et al.* (2012a) surveyed the groundnut genome for *AhMITE1* using transposon display. *AhMITE1* exhibited a mean length of 205.5 bp and a GC content of 30.1 per cent, with AT-rich, 9 bp target site duplications and 25 bp terminal inverted repeats. They developed 504 AhTE markers using *AhMITE1*-enriched libraries. Additional 535 AhTE markers were developed using transposon-enriched libraries of other cultivars (Shirasawa *et al.*, 2012b).

TE markers have been successfully used for cultivar identification in Japanese pear (Kim *et al.*, 2012), studying genetic relationships in groundnut (Hui *et al.*, 2013), construction of linkage maps in sweet potato (Monden *et al.*, 2015), wheat (Queen *et al.*, 2004), diploid avena, and genomics in rice (Monden *et al.*, 2009) and other crops (Monden *et al.*, 2014a; Monden *et al.*, 2014b). *BARE1* retrotransposon markers have been used to map a major resistance gene for net blotch in barley (Manninen *et al.*, 2000).

Retrotransposons have also been used in generating insertion inactivation tagged mutants. *Tos17* is involved in mutations induced by tissue culture in rice (Hirochika *et al.*, 1996), and it contributed immensely for rice functional genomics (Hirochika, 2001). Similarly, the endogenous Lotus retrotransposon 1 (*LORE1*) transposes in the germ line of *Lotus japonicus*. This feature of *LORE1* has been exploited for generation of a large non-transgenic insertion mutant population, where insertions have been annotated using next-generation sequencing approaches (Fukai *et al.*, 2014). Endogenous retrotransposons are also active in many other plant species. Based on the methods developed for *LORE1* mutagenesis, it should be simple to establish similar systems in other species, once an appropriate element has been identified.

2.3 Mapping populations

Various mapping populations have been used in groundnut for mapping the traits. F_2 populations were used to construct the linkage maps in wild (Halward *et al.*, 1993; Milla, 2003) as well as cultivated groundnut (Herselman *et al.*, 2004). Considering the advantages of recombinant inbred lines (RILs), such populations were used for mapping the productivity (Luo *et al.*, 2017a; Luo *et al.*, 2017b), abiotic stress (Ravi *et al.*, 2011) and disease resistance traits (Sujay *et al.*, 2012; Kolekar *et al.*, 2016). RIL populations have been commonly used in groundnut for mapping several traits (Ravi *et al.*, 2011; Zhou *et al.*, 2014; Kolekar *et al.*, 2016; Zhou *et al.*, 2016b; Luo *et al.*, 2017a; Pandey *et al.*, 2017). Backcross populations were also used for mapping in *Arachis stenosperma* × (*Arachis stenosperma* × *A. cardenasii*) (Garcia *et al.*, 2005). AB-QTL population, which facilitates simultaneous discovery of QTLs and development of elite genotypes, was developed for pod morphology, plant architecture, yield components and days to flowering (Fonceka *et al.*, 2012a). Chromosome segment

substitution lines (CSSLs) were developed to facilitate characterization of different segments of wild species contributing for resistance to foliar diseases and/or any other desirable traits (Fonceka *et al.*, 2012b).

Afore-mentioned mapping populations are generally used for linkage mapping. However, association mapping, which is a powerful approach for exploring the molecular basis of phenotypic variations in plants, employs a population which is different than those used for linkage mapping. A germplasm collection, like groundnut minicore (US) containing 112 accessions was used to determine the population structure and its impact on marker–trait association for seed quality traits (including oil content, fatty acid composition, flavonoids, and resveratrol) (Wang *et al.*, 2011). Genetic analysis demonstrated that the groundnut minicore panel was suitable for association mapping. Further, linkage disequilibrium was worked for the same population to identify the marker-trait associations (Belamkar *et al.*, 2011).

Similarly, groundnut minicore (China) comprising 298 accessions was genotyped using 109 SSR markers. The accessions exhibited abundant genetic and phenotypic diversity over three environments for 15 agronomic traits. In total, 89 SSR alleles were identified to be associated with 15 agronomic traits of three environments by the Q + K model-based association analysis (Jiang *et al.*, 2014).

A ‘reference set’ of groundnut, consisting of representative genotypes from 48 countries including different genomes (AA, BB, EE, EX, PP and AABB) along with four additional elite genotypes, was employed for high-resolution genotyping and multiple season phenotyping data for 50 important agronomic, disease and quality traits. Distinctness of all the genotypes could be established using either a unique allele detected by a single SSR or a combination of unique alleles by two or more than two SSR markers. Allelic diversity, population structure, linkage disequilibrium decay and marker-trait association (MTA) were analysed. A total of 524 highly significant MTAs (p value $>2.1\times10^{-6}$) with wide phenotypic variance (PV) range (5.81–90.09 %) were identified for 36 traits. These MTAs are useful in improving biotic resistance, oil/seed/nutritional quality, drought tolerance related traits, and yield/yield components in groundnut (Pandey *et al.*, 2014a)

The majority of agronomic traits are controlled by multiple genes that cause minor phenotypic effects, making the identification of these genes difficult. MutMap, a method based on whole genome re-sequencing of pooled DNA from a segregating population of plants that show a useful phenotype, was proposed (Abe *et al.*, 2012). In MutMap, a mutant is crossed directly to the original wild-type line and then selfed, allowing unequivocal segregation in second filial generation (F_2) progeny of subtle phenotypic differences. This approach is particularly amenable to crop species because it minimizes the number of genetic crosses (n=1 or 0) and mutant F_2 progeny that are required. MutMap was applied to seven mutants of a Japanese elite rice cultivar to identify the unique genomic positions most probable to harbor mutations causing pale green leaves and semi-dwarfism (Abe *et al.*, 2012).

Genotypes differing for a few genetic factors help in identifying the markers for traits by reducing the number of candidate genomic regions or genes (Andersen and Lubberstedt, 2003). Backcrossing of mutants to their non-mutagenized progenitor, and analyzing their isogenic lines could be one way of drastically reducing the background noise Abe *et al.* (2012). Near isogenic line (NIL) population provides more accurate estimation of genetic effects because these lines are almost identical, and the background noise due to variable genome regions is minimum.

Zhang *et al.* (2006) developed trait-performance derived near-isogenic lines in rice using two recombinant inbred lines contrasting for the traits. These near isogenic lines segregated only for 0.9 per cent of the genetic background (apart from the QTL region). QTL with very high contribution towards panicle size, heading date and plant height were detected. In maize, near isogenic lines differing for resistance to sugarcane mosaic virus resistance (SCMV) were employed for suppression subtractive hybridization to identify the resistance genes (Shi *et al.*, 2005).

Reducing the background noise to increase the power of QTL detection was attempted not only by using appropriate genetic material, but also standardizing the method of QTL analysis (Jansen and Stam, 1994; Zeng, 1994). Different biometrical models used for joint linkage association mapping (JLAM), which combines the advantages of linkage mapping and association mapping, were compared for the QTL

detection power, and the model which help reduce the background noise and result in high QTL detection power was proposed (Wurschum *et al.*, 2012).

Recently, a new method of mapping-by-sequencing was attempted to demonstrate candidate gene identification using mutagen-induced changes as segregating markers in the same genetic background (Hartwig *et al.*, 2012). Using this method, the mutation responsible for the suppression of *heterochromatin protein1* (*lhp1*) involved in chromatin-mediated gene repression were identified. This study also demonstrated that the genotypes with similar background would help in identifying specific genetic factors governing a trait.

Exome sequencing, the targeted sequencing of the subset of the genome coding for proteins, is a powerful and cost-effective new tool for dissecting the genetic basis of traits that have proved to be intractable to conventional gene-discovery strategies. Additionally, exome sequencing is being adapted to explore the extent to which rare alleles explain the heritability of traits (Bamshad *et al.*, 2011). Thus, exome sequencing can be very well applied to mutants for gene discovery (Bolon *et al.*, 2011; Wang *et al.*, 2013b; Henry *et al.*, 2014).

Comparative genomic hybridization (CGH) detects lesion-induced mutations. A midoleate x-ray mutant, M23, with a known *FAD2-1A* (for fatty acid desaturase) gene deletion was detected using CGH (Bolon *et al.*, 2011). Further, fast neutron-induced deletions were detected by CGH, and confirmed by exome resequencing and sequencing of PCR products.

High-throughput TILLING (Targeting Induced Local Lesions in Genomes) allows the rapid and low-cost discovery of induced point mutations in populations of chemically mutagenized individuals (Till *et al.*, 2003; Bhat *et al.*, 2007). It has been successfully used for improving shelf life in melon (Dahmani-Mardas *et al.*, 2010), nitrogen assimilation and fixation in *Lotus japonicas* (Horst *et al.*, 2007), erucic acid synthesis in rapeseed (Wang *et al.*, 2008) etc. Thus, induced mutants provide an ideal genotype for gene discovery directly or indirectly by developing appropriate experimental populations.

2.4 Trait mapping

In groundnut, several traits have been mapped. They include plant morphological traits (Kayam *et al.*, 2017), productivity traits (Faye *et al.*, 2015; Huang *et al.*, 2015; Luo *et al.*, 2017a; Luo *et al.*, 2017b), resistance to diseases and insects (Khedikar *et al.*, 2010; Sarvamangala *et al.*, 2011; Shoba *et al.*, 2012; Sujay *et al.*, 2012; Shoba *et al.*, 2013; Kolekar *et al.*, 2016; Leal-Bertioli *et al.*, 2016; Zhou *et al.*, 2016b; Pandey *et al.*, 2017), tolerance to abiotic stress (Ravi *et al.*, 2011; Gautami *et al.*, 2012) and nutritional quality traits (Sarvamangala *et al.*, 2011; Pandey *et al.*, 2014b; Mondal *et al.*, 2015). QTL/markers have been identified for these traits.

Genomic resources with significant contribution towards the trait are used for marker-assisted breeding. For example, the QTL and their flanking markers were successfully identified for LLS and rust resistance (Khedikar *et al.*, 2010; Sarvamangala *et al.*, 2011; Sujay *et al.*, 2012; Kolekar *et al.*, 2016). A genomic region on A03 had significantly high PVE for LLS (44.5 %) and rust (70.4 %) resistance, while the region on A02 contributed significantly for LLS resistance (62.3 %). SSR and AhTE markers linked to these QTL were identified. They were extensively validated using near isogenic lines and other mapping populations (Yeri *et al.*, 2014; Sukruth *et al.*, 2015) and used to develop LLS and rust resistant genotypes in groundnut (Varshney *et al.*, 2014; Yeri and Bhat, 2016; Kolekar, 2017). Therefore, successful marker-assisted breeding requires identification and validation of markers, which depends on the number and type of markers, and the mapping population.

3. MATERIAL AND METHODS

An attempt was made to identify the markers linked/associated with taxonomic, agronomic, disease resistance, productivity, nutritional and physiological traits in groundnut. For this purpose, a recombinant inbred line (RIL) population and a large collection of independent mutants were employed along with Arachis hypogaea transposable element (AhTE) markers and phenotypic data collected over the rainy seasons of 2014 and 2015. The material and methods used in this study are described in this chapter under the following headings:

3.1 RIL mapping

3.2 Mutant population

3.3 Experimental site

3.4 Raising RIL and mutant population

3.5 Phenotyping of RIL and mutant populations

3.6 Statistical analysis

3.7 Genotyping with AhTE markers

3.8 Double-digest restriction site-associated DNA sequencing (ddRAD- Seq)

3.9 Marker-trait association analysis with RIL population

3.10 Marker-trait association analysis with RIL population

3.1 RIL mapping population

The mapping population consisting of 432 recombinant inbred lines (Appendix I) was developed from TMV 2 × TMV 2-NLM at the University of Agricultural Sciences (UAS), Dharwad (Pattanashetti, 2005). TMV 2 is a high yielding Spanish bunch cultivar with erect growth habit, sequential branching pattern and wide elliptic leaflet. TMV 2-NLM (Prasad *et al.,* 1984) is a EMS derived mutant of TMV 2. TMV 2-NLM has semi-spreading growth habit, alternate branching pattern and lanceolate leaflet (Plate 1). TMV 2 and TMV 2-NLM were crossed, and the F_1s were selfed. Four hundred and thirty-two F_2 plants were advanced through single seed descent method till F_{14} generation.

a. TMV 2

b. TMV 2-NLM

Plate 1: Morphology of TMV 2 (a) and TMV 2-NLM (b)

3.2 Mutant population

The mutant population (98 genotypes) (Appendix V) consisted of parents and their independent mutants developed at UAS, Dharwad and Bhabha Atomic Research Centre (BARC), Mumbai. The mutants from UAS, Dharwad included 42 primary mutants, 7 secondary mutants and 4 tertiary mutants from EMS mutagenesis of Dharwad Early Runner (DER) which was derived from a cross between two *fastigiata* cultivars, *viz.* Dh3-20 and CGC-1 (Gowda *et al.*, 1989). The mutants from BARC, Mumbai were developed by gamma and x-ray mutagenesis.

3.3 Experimental site

RIL and mutant populations were evaluated at IABT Garden (E115) of Main Agricultural Research Station, UAS, Dharwad. This experimental site was located in the transitional tract of Karnataka at 15^0 13' north latitude and 75^0 07' east longitude with an altitude of 678 m above mean sea level. The soil type of the experimental block was vertisol with pH ranging from 7.0 to 7.5.

3.4 Raising RIL and mutant populations

The RILs, mutants and the parents were grown during the rainy season of 2014 and 2015 in a randomized complete block design (RCBD) with a spacing of 30 cm between the rows and 10 cm between the plants in two replications. During the first season, the crop was sown on 6th July 2014 and harvested on 25th October 2014. During the second season, the crop was sown on the 2nd July 2015 and harvested on 26th October 2015. Care was taken to grow healthy crop with necessary agronomic practices during both the seasons.

3.5 Phenotyping of RIL and mutant populations

3.5.1 Taxonomic trait

3.5.1.1 Main stem flowering

Based on the presence or absence of flower on the main axis, main stem flowering was recorded as 'present' or 'absent'.

3.5.1.2 Inflorescence type (INF)

Based on the number of pegs on the reproductive node, inflorescence type was recorded as ‘simple’ or ‘compound’. A reproductive node bearing single peg was classified as simple inflorescence, while the reproductive node with more than one peg was regarded as compound inflorescence.

3.5.1.3 Branching pattern

Branching pattern was observed and classified as (i) alternate, (ii) sequential, (iii) irregular with flowers on main stem, and (iv) irregular without flowers on main stem based on the standard chart (Fig. 1) (IBPGR/ICRISAT, 1992).

3.5.2 Agronomic traits

3.5.2.1 Growth habit

Plant growth habit was observed at the pod-setting stage, and recorded as either procumbent-1, procumbent-2, decumbent-1, decumbent-2, decumbent-3 or erect using the standard chart (Fig. 2) (IBPGR/ICRISAT, 1992).

3.5.2.2 Plant height

The height of the main stem was measured from ground level to terminal bud in centimeter (cm) from five representative plants of each line at 60-85 days after emergence, and the mean was calculated.

3.5.2.3 Number of primary branches

Number of branches borne on the main stem was recorded from five representative plants of each line at 60-85 days after emergence, and the mean was calculated.

3.5.2.4 Number of secondary branches

Number of branches borne on the primary branches was recorded from five representative plants of each line at 60-85 days after emergence, and the mean was calculated.

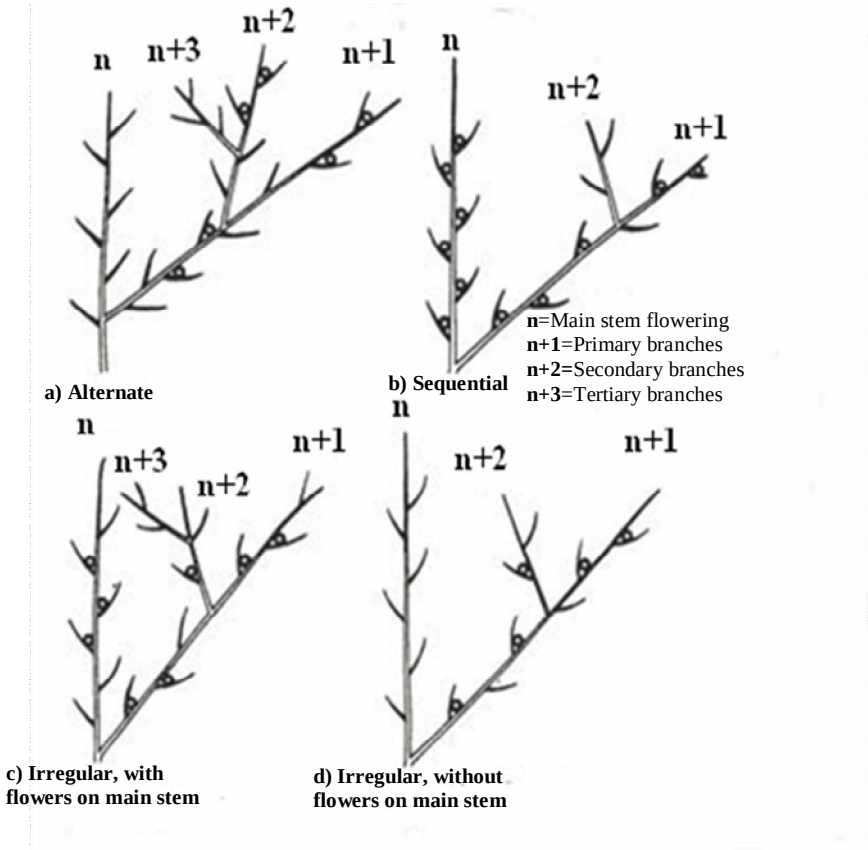


Fig. 1: Branching pattern in groundnut

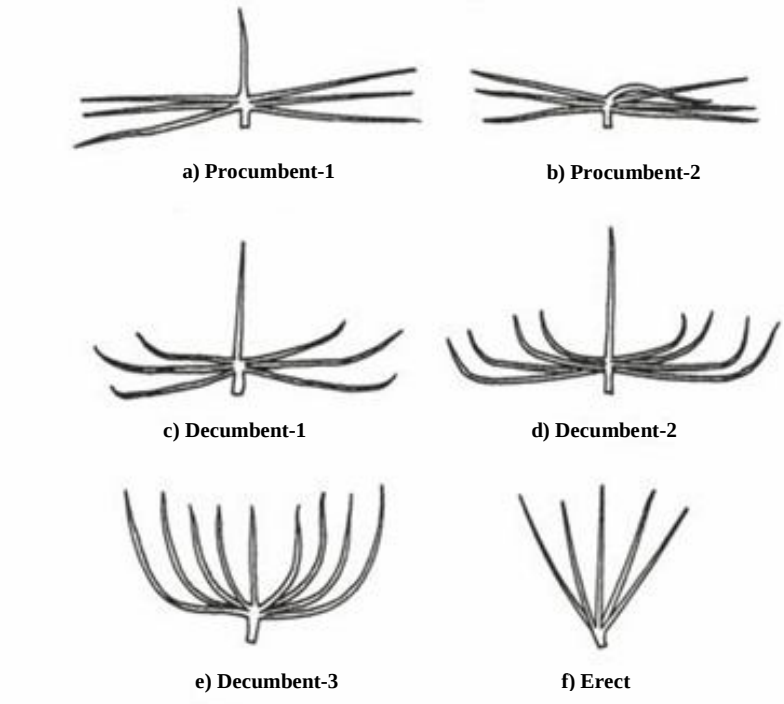


Fig. 2: Growth habit in groundnut

3.5.2.5 Leaflet length

Length of the apical leaflet on the fully expanded third leaf on the main stem was measured in centimeter (cm) from five representative plants of each line at 60-85 days after emergence, and the mean was calculated.

3.5.2.6 Leaflet width

Width of the apical leaflet on the fully expanded third leaf on the main stem was measured in centimeter (cm) from five representative plants of each line at 60-85 days after emergence, and the mean was calculated.

3.5.2.7 Leaflet shape

Shape of the fully expanded apical leaflet of the third leaf on the main stem was recorded in 14 classes (Fig. 3).

3.5.2.8 Leaflet colour

Leaflet colour of the fully expanded apical leaflet of the third leaf on the main stem was recorded into different classes based on intensity of colour distribution.

3.5.2.9 Days to 50 per cent flowering

Number of days taken from sowing to the day on which 50 per cent of the plants in each line flowered was recorded.

3.5.3 Disease resistance traits (LLS and rust)

Inoculum of late leaf spot (LLS) and rust pathogen were maintained on susceptible genotypes (TMV 2 and JL 24). The artificial epiphytotic condition for LLS and rust was created in the field using 'Spreader Row Technique' (Subrahmanyam *et al.*, 1995) in which the disease spreader plants (TMV 2 and JL 24) were planted at every 10^{th} row in the experimental plot. The infected leaves from susceptible plants grown in the growth chamber were collected and soaked in water for 30 min. LLS conidia and rust uredinospores were released by rubbing the infected leaves in the water. The inoculum containing 20,000 conidia/urediniospores per ml water was mixed with

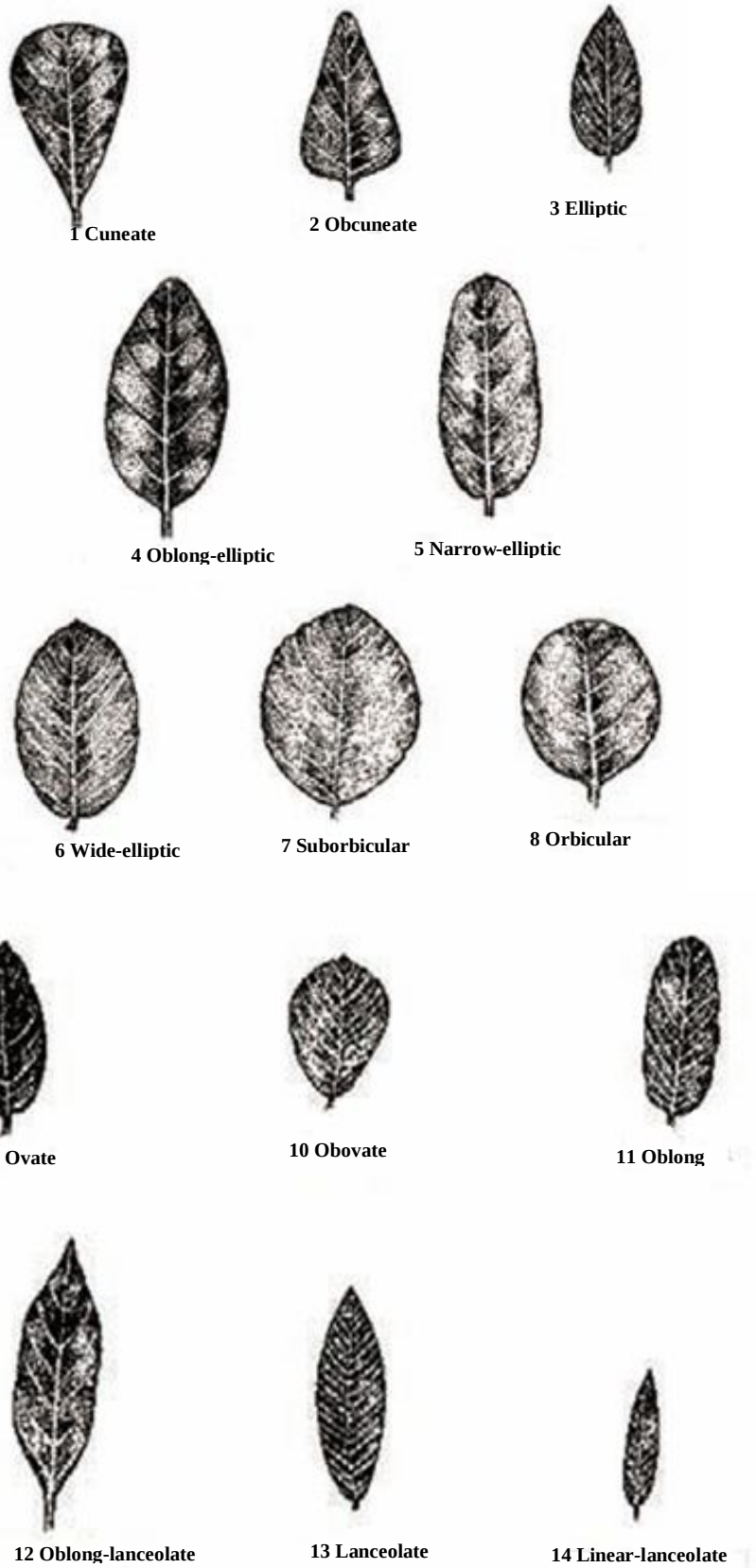


Fig. 3: Leaflet shapes in groundnut

Tween 80 (0.2 ml/1,000 ml of water) as a mild surfactant. The field-grown plants, when they were 35 days old, were sprayed in the evening with the inoculum using a Knapsack sprayer for a week. High humidity was maintained by irrigating the field in the night with sprinkler or furrow irrigation. Additional inoculum was provided by placing pots containing diseased plants at every 20 rows. Modified 9 point scale (1-9 score) (Subbarao *et al.*, 1990) was used for scoring rust (Table 1, Fig. 4) and LLS (Table 2, Fig. 5) disease at three stages of growth (70 DAS, 80 DAS and 90 DAS).

3.5.4 Productivity traits

3.5.4.1 Number of pods per plant

Number of pods per plants was counted for five representative plants of each line, and the average was recorded.

3. 5.4.2 Pod yield per plant

Weight of the dried pods per plant was recorded in gram (g) from five representative plants of each line, and the average was calculated.

3.5.4.3 Pod yield

Pod yield per hectare was expressed in kilogram per hectare (kg/ha) and worked out using the formula:

$$\text{Pod yield (kg/ha)} = \frac{\text{Pod yield per plot (kg)}}{\text{Plot area (m}^2\text{)}} \times 1000$$

3.5.4.4 Pod length

The length of five dried and cleaned pods was measured in centimeter (cm) using vernier caliper, and the mean length was recorded.

3.5.4.5 Pod width

The width of five dried and cleaned pods were measured in centimeter (cm) using vernier caliper, and the mean width was recorded.

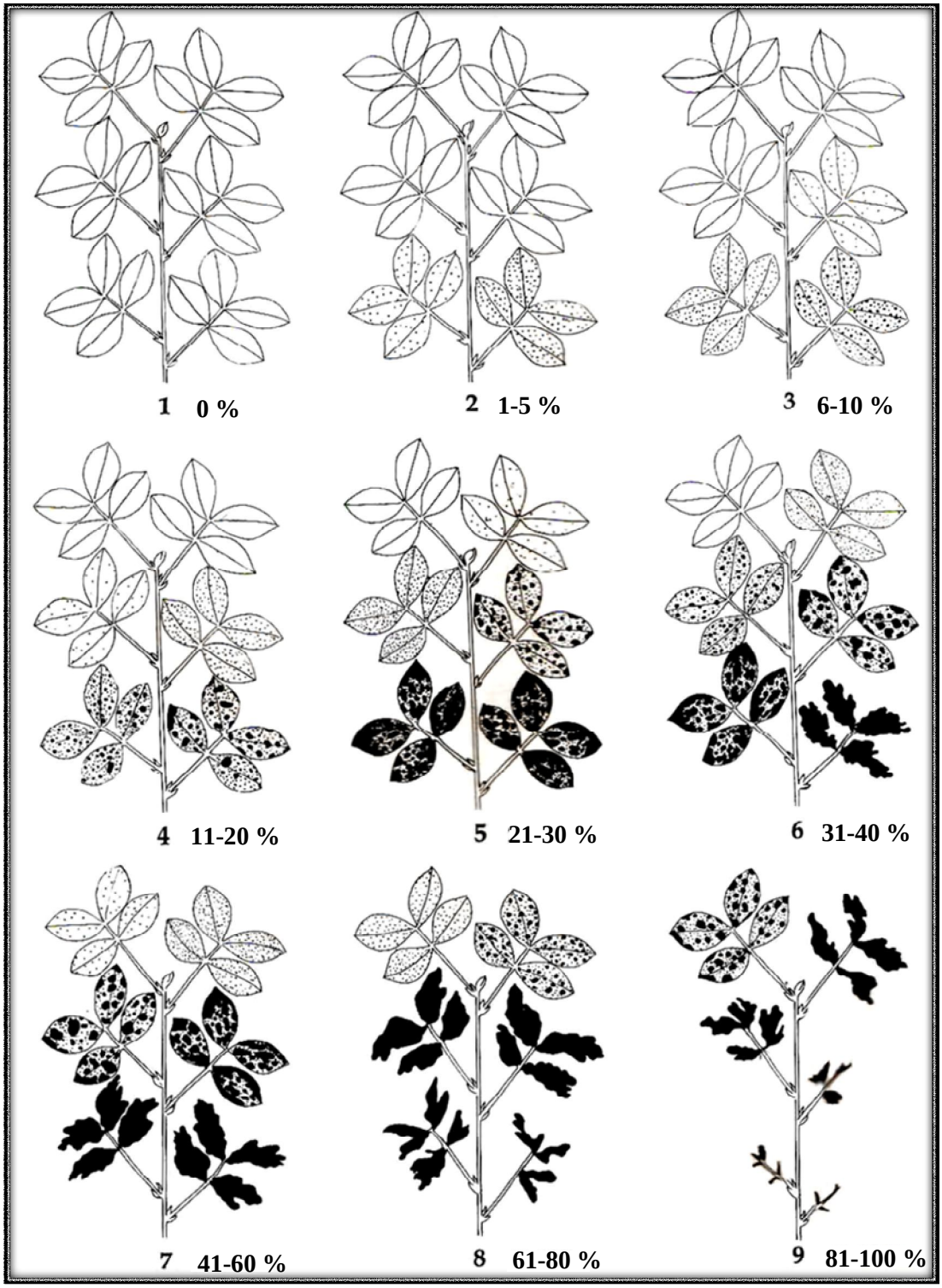


Fig. 4: Modified 9 point scale used for field evaluation of rust in groundnut

Table 1: Modified 9 point scale used for field screening of groundnut genotypes for resistance to rust disease`

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 of lower and middle leaves, pustules may be present on top leaves but less severe	21 - 30
6	Extensive damage to lower leaves, middle leaves, necrotic 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

***-** Per cent leaf area damaged by the disease

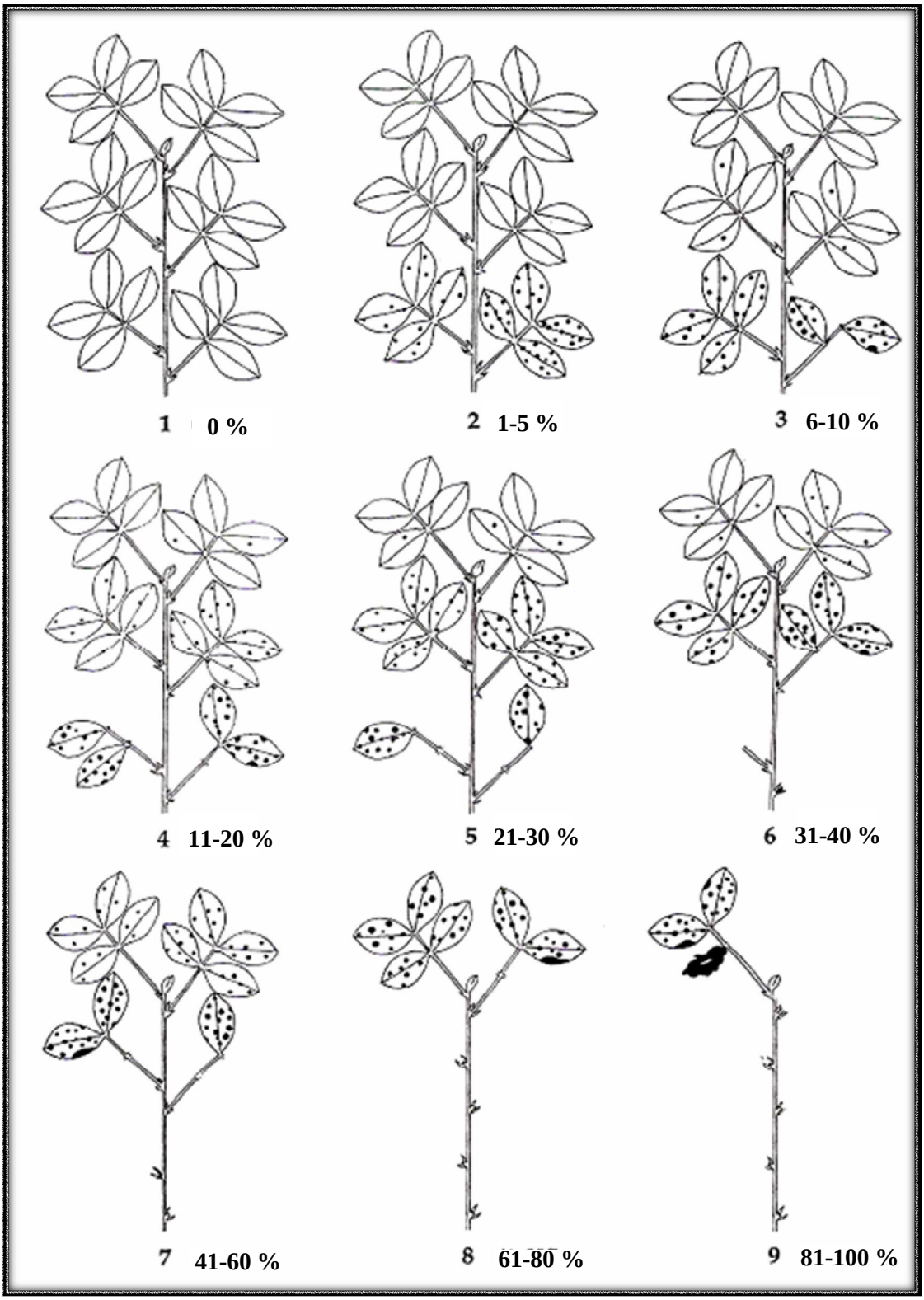


Fig. 5: Modified 9 point scale used for field evaluation of late leaf spot in groundnut

Table 2: Modified 9 point scale used for field screening of groundnut genotypes for resistance to late leaf spot disease

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 present on lower and middle leaves but severe 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	Severe lesions on lower and middle leaves; lesions present but less severe on top leaves; extensive defoliation of lower leaves; defoliation of some defoliation 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; severe lesions on top leaves; some defoliation of top leaves evident.	61 - 80
9	Almost leaves defoliated, leaving bare stem; some leaflets may remain, but show severe leaf spots.	81 - 100

*- Per cent leaf area damaged by the disease

3.5.4.6 Test weight

Weight of 100 representative kernels from each line was recorded in gram (g) as test weight.

3.5.4.7 Shelling percentage

The ratio of weight of kernels to weight of pods was worked out for each line, and expressed in percentage (%).

3.5.4.8 Sound mature kernel weight percentage

The ratio of sound mature kernel weight to weight of total kernels (immature /shriveled kernels) was worked out, and expressed in percentage (%).

3.5.4.9 Seeds per pod

The pods of each genotype were observed for the number of kernels. Depending on the order of the frequency of kernels, the genotypes were given with scores by following the Groundnut Descriptors (IBPGR/ICRISAT, 1992).

3.5.4.10 Seed colour

Kernel colour was observed within one month after harvest. The colour was recorded by following the Groundnut Descriptors (IBPGR/ICRISAT, 1992).

3.5.4.11 Pod constriction

Intensity of constriction on the mature pods was observed, and recorded as absent, shallow, medium, deep and very deep according to the scale of Groundnut Descriptors (IBPGR/ICRISAT, 1992).

3.5.4.12 Pod reticulation

Intensity of reticulation on the mature pods was observed, and recorded as absent, slight, moderate, prominent, and very prominent according to the scale of Groundnut Descriptors (IBPGR/ICRISAT, 1992).

3.5.4.13 Pod beak

The intensity of beak on mature pods was observed. Genotypes were scored as absent, slight, moderate, prominent, and very prominent according to Groundnut Descriptors (IBPGR/ICRISAT, 1992).

3.5.5 Nutritional traits

3.5.5.1 Oil content

Per cent oil content (%) of each genotype was estimated by near infrared spectroscopy (NIRS) using FOSS NIR System, 6500 Composite (FOSS Analytical A/S, Denmark) at Seed Quality Testing and Research Laboratory, Seed Unit, UAS, Dharwad.

3.5.5.2 Protein content

Per cent protein content (%) of each genotype was estimated by NIRS at Seed Quality Testing and Research Laboratory, Seed Unit, UAS, Dharwad.

3.5.5.3 Fatty acid profile

Eight fatty acids *viz.*, arachidic acid, behenic acid, eicosenoic acid, lignoseric acid, linoleic acid, oleic acid, palmitic acid and stearic acid of each genotype were estimated from well matured equal sized kernels using NIRS at Seed Quality Testing and Research Laboratory, Seed Unit, UAS, Dharwad.

3.5.6 Physiological traits

3.5.6.1 Relative chlorophyll content (SPAD values)

Relative chlorophyll content was measured in terms of SPAD chlorophyll meter reading (SCMR) with the help of SPAD meter on 37 DAS.

3.5.6.2 Seed dormancy

Seed dormancy test was conducted by subjecting the dried seeds for germination after 15 days of harvesting, and observing for the number of seeds germinated on each

day for 14 consecutive days. Percentage of seeds germinated was used to record the level of seed dormancy using the score provided by Landfort *et al.* (1965).

3.6 Statistical analysis

The data collected during 2014 and 2015 for various traits were subjected for statistical analysis using Windostat Version 8.1 available at the Department of Biotechnology, University of Agricultural Sciences, Dharwad. The following statistical parameters were calculated.

3.6.1 Mean and range

Mean for each genotype in a replication was calculated using the observations recorded from the sample of five plants. The overall mean for each genotype was calculated using the values from each replication. Minimum and maximum means of the genotypes were considered to record the range.

3.6.2 Analysis of variance

Analysis of variance (ANOVA) was carried out in order to partition the variation due to different sources following the method of Panse and Sukhatme (1954).

Source of variation	**Df**	**MSS**	**EMSS**	**F**
Replication (r)	(r-1)	M_1	-	M_1/M_3
Genotypes (g)	(g-1)	M_2	$\sigma^2_e + r\sigma^2_g$	M_2/M_3
Error	(r-1) (g-1)	M_3	σ^2_e	
Total	**(rg-1)**			

3.6.3 Two-way analysis of variance

The data over the two seasons were subjected for two-way analysis of variance using the method given by Sundararaj *et al.* (1972) to find out the variation due to genotype, environment and genotype × environment interaction.

Source of variation	Df	MSS	EMSS	F
Replication (r)	(r-1)			
Environment (t)	(t-1)	M_1	$\sigma^2_e + r\sigma^2_{g \times e} + rg\sigma^2_e$	M_1/M_4
Genotypes (g)	(g-1)	M_2	$\sigma^2_e + r\sigma^2_{g \times e} + rg\sigma^2_g$	M_2/M_4
Genotype × environment	(g-1) (t-1)	M_3	$\sigma^2_e + r\sigma^2_{g \times e}$	M_3/M_4
Pooled error	gt (r-1)	M_4	σ^2_e	
Total	**t (rg-1)**			

3.6.4 Estimation of components of variance

Phenotypic and genotypic variances were calculated for the traits as suggested by Singh and Chaudhary (1979).

3.6.5 Coefficient of variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed as per the method suggested by Burton and De Vane (1953).

$$PCV\ (\%) = \frac{\sigma_p}{\overline{X}} \times 100$$

$$GCV\ (\%) = \frac{\sigma_g}{\overline{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\overline{X}$ = General mean of the character

PCV and GCV values were categorized as low (0 - 10 %), moderate (10 - 20 %) and high (> 20 %) as indicated by Sivasubramanian and Menon (1973).

3.6.6 Heritability (h^2_{bs})

Heritability in broad sense (h^2_{BS}) was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability } (h^2_{bs})\ (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability in broad sense was categorized as low (0-30 %), moderate (30-60 %) and high (> 60 %) as indicated by Robinson *et al.* (1949).

3.6.7 Genetic advance (GA)

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

$$GA = ih^2_{bs}\,\sigma_p$$

Where,

h^2_{bs}: Heritability in broad sense

K: Selection differential which is equal to 2.06 at 5 per cent intensity of selection (Lush, 1940)

σ_p: Phenotypic standard deviation.

3.6.8 Genetic advance as per cent of mean (GAM)

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

Where,

GA = Genetic advance

$\overline{X}$ = General mean of the character

Genetic advance as Per cent mean were categorized as low (0 - 10 %), moderate (10 - 20 %) and high (> 20 %) as indicated by Johnson *et al.* (1955).

3.6.9 Correlation analysis

Phenotypic correlation was computed to determine the degree of association among the traits using the formula given by Weber and Moorthy (1952).

$$r_{xy}(p) = \frac{Cov_{xy}(p)}{\sqrt{V_y(p) \times V_y(p)}}$$

Where,

$Cov_{xy}(p)$ = Phenotypic covariance between characters x and y

$V_x(p)$ = Phenotypic variance of character x

$V_y(p)$ = Phenotypic variance of character y

$r_{xy}(p)$ = Phenotypic correlation coefficient between characters x and y

Phenotypic correlation coefficients were compared against table value at (n-2) degrees of freedom at the probability levels of 0.05 to test their significance (Fisher and Yates, 1963).

3.6.10 Frequency distribution

The frequency distribution of the RILs and mutants was studied for the mean values of agronomic, productivity, disease resistance, nutritional and physiological traits for two seasons (2014 and 2015). Frequency distribution was worked out using the statistical package SPSS version 16.0. The genotypes were said to be normally distributed when the skewness values ranged from -2.00 to +2.00, and the kurtosis from -3.00 to +3.00.

3.7 Genotyping with AhTE markers

3.7.1 DNA isolation

DNA was isolated from the young leaves of the genotypes of both the populations by following the modified cetyltrimethyl ammonium bromide (CTAB) method (Mace *et al.*, 2003).

1. A 100 mg of young leaves were transferred to 1.5 ml microcentrifuge tube, and ground to a fine powder in liquid nitrogen using a micropestle.

2. Pre-heated CTAB buffer (1,000 µl) was immediately added to microcentrifuge containing fine powder of leaves. The contents were mixed vigorously by vortexing and inverting. The tube was incubated at 65 ^{0}C for 40 min with occasional inversion.

3. The samples were cooled on the bench to room temperature and were centrifuged at 13,000 rpm for 20 min to pellet the cellular debris, proteins and polysaccharides.

4. An equal volume of phenol: chloroform: isoamyl alcohol (25:24:1) was added to the extract and mixed by gentle inversion for 5 to 10 min to form a uniform milky white emulsion.

5. The mixture was centrifuged at 13,000 rpm for 20 min.

6. The aqueous phase was pipetted out gently, avoiding the interface and added with an equal volume of pre-chilled isopropanol. The contents were mixed gently by inverting the microcentrifuge tube and incubated overnight at -20 ^{0}C.

7. The content was centrifuged at 13,000 rpm for 20 min. Supernatant was discarded.

8. The pellet was washed with 70 per cent ethyl alcohol by spinning at 13,000 rpm for 10 min. Alcohol was completely discarded to get clear pellet. The pellet was dried by using vacuum concentrator for 5 min.

9. The pellet was dissolved in 100 µl of $T_{10}E_1$ buffer.

3.7.2 Quality and quantification of DNA

Quantification of DNA was done by UV-Spectrophotometer (at 260 nm) and the quality of DNA was checked by agarose gel electrophoresis (Sub-Cell, model 192, BIO-RAD) according to Sambrook and Russell (2001). Genomic DNA was electrophorated on 0.8 per cent agarose gel at voltage of 5 V/cm using 1X TAE buffer and ethidium bromide (0.5 µg/ml) staining. On the completion of run, gel was image was captured using GBOX F3 (SYNGENE). The concentration of DNA and quality was determined by nanospectrophotometer. The good quality DNA samples with a ratio of 1.8 at OD 260/280 were diluted to a final concentration of 50 ηg/µl and used for genotyping.

3.7.3 Polymerase chain reaction (PCR)

The members of the RIL population and mutant population were genotyped with 105 and 110 *Arachis hypogaea* transposable element (AhTE) markers, respectively (Shirasawa *et al.*, 2012a; Shirasawa *et al.*, 2012b). DNA amplification was performed in a 20 µl reaction mixture (Table 3) with appropriate PCR profile (Table 4) using eppendorf Mastercycler® pro and BIO-RAD T100^{TM} Thermal cyclers.

3.7.4 Separation of PCR products

The PCR products were mixed with 2 µl of loading dye (Bromophenol blue) and loaded on 1.8 per cent agarose gel prepared in 1X TAE buffer containing ethidium bromide (50 µg/100 ml). Products were separated at 80 volts till they were clearly resolved. The gel was observed and documented with image capturing system.

3.7.5 Scoring the alleles

Alleles differing for 205 bp (equal to the size of *AhMITE1*) were scored as A [homozygote as the first parent (TMV 2)], B [homozygote as the second parent (TMV 2-NLM)], H (heterozygote), C [not genotype a (b-allele is dominant)] and D [not genotype b (a-allele is dominant)] as per JoinMap 4 format (Van Ooijen, 2006) for the RILs. Mutants were scored as A [homozygote with *AhMITE1* insertion], B [homozygote without *AhMITE1* insertion] and H (heterozygote).

Table 3: PCR reaction mixture used for AhTE-PCR

Component	Stock	Working concentration	Quantity (µl)
Water (HPLC grade)	-	-	13.8
PCR buffer (with 15 mM $MgCl_2$)	10 X	1 X	2.0
dNTPs	2 mM	0.2 mM	2.0
AhTE primer (Forward)	10 pmol/ul	5 pmol	0.5
AhTE primer (Reverse)	10 pmol/ul	5 pmol	0.5
DNA template	50 ng/ ul	50 ng	1.0
Taq DNA Polymerase	5 U/ul	1 U	0.2
Total			20.0

Table 4: PCR profile for AhTE-PCR

S.N.	Step	Temperature (^{0}C)	Duration (min)	No of cycles
1	Denaturation	94	5	1
2	Denaturation Annealing Primer extension	94 53 72	2 1 2	35
3	Final extension	72	10	1
4	Hold	4		

3.7.6 Marker localization and prediction of candidate genes

The physical location of AhTE marker loci was decided by subjecting the sequences flanking the *AhMITE1* for BLASTn at peanut database (https://peanutbase.org/gbrowse) against the reference genomes of *A. duranensis* (A genome, 2n=2x=20) and *A.ipaensis* (B genome, 2n=2x=20) (Bertioli *et al.*, 2016). The result with highest BLAST score was used to decide the chromosomal location. Gene content in the marker loci was checked using the genome browser at PeanutBase (https://peanutbase.org/gbrowse).

3.8 Double-digest restriction site-associated DNA sequencing (ddRAD-Seq)

DNA was subjected for restriction digestion with *Pst*I and *Msp*I. The ddRAD-Seq libraries were constructed and sequenced on a MiSeq (Illumina) in paired-end 251 bp mode (Shirasawa *et al.*, 2016a). The reads were employed to discover SNPs and copy number variations (Shirasawa *et al.*, 2016a). SNP sites were checked for gene content using SnpEff (http://snpeff.sourceforge.net/).

3.9 Marker-trait association analysis with RIL population

3.9.1 Linkage map construction

Linkage analysis was performed with JoinMap 4.0 (Van Ooijen, 2006). Markers were placed on to linkage groups with the “LOD groupings” and “Create groups for mapping” command using the Kosambi map function (Kosambi, 1943). Calculation parameters were set for a minimum LOD threshold of 3.0, and the marker order in the linkage groups was established by “Calculate Map” command. After developing the framework genetic map, the unmapped markers were placed into different linkage groups. The linkage maps were graphically represented using the software MapChart 2.2 (Voorrips, 2002).

3.9.2 Single marker analysis (SMA)

Single marker analysis was performed in the RILs of TMV 2 × TMV 2-NLM to find out the association between the markers and various traits using the phenotypic

data. SMA was carried out using F-statistic and simple linear regression method (Haley and Knott, 1992) available at WinQTL Cartographer version 2.5 (Wang *et al.*, 2007).

3.9.3 Quantitative trait loci analysis

Linkage map of TMV 2 × TMV 2-NLM was used for QTL analysis along with the phenotypic data of two seasons (*kharif* 2014 and 2015). QTL analysis was carried out using WinQTL Cartographer, version 2.5 (Wang *et al.*, 2007). Composite interval mapping was performed using Model 6, with scanning intervals of 2.0 cM between markers and putative QTL with a window size of 10.0 cM. The number of marker cofactors for the background control was set by forward backward stepwise regression. "Automatically Locate QTLs'' option was used with a minimum of 5.0 cM between QTL to define a QTL region. Permutation for 1000 times was also employed while determining the QTL using the option ''permutations times'' with 0.05 significance level. The percentage of phenotypic variance explained (PVE) by each QTL region was estimated based on the partial correlation of putative QTL with observed variable (Kendall and Stuart, 1961). Significant QTLs were identified by comparing the LOD scores with the threshold LOD. The additive effect was calculated as half the differences between genotypic values of two homozygotes (Falconer, 1975).

3.10 Marker-trait association analysis with mutant population

3.10.1 Diversity analysis

3.10.1.1 Polymorphism information content (PIC) analysis

Polymorphic information content indicating the ability of the marker to distinguish the individuals was computed for each marker using PowerMarker V3.25 (Liu and Muse, 2005), and classified as low (≤ 0.25), moderate (0.26 - 0.49) and high (≥ 0.5) (Hildebrand *et al.*, 1994).

3.10.1.2 Major allele frequency

The frequency of the major allele at each marker loci was computed using PowerMarker V3.25 (Liu and Muse, 2005).

3.10.1.3 Minor allele frequency

Minor allele frequency refers to the frequency at which the second most common allele at a locus occurs in a given population. It was computed for each marker using PowerMarker V3.25 (Liu and Muse, 2005).

3.10.1.4 Heterozygosity of a locus

The observed heterozygosity of a locus indicating the number of heterozygous individuals in the population at that locus was computed for each marker using PowerMarker V3.25 (Liu and Muse, 2005).

3.10.1.5 Gene diversity of a locus

Gene diversity of a locus indicating the expected heterozygosity of the locus was computed for each marker using PowerMarker V3.25 (Liu and Muse, 2005).

3.10.1.6 Principal co-ordinate analysis (PCoA)

It is a method to explore and to visualize similarities or dissimilarities of genotypes. Genotypes ordinated closer to one another are more similar than those ordinated further away. Principal co-ordinate analysis was computed for mutant population using DARwin 6.0.14 (Perrier *et al.*, 2003).

3.10.1.7 Population structure analysis

Model-based cluster analysis was performed to infer genetic structure and define the number of clusters (gene pools) in the datasets using software STRUCTURE version 2.3.1 (Pritchard *et al.*, 2000). The number of presumed populations (K) was set from 1 to 15, and each was repeated two times. For each run, burn-in and iterations were set to 1,00,000 and 2,00,000, respectively, and a model without admixture and correlated allele frequencies was used. The run with maximum likelihood was used to assign individual genotypes into groups. Delta K (ΔK) value was computed according to Evanno's method (Evanno *et al.*, 2005). The Q matrix obtained for the highest ΔK was used for association analysis along with the genotypic and phenotypic data.

3.10.2 Genome-wide marker-trait association analysis

Marker-trait association in the mutant population was analyzed using Genomic Association and Prediction Integrated Tool (GAPIT) available at the computer package EMMA (Lipka *et al.*, 2012). AhTE markers with genomic positions were used for analysis. Quantile-quantile (QQ) plots were generated to check the significance of association. A marker-trait association was declared significant when the p value was ≤ 0.05.

4. EXPERIMENTAL RESULTS

In an attempt to map the important taxonomic, agronomic, productivity and nutritive traits in groundnut, TMV 2 and its EMS-derived mutant, TMV 2-NLM were compared for the genetic changes, and the recombinant inbred line (RIL) population of TMV 2 × TMV 2-NLM was employed to construct the linkage map and QTL map. Marker-trait associations were also studied using a panel consisting of parents and their independent mutants. The results of these experiments are presented in this chapter under following headings:

4.1 Phenotypic and genotypic differences between TMV 2 and TMV 2-NLM

4.2 Genetic mapping with the RILs of TMV 2 × TMV 2-NLM

4.3 Selection of superior RILs

4.4 Association studies using a mutant population

4.1 Phenotypic and genotypic differences between TMV 2 and TMV 2-NLM

TMV 2 and TMV 2-NLM were grown in the field during the rainy seasons of 2014 and 2015, and observed for the differences with respect to taxonomic, agronomic, productivity, nutritional and physiological traits. TMV 2 was a typical Spanish bunch variety, while TMV 2-NLM had Virginia runner growth habit (decumbent-3, semi-spreading). TMV 2 had sequential branching pattern, early flowering, light green leaves and absence of seed dormancy, while TMV 2-NLM had alternate branching pattern, late flowering, dark green leaves and seed dormancy. The parents also differed for important qualitative traits like leaflet shape, pod size, pod beak and kernel colour (Table 5). TMV 2 had wide elliptic leaflet, medium pod size, slight pod beak and light tan kernel colour, while TMV 2-NLM had lanceolate leaflet, large pod size, medium pod beak and dark tan kernel colour. Phenotypically, the parents differed significantly for important quantitative traits like number of pods per plant, pod yield, test weight, shelling percentage, protein and oil content, oleic acid and chlorophyll content.

TMV 2 and TMV 2-NLM were subjected to ddRAD-Sequencing with an average depth of 3.4X. Of the 3,76,957 paired-end reads of 251 bp for TMV 2, 3,33,114

Table 5: Distinguishing features of TMV 2 and TMV 2-NLM

Sl. No.	Name of the trait	TMV 2	TMV 2-NLM
Taxonomic traits			
1	Branching pattern	Sequential	Alternate
Morphological traits			
2	Growth habit	Erect	Decumbent-3 (Semi-spreading)
3	Days to 50 per cent flowering	31	36
4	Leaflet shape	Wide-elliptic	Linear lanceolate
5	Leaflet colour	Light green	Dark green
6	Leaflet length (cm)	5.57	4.76
7	Leaflet width (cm)	2.48	1.25
8	Number of primary branches	5.73	9.00
9	Plant height (cm)	35.58	28.69
10	Number of secondary branches	0.00	9.25
Physiological traits			
11	Seed dormancy Score (0 to 8)	Absent (6)	Present (3)
12	SPAD Chlorophyll Meter Reading	24.59	44.56
Productivity traits			
13	Pod size	Medium	Large
14	Number of pods per plant	24.58	11.9
15	Pod yield per plant (g)	16.55	7.83
16	Pod yield (kg/ha)	4883	2043
17	Test weight (g)	37.00	45.93
18	Shelling percentage	74.60	66.53
19	Kernel colour	Light tan	Dark tan
20	Pod beak	slight	Moderate
Nutritional traits			
21	Protein (%)	32.27	27.50
22	Oil (%)	46.58	43.94
23	Linoleic acid (%)	35.82	27.76
24	Oleic acid (%)	42.38	54.47
25	Arachidic acid (%)	1.99	1.55
26	Behenic acid (%)	3.52	2.75
27	Palmitic acid (%)	12.37	11.50
28	Stearic acid (%)	4.00	3.15

aligned with the reference genome [(*Arachis duranensis* (A genome) and *Arachis ipaensis* (B genome)] in pairs, while 20,033 aligned as single reads. Thus, the total reads aligned with the reference genomes was 3,53,147 which accounted for an alignment rate of 93.68 per cent. Similarly, a total of 3,69,416 reads of 251 bp were obtained for TMV 2-NLM, of which 3,18,728 reads aligned in pairs, while 20,962 aligned as single reads with a total aligned sequence of 3,39,690 accounting to 91.95 per cent alignment rate. These reads were subjected for SNP discovery and copy number variation (CNV) analysis. In total, 31 SNPs were observed between TMV 2 and its mutant TMV 2-NLM (Table 6). These SNPs were spread across seven chromosomes with a non-random distribution. Both genic and intergenic SNPs were observed. The genic SNPs were observed all along (promoter to 3′ UTR) the genes with low to high impact on the gene function. Of the 29 genic SNPs, four were non-synonymous in three genes. A few genes accumulated considerably more number of single nucleotide mutations. For example, *Araip NZ9YG* gene on B04 chromosome, accumulated 14 SNPs. SNPs were analyzed for functional annotation. Gene annotation in terms of cDNA was available in the database for four genes, and the probable functions are listed in Table 6. Apart from the single nucleotide mutations, an effort was made to compare for CNVs over 10 kb genomic regions. CNVs with more than 5-fold increase or decrease of $\log_2$ ratio were observed at 5 regions on three chromosomes (A03, A09 and B03), however, only one (121135001-121145000 bp region on A04) was statistically significant (Table 7 and Fig. 6).

4.2 Genetic mapping with the RILs of TMV 2 × TMV 2-NLM

The mapping population was field evaluated for 41 and 43 taxonomic, agronomic, disease resistance, productivity, nutritional and physiological traits during the rainy seasons of 2014 and 2015, respectively. ANOVA across two years indicated significant differences among the RILs for all the traits (Table 8). Environmental effect was significant for all the traits except plant height, leaflet length, protein content, behenic acid, O/L ratio and seed dormancy.

Table 6: Single nucleotide polymorphism between TMV 2 and TMV 2-NLM

SN	Gene	Chrom-osome	No of SNPs	SNP location	Annotation	Transcript
1	*Aradu.EGH8I*	A01	01	Intron	Adenine phosphoribosyltransferase-like protein	EZ725386.1 (Guo *et al*., 2008)
2	*Aradu.KAB8X*	A07	01	3'UTR (954 bp apart)	Disease resistance protein (CC-Nbs-LRR class) family protein; IPR002182 (NB-ARC), IPR027417 (P-loop containing nucleoside triphosphate hydrolase); GO:0043531 (ADP binding)	EZ742624.1 (Guo *et al*., 2008)
3	*Aradu.MA5IZ*	A06	01	Exon (synonymous)	GYF domain-containing protein; IPR003169 (GYF); GO:0005515 (protein binding)	Adur5580_comp0_c0_seq5 (Clevenger *et al*. 2016)
4	*Araip.G5J45*	B10	01	Exon (non-synonymous)	Transmembrane protein, putative	Aipa26504_comp0_c0_seq1 (Clevenger *et al*., 2016)
5	*Araip.K4U0Q*	B10	05	Downstream (2546 to 2692 bp apart)	Pentatricopeptide repeat (PPR) superfamily protein; IPR002885 (Pentatricopeptide repeat), IPR011990 (Tetratricopeptide-like helical), IPR027434 (Homing endonuclease); GO:0004519 (endonuclease activity), GO:0005515 (protein binding)	gi|372391829|gb|JR544303.1| (Zhang *et al*., 2012)
6	*Araip.NZ9YG*	B04	14	Intron	F-box protein interaction domain protein; IPR001810 (F-box domain), IPR011043 (Galactose oxidase/kelch, beta-propeller), IPR017451 (F-box associated interaction domain); GO:0005515 (protein binding)	Aipa36174_comp0_c1_seq4 (Clevenger *et al*., 2016)
7	*Araip.X5KQ1*	B01	05	Exon [synonymous (1) and non-synonymous (2)], intron (2)	Probable sugar phosphate/phosphate translocator [Glycine max]; IPR004853 (Triose-phosphate transporter domain)	GG14274|comp0_c0_seq1 (Clevenger *et al*., 2016)
8	*Araip.ZEW2Y*	B10	1	Exon (non-synonymous)	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein; IPR002130 (Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain), IPR011990 (Tetratricopeptide-like helical); GO:0003755 (peptidyl-prolyl cis-trans isomerase activity), GO:0005515 (protein binding), GO:0006457 (protein folding)	EZ734646.1 (Guo *et al*., 2008)

Table 7: Copy number variations between TMV 2 and TMV 2-NLM

Site of CNV	No of loci showing CNV/s		CNV position		log2	P value
	NLM	TMV2	Start	End		
A04	34	1	121135001	121145000	5.27	0.04
B03	37	1	127715001	127725000	5.19	0.13
B03	34	1	127720001	127730000	5.07	0.13
A03	1	44	6915001	6925000	-5.27	0.11
A09	1	44	6920001	6930000	-5.27	0.11

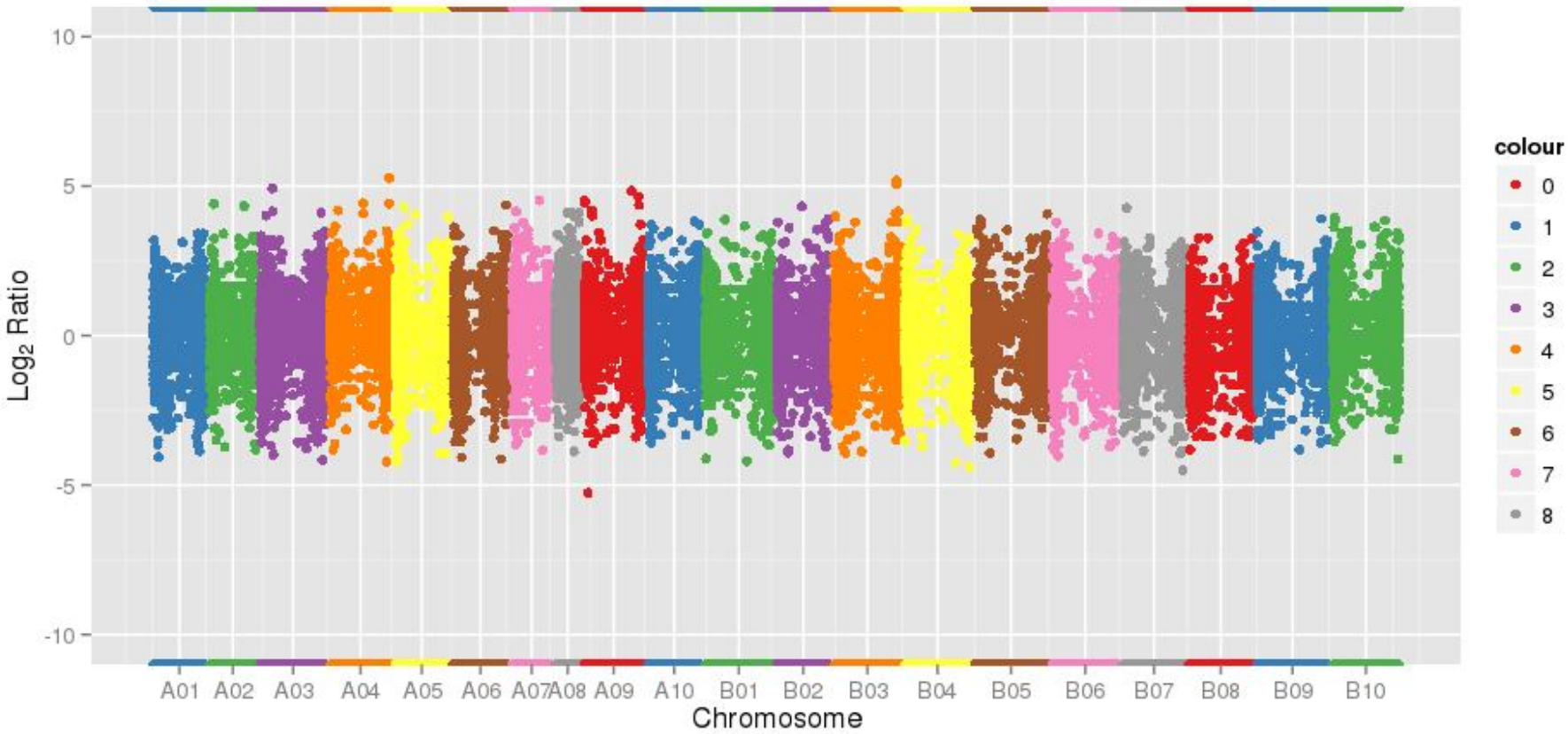


Fig. 6: Copy number variation in TMV 2-NLM when compared to TMV 2

Table 8: ANOVA for disease resistance, productivity, agronomic, nutritional and physiological traits among RILs of TMV 2 × TMV 2-NLM

Sl. No.	Trait/Source of variation	Genotype (G)	Season (E)	G × E	Pooled Error	CV
	Degree of freedom	**433**	**1**	**433**	**866**	
1	Days to 50 per cent flowering	70.28**	499.50**	16.21**	0.19	3.23
2	Plant height (cm)	4.11**	5.43^{NS}	1.72**	28.31	17.90
3	Number of primary branches	2.51**	98.58**	1.29**	3.07	24.43
4	Number of secondary branches	3.63**	69.23**	1.52**	12.17	19.00
5	Leaflet length (cm)	4.97**	0.17^{NS}	2.78**	0.24	15.06
6	Leaflet width (cm)	6.93**	7.10**	2.62**	0.07	16.57
7	LLS score at 70 DAS	3.85**	472.78**	2.55**	0.60	24.29
8	LLS score at 80 DAS	24.28**	614.08**	11.67**	0.20	22.51
9	LLS score at 90 DAS	15.60**	401.65**	4.11**	0.28	10.91
10	Rust score at 70 DAS	20.63**	707.01**	13.95**	0.05	21.79
11	Rust score at 80 DAS	13.23**	705.93**	8.41**	0.19	20.07
12	Rust score at 90 DAS	13.82**	67.74**	6.41**	0.20	11.71
13	Number of pods per plant	9.86**	29.25**	4.88**	5.22	24.34
14	Pod yield per plant (g)	6.46**	54.62**	2.33**	8.88	24.21
15	Shelling percentage (%)	2.41**	22.33**	1.27**	32.31	8.57
16	Test weight (g)	10.69**	799.64**	1.56**	21.31	12.00
17	Sound mature kernel weight (g)	1.34**	224.51**	1.01^{NS}	19.70	4.60
18	Pod length (cm)	13.96**	80.15**	1.54**	0.04	7.07
19	Pod width (cm)	9.96**	248.53**	1.96**	0.01	8.39
20	Protein (%)	12.68**	0.00^{NS}	0.28^{NS}	1.94	4.73
21	Oil (%)	9.81**	144.09**	0.16^{NS}	1.25	2.47
22	Palmitic acid (%)	6.20**	17.38**	0.14^{NS}	0.24	4.09
23	Stearic acid (%)	5.35**	43.94**	0.22^{NS}	0.10	9.13
24	Oleic acid (%)	7.61**	16.47**	0.01^{NS}	11.37	7.24
25	Linoleic acid (%)	7.66**	19.33**	0.00^{NS}	6.77	7.93
26	Arachidic acid (%)	7.34**	12.40**	0.08^{NS}	0.01	6.85
27	Eicosenoic acid (%)	7.16**	318.86**	0.00^{NS}	0.00	5.45
28	Behenic acid (%)	7.22**	1.30^{NS}	0.03^{NS}	0.04	6.34
29	Lignoseric acid (%)	5.70**	9.82**	0.02^{NS}	0.01	5.81
30	Oleic to linoleic acid ratio	2.42**	0.21^{NS}	0.00^{NS}	0.08	9.86
31	Seed dormancy	16.27**	0.99^{NS}	0.99^{NS}	0.76	24.94
32	Relative Relative chlorophyll content (SPAD values)	6.38**	48.49**	0.02^{NS}	1.45	9.40

:** Significant at 0.05 level of probability, *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

Genotype × environment (G × E) interactions were significant for all the traits including agronomic, productivity and disease resistance except sound mature kernel weight and nutritional traits. The mapping population showed very high PCV and GCV for LLS at 80 and 90 DAS, number of pods per plant, pod yield, number of secondary branches and seed dormancy (Table 9). The RILs showed normal distribution for most of the traits, except LLS score at 90 DAS, shelling percentage and sound mature kernel weight based on the kurtosis and skewness values (Table 10, Fig. 7).

Four hundred and thirty-two RILs of TMV 2 × TMV 2-NLM were genotyped with 105 AhTE markers (Plate 2). A linkage map of 1,205.66 cM was constructed with 91 mapped markers (Fig. 8). The features of the linkage map are presented in the Table 11. Based on the physical position of the mapped AhTE marker loci, the nomenclature of the linkage groups was decided. However, there were a few discrepancies since the BLAST results showed multiple hits.

Genotypic and phenotypic data were employed for marker-trait association (MTA) studies [single marker analysis (SMA) and QTL analysis]. A total of 41 and 43 traits from 2014 and 2015, respectively were subjected for SMA. Three markers (AhTE0357, AhTE0391 and AhTE0523) showed significant association and R^2 more than 10 per cent with eleven traits during 2014 and/or 2015 (Table 12). The MTA AhTE0357-branching pattern had the highest R^2 (32.8 %) followed by AhTE0357-days to 50 per cent flowering (14.2 %), AhTE0391-linoleic acid (13.5 %) and AhTE0391-oleic acid (12.1 %). During 2015, the association between AhTE0357-branching pattern was highest (32.8 %) followed by AhTE0357-number of secondary branches (23.3 %), AhTE0357-number of primary branches (20.0 %), AhTE0523-eicosenoic acid (13.8 %), AhTE0391-linoleic acid (13.4 %) and AhTE0391-oleic acid (13.1 %). Eight marker-trait associations involving three markers were common between 2014 and 2015. The marker locus corresponding to AhTE0391 coincided with the gene *Aradu.7N61X*. The *AhMITE1* transposition site was at 2,129 bp of the second intronic region of *Aradu.7N61X* (Fig. 9). Function prediction revealed that *Aradu.7N61X* codes for alpha glucosidase. However, the marker AhTE0523 showed several significant hits upon BLAST, therefore the exact position could not be decided. At AhTE0357 locus, *AhMITE1* was inserted at 79 bp downstream region of the gene *Araip.TG1BL*. Functional prediction revealed that *Araip.TG1BL* codes for galactose oxidase/keltch,

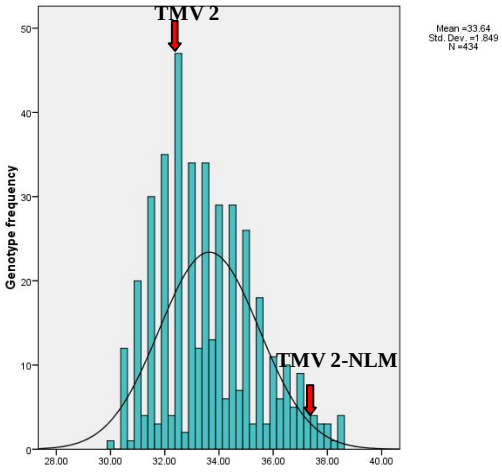
Table 9: Mean, range and genetic variability components for agronomic, productivity, nutritional and disease resistance traits among the RILs of TMV 2 × TMV 2-NLM

SN	Trait	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GAM (%)
			Min	Max					
1	Days to 50 per cent flowering	33.64	30.00	38.50	6.17	5.25	72.50	3.97	11.81
2	Plant height (cm)	33.96	17.50	54.80	22.19	13.11	34.90	6.94	20.44
3	Number of primary branches	6.34	3.88	12.00	33.60	16.21	23.30	1.31	20.66
4	Number of secondary branches	3.20	0.00	19.88	146.22	84.85	33.70	4.17	129.90
5	Leaflet length (cm)	4.12	2.51	6.05	18.52	10.77	33.80	0.68	16.53
6	Leaflet width (cm)	2.03	1.02	2.85	22.57	15.32	46.10	0.56	27.48
7	LLS score at 70 DAS	2.63	1.00	4.00	42.69	22.48	27.70	8.24	31.25
8	LLS score at 80 DAS	4.27	1.00	6.50	32.47	23.39	51.90	1.90	44.50
9	LLS score at 90 DAS	6.99	1.00	8.75	17.80	14.06	62.40	2.05	29.34
10	Rust score at 70 DAS	2.40	1.00	4.00	28.59	18.50	41.90	0.76	31.63
11	Rust score at 80 DAS	4.05	1.00	6.00	26.15	16.76	41.10	1.15	28.38
12	Rust score at 90 DAS	6.48	1.75	8.25	16.45	11.55	49.30	1.04	21.41
13	Number of pods per plant	13.35	5.33	27.08	35.81	23.13	41.70	5.27	39.46
14	Pod yield per plant (g)	11.76	4.16	22.01	39.34	23.26	34.90	4.27	36.30
15	Shelling percentage (%)	69.43	45.44	77.67	9.77	4.70	23.10	4.14	5.97
16	Test weight (g)	41.91	24.59	69.04	20.79	16.98	66.70	15.34	36.60
17	Sound mature kernel weight (g)	96.55	71.12	100.00	4.79	1.34	7.90	0.96	0.99
18	Pod length (cm)	2.88	1.80	4.04	13.59	11.61	72.90	0.75	26.17
19	Pod width (cm)	1.20	0.88	1.61	13.59	10.69	61.90	0.27	22.20
20	Protein (%)	29.48	18.55	35.85	9.36	8.08	74.50	5.42	18.41
21	Oil (%)	45.13	40.65	50.25	4.43	3.67	68.80	3.63	8.04
22	Palmitic acid (%)	11.87	8.94	13.52	6.20	4.66	56.50	1.09	9.26
23	Stearic acid (%)	3.53	2.24	4.57	13.19	9.52	52.10	0.64	18.14
24	Oleic acid (%)	46.58	34.07	60.63	11.79	9.81	62.30	9.04	19.40
25	Linoleic acid (%)	32.82	22.28	42.59	12.95	10.24	62.50	7.01	21.36
26	Arachidic acid (%)	1.72	1.24	2.22	11.01	8.62	61.30	0.31	17.83
27	Eicosenoic acid (%)	0.94	0.73	1.18	8.69	6.77	60.70	0.13	13.92
28	Behenic acid (%)	3.28	2.25	4.24	10.14	7.91	60.90	0.53	16.29
29	Lignoseric acid (%)	1.24	0.98	1.49	8.56	6.30	54.00	0.15	12.22
30	Oleic to linoleic acid ratio	1.47	0.80	2.87	25.97	16.74	41.52	0.33	22.41
31	Seed dormancy	1.35	0.00	8.00	142.25	126.90	79.20	4.02	298.20
32	Relative chlorophyll content (SPAD values)	33.80	17.35	49.25	18.07	15.42	72.90	9.17	27.13

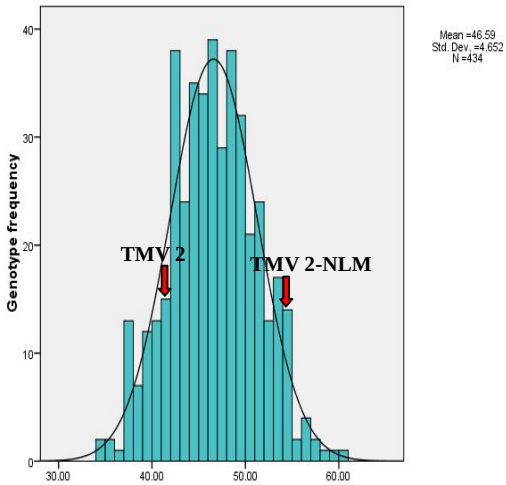
GCV: Genotypic coefficient of variation, **PCV**: Phenotypic coefficient of variation, $\mathbf{h^2_{bs}}$: Heritability (broad sense), **GA**: Genetic advance, **GAM**: Genetic advance as per cent of mean

Table 10: Frequency distribution of the RILs of TMV 2 × TMV 2-NLM for agronomic, disease resistance, physiological, productivity and nutritional traits

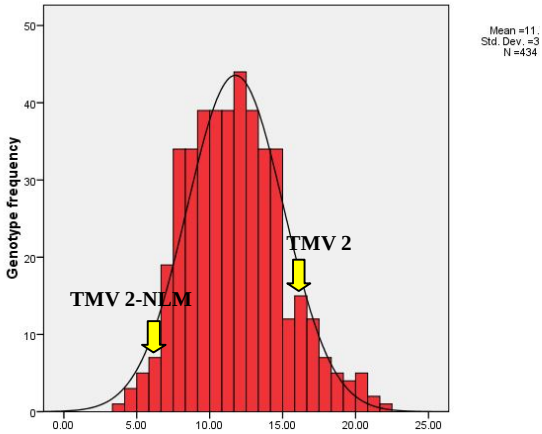
Sl. No.	Trait	Skewness	Kurtosis	Distribution
1	Days to 50 per cent flowering	0.466	-0.379	Normal
2	Plant height (cm)	0.378	0.930	Normal
3	Number of primary branches	0.995	0.944	Normal
4	Number of secondary branches	1.248	1.627	Normal
5	Leaflet length (cm)	0.450	0.698	Normal
6	Leaflet width (cm)	-0.679	0.282	Normal
7	LLS score at 70 DAS	-0.311	0.123	Normal
8	LLS score at 80 DAS	-0.906	0.799	Normal
9	LLS score at 90 DAS	-2.439	9.867	Skewed kurtosis
10	Rust score at 70 DAS	-0.083	0.221	Normal
11	Rust score at 80 DAS	-0.553	1.082	Normal
12	Rust score at 90 DAS	-0.747	2.048	Normal
13	Number of pods per plant	0.600	0.372	Normal
14	Pod yield per plant (g)	0.318	-0.173	Normal
15	Shelling percentage (%)	-1.363	3.640	Kurtosis
16	Test weight (g)	0.382	-0.165	Normal
17	Sound mature kernel weight (g)	-4.724	40.124	Skewed kurtosis
18	Pod length (cm)	0.370	0.194	Normal
19	Pod width (cm)	0.410	0.147	Normal
20	Protein (%)	-0.134	0.543	Normal
21	Oil (%)	0.056	-0.393	Normal
22	Palmitic acid (%)	-0.381	0.940	Normal
23	Stearic acid (%)	0.104	-0.044	Normal
24	Oleic acid (%)	0.012	-0.199	Normal
25	Linoleic acid (%)	-0.020	-0.263	Normal
26	Arachidic acid (%)	0.162	-0.102	Normal
27	Eicosenoic acid (%)	-0.035	0.074	Normal
28	Behenic acid (%)	0.207	0.634	Normal
29	Lignoseric acid (%)	0.068	-0.145	Normal
30	Oleic to linoleic acid ratio	0.636	0.528	Normal
31	Seed dormancy	1.484	1.670	Normal
32	Relative chlorophyll content (SPAD values)	0.089	-0.148	Normal



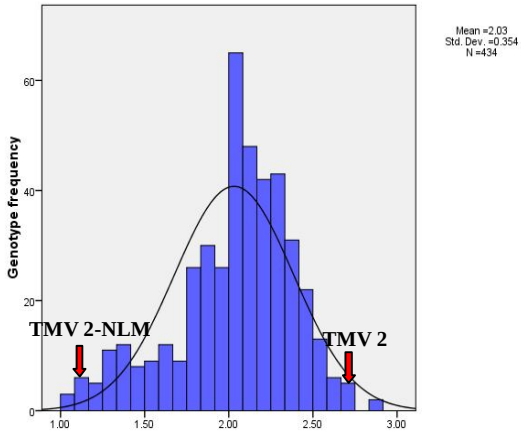
a) Days to 50% flowering



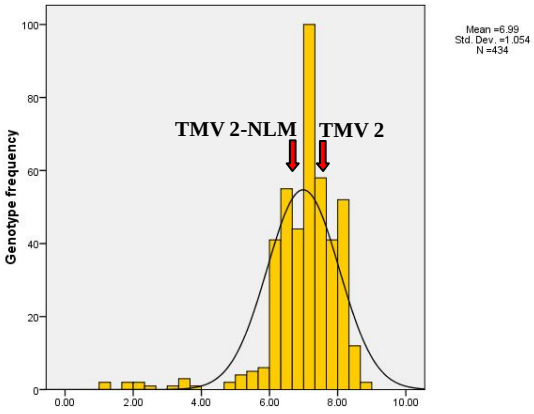
b) Oleic acid



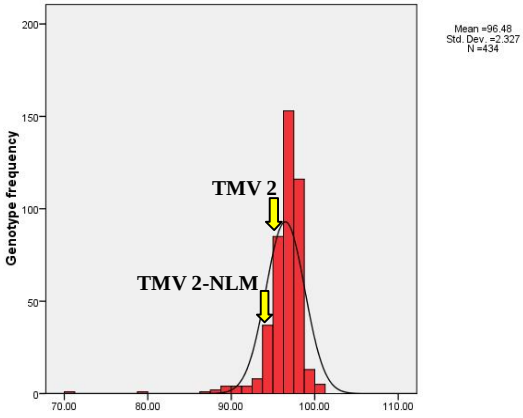
c) Pod yield per plant



d) Leaflet width



d) Late leaf spot at 90 DAS



f) Sound mature kernel weight

Fig. 7: Frequency distribution of RILs of TMV 2 × TMV 2-NLM

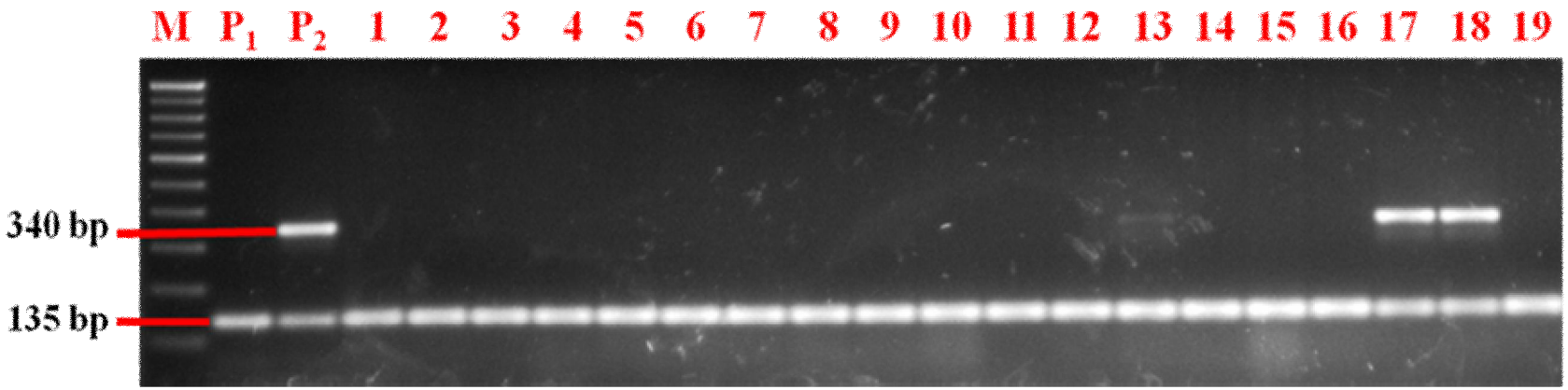


Plate 2: PCR amplification with AhTE0572 in a few RILs of TMV 2 × TMV 2-NLM

M: 100 bp DNA ladder, **P_1**: TMV 2, **P_2**: TMV 2-NLM and **1-19:** RILs of TMV 2 × TMV 2-NLM

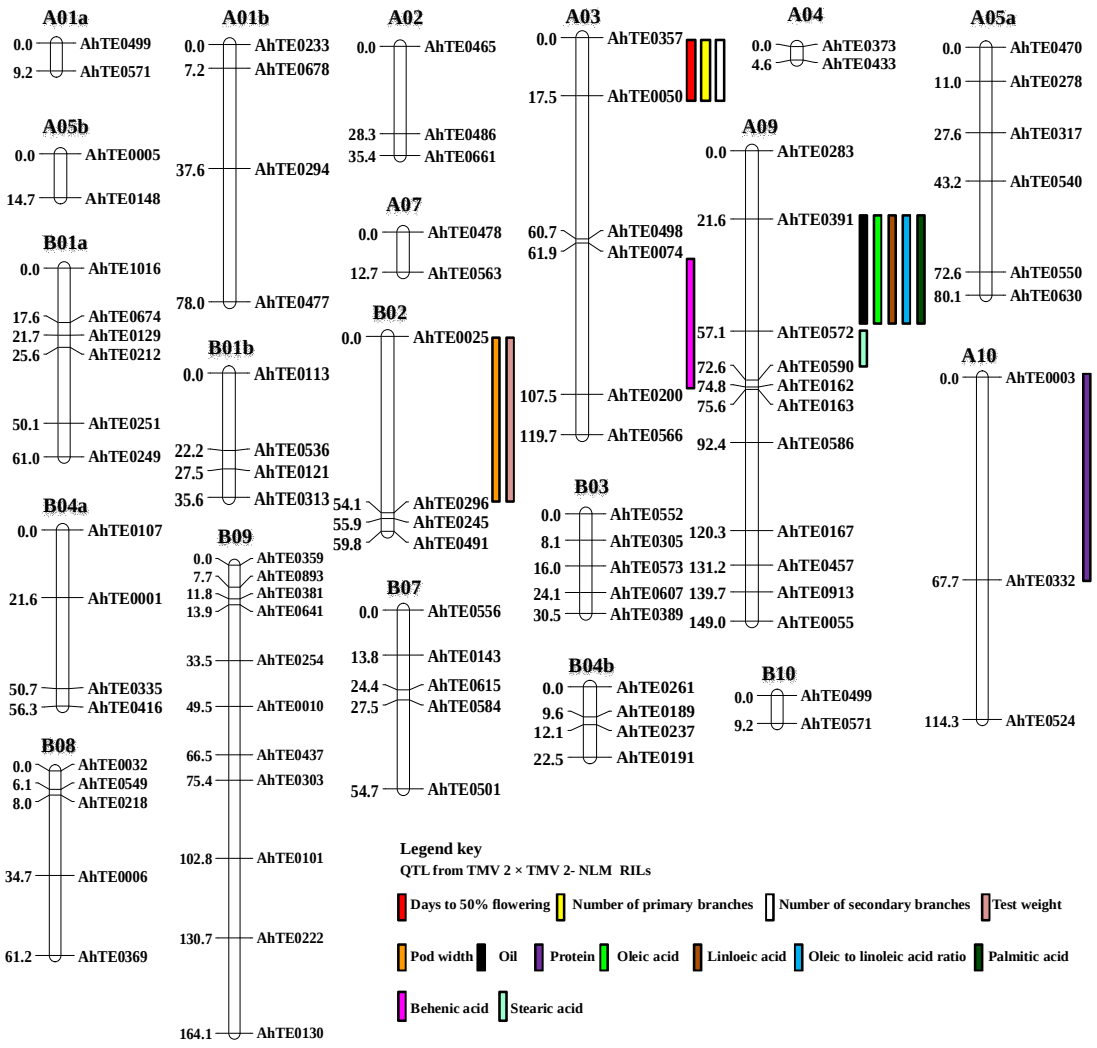


Fig. 8: QTL map for agronomic, productivity and nutritional traits

Table 11: Features of linkage map constructed using the RILs of TMV 2 × TMV 2-NLM

Sl. No.	Linkage group	Map length (cM)	No. of mapped markers	Map density (cM)	Inter-locus gap distance (cM)
1	A01a	9.15	2	4.57	9.15
2	A01b	77.97	4	19.49	25.99
3	A02	35.38	3	11.79	17.69
4	A03	119.68	6	19.95	23.94
5	A04	4.59	2	2.29	4.59
6	A05a	80.08	6	13.35	16.02
7	A05b	14.69	2	7.35	14.69
8	A07	12.72	2	6.36	12.72
9	A09	148.97	11	13.54	14.9
10	A10	114.25	3	38.08	57.12
11	B01a	60.97	6	10.16	12.19
12	B01b	35.56	4	8.89	11.85
13	B02	59.81	4	14.95	19.94
14	B03	30.53	5	6.11	7.63
15	B04a	56.25	4	14.06	18.75
16	B04b	22.54	4	5.64	7.51
17	B07	54.68	5	10.94	13.67
18	B08	61.19	5	12.24	15.3
19	B09	164.12	11	14.92	16.41
20	B10	42.53	2	21.27	42.53
	Mean	**60.28**	**5**	**12.8**	**18.13**
	Total	**1205.66**	**91**	**255.94**	**362.59**

Table 12: Markers identified from single marker analysis for significant association with important agronomic, productivity and nutritional traits

Sl. No.	Marker	Trait	Rainy (2014)			Rainy (2015)		
			F	p	PVE (%)	F	p	PVE (%)
1	AhTE0357	Branching pattern	198.7	0.0	32.3	198.7	0.0	32.3
		Leaflet shape	52.2	0.0	10.0	52.2	0.0	10.0
		Days to 50 per cent flowering	70.3	0.0	14.2	64.2	0.0	12.4
		Number of primary branches	12.9	0.0	2.8	112.8	0.0	20.0
		Number of secondary branches	53.2	0.0	10.8	125.8	0.0	23.3
2	AhTE0391	Oil	36.1	0.0	7.7	26.5	0.0	5.7
		Oleic acid	61.3	0.0	12.4	65.0	0.0	13.1
		Linoleic acid	67.8	0.0	13.5	66.9	0.0	13.4
		O/L ratio	59.3	0.0	12.1	59.8	0.0	12.1
		Palmitic acid	48.7	0.0	10.2	45.2	0.0	9.5
3	AhTE0523	Eicosenoic acid	72.4	0.0	14.4	68.9	0.0	13.8
		Stearic acid	56.2	0.0	11.6	6.6	0.0	1.5
		Protein	49.1	0.0	10.2	16.7	0.0	3.7
		Pod width	11.2	0.0	2.5	55.2	0.0	11.4
		Lignoceric acid	39.2	0.0	8.4	65.8	0.0	13.3
		Linoleic acid	50.4	0.0	10.5	43.6	0.0	9.2
4	AhTE0025	Test weight	31.8	0.0	6.9	36.6	0.0	7.8
		Pod width	45.6	0.0	9.6	39.6	0.0	8.4

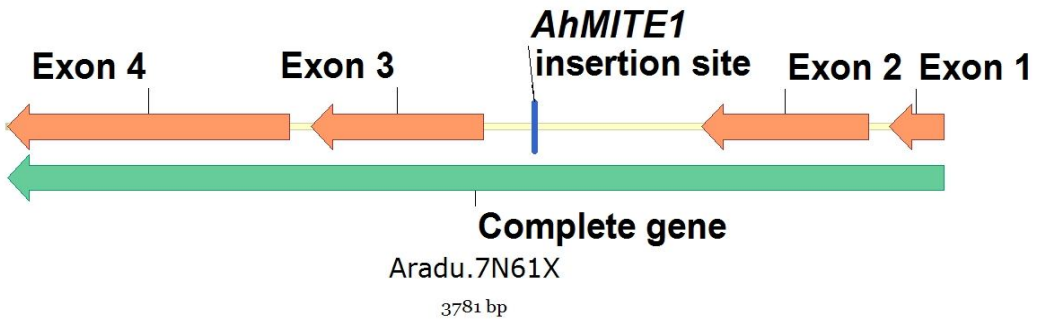


Fig. 9: Insertion of *AhMITE1* in the intronic region of the gene *Aradu.7N61X*

beta-propeller protein. AhTE0025 showed significant association with test weight (6.9-7.8 % R^2) and pod width (8.9-9.6 % R^2). At AhTE0025 locus, *AhMITE1* was inserted in the intronic region of *Aradu.7065G* on A07 chromosome coding for aldo/keto reductase family oxidoreductase.

QTL analysis was attempted using the linkage map and the phenotypic data for 31 traits in 2014, and 33 traits in 2015. The QTL map showed seven major QTL regions (PVE more than 10 %) for 22 traits across the years (Table 13 and Fig. 8). The number of traits governed by these QTL ranged from one (AhTE0074-AhTE0200 and AhTE0005-AhTE0148) to nine (AhTE0391-AhTE0572). The QTL (AhTE0357-AhTE0050) showed the highest PVE of 28.4 per cent for number of secondary branches followed by QTL (AhTE0003-AhTE0332) for protein content (26.4 %). QTL (AhTE0357-AhTE0050) governed days to 50 per cent flowering (PVE 22.0 %) and number of primary branches (PVE 19.9 %). Similarly, QTL (AhTE0391-AhTE0572) governed linoleic acid (PVE 15.5 %) and oleic acid (PVE 15.1 %). QTL (AhTE0025-AhTE0296) governed test weight with a PVE of 13.6 per cent. TMV 2 contributed the favourable allele at AhTE0003-AhTE0332 for protein content. The allele contributed by TMV 2 at AhTE0357-AhTE0050 resulted in reduced days to 50 per cent flowering and number of primary branches. TMV 2-NLM contributed favourable allele at AhTE0391-AhTE0572 for oleic acid content. For test weight, TMV 2-NLM contributed the favourable allele at AhTE0025-AhTE0296.

An effort was made to find out the gene content in the QTL region AhTE0391-AhTE0572 (on A09). A total of 256 genes were predicted in the region homeologous to AhTE0391-AhTE0572 on B09 chromosome. Of 256 genes, 14 were related to fatty acid metabolism (Table 14).

4.3 Selection of superior RILs

With an objective of selecting the superior RILs, heritability was estimated for all the traits across two years. Highest heritability was observed for LLS score at 90 DAS followed by days to 50 per cent flowering, test weight, pod length, pod width, oil and protein content, oleic acid, linoleic acid, arachidic acid, behenic acid, eicosenoic acid, SCMR and seed dormancy (Table 9). To know the extent of gain with the

Table 13: Details of major effect QTLs identified for important agronomic, productivity and nutritional traits in groundnut

Sl. No.	QTL in the marker interval	Linkage group	Marker interval distance (cM)	Trait	Rainy (2014)			Rainy (2015)		
					LOD	Ae	PVE (%)	LOD	Ae	PVE (%)
1	AhTE0357-AhTE0050	A03	0.00-17.52	Days to 50 per cent flowering	13.8	-0.8	18.5	14.3	-1.0	22.0
			0.00-17.52	Number of primary branches	11.6	-0.1	1.0	22.8	-1.7	19.9
			0.00-17.52	Number of primary branches	18.5	-2.9	10.8	26.2	-1.0	28.4
2	AhTE0003-AhTE0332	A10	0.00-67.66	Protein	9.5	1.4	25.4	11.2	1.8	26.4
3	AhTE0391-AhTE0572	A09	21.57-57.11	Oil	9.1	0.5	10.4	6.1	0.5	6.7
			21.57-57.11	Oleic acid	10.4	-1.2	12.4	11.6	-1.4	15.1
			21.57-57.11	Linoleic acid	11.4	0.6	15.5	11.1	0.6	14.8
			21.57-57.11	O/L ratio	10.8	0.0	15.0	11.0	0.0	15.2
			21.57-57.11	Palmitic acid	9.8	0.2	14.8	10.7	0.2	15.3
4	AhTE0572-AhTE0590	A09	57.11-72.62	Stearic acid	7.4	0.1	12.2	2.9	0.1	4.6
			57.11-72.62	Pod width	*	*	*	7.8	-0.1	10.9
5	AhTE0025-AhTE0296	B02	0.00-54.14	Test weight	8.2	-2.3	8.9	10.6	-4.0	13.6
			0.00-54.14	Pod width	9.8	0.0	9.3	12.0	-0.1	11.6
6	AhTE0074-AhTE0200	A03	61.94-107.48	Behenic acid	4.5	0.1	7.1	4.5	0.1	11.8
7	AhTE0005-AhTE0148	A05	0.00-14.69	Pod width	*	*	*	13.32	-0.1	15.9

cM: centi Morgan, **LOD**: logarithm of the odds, **Ae**: Additive effect, **PVE**: Phenotypic variance explained, and '*' : QTL was not detected

Table 14: Annotation of genes related to fatty acid metabolism

Gene	Annotation
Araip.M2BYP	Lipid transfer protein, IPR000528 (Plant lipid transfer protein/Par allergen), IPR016140 (Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain) GO:0006869 (lipid transport) GO:0008289 (lipid binding)
Araip.A4865	Lipid phosphate phosphatase, IPR000326 (Phosphatidic acid phosphatase type 2/haloperoxidase), IPR028681 (Lipid phosphate phosphatase, plant) GO:0003824 (catalytic activity) GO:0016020 (membrane)
Araip.Q09LN	Phosphate phosphatase 3, IPR000326 (Phosphatidic acid phosphatase type 2/haloperoxidase) IPR028681 (Lipid phosphate phosphatase), GO:0003824 (catalytic activity) GO:0016020 (membrane)
Araip.WB0T6	Phosphatidylinositol C5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN-like isoform X2 [Glycine max], IPR014020 (Tensin phosphatase C2 domain) GO:0005515 (protein binding)
Araip.D6PZJ	Seed linoleate 9S-lipoxygenase, IPR000907 (Lipoxygenase) IPR008976 (Lipase/lipooxygenase PLAT/LH2) IPR027433 (Lipoxygenase domain 3) GO:0005506 (iron ion binding) GO:0005515 (protein binding) GO:0016165 (linoleate 13S-lipoxygenase activity) GO:0046872 (metal ion binding) GO:0055114 (oxidation-reduction process)
Araip.S0CWL	Sec14p-like phosphatidylinositol transfer family protein IPR001251 (CRAL-TRIO domain), IPR011074 (CRAL/TRIO N-terminal domain)
Araip.E6C1Q	Homeobox-leucine zipper protein ANTHOCYANINLESS 2-like isoform X2 [Glycine max], IPR002913 (START domain) IPR009057 (Homeodomain-like) ,GO:0003700 (sequence-specific DNA binding transcription factor activity) GO:0008289 (lipid binding)
Araip.PD5F8	Probable carboxylesterase 13-like [*Glycine max*], IPR013094 (Alpha/beta hydrolase fold-3) GO:0008152 (metabolic process)
Araip.Y8ZPE	Probable carboxylesterase 13-like [*Glycine max*], IPR013094 (Alpha/beta hydrolase fold-3) GO:0008152 (metabolic process) GO:0016787 (hydrolase activity)
Araip.38XYU	Probable carbohydrate esterase At4g34215-like isoform X1 [*Glycine max*] IPR005181 (Domain of unknown function DUF303 acetylesterase putative) IPR013831 (SGNH hydrolase-type esterase domain) GO:0016787 (hydrolase activity)
Araip.LY5JJ	Lipase 1, IPR000073 (Alpha/beta hydrolase fold-1) IPR006693 (Partial AB-hydrolase lipase domain) IPR025483 (Lipase eukaryotic) GO:0006629 (lipid metabolic process)
Araip.S1TFK	Acyl-ACP thioesterase IPR002864 (Acyl-ACP thioesterase) GO:0006633 (fatty acid biosynthetic process) GO:0016790 (thiolester hydrolase activity)
Araip.4E9NM	Glycosyl hydrolase superfamily protein IPR001000 (Glycoside hydrolase family 10) IPR017853 (Glycoside hydrolase superfamily) GO:0005975 (carbohydrate metabolic process)
Araip.HF8ER	Lipoyl (Octanoyl) transferase Taxgut metagenome RepIDJ9CQW6_9ZZZZ IPR000544 (Octanoyltransferase) GO:0003824 (catalytic activity) GO:0005737 (cytoplasm) GO:0006464 (cellular protein modification process) GO:0009107 (lipoate biosynthetic process) GO:0016415 (octanoyltransferase activity)

selection, genetic advance over mean (GAM) was calculated. High GAM was observed for LLS and rust reaction, plant height, number of primary branches, number of secondary branches, number of pods per plant, pod yield, pod yield per plant, test weight, pod length and width, linoleic acid, O/L ratio, SCMR and seed dormancy (Table 9).

Correlation coefficients were computed to assess the magnitude and direction of association between the traits (Table 15a and 15b). Number of pods per plant showed significant and positive correlation with pod yield per plant, shelling percentage, sound mature kernel weight, branching pattern, growth habit, oil content, eicosenoic acid and lignoceric acid, while it showed significant negative correlation with LLS, days to 50 per cent flowering, number of secondary branches, test weight, pod length, pod width and pod quality traits.

Test weight was positively and significantly correlated with pod size, sound mature kernel weight and pod yield per plant. Protein and oil content were positively and significantly associated. Oleic acid content showed negative but non-significant correlation with protein and oil content.

Scores at different stages (70, 80 and 90 DAS) of LLS and rust exhibited highly significant and positive correlations. LLS and rust showed significant and positive correlations at 70, 80 and 90 DAS. Both LLS and rust score at 90 DAS showed significant positive association with days to 50 per cent flowering, number of secondary branches and seed dormancy while negative association with number of pods per plant, pod yield, test weight, sound mature kernel weight, protein content, oil content, linoleic acid and palmitic acid.

RIL [2-19(f)] was significantly superior over TMV 2 for pod yield (kg/ha), and fourteen RILs were marginally superior (Table 16). Some of these superior lines were also superior for sound mature kernel weight, oleic acid, test weight, days to 50 per cent flowering, seed dormancy (moderate), LLS and rust resistance, protein content and shelling percentage. The RIL 2-45(a) was superior over TMV 2 for pod yield (kg/ha), days to 50 per cent flowering (early), test weight, sound mature kernel weight, protein content, oil content, oleic acid, O/L ratio and LLS and rust resistance. Another RIL 1-11(b) was superior over TMV 2 for pod yield (kg/ha), seed dormancy (moderate), days

Table 15a: Correlation coefficients for disease resistance, productivity, agronomic, taxonomic, physiological and nutritional traits in the RILs of TMV 2 × TMV 2-NLM

Correlation	Late leaf spot score at 70 DAS	Late leaf spot score at 80 DAS	Late leaf spot score at 90 DAS	Rust score at 70 DAS	Rust score at 80 DAS	Rust score at 90 DAS	Number of pods per plant	Pod yield per plant	Shelling percentage (%)	Test weight	Sound mature kernel weight	Pod length	Pod width	Pod constriction	Pod reticulation	Pod beak	Pod size
LLS 70	1.000																
LLS 80	0.793**	1.000															
LLS 90	0.560**	0.732**	1.000														
R 70	0.493**	0.580**	0.470**	1.000													
R 80	0.499**	0.656**	0.496**	0.886**	1.000												
R 90	0.459**	0.600**	0.667**	0.596**	0.664**	1.000											
NPPP	-0.007NS	-0.085NS	-0.134**	-0.059NS	-0.080NS	0.022NS	1.000										
PY	-0.051NS	-0.144**	-0.154**	-0.055NS	-0.128**	-0.096*	0.602**	1.000									
SP	-0.086NS	-0.049NS	-0.047NS	-0.102*	-0.077NS	0.037NS	0.154**	0.157**	1.000								
TW	-0.072NS	-0.097*	-0.141**	-0.004NS	-0.032NS	-0.097*	-0.208**	0.281**	0.029NS	1.000							
SMKW	-0.106*	-0.101*	-0.103*	-0.120*	-0.142**	-0.141**	0.192**	0.269**	0.244**	-0.030NS	1.000						
PL	0.104*	0.089NS	0.044NS	0.127**	0.082NS	0.045NS	-0.257**	0.043NS	-0.234**	0.643**	-0.247**	1.000					
PW	0.010NS	-0.000NS	-0.029NS	0.016NS	0.000NS	-0.005NS	-0.121*	0.231**	-0.138**	0.691**	-0.036NS	0.564**	1.000				
PC	0.124**	0.163**	0.143**	0.127**	0.185**	0.192**	-0.123*	-0.149**	-0.260**	0.180**	-0.261**	0.412**	0.038NS	1.000			
PR	0.009NS	0.057NS	0.046NS	0.012NS	0.025NS	0.046NS	0.045NS	0.112*	-0.080NS	0.083NS	0.060NS	0.109*	0.080NS	-0.026NS	1.000		
PB	0.106*	0.140**	0.056NS	0.148**	0.145**	0.051NS	-0.057NS	-0.047NS	-0.119*	0.147**	-0.106*	0.332**	-0.036NS	0.296**	0.215**	1.000	
PS	0.010NS	0.002NS	-0.019NS	0.037NS	-0.005NS	0.008NS	-0.119*	0.142**	-0.154**	0.580**	-0.162**	0.693**	0.495**	0.249**	0.170**	0.305**	1.000
50 % F	-0.137**	-0.155**	-0.139**	-0.037NS	-0.029NS	-0.110*	-0.168**	-0.232**	-0.189**	0.063NS	-0.161**	0.151**	0.110*	0.137**	-0.010NS	-0.039NS	0.110*
PH	0.139**	0.144**	0.038NS	0.070NS	0.073NS	0.042NS	0.058NS	0.055NS	-0.039NS	0.102*	-0.078NS	0.204**	0.208**	0.117*	0.073NS	0.129**	0.157**
NPB	-0.069NS	-0.092NS	-0.134**	-0.024NS	0.005NS	-0.061NS	-0.026NS	-0.159**	-0.130**	0.012NS	-0.152**	0.240**	0.048NS	0.206**	0.125**	0.126**	0.209**
NSB	-0.028NS	-0.032NS	-0.069NS	-0.012NS	-0.006NS	-0.072NS	-0.150**	-0.273**	-0.160**	0.031NS	-0.165**	0.216**	0.015NS	0.223**	0.064NS	0.114*	0.149**
BP	0.069NS	0.071NS	0.038NS	-0.006NS	-0.000NS	0.061NS	0.228**	0.223**	0.152**	-0.152**	0.189**	-0.253**	-0.135**	-0.186**	-0.059NS	-0.081NS	-0.201**
GH	0.016NS	-0.009NS	-0.034NS	-0.016NS	-0.020NS	-0.063NS	0.196**	0.131**	0.065NS	-0.034NS	0.048NS	0.050NS	-0.033NS	-0.019NS	-0.028NS	0.150**	0.058NS
LS	0.147**	0.234**	0.207**	0.017NS	0.080NS	0.180**	-0.139**	-0.274**	-0.072NS	-0.051NS	-0.232**	0.172**	-0.033NS	0.131**	0.056NS	0.084NS	0.092NS
LC	-0.041NS	-0.090NS	-0.205**	-0.067NS	-0.032NS	-0.265**	-0.137**	-0.104*	-0.119*	0.026NS	-0.079NS	0.050NS	-0.062NS	0.050NS	-0.081NS	0.055NS	0.069NS
LL	-0.185**	-0.218**	-0.274**	-0.128**	-0.158**	-0.285**	-0.053NS	0.102*	-0.080NS	0.188**	-0.030NS	0.068NS	0.061NS	-0.045NS	-0.025NS	-0.040NS	0.053NS
LW	-0.178**	-0.243**	-0.259**	-0.131**	-0.153**	-0.285**	0.081NS	0.207**	0.029NS	0.078NS	0.184**	-0.117*	0.040NS	-0.122*	-0.037NS	-0.055NS	-0.052NS
DORM	0.045NS	0.088NS	0.099*	0.076NS	0.065NS	0.160**	0.049NS	0.018NS	0.075NS	-0.045NS	-0.000NS	-0.031NS	-0.050NS	0.012NS	0.017NS	-0.032NS	0.020NS
SCMR	0.009NS	0.028NS	0.024NS	-0.010NS	-0.016NS	0.031NS	-0.019NS	0.010NS	0.074NS	0.075NS	-0.014NS	0.090NS	0.017NS	0.043NS	-0.064NS	0.095*	0.017NS
OIL	-0.117*	-0.184**	-0.186**	-0.129**	-0.187**	-0.148**	0.157**	0.183**	0.189**	0.015NS	0.172**	-0.158**	-0.052NS	-0.190**	0.059NS	-0.041NS	-0.108*
PROTEIN	-0.075NS	-0.152**	-0.180**	-0.104*	-0.135**	-0.162**	0.039NS	0.086NS	0.172**	-0.041NS	0.097*	-0.258**	-0.207**	-0.196**	-0.113*	-0.052NS	-0.202**
ARA	0.032NS	0.046NS	0.084NS	-0.015NS	-0.002NS	0.034NS	0.136**	-0.058NS	0.127**	-0.409**	0.092NS	-0.406**	-0.416**	-0.128**	-0.066NS	-0.091NS	-0.359**
BEH	0.029NS	-0.001NS	0.043NS	0.010NS	-0.016NS	-0.004NS	0.085NS	-0.055NS	0.163**	-0.288**	0.136**	-0.380**	-0.265**	-0.177**	-0.106*	-0.133**	-0.323**
ECO	-0.050NS	-0.110*	-0.148**	-0.077NS	-0.116*	-0.019NS	0.151**	0.129**	0.050NS	0.057NS	0.042NS	0.051NS	0.154**	-0.080NS	0.030NS	-0.016NS	0.021NS
LIG	-0.133**	-0.195**	-0.238**	-0.163**	-0.202**	-0.155**	0.132**	0.150**	0.106*	0.060NS	0.113*	-0.013NS	0.125**	-0.146**	0.050NS	-0.049NS	-0.048NS
LIN	-0.045NS	-0.090NS	-0.017NS	-0.041NS	-0.061NS	-0.109*	0.064NS	-0.000NS	0.089NS	-0.203**	0.155**	-0.394**	-0.201**	-0.224**	-0.105*	-0.187**	-0.274**
OLE	0.005NS	0.048NS	-0.029NS	-0.009NS	0.023NS	0.027NS	-0.055NS	-0.022NS	-0.105*	0.109*	-0.132**	0.300**	0.107*	0.173**	0.068NS	0.144**	0.178**
PAL	-0.110*	-0.168**	-0.135**	-0.067NS	-0.104*	-0.193**	-0.047NS	0.070NS	0.011NS	0.117*	0.093NS	-0.104*	-0.007NS	-0.093NS	-0.000NS	-0.065NS	-0.009NS
STE	0.093NS	0.126**	0.149**	0.063NS	0.072NS	0.130**	0.079NS	-0.150**	0.057NS	-0.439**	0.048NS	-0.381**	-0.374**	-0.019NS	-0.081NS	-0.097*	-0.370**
O/L	0.021NS	0.070NS	-0.006NS	0.020NS	0.042NS	0.067NS	-0.063NS	-0.011NS	-0.102*	0.154**	-0.151**	0.355**	0.149**	0.200**	0.089NS	0.170**	0.237**

:** Significant at 0.05 level of probability, *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

Table 15b: Correlation coefficients for agronomic, taxonomic, productivity, physiological and nutritional, traits in the RILs of TMV 2 × TMV 2-NLM

	Days to 50 per cent flowering	Plant height (cm)	Number of primary branches (cm)	Number of secondary branches (cm)	Branching pattern	Growth habit	Leaflet shape	Leaflet colour	Leaflet length (cm)	Leaflet width (cm)	Seed dormancy	Relative chlorophyll content (µg/cm2)	Oil content	Protein content	Arachidic acid	Behenic acid	Eicosenoic acid	Lignoseric acid	Linoleic acid	Oleic acid	Palmitic acid	Stearic acid
50 % F	1.000																					
PH	0.014^{NS}	1.000																				
NPB	0.533**	0.202**	1.000																			
NSB	0.554**	0.143**	0.699**	1.000																		
BP	-0.608*	-0.071^{NS}	-0.556**	-0.646**	1.000																	
GH	-0.030^{NS}	0.242**	0.198**	-0.013^{NS}	0.037^{NS}	1.000																
LS	0.208**	0.013^{NS}	0.277**	0.352**	-0.339**	0.057^{NS}	1.000															
LL	-0.040^{NS}	0.144**	-0.061^{NS}	0.018^{NS}	0.095*	0.028^{NS}	-0.242**	1.000														
LW	-0.206**	0.075^{NS}	-0.209**	-0.253**	0.266**	-0.045^{NS}	-0.616**	0.536**	1.000													
DORM	0.063^{NS}	0.009^{NS}	-0.036^{NS}	-0.049^{NS}	0.079^{NS}	-0.021^{NS}	-0.006^{NS}	0.016^{NS}	0.025^{NS}	1.000												
SCMR	-0.033^{NS}	0.023^{NS}	0.044^{NS}	0.066^{NS}	-0.060^{NS}	0.055^{NS}	0.103*	-0.071^{NS}	-0.129**	0.120*	1.000											
OIL	-0.034^{NS}	-0.025^{NS}	-0.084^{NS}	-0.058^{NS}	0.033^{NS}	-0.038^{NS}	-0.171**	0.162**	0.171**	0.092^{NS}	-0.053^{NS}	1.000										
PROT	-0.169**	-0.222**	-0.228**	-0.196**	0.166**	-0.040^{NS}	-0.179**	0.149**	0.144**	-0.014^{NS}	-0.072^{NS}	0.378**	1.000									
ARA	-0.143**	-0.245**	-0.130**	-0.079^{NS}	0.111*	-0.120*	-0.076^{NS}	-0.045^{NS}	0.045^{NS}	0.040^{NS}	-0.082^{NS}	0.230**	0.455**	1.000								
BEH	-0.188**	-0.255**	-0.210**	-0.179**	0.114*	-0.140**	-0.126**	-0.075^{NS}	0.094*	0.039^{NS}	-0.112*	0.289**	0.468**	0.711**	1.000							
ECO	-0.066^{NS}	0.126**	0.041^{NS}	-0.039^{NS}	0.007^{NS}	0.110*	0.016^{NS}	0.018^{NS}	0.019^{NS}	0.087^{NS}	0.101*	0.212**	0.015^{NS}	-0.311**	-0.143**	1.000						
LIG	-0.012^{NS}	0.073^{NS}	0.076^{NS}	-0.008^{NS}	-0.006^{NS}	0.081^{NS}	-0.035^{NS}	0.024^{NS}	0.042^{NS}	0.063^{NS}	0.106*	0.306**	0.009^{NS}	-0.273**	-0.095*	0.850**	1.000					
LIN	-0.129**	-0.237**	-0.248**	-0.173**	0.137**	-0.099*	-0.172**	0.026^{NS}	0.187**	0.023^{NS}	-0.099*	0.247**	0.346**	0.379**	0.674**	-0.244**	-0.199**	1.000				
OLE	0.154**	0.207**	0.246**	0.176**	-0.124**	0.126**	0.156**	0.003^{NS}	-0.164**	-0.060^{NS}	0.104*	-0.288*	-0.350**	-0.385**	-0.721**	0.206**	0.208**	-0.958**	1.000			
PAL	-0.052^{NS}	-0.183**	-0.144**	-0.086^{NS}	0.057^{NS}	-0.075^{NS}	-0.128**	0.183**	0.215**	-0.009^{NS}	-0.066^{NS}	0.294**	0.262**	-0.029^{NS}	0.313**	-0.157**	-0.096*	0.764**	-0.772**	1.000		
STE	-0.112*	-0.168**	-0.130**	-0.091^{NS}	0.118*	-0.106*	-0.045^{NS}	-0.089^{NS}	0.018^{NS}	-0.062^{NS}	-0.086^{NS}	-0.013^{NS}	0.302**	0.651**	0.462**	-0.430**	-0.484**	0.312**	-0.288**	0.027^{NS}	1.000	
O/L	0.159**	0.227**	0.261**	0.191**	-0.134**	0.111*	0.178**	-0.003^{NS}	-0.184**	-0.039^{NS}	0.099*	-0.268**	-0.350**	-0.367**	-0.685**	0.214**	0.192**	-0.980**	0.977**	-0.772**	-0.294**	**1.000**

:** Significant at 0.05 level of probability, *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

Table 16: Performance of superior RILs from TMV 2 × TMV 2-NLM mapping population

SN	RIL	Pod yield (kg/ha),	Number of pods per plant	Shelling percentage (%)	Test weight	Sound mature kernel weight	Late leaf spot at 90 DAS	Rust at 90 DAS	Days to 50 per cent flowering	Seed dormancy	Oil content	Protein content	Oleic acid	Oleic to linoleic acid ratio	Pod constriction	Pod reticulation	Pod beak and	Pod size
1	2-19(f)	6,508.52	22.39	69.42	48.02	98.23	7.50	7.00	33.25	3.00	44.99	29.14	54.64	1.99	Moderate	Prominent	Slight	Medium
2	1-31(f)	5,849.89	14.00	72.18	46.38	97.42	7.00	5.50	33.50	3.50	45.20	31.80	45.75	1.36	Moderate	Slight	Slight	Medium
3	2-14(a)(i)	5,471.71	13.58	71.84	49.53	97.47	7.25	4.50	31.00	1.00	43.35	28.59	46.49	1.41	Slight	Moderate	Absent	Large
4	2-24(c)	5,561.45	18.80	70.63	55.44	97.93	3.50	4.00	35.00	0.00	46.09	31.10	57.14	2.44	Moderate	Moderate	Moderate	Large
5	2-14(a)(ii)	5,597.27	20.28	70.02	42.73	99.90	7.00	5.25	31.00	1.50	46.08	28.25	47.80	1.49	Moderate	Moderate	Slight	Large
6	2-33(a)	5,387.88	22.68	72.56	35.38	98.97	5.00	5.50	31.50	0.00	48.45	29.40	47.58	1.45	Moderate	Slight	Slight	Medium
7	2-13(a)	5,851.11	17.88	66.09	39.82	98.78	7.00	6.50	33.00	3.50	47.62	33.56	40.65	1.10	Moderate	Slight	Slight	Medium
8	2-29(g)	5,234.94	22.08	73.14	50.08	98.14	6.75	6.75	31.00	3.00	47.65	30.44	48.52	1.57	Moderate	Slight	Slight	Large
9	2-76(b)	5,364.43	15.65	70.99	56.54	98.92	4.75	3.50	35.25	0.00	44.12	28.08	46.25	1.37	Slight	Slight	Absent	Large
10	2-45(a)	5,209.09	18.80	73.09	58.25	99.06	1.75	4.75	31.00	0.00	46.67	32.79	47.90	1.58	Moderate	Slight	Slight	Large
11	1-11(b)	5,027.00	10.17	75.71	52.89	99.11	7.00	5.75	31.25	4.00	44.96	31.94	49.08	1.63	Moderate	Moderate	Slight	Medium
12	2-60(f)	5,573.46	22.30	68.11	47.34	95.04	6.75	6.75	34.00	0.00	45.93	30.63	50.26	1.67	Moderate	Slight	Slight	Large
13	2-5 (c)	5,033.05	18.98	73.45	31.30	96.31	7.50	6.75	32.50	0.00	49.60	31.36	53.39	1.83	Moderate	Slight	Slight	Medium
14	2-72(f)	4,925.06	19.20	75.01	41.01	97.72	8.00	7.00	32.00	0.00	47.45	34.83	37.84	1.02	Moderate	Slight	Slight	Medium
15	2-23(c)	5,309.72	20.13	68.89	45.37	98.67	7.25	7.00	35.00	3.00	46.60	32.05	51.26	1.75	Moderate	Slight	Slight	Medium
	TMV 2	4,883.52	24.59	74.12	36.25	95.84	7.13	6.25	32.50	2.75	46.58	32.13	42.48	1.20	Moderate	Slight	Slight	Medium

to 50 per cent flowering (early), test weight, sound mature kernel weight, oleic acid, and O/L ratio. RILs 2-14(a)(ii), 2-29(g), 2-33(a) and 2-23(c) were superior over TMV 2 for pod yield (kg/ha), oil content, oleic acid, test weight, sound mature kernel weight and days to 50 per cent flowering (early).

Of these 15 RILs, four foliar disease resistant lines [2-45 (a), 2-25 (a), 2-14(a)(i) and 2-76(b)] were subjected for ddRAD-Seq, and compared with TMV 2 at nearly 28 Mb random nucleotide positions. RIL 2-45 (a) showed the highest similarity (only 4 SNP) with TMV 2 followed by 2-25 (a) (5 SNP), 2-14(a)(i) (8 SNP) and 2-76(b) (30 SNP). At Aradu.A01_2581365, Aradu.A06_112199516, Araip.B02_34272578 and Araip.B10_2552983 SNP sites, the four-foliar disease resistant lines shared the same nucleotide in contrast to TMV 2 (Table 6).

4.4 Association studies using a mutant population

The association panel consisted of 98 genotypes representing the parents and mutants. Many of the mutants were independent in origin. For example, 49, 18, 11, 4 and 2 mutants originated independently from the parents DER, TAG 24, TG 66, TG 18A and Spanish Improved, respectively. Field evaluation of the mutant population during the rainy seasons of 2014 and 2015 showed significant differences among the genotypes for the taxonomic, agronomic, productivity, nutritional traits along with foliar disease resistance (Table 17). Environmental effect was significant for all the traits except for pod length, palmitic acid and seed dormancy. Genotype × environment (G×E) interactions were significant for disease resistance and most of the agronomic and productivity traits except for the number of secondary branches, leaflet width, seed dormancy and pod yield (kg/ha). G×E interactions were significant for oil and protein content, but non-significant for all fatty acids.

High variability (PCV and GCV) were observed for LLS and rust score at 70, 80 and 90 DAS, number of pods per plant, pod yield per plant, plant height, number of primary and secondary branches, O/L ratio and seed dormancy (Table 18). Genotypes showed normal frequency distribution for all the traits except for the number of primary and secondary branches, and sound mature kernel weight (Table 19, Fig. 10). Productivity traits like pod yield, pod size and sound mature kernel weight were positively and significantly correlated. LLS and rust resistance were also positively and significantly correlated (Table 20a and 20b).

Table 17: ANOVA for disease resistance, productivity, agronomic and nutritional traits in mutant population

Sl. No.	Trait/Source of variation	Genotype (G)	Season (E)	G × E	Pooled error	CV (%)
		97	1	97	194	
1	Days to 50 per cent flowering	34.75**	7209**	8.85**	0.25	3.55
2	Plant height (cm)	28.44**	16.28**	1.49**	11.65	16.37
3	Number of primary branches	7.57**	12.81**	2.67**	1.32	23.44
4	Number of secondary branches	13.35**	2.34**	1.60^{NS}	1.87	24.72
5	Leaflet length (cm)	7.42**	90.45**	1.79**	0.22	12.67
6	Leaflet width (cm)	3.52**	38.58**	1.15^{NS}	0.08	12.86
7	LLS score at 70 DAS	12.84**	158.78**	3.83**	0.46	18.10
8	LLS score at 80 DAS	44.48**	368.36**	12.61**	0.24	24.68
9	LLS score at 90 DAS	35.33**	46.02**	5.20**	0.42	18.40
10	Rust score at 70 DAS	12.58**	293.56**	10.58**	0.24	18.18
11	Rust score at 80 DAS	32.27**	310.18**	8.79**	0.25	19.94
12	Rust score at 90 DAS	30.25**	100.85**	5.92**	0.42	23.40
13	Number of pods per plant	3.23**	61.93**	1.84**	12.01	24.05
14	Pod yield per plant (g)	4.00**	46.65**	1.38^{NS}	999.5	24.71
15	Shelling percentage (%)	3.72**	17.01**	1.60**	12.08	5.43
16	Test weight (g)	17.72**	384.83**	3.50**	14.85	12.53
17	Sound mature kernel weight (g)	1.94**	132.02**	1.72**	7.21	3.13
18	Pod length (cm)	9.95**	0.08^{NS}	1.73**	0.07	10.45
19	Pod width (cm)	7.62**	148.02**	2.40**	0.01	11.29
20	Protein (%)	46.58**	50.23**	2.46**	2.04	6.19
21	Oil (%)	10.55**	64.38**	1.69**	1.91	3.40
22	Palmitic acid (%)	9.99**	0.04^{NS}	1.22^{NS}	0.36	5.18
23	Stearic acid (%)	11.74**	324.15**	1.39^{NS}	0.13	11.56
24	Oleic acid (%)	9.84**	97.71**	1.48^{NS}	10.41	7.40
25	Linoleic acid (%)	8.08**	310.66**	1.48^{NS}	7.33	8.06
26	Arachidic acid (%)	8.79**	197.25**	1.25^{NS}	0.03	10.29
27	Eicosenoic acid (%)	8.96**	46.78**	1.26^{NS}	0.00	6.05
28	Behenic acid (%)	11.23**	44.45**	1.45^{NS}	0.05	6.41
29	Lignoseric acid (%)	8.38**	27.35**	1.31^{NS}	0.01	6.24
30	Oleic to linoleic acid ratio	8.87**	60.30**	1.45^{NS}	0.05	17.33
31	Seed dormancy	20.95**	0.11^{NS}	0.06^{NS}	0.45	15.39

:** Significant at 0.05 level of probability and *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

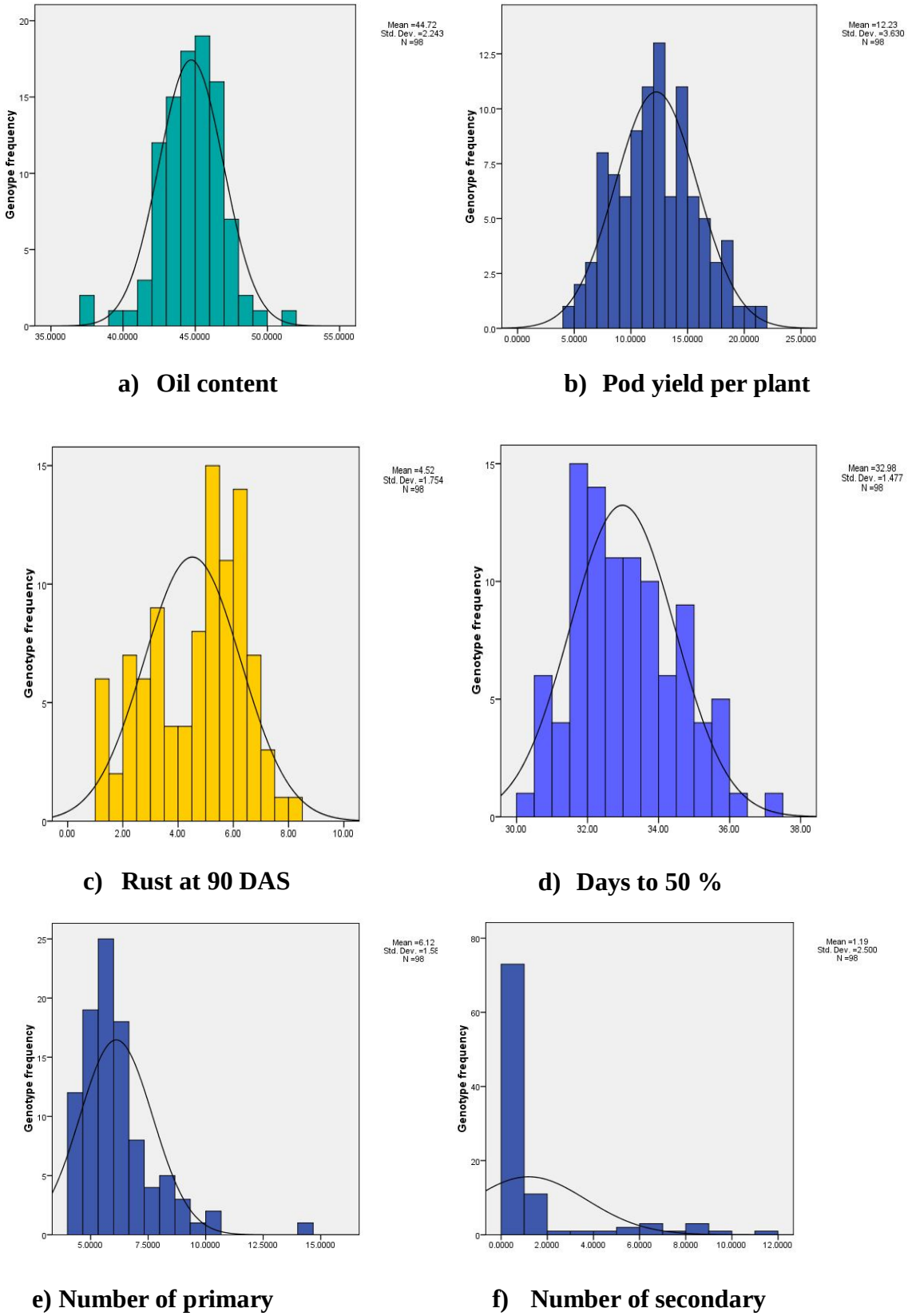
Table 18: Mean, range and genetic variability components for agronomic, disease resistance, productivity and nutritional traits in mutant population

Sl. No.	Trait	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GAM (%)
			Min	Max					
1	Days to 50 per cent flowering	33.00	30.00	37.25	5.45	4.13	57.50	2.73	8.26
2	Plant height (cm)	24.73	9.08	43.42	39.44	35.88	82.80	21.31	86.17
3	Number of primary branches	6.11	4.08	14.67	32.90	23.07	49.20	2.61	42.73
4	Number of secondary branches	1.19	0.00	11.33	236.55	200.37	71.80	5.33	94.07
5	Leaflet length (cm)	4.20	2.45	5.55	18.81	13.90	54.60	1.14	27.12
6	Leaflet width (cm)	2.18	1.45	2.83	16.42	10.21	38.70	0.37	16.77
7	LLS score at 70 DAS	2.48	1.00	5.25	58.90	44.91	58.10	2.25	90.41
8	LLS score at 80 DAS	4.13	1.00	6.75	46.25	37.79	66.70	3.37	81.49
9	LLS score at 90 DAS	5.59	1.00	8.25	37.91	33.14	76.40	4.28	76.49
10	Rust score at 70 DAS	2.08	1.00	4.00	59.26	34.36	33.60	1.10	52.60
11	Rust score at 80 DAS	3.21	1.00	6.00	51.87	42.36	66.70	2.94	91.30
12	Rust score at 90 DAS	4.49	1.00	8.00	44.29	37.60	72.10	3.79	84.29
13	Number of pods per plant	14.01	7.57	23.17	32.93	17.26	27.50	3.34	23.88
14	Pod yield per plant (g)	12.26	4.70	21.67	39.63	25.27	40.70	5.22	42.54
15	Shelling percentage (%)	70.08	59.50	77.09	6.71	3.93	34.40	4.27	6.09
16	Test weight (g)	41.85	21.44	56.12	22.21	18.34	68.20	3.83	40.00
17	Sound mature kernel weight (g)	96.99	88.59	100.00	3.33	1.13	11.60	0.99	1.02
18	Pod length (cm)	2.90	1.81	3.70	17.13	13.58	62.80	0.82	28.43
19	Pod width (cm)	1.23	0.86	1.81	16.47	11.99	53.00	0.28	23.04
20	Protein (%)	27.18	16.55	34.07	18.75	17.70	89.10	11.98	44.09
21	Oil (%)	44.72	37.45	51.04	5.81	4.72	66.00	4.53	10.12
22	Palmitic acid (%)	11.59	8.59	13.65	9.34	7.77	69.20	1.98	17.06
23	Stearic acid (%)	3.25	1.61	4.83	21.15	17.71	70.10	1.27	39.15
24	Oleic acid (%)	45.92	34.44	60.59	12.75	10.38	8.00	17.41	45.92
25	Linoleic acid (%)	33.59	23.76	43.42	13.42	10.73	63.90	7.60	22.63
26	Arachidic acid (%)	1.55	1.05	2.22	17.66	14.35	66.10	0.48	30.80
27	Eicosenoic acid (%)	0.97	0.78	1.15	10.46	8.54	66.50	0.18	18.38
28	Behenic acid (%)	3.37	2.50	4.24	12.08	10.25	71.90	0.77	22.94
29	Lignoseric acid (%)	1.24	0.99	1.49	10.10	7.95	61.80	0.20	16.49
30	Oleic to linoleic acid ratio	1.42	0.83	2.40	27.19	20.95	59.40	0.61	42.63
31	Seed dormancy	1.07	0.00	7.25	150.50	135.50	81.10	3.46	96.30

GCV: Genotypic coefficient of variation, **PCV**: Phenotypic coefficient of variation, $\mathbf{h^2_{bs}}$: Heritability (broad sense), **GA**: Genetic advance, **GAM**: Genetic advance as per cent of mean

Table 19: Frequency distribution of genotypes in the mutant population for the disease resistance, agronomic, productivity and nutritional traits

Sl. No.	Trait	Skewness	Kurtosis	Distribution
1	Days to 50 per cent flowering	0.404	-0.332	Normal
2	Plant height (cm)	-0.081	-0.895	Normal
3	Number of primary branches	2.169	8.106	Skewed kurtosis
4	Number of secondary branches	2.440	5.089	Skewed kurtosis
5	Leaflet length (cm)	-0.309	-0.093	Normal
6	Leaflet width (cm)	-0.376	0.240	Normal
7	LLS score at 70 DAS	0.326	-1.080	Normal
8	LLS score at 80 DAS	-0.535	-0.867	Normal
9	LLS score at 90 DAS	-0.773	-0.399	Normal
10	Rust score at 70 DAS	0.283	-1.013	Normal
11	Rust score at 80 DAS	-0.085	-1.090	Normal
12	Rust score at 90 DAS	-0.411	-0.805	Normal
13	Number of pods per plant	0.556	0.107	Normal
14	Pod yield per plant (g)	0.121	-0.082	Normal
15	Shelling percentage (%)	-0.433	0.567	Normal
16	Test weight (cm)	-0.316	-0.656	Normal
17	Sound mature kernel weight (g)	-1.727	4.447	Kurtosis
18	Pod length (cm)	-0.327	-0.254	Normal
19	Pod width (cm)	0.422	0.735	Normal
20	Protein (%)	-0.819	-0.833	Normal
21	Oil (%)	-0.379	1.336	Normal
22	Palmitic acid (%)	-1.039	1.235	Normal
23	Stearic acid (%)	-0.666	0.440	Normal
24	Oleic acid (%)	-0.023	0.406	Normal
25	Linoleic acid (%)	-0.067	0.725	Normal
26	Arachidic acid (%)	0.472	-0.097	Normal
27	Eicosenoic acid (%)	-0.072	-0.534	Normal
28	Behenic acid (%)	0.232	0.142	Normal
29	Lignoseric acid (%)	0.287	-0.411	Normal
30	Oleic to linoleic acid ratio	1.031	1.809	Normal
31	Seed dormancy	1.615	2.907	Normal



a) Oil content **b) Pod yield per plant**

c) Rust at 90 DAS **d) Days to 50 %**

e) Number of primary **f) Number of secondary**

Fig. 10: Frequency distribution of genotypes in mutant population

Table 20a: Correlation coefficients for disease resistance, productivity, agronomic, taxonomic, and nutritional traits in the mutant population

	Late leaf spot score at 70 DAS	Late leaf spot score at 80 DAS	Late leaf spot score at 90 DAS	Rust score at 70 DAS	Rust score at 80 DAS	Rust score at 90 DAS	Number of pods per plant	Pod yield per plant	Shelling percentage (%)	Test weight	Sound mature kernel weight	Pod length	Pod width	Pod constriction	Pod reticulation	Seeds per pod	Pod beak	Pod size	Kernel colour	Seed shape	Main stem flowering	Growth habit	Leaf let shape
LLS 70	1.000																						
LLS 80	0.811**	1.000																					
LLS 90	0.750**	0.933**	1.000																				
R 70	0.414**	0.540**	0.562**	1.000																			
R 80	0.349**	0.584**	0.603**	0.829**	1.000																		
R 90	0.346**	0.540**	0.580**	0.798**	0.927**	1.000																	
NPPP	-0.233*	-0.177NS	-0.140NS	0.032NS	0.007NS	0.049NS	1.000																
PYPP	-0.144NS	-0.168NS	-0.202*	-0.083NS	-0.177NS	-0.166NS	0.404**	1.000															
SP	-0.206*	-0.140NS	-0.067NS	-0.030NS	-0.006NS	-0.003NS	0.380**	-0.067NS	1.000														
TW	0.103NS	0.152NS	0.142NS	0.174NS	0.170NS	0.184NS	-0.269**	0.420**	-0.213*	1.000													
SMKW	-0.119NS	-0.181NS	-0.172NS	-0.101NS	-0.116NS	-0.082NS	0.138NS	0.380**	0.270**	0.377**	1.000												
PL	0.215*	0.340**	0.362**	0.289**	0.316**	0.291**	-0.123NS	0.260**	-0.314**	0.664**	0.133NS	1.000											
PW	0.009NS	-0.039NS	-0.087NS	-0.075NS	-0.134NS	-0.190NS	-0.401**	0.465**	-0.399**	0.707**	0.270**	0.424**	1.000										
PC	0.124NS	0.147NS	0.203*	0.337**	0.401**	0.480**	0.162NS	-0.029NS	-0.010NS	0.264**	-0.044NS	0.309**	-0.147NS	1.000									
PR	0.135NS	-0.020NS	-0.032NS	-0.159NS	-0.142NS	-0.158NS	0.009NS	0.178NS	-0.078NS	-0.052NS	-0.043NS	0.017NS	0.043NS	-0.051NS	1.000								
SPP	0.050NS	0.005NS	0.010NS	-0.288**	-0.342**	-0.415**	-0.275**	0.265**	-0.151NS	0.162NS	0.160NS	0.286**	0.394**	-0.421**	0.276**	1.000							
PB	0.083NS	0.220*	0.257*	0.258*	0.357**	0.369**	0.218*	0.002NS	0.154NS	0.171NS	-0.052NS	0.372**	-0.162NS	0.509**	0.216*	-0.166NS	1.000						
PS	0.198NS	0.309**	0.325**	0.200*	0.199*	0.156NS	-0.251*	0.348**	-0.283**	0.685**	0.140NS	0.829**	0.542**	0.152NS	0.115NS	0.454**	0.236*	1.000					
KC	-0.240*	-0.331**	-0.365**	-0.268**	-0.344**	-0.296**	0.109NS	0.037NS	0.034NS	-0.149NS	0.002NS	-0.096NS	-0.065NS	0.023NS	0.114NS	-0.127NS	-0.000NS	-0.113NS	1.000				
SS	0.090NS	-0.010NS	-0.012NS	0.135NS	0.106NS	0.100NS	-0.079NS	-0.040NS	-0.108NS	-0.034NS	0.040NS	-0.085NS	0.027NS	0.162NS	0.303**	-0.107NS	0.081NS	-0.121NS	0.159NS	1.000			
MSF	0.188NS	0.206*	0.139NS	-0.042NS	-0.097NS	-0.082NS	0.133NS	0.018NS	0.025NS	-0.150NS	-0.059NS	0.061NS	-0.082NS	0.119NS	-0.030NS	-0.005NS	0.039NS	0.050NS	0.095NS	0.019NS	1.000		
GH	-0.178NS	-0.084NS	-0.079NS	0.113NS	0.124NS	0.165NS	-0.174NS	-0.064NS	-0.085NS	0.010NS	0.005NS	0.055NS	-0.023NS	0.174NS	0.081NS	0.005NS	0.077NS	-0.013NS	-0.110NS	0.139NS	-0.066NS	1.000	
LS	-0.001NS	0.116NS	0.163NS	0.033NS	0.085NS	0.074NS	0.033NS	-0.033NS	-0.032NS	0.027NS	0.016NS	-0.027NS	-0.070NS	0.024NS	-0.188NS	-0.086NS	-0.073NS	-0.076NS	-0.115NS	-0.115NS	-0.217*	0.017NS	1.000
LC	-0.323**	-0.403**	-0.360**	-0.281**	-0.209*	-0.232*	-0.049NS	0.178NS	-0.116NS	0.078NS	0.109NS	-0.056NS	0.212*	-0.042NS	-0.189NS	0.037NS	-0.209*	-0.050NS	0.013NS	-0.179NS	-0.036NS	0.170NS	-0.001NS
LL	-0.122NS	-0.278**	-0.299**	-0.226*	-0.293**	-0.289**	-0.145NS	0.435**	-0.198NS	0.270**	0.233*	0.039NS	0.492**	-0.298**	0.276**	0.403**	-0.175NS	0.230*	-0.054NS	0.104NS	-0.057NS	0.160NS	-0.028NS
LW	0.084NS	-0.096NS	-0.138NS	-0.153NS	-0.232*	-0.212*	-0.120NS	0.470**	-0.266**	0.247*	0.147NS	0.068NS	0.434**	-0.115NS	0.294**	0.365**	-0.102NS	0.280**	-0.116NS	0.029NS	0.126NS	0.122NS	-0.176NS
50 % F	0.128NS	0.085NS	0.035NS	0.134NS	0.127NS	0.057NS	-0.160NS	-0.200*	0.129NS	-0.129NS	-0.120NS	-0.264**	-0.112NS	-0.109NS	-0.090NS	-0.008NS	-0.138NS	-0.177NS	-0.059NS	0.305**	0.030NS	0.102NS	-0.106NS
PH	-0.087NS	0.066NS	0.060NS	-0.036NS	-0.124NS	-0.157NS	0.002NS	-0.176NS	0.011NS	-0.150NS	-0.094NS	-0.025NS	-0.145NS	-0.058NS	-0.047NS	-0.011NS	0.040NS	-0.049NS	0.011NS	-0.072NS	0.043NS	-0.080NS	0.027NS
NPB	0.042NS	0.045NS	0.062NS	-0.008NS	0.020NS	0.042NS	0.046NS	0.013NS	0.038NS	0.151NS	0.107NS	0.113NS	0.024NS	0.073NS	-0.002NS	-0.101NS	0.079NS	0.074NS	-0.010NS	-0.086NS	0.051NS	-0.066NS	-0.015NS
NSB	-0.125NS	-0.053NS	0.022NS	0.105NS	0.162NS	0.144NS	-0.105NS	-0.074NS	0.074NS	0.063NS	-0.002NS	-0.002NS	0.001NS	-0.109NS	-0.090NS	-0.008NS	-0.027NS	-0.035NS	-0.059NS	-0.051NS	-0.341**	0.102NS	0.456**
DORM	-0.090NS	-0.206*	-0.280**	-0.289**	-0.322**	-0.325**	-0.077NS	0.491**	-0.252*	0.155NS	0.118NS	-0.131NS	0.432**	-0.278**	0.403**	0.270**	-0.191NS	0.080NS	-0.039NS	0.110NS	-0.025NS	0.046NS	-0.031NS
OIL	-0.188NS	-0.158NS	-0.175NS	0.122NS	0.141NS	0.181NS	0.136NS	0.048NS	0.024NS	0.100NS	0.016NS	-0.041NS	-0.037NS	0.007NS	-0.125NS	-0.261**	0.048NS	-0.112NS	-0.036NS	-0.213*	-0.628**	0.031NS	0.137NS
PROT	-0.238*	-0.201*	-0.256*	-0.100NS	-0.036NS	-0.075NS	-0.104NS	-0.094NS	-0.065NS	-0.044NS	-0.056NS	-0.170NS	0.061NS	-0.244*	0.090NS	-0.143NS	-0.109NS	-0.176NS	0.142NS	0.031NS	-0.560**	0.085NS	0.143NS
ARA	-0.050NS	-0.149NS	-0.205*	-0.208*	-0.210*	-0.228*	-0.131NS	0.380**	-0.280**	0.085NS	-0.071NS	-0.095NS	0.364**	-0.199*	0.385**	0.247*	-0.114NS	0.054NS	-0.080NS	0.110NS	-0.025NS	0.271**	0.026NS
BEH	0.114NS	-0.007NS	-0.047NS	-0.121NS	-0.130NS	-0.149NS	-0.166NS	-0.035NS	-0.091NS	-0.134NS	-0.010NS	-0.140NS	0.056NS	-0.067NS	0.173NS	0.134NS	-0.172NS	-0.098NS	-0.082NS	0.131NS	0.073NS	0.031NS	0.012NS
ECO	-0.243*	-0.357**	-0.403**	-0.287**	-0.250*	-0.255*	0.235*	0.139NS	0.242*	-0.239*	0.109NS	-0.262**	-0.191NS	-0.025NS	0.084NS	-0.072NS	0.020NS	-0.206*	0.169NS	-0.134NS	0.005NS	-0.012NS	-0.134NS
LIG	0.201*	0.334**	0.304**	0.277**	0.350**	0.333**	-0.186NS	0.003NS	-0.094NS	0.228*	-0.044NS	0.038NS	0.145NS	0.024NS	-0.136NS	0.043NS	0.008NS	0.144NS	-0.805**	-0.159NS	-0.018NS	0.132NS	0.071NS
LIN	0.254*	0.331**	0.328**	0.406**	0.390**	0.354**	0.044NS	-0.360**	0.108NS	-0.353**	-0.102NS	-0.273**	-0.357**	-0.115NS	0.055NS	-0.236*	0.026NS	-0.256*	-0.231*	0.155NS	0.047NS	-0.047NS	-0.017NS
OLE	0.056NS	-0.012NS	-0.027NS	0.077NS	0.003NS	-0.010NS	0.094NS	-0.090NS	0.147NS	-0.444**	0.007NS	-0.549**	-0.235*	-0.333**	0.220*	-0.057NS	-0.221*	-0.382**	-0.150NS	0.134NS	0.060NS	-0.052NS	-0.025NS
PAL	-0.237*	-0.420**	-0.440**	-0.480**	-0.466**	-0.419**	0.034NS	0.116NS	-0.037NS	-0.120NS	-0.023NS	-0.152NS	0.051NS	-0.016NS	0.134NS	-0.083NS	-0.057NS	-0.132NS	0.621**	0.163NS	0.011NS	-0.017NS	-0.025NS
STE	-0.264**	-0.332**	-0.337**	-0.415**	-0.366**	-0.333**	0.127NS	0.018NS	0.030NS	-0.207*	-0.119NS	-0.172NS	-0.156NS	0.072NS	-0.111NS	-0.126NS	-0.022NS	-0.192NS	0.350**	-0.064NS	0.033NS	0.073NS	0.020NS
O/L	0.170NS	0.160NS	0.212*	0.127NS	0.067NS	0.057NS	0.174NS	0.061NS	0.131NS	-0.164NS	0.093NS	-0.085NS	-0.222*	-0.115NS	0.021NS	0.170NS	-0.118NS	-0.036NS	-0.437**	-0.238*	0.055NS	-0.038NS	0.069NS

:** Significant at 0.05 level of probability and *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

Table 20b: Correlation coefficients for agronomic and nutritional traits in the mutant population

Correlation	Leaflet colour	Leaflet length (cm)	Leaflet width (cm)	Days to 50 per cent flowering	Plant height (cm)	Number of primary branches (cm)	Number of secondary branches (cm)	Seed dormancy	Oil content	Protein content	Arachidic acid	Behenic acid	Eicosenoic acid	Lignoseric acid	Linoleic acid	Oleic acid	Palmitic acid	Stearic acid	Oleic to linoleic acid ratio
LC	1.000																		
LL	0.162^{NS}	1.000																	
LW	0.213^{*}	0.733^{**}	1.000																
50 % F	0.061^{NS}	-0.029^{NS}	0.018^{NS}	1.000															
PH	-0.098^{NS}	-0.233^{*}	-0.242^{*}	-0.015^{NS}	1.000														
NPB	-0.067^{NS}	-0.148^{NS}	-0.098^{NS}	-0.017^{NS}	-0.025^{NS}	1.000													
NSB	0.061^{NS}	0.172^{NS}	-0.284^{**}	-0.010^{NS}	-0.015^{NS}	-0.017^{NS}	1.000												
DORM	0.053^{NS}	0.757^{**}	0.693^{**}	-0.057^{NS}	-0.241^{*}	-0.135^{NS}	-0.065^{NS}	1.000											
OIL	-0.024^{NS}	-0.084^{NS}	-0.220^{*}	-0.126^{NS}	-0.034^{NS}	-0.052^{NS}	0.250^{*}	-0.023^{NS}	1.000										
PROT	-0.144^{NS}	0.032^{NS}	-0.135^{NS}	-0.049^{NS}	-0.069^{NS}	-0.082^{NS}	0.207^{*}	0.203^{*}	0.540^{**}	1.000									
ARA	0.050^{NS}	0.703^{**}	0.665^{**}	-0.026^{NS}	-0.253^{*}	-0.118^{NS}	0.008^{NS}	0.889^{**}	-0.079^{NS}	0.208^{*}	1.000								
BEH	-0.052^{NS}	0.229^{*}	0.206^{*}	-0.073^{NS}	-0.103^{NS}	-0.103^{NS}	-0.073^{NS}	0.325^{**}	-0.276^{**}	0.063^{NS}	0.378^{**}	1.000							
ECO	0.189^{NS}	0.149^{NS}	0.202^{*}	-0.035^{NS}	0.035^{NS}	-0.047^{NS}	-0.035^{NS}	0.095^{NS}	-0.014^{NS}	-0.029^{NS}	0.058^{NS}	0.150^{NS}	1.000						
LIG	-0.011^{NS}	0.137^{NS}	0.194^{NS}	0.101^{NS}	-0.051^{NS}	-0.062^{NS}	0.048^{NS}	0.228^{*}	0.047^{NS}	-0.040^{NS}	0.261^{**}	0.111^{NS}	-0.176^{NS}	1.000					
LIN	-0.374^{**}	-0.219^{*}	-0.250^{*}	0.067^{NS}	0.107^{NS}	-0.049^{NS}	0.028^{NS}	-0.194^{NS}	-0.126^{NS}	0.008^{NS}	-0.168^{NS}	0.066^{NS}	-0.178^{NS}	0.244^{*}	1.000				
OLE	-0.238^{*}	0.164^{NS}	0.113^{NS}	0.043^{NS}	-0.028^{NS}	-0.107^{NS}	0.023^{NS}	0.274^{**}	-0.195^{NS}	-0.008^{NS}	0.258^{*}	0.317^{**}	0.142^{NS}	0.244^{*}	0.739^{**}	1.000			
PAL	0.187^{NS}	0.170^{NS}	0.111^{NS}	0.097^{NS}	-0.028^{NS}	-0.049^{NS}	-0.090^{NS}	0.187^{NS}	-0.078^{NS}	0.149^{NS}	0.200^{*}	0.011^{NS}	0.203^{*}	-0.578^{**}	-0.443^{**}	-0.231^{*}	1.000		
STE	0.249^{*}	0.019^{NS}	0.053^{NS}	0.147^{NS}	0.101^{NS}	-0.018^{NS}	-0.072^{NS}	-0.001^{NS}	-0.028^{NS}	-0.025^{NS}	0.069^{NS}	-0.065^{NS}	0.378^{**}	-0.377^{**}	-0.580^{**}	-0.349^{**}	0.774^{**}	1.000	
O/L	-0.122^{NS}	-0.072^{NS}	0.099^{NS}	-0.062^{NS}	0.167^{NS}	-0.003^{NS}	0.040^{NS}	-0.091^{NS}	-0.107^{NS}	-0.331^{**}	-0.076^{NS}	0.075^{NS}	0.330^{**}	0.206^{*}	0.166^{NS}	0.311^{**}	-0.389^{**}	-0.078^{NS}	1.000

:** Significant at 0.05 level of probability and *:** Significant at 0.01 level of probability and NS: Non-significant at 0.05 level of probability

The mutants and their parents were genotyped with 110 AhTE markers to assess marker-trait associations (Plate 3). The allele frequency ranged from 0.50 to 1.00 with a mean of 0.73 across 110 marker loci, indicating that some mutants were heterozygous at a few loci (Table 21). Most of the mutants were homozygous, and the heterozygosity ranged from 0.00 to 0.68 with a mean of 0.02 across the genotypes. The polymorphism information content (PIC) for the AhTE markers ranged from 0.00 to 0.38 with a mean of 0.27, indicating low to moderate ability of the markers to differentiate the genotypes. AhTE0343 and AhTE0372 recorded the highest PIC value followed by a total of 22 markers showing PIC value of 0.37. Fifty markers had a PIC of 0.26 to 0.36. The gene diversity index ranged from 0.00 to 0.50 with an average of 0.35, indicating low to moderate genetic diversity in the population. Four mutant-specific markers were identified in this study for the unique identification. AhTE0012 could differentiate 104-9 VL 1 type from rest of the genotypes. Similarly, AhTE0190 (TGM 221), AhTE0227 [VR 1 (a)] and AhTE0445 (110) were also mutant-specific.

The population structure analysis revealed the presence of the highest ΔK value at K=3 followed by K=7, indicating the presence of three major groups with seven sub-groups in the population (Fig. 11a and 11b). Principal co-ordinate analysis (PCoA) also revealed the presence of seven sub-clusters, which was further supported by radial type of tree diagram generated by hierarchical clustering (Fig. 11c and 11d). Diversity analysis indicated the grouping of mutants derived from each parent in respective subgroups (Table 22). The subgroups II and III consisted of the independent mutants of VL 1 genotype, whereas subgroup VI had the independent mutants of TG 66, and subgroup VII had the independent mutants of TAG 24. It was interesting to note that most of the LLS resistant mutants derived from VL 1 parent were grouped in the subgroup III. When the independent mutants were compared with their respective parents, a wide range of Per cent polymorphism (2.7 to 66.1 %) was observed in all the cases, except for TG 66 (1.8 to 17.1 %).

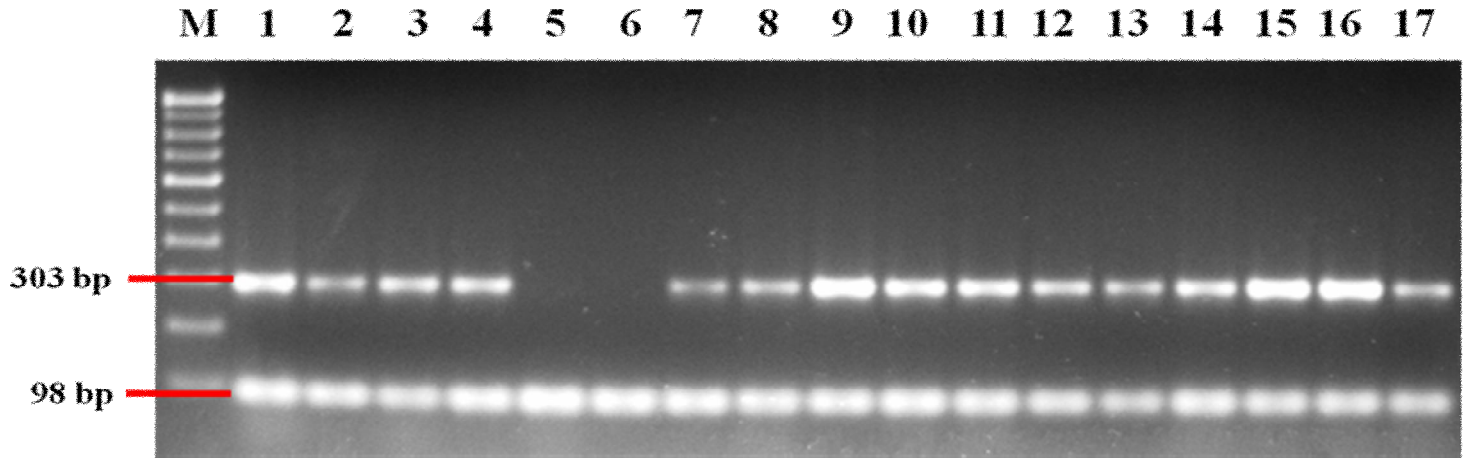


Plate 3: PCR amplification with AhTE0233 among a few genotypes of mutant population

M: 100 bp DNA ladder, **1**: Spanish Improved, **2**: TGM-8, **3**: TGM-14, **4**: TGM-16, **5**: TGM-17, **6**: TGM-19, **7**: TGM-44, **8**: TGM-46, **9**: TGM-47, **10**: TGM-49, **11**: TGM-50, **12**: TGM-51, **13**: TGM-54, **14**: TGM-20, **15**: TGM-25, **16:** TGM-101 and **17:** TGM-111

Table 21: Major allele frequency, gene diversity, heterozygosity and polymorphic information content of AhTE markers used in the mutant population

Sl. No.	Marker	Major allele frequency	Gene diversity	Heterozygosity	Polymorphic information content
1	AhTE0001	0.68	0.43	0.00	0.34
2	AhTE0005	0.86	0.24	0.00	0.21
3	AhTE0006	0.55	0.49	0.00	0.37
4	AhTE0010	0.90	0.18	0.00	0.17
5	AhTE0012	0.99	0.02	0.00	0.02
6	AhTE0025	0.99	0.02	0.00	0.02
7	AhTE0029	1.00	0.00	0.00	0.00
8	AhTE0032	0.65	0.45	0.00	0.35
9	AhTE0045	0.55	0.49	0.00	0.37
10	AhTE0050	0.80	0.32	0.00	0.27
11	AhTE0060	0.96	0.08	0.00	0.08
12	AhTE0074	0.76	0.37	0.00	0.30
13	AhTE0101	0.64	0.46	0.00	0.35
14	AhTE0107	0.83	0.28	0.03	0.24
15	AhTE0113	0.68	0.44	0.03	0.34
16	AhTE0119	0.64	0.46	0.00	0.35
17	AhTE0121	0.64	0.46	0.03	0.36
18	AhTE0129	0.61	0.47	0.00	0.36
19	AhTE0130	0.63	0.47	0.01	0.36
20	AhTE0143	0.60	0.48	0.00	0.36
21	AhTE0148	0.67	0.44	0.00	0.34
22	AhTE0159	0.96	0.08	0.00	0.08
23	AhTE0163	0.70	0.42	0.56	0.33
24	AhTE0164	0.52	0.50	0.05	0.37
25	AhTE0180	0.90	0.18	0.04	0.17
26	AhTE0181	0.51	0.50	0.01	0.37
27	AhTE0189	0.66	0.45	0.00	0.35
28	AhTE0190	0.99	0.02	0.00	0.02
29	AhTE0191	0.64	0.46	0.01	0.36
30	AhTE0202	0.96	0.08	0.00	0.08
31	AhTE0205	0.52	0.50	0.00	0.37
32	AhTE0212	0.54	0.50	0.00	0.37
33	AhTE0218	0.62	0.47	0.01	0.36
34	AhTE0222	0.54	0.50	0.17	0.37
35	AhTE0227	0.99	0.02	0.00	0.02
36	AhTE0232	0.94	0.11	0.00	0.11

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Sl. No.	Marker	Major allele frequency	Gene diversity	Heterozygosity	Polymorphic information content
37	AhTE0233	0.51	0.50	0.00	0.37
38	AhTE0237	0.66	0.45	0.00	0.35
39	AhTE0245	0.72	0.40	0.01	0.32
40	AhTE0248	0.96	0.08	0.02	0.08
41	AhTE0249	0.52	0.50	0.00	0.37
42	AhTE0251	0.54	0.50	0.00	0.37
43	AhTE0254	0.65	0.46	0.01	0.35
44	AhTE0261	0.73	0.39	0.00	0.31
45	AhTE0268	0.97	0.05	0.01	0.05
46	AhTE0278	0.66	0.45	0.02	0.35
47	AhTE0283	0.71	0.41	0.00	0.32
48	AhTE0296	0.70	0.42	0.02	0.33
49	AhTE0303	0.77	0.35	0.01	0.29
50	AhTE0305	0.59	0.48	0.00	0.37
51	AhTE0317	0.86	0.24	0.02	0.21
52	AhTE0324	0.62	0.47	0.00	0.36
53	AhTE0328	0.60	0.48	0.67	0.36
54	AhTE0332	0.92	0.15	0.00	0.14
55	AhTE0333	0.93	0.12	0.01	0.12
56	AhTE0335	0.80	0.32	0.01	0.27
57	AhTE0343	0.50	0.50	0.00	0.38
58	AhTE0357	0.62	0.47	0.00	0.36
59	AhTE0359	0.58	0.49	0.01	0.37
60	AhTE0360	0.54	0.50	0.01	0.37
61	AhTE0361	1.00	0.00	0.00	0.00
62	AhTE0369	0.79	0.33	0.01	0.28
63	AhTE0372	0.50	0.50	0.00	0.38
64	AhTE0373	0.85	0.25	0.01	0.22
65	AhTE0378	0.85	0.25	0.05	0.22
66	AhTE0381	0.73	0.39	0.00	0.31
67	AhTE0391	0.81	0.31	0.00	0.26
68	AhTE0398	0.94	0.11	0.01	0.10
69	AhTE0416	0.69	0.42	0.04	0.33
70	AhTE0417	1.00	0.00	0.00	0.00
71	AhTE0422	0.66	0.45	0.06	0.35
72	AhTE0426	0.64	0.46	0.01	0.36
73	AhTE0429	0.84	0.27	0.00	0.24
74	AhTE0433	0.85	0.26	0.00	0.23
75	AhTE0437	0.75	0.38	0.01	0.30
76	AhTE0442	1.00	0.00	0.00	0.00

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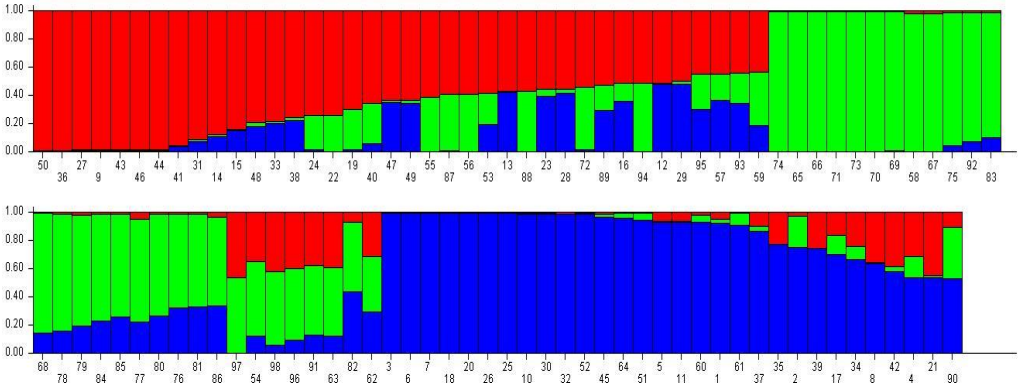
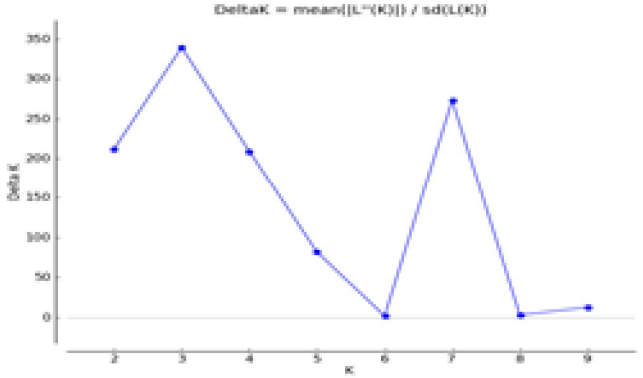
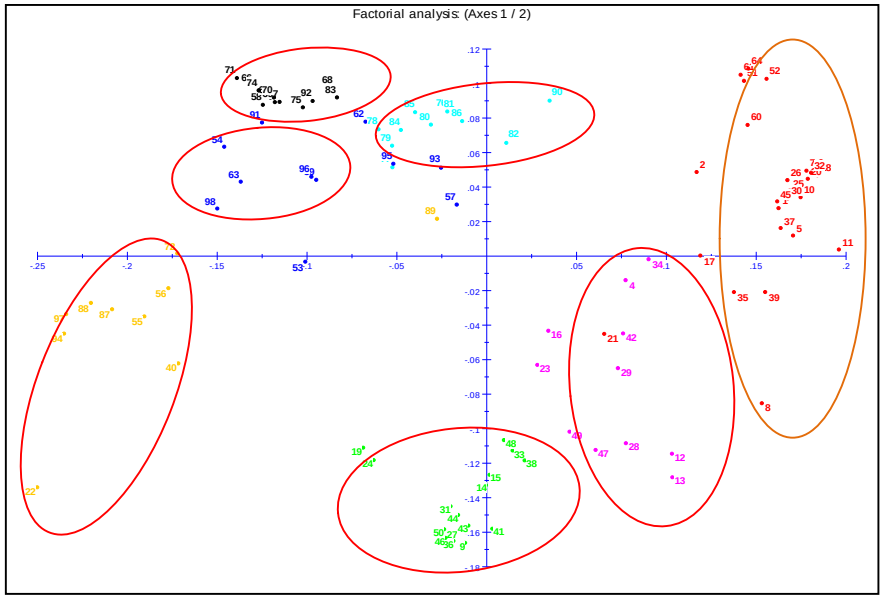
Sl. No.	Marker	Major allele frequency	Gene diversity	Heterozygosity	Polymorphic information content
77	AhTE0445	0.99	0.02	0.00	0.02
78	AhTE0446	0.51	0.50	0.02	0.37
79	AhTE0459	0.77	0.35	0.01	0.29
80	AhTE0465	0.73	0.39	0.00	0.31
81	AhTE0467	0.90	0.18	0.04	0.17
82	AhTE0470	0.68	0.43	0.02	0.34
83	AhTE0477	0.84	0.27	0.00	0.24
84	AhTE0482	0.62	0.47	0.00	0.36
85	AhTE0483	0.90	0.18	0.00	0.17
86	AhTE0486	0.77	0.36	0.00	0.29
87	AhTE0487	0.84	0.27	0.00	0.24
88	AhTE0489	0.61	0.48	0.01	0.36
89	AhTE0491	0.70	0.42	0.02	0.33
90	AhTE0498	0.53	0.50	0.00	0.37
91	AhTE0501	0.56	0.49	0.00	0.37
92	AhTE0504	0.72	0.40	0.00	0.32
93	AhTE0517	0.51	0.50	0.00	0.37
94	AhTE0523	0.90	0.18	0.01	0.16
95	AhTE0524	0.72	0.40	0.00	0.32
96	AhTE0536	0.87	0.23	0.00	0.20
97	AhTE0540	0.90	0.18	0.00	0.17
98	AhTE0547	0.65	0.45	0.00	0.35
99	AhTE0550	0.80	0.32	0.08	0.27
100	AhTE0552	0.55	0.49	0.04	0.37
101	AhTE0563	0.93	0.13	0.00	0.12
102	AhTE0571	0.62	0.47	0.03	0.36
103	AhTE0572	0.86	0.24	0.00	0.21
104	AhTE0586	0.57	0.49	0.00	0.37
105	AhTE0590	0.52	0.50	0.00	0.37
106	AhTE0599	0.63	0.46	0.00	0.36
107	AhTE0607	0.59	0.48	0.00	0.37
108	AhTE0630	0.75	0.38	0.15	0.30
109	AhTE0661	0.53	0.50	0.00	0.37
110	AhTE0674	0.64	0.46	0.00	0.35
	Mean	0.73	0.35	0.02	0.27



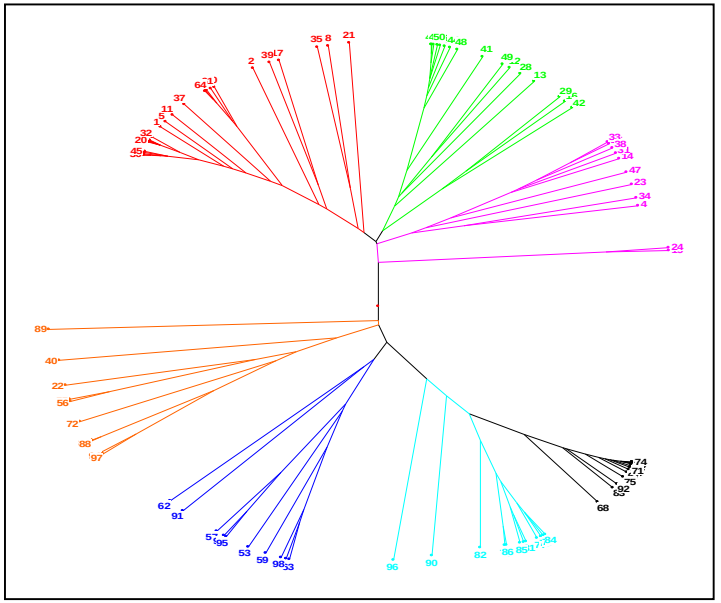
a. Structure plot of mutant population of groundnut at K=3



b. Estimation of delta K value using Evanno's method



c. Principal co-ordinate analysis (PCoA)



d. Grouping of the genotypes based on AhTE marker genotyping data

Subgroup I (DER derivatives)
Subgroup II (VL 1 derivatives)
Subgroup III (VL 1 derivatives)
Subgroup IV (Admixtures)
Subgroup V (Admixtures)
Subgroup VI (TG 66 derivatives)
Subgroup VII (TAG 24 derivatives)

Fig. 11: Population structure and diversity analysis of mutant population

Table 22: Major allele frequency, gene diversity, heterozygosity, polymorphic information content and percent polymorphism in subgroups of mutant population

Sl. No.	Group	Major allele frequency	Gene diversity	Hetero-zygosity	Polymorphism information content	Polymorphism (%)
1	DER	0.80	0.27	0.019	0.22	4.5-66.1
2	VL 1	0.79	0.28	0.020	0.21	2.7-36.6
3	Spanish Improved	0.84	0.22	0.021	0.17	2.7-47.7
4	TAG 24	0.80	0.30	0.035	0.24	4.5-44.1
5	TG 66	0.92	0.10	0.016	0.08	1.8-17.1
6	TG 18A	0.84	0.22	0.022	0.18	33.3-47.7

4.4.1 Marker-trait associations (MTAs)

MTA analysis among 110 markers and 40 traits (mean of two years) identified 132 highly significant MTAs represented by 58 AhTE markers and 39 traits (Table 23, Fig. 12). Highest number of MTAs (38) was detected for nutritional traits, followed by agronomic traits (35), productivity traits (31), foliar disease resistance (23), and taxonomic traits (5). Seventeen MTAs with five traits showed phenotypic variance explained (PVE) of more than 50 per cent. AhTE0501-plant height recorded the highest PVE (69.66 %) followed by AhTE0233-LLS score at 90 DAS (59.39 %), AhTE0504-pod width (53.52 %), AhTE0233-rust score at 90 DAS (52.20 %) and AhTE0674-LLS score at 80 DAS (50.40 %). Further, thirty-seven MTAs with ten traits had a PVE of 30-50 per cent.

Of the 58 AhTE markers showing significant associations, a few were associated with multiple traits. For example, AhTE0523 showed strong association with productivity traits like pod yield, pod size and sound mature kernel weight. Similarly, AhTE0233 showed strong association with LLS and rust resistance.

Of the 58 AhTE markers showing significant associations, 29 were genic with a distribution across 15 chromosomes (Table 24). AhTE0233 marker, with *AhMITE1* transposition site in the exonic region of the gene *Aradu.BZ12G* on chromosome A01, was associated with resistance to LLS and rust, and contents of protein and fatty acids like oleic and linoleic acid. Database search identified a groundnut transcript (GG11555|comp0_c0_seq1) (Clevenger *et al.*, 2016) corresponding to *Aradu.BZ12G*. *Aradu.BZ12G* codes for sterol C4-methyl oxidase 1-2 involved in biosynthesis of sterol and fatty acids.

AhTE0486 showed significant association with LLS resistance as well as growth habit. *AhMITE1* activity was found at 61 bp upstream region of the gene *Aradu.WK4VE* on chromosome A02. This gene was annotated with a transcript Adur41444_comp0_c0_seq2 (Clevenger *et al.*, 2016). *Aradu.WK4VE* codes for 4-coumarate: CoA ligase had catalytic activity and involved in various metabolic processes.

Table 23: Marker-trait associations identified for taxonomic, disease resistance, agronomic, nutritional and productivity traits

Trait	Marker/s with phenotypic variance explained (PVE)	p value	Minor allele frequency (%)
Taxonomic trait			
Main stem flowering	AhTE0335 (14.73 %), AhTE0129 (14.33 %), AhTE0360 (12.28 %), AhTE0498 (10.50 %), AhTE0113 (10.44 %)	0.00-0.04	19.90-32.44
Disease resistance traits			
Late leaf spot at 70 DAS	AhTE0233 (35.88 %), AhTE0674 (35.82 %), AhTE0181 (34.93 %), AhTE0372 (33.25 %), AhTE0523 (33.09 %), AhTE0148 (32.84 %), AhTE0524 (32.79 %)	0.01-0.05	9.69-50.00
Late leaf spot at 80 DAS	AhTE0674 (50.40 %), AhTE0437 (50.025 %), AhTE0523 (49.72 %), AhTE0233 (49.40 %)	0.02-0.04	9.69-48.98
Late leaf spot at 90 DAS	AhTE0233 (59.39 %), AhTE0074 (58.18 %), AhTE0674 (58.09 %), AhTE0486 (57.68 %), AhTE0563 (57.64 %), AhTE0524 (57.43 %)	0.01-0.05	7.14-48.98
Rust at 70 DAS	AhTE0233 (37.68 %), AhTE0005 (35.48 %)	0.01-0.03	14.29-48.98
Rust at 80 DAS	AhTE0233 (46.88 %), AhTE0333 (44.64 %)	0.00-0.02	6.63-48.98
Rust at 90 DAS	AhTE0233 (52.20 %), AhTE0674 (47.72 %)	0.00-0.04	35.71-48.98
Agronomic traits			
Growth habit	AhTE0486 (18.30 %), AhTE0536 (4.57 %), AhTE0391 (3.94 %)	0.02-0.04	13.27-23.47
Seed dormancy	AhTE0181 (26.22 %), AhTE0148 (26.73 %), AhTE0113 (25.94 %), AhTE0433 (23.59 %), AhTE0254 (23.28 %), AhTE0050 (22.86 %)	0.01-0.04	15.31-49.49
Days to 50 per cent flowering	AhTE0261 (19.45 %), AhTE0335 (18.80 %), AhTE0317 (18.51 %)	0.02-0.04	14.29-26.53
Plant height	AhTE0501 (69.66 %), AhTE0148 (69.20 %), AhTE0536 (69.05 %), AhTE0586 (68.99 %), AhTE0599 (68.80 %)	0.01-0.05	13.27-43.88
Number of primary branches	AhTE0501 (13.83 %), AhTE0129 (10.98 %), AhTE0050 (10.66 %), AhTE0489 (10.17 %)	0.01-0.05	20.41-43.88

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Trait	Marker/s with phenotypic variance explained (PVE)	p value	Minor allele frequency (%)
Number of secondary branches	AhTE0489 (19.72 %), AhTE0233 (18.35 %), AhTE0317 (17.84 %), AhTE0129 (17.92 %), AhTE0467 (17.42 %), AhTE0483 (17.15 %)	0.01-0.03	10.20-48.98
Leaflet length	AhTE0317 (49.01 %), AhTE0005 (47.94 %), AhTE0191 (47.87 %)	0.01-0.02	14.29-36.22
Leaflet width	AhTE0547 (42.31 %), AhTE0504 (40.42 %)	0.00-0.02	27.55-34.69
Leaflet colour	AhTE0373 (11.82 %), AhTE0599 (11.67 %)	0.03	14.80-36.73
Leaflet shape	AhTE0459 (11.19 %)	0.00	22.96
Nutritional traits			
Oil content	AhTE0045 (30.87 %)	0.01	44.90
Protein content	AhTE0540 (30.23 %), AhTE0233 (29.34 %), AhTE0674 (28.97 %), AhTE0317 (28.85 %), AhTE0129 (28.56 %), AhTE0459 (28.53 %), AhTE0369 (27.90 %)	0.02-0.05	10.20-48.98
Arachidic acid	AhTE0630 (33.75)	0.00	25.00
Behenic acid	AhTE0630 (46.18)	0.00	25.00
Eicosenoic acid	AhTE0233 (20.19 %), AhTE0630 (19.19 %), AhTE0459 (18.49 %), AhTE0446 (18.39 %), AhTE0572 (17.61 %), AhTE0163 (17.52 %), AhTE0107 (17.21 %)	0.01-0.05	14.29-48.98
Lignoseric acid	AhTE0163 (16.60 %), AhTE0572 (14.33 %)	0.01-0.03	14.2930.10
Linoleic acid	AhTE0459 (19.13 %), AhTE0563 (15.56 %), AhTE0524 (15.46 %), AhTE0233 (14.13 %)	0.00-0.03	7.14-48.98
Oleic acid	AhTE0459 (22.77 %), AhTE0563 (21.34 %), AhTE0524 (19.90 %), AhTE0233 (19.33 %), AhTE0359 (19.22 %)	0.00-0.03	7.14-48.98
Palmitic acid	AhTE0674 (30.23 %), AhTE0524 (11.20 %), AhTE0459 (11.18 %), AhTE0233 (6.15 %)	0.00-0.05	10.20-48.98
Stearic acid	AhTE0343 (23.34 %)	0.04	50.00
Oleic to linoleic acid ratio	AhTE0459 (19.77 %), AhTE0563 (19.65 %), AhTE0524 (18.21 %), AhTE0130 (16.85 %), AhTE0599 (16.69 %)	0.01-0.04	7.14-37.24

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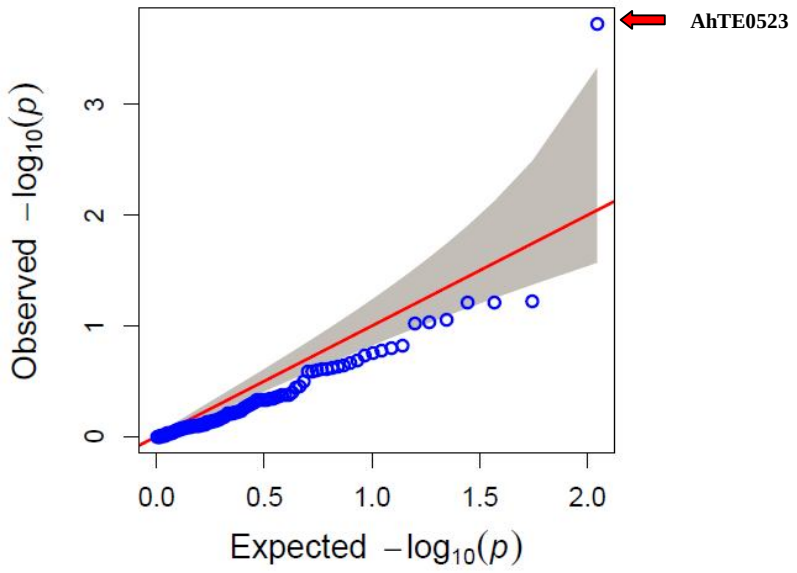
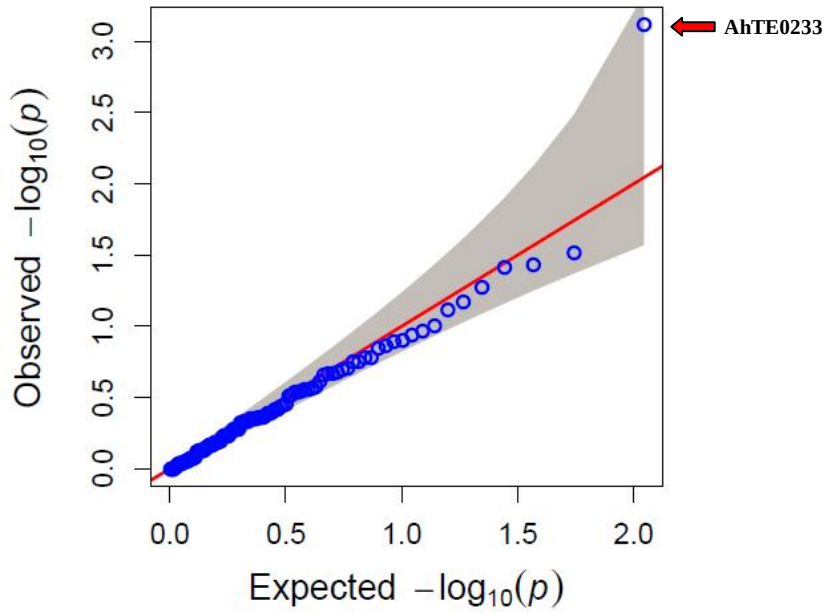
Trait	Marker/s with phenotypic variance explained (PVE)	p value	Minor allele frequency (%)
Productivity traits			
Number of pods per plant	AhTE0491 (17.84 %), AhTE0317 (17.62 %), AhTE0249 (16.77 %)	0.03-0.05	14.29-47.96
Pod yield	AhTE0523 (25.96 %)	0.00	9.69
Shelling percentage	AhTE0477 (14.76 %)	0.05	16.33
Sound mature kernel weight	AhTE0523 (14.29 %), AhTE0524 (11.83 %), AhTE0674 (11.66 %), AhTE0101 (11.41 %)	0.01-0.03	9.69-35.71
Pod constriction	AhTE0674 (36.19 %), AhTE0233 (35.90 %), AhTE0101 (35.88 %), AhTE0107 (35.33 %)	0.02-0.03	16.84-48.98
Pod reticulation	AhTE0674 (21.79 %), AhTE0599 (19.03 %), AhTE0296 (18.66 %)	0.00-0.01	29.59-35.71
Pod beak	AhTE0328 (32.43 %), AhTE0233 (31.37 %), AhTE0674 (30.56 %), AhTE0586 (30.24 %)	0.01-0.05	35.71-48.98
Pod length	AhTE0305 (43.68 %), AhTE0437 (41.97 %)	0.01-0.03	25.00-40.82
Pod width	AhTE0504 (53.52 %), AhTE0278 (53.23 %), AhTE0010 (52.47 %)	0.01-0.03	10.20-33.67
Pod size	AhTE0143 (32.83 %), AhTE0523 (32.17 %), AhTE0398 (31.74 %)	0.02-0.05	5.61-39.80
Seed shape	AhTE0524 (23.58 %), AhTE0459 (23.17 %), AhTE0674 (22.56 %)	0.00	22.96-27.55



A) AhTE0523 with pod yield



B) AhTE0233 with rust score at 90 DAS

Fig. 12: QQ plot showing marker-trait association

Table 24: Prediction and annotation of candidate genes for associated markers

Sl. No.	Marker	Site of insertion	Chrom-osome	Gene	Transcript	Annotation (peanutbase.org)
1	AhTE0005	UTR	A05	*Aradu.94ETY*	Adur18876_comp0_c0_seq1	U-box domain-containing protein 4-like [Glycine max]; IPR016024 (Armadillo-type fold); GO:0005488 (binding), GO:0005515 (protein binding)
2	AhTE0101	Downstream	B09	*Araip.F8RKD*	Aipa20005_comp0_c0_seq2	MYB transcription factor; IPR009057 (Homeodomain-like); GO:0003677 (DNA binding), GO:0003682 (chromatin binding)
3	AhTE0107	Downstream	B04	*Araip.4L2RH*	EZ744843.1	Transmembrane protein, putative
4	AhTE0129	Upstream	B01	*Araip.YRL80*	Aipa52545_comp1_c0_seq1	Cysteine proteinases superfamily protein; IPR013128 (Peptidase C1A); GO:0006508 (proteolysis), GO:0008234 (cysteine-type peptidase activity)
5	AhTE0130	Upstream	B01	*Araip.Q5AP6*	EZ756272.1, Adur8212_comp1_c0_seq14	Calcium-transporting ATPase 8, plasma membrane-type protein; IPR001757 (Cation-transporting P-type ATPase), IPR023214 (HAD-like domain), IPR023298 (P-type ATPase, transmembrane domain), IPR024750 (Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain); GO:0000166 (nucleotide binding), GO:0005388 (calcium-transporting ATPase activity), GO:0005516 (calmodulin binding), GO:0005524 (ATP binding), GO:0006812 (cation transport), GO:0016020 (membrane), GO:0016021 (integral component of membrane), GO:0019829 (cation-transporting ATPase activity), GO:0046872 (metal ion binding), GO:0070588 (calcium ion transmembrane transport)
6	AhTE0148	UTR	A05	*Aradu.4RE2S*	Adur32853_comp0_c0_seq3	12-oxophytodienoate reductase 2; IPR013785 (Aldolase-type TIM barrel); GO:0003824 (catalytic activity), GO:0010181 (FMN binding), GO:0016491 (oxidoreductase activity), GO:0055114 (oxidation-reduction process)
7	AhTE0191	Exon	B04	*Araip.Q2YHX*	Aipa18069_comp0_c0_seq1	Disease resistance protein (TIR-Nbs-LRR class), putative; IPR000157 (Toll/interleukin-1 receptor homology (TIR) domain), IPR000767 (Disease resistance protein), IPR027417 (P-loop containing nucleoside triphosphate hydrolase); GO:0005515 (protein binding), GO:0006952 (defense response), GO:0007165 (signal transduction), GO:0043531 (ADP binding)
8	AhTE0233	Exon	A01	*Aradu.BZ12G*	GG11555|comp0_c0_seq1	Sterol C4-methyl oxidase 1-2; IPR006694 (Fatty acid hydroxylase); GO:0005506 (iron ion binding), GO:0006633 (fatty acid biosynthetic process), GO:0016491 (oxidoreductase activity), GO:0055114 (oxidation-reduction process)
9	AhTE0261	UTR	B04	*Araip.FJW22*	gi|372445500|gb|JR586420.1|, GG8772|comp0_c0_seq1	RING/U-box superfamily protein; IPR013083 (Zinc finger, RING/FYVE/PHD-type)

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Sl. No.	Marker	Site of insertion	Chrom-osome	Gene	Transcript	Annotation (peanutbase.org)
10	AhTE0305	UTR	B03	*Araip.WT1Z7*	Aipa17307_comp0_c0_seq1	Cinnamyl alcohol dehydrogenase 9; IPR002085 (Alcohol dehydrogenase superfamily, zinc-type), IPR016040 (NAD(P)-binding domain), IPR020843 (Polyketide synthase, enoylreductase); GO:0008270 (zinc ion binding), GO:0016491 (oxidoreductase activity), GO:0055114 (oxidation-reduction process)
11	AhTE0317	Intron	B05	*Araip.AP706*	Aipa895_comp1_c0_seq1	MYB transcription factor; IPR009057 (Homeodomain-like); GO:0003677 (DNA binding), GO:0003682 (chromatin binding)
12	AhTE0333	Upstream	A05	*Aradu.ZV9U0*	Adur12927_comp0_c0_seq1	Kunitz trypsin inhibitor 1; IPR002160 (Proteinase inhibitor I3, Kunitz legume); GO:0004866 (endopeptidase inhibitor activity)
13	AhTE0369	Upstream	A01	*Aradu.06HG0*	Adur28540_comp0_c0_seq1	Glycerophosphodiester phosphodiesterase GDE1 n=2 Tax=Triticeae RepID=M8BLH1_AEGTA; IPR004129 (Glycerophosphoryl diester phosphodiesterase); GO:0006071 (glycerol metabolic process), GO:0006629 (lipid metabolic process), GO:0008081 (phosphoric diester hydrolase activity), GO:0008889 (glycerophosphodiester phosphodiesterase activity)
14	AhTE0372	Intron	B06	*Araip.MKC7R*	Aipa16862_comp0_c0_seq12	Calcium-dependent lipid-binding (CaLB domain) family protein; IPR000008 (C2 domain); GO:0005515 (protein binding)
15	AhTE0373	Downstream	A04	*Aradu.P34U4*	EZ750116.1, gi|372396699|gb|JR547173.1|	Pseudouridine synthase family protein; IPR020103 (Pseudouridine synthase, catalytic domain); GO:0001522 (pseudouridine synthesis), GO:0003723 (RNA binding), GO:0009451 (RNA modification), GO:0009982 (pseudouridine synthase activity)
16	AhTE0391	Intron	A09	*Aradu.7N61X*	-	Alpha-glucosidase; IPR000322 (Glycoside hydrolase, family 31), IPR011013 (Galactose mutarotase-like domain), IPR013785 (Aldolase-type TIM barrel); GO:0003824 (catalytic activity), GO:0005975 (carbohydrate metabolic process), GO:0030246 (carbohydrate binding)
17	AhTE0446	Upstream	B05	*Araip.ZL45M*	EZ739845.1, EZ740561.1	UDP-glucosyltransferase family protein; IPR002213 (UDP-glucuronosyl/UDP-glucosyltransferase); GO:0008152 (metabolic process)
18	AhTE0483	Intron	A08	*Aradu.22X1P*	Adur3313_comp2_c0_seq1	MADS-box transcription factor family protein; IPR002100 (Transcription factor, MADS-box), IPR002487 (Transcription factor, K-box); GO:0003677 (DNA binding), GO:0003700 (sequence-specific DNA binding transcription factor activity), GO:0005634 (nucleus), GO:0046983 (protein dimerization activity)
19	AhTE0486	Upstream	A02	*Aradu.WK4VE*	Adur41444_comp0_c0_seq2	4-coumarate:CoA ligase 3; IPR000873 (AMP-dependent synthetase/ligase), IPR025110 (AMP-binding enzyme C-terminal domain); GO:0003824 (catalytic activity), GO:0008152 (metabolic process)
20	AhTE0489	Intron	B01	*Araip.64470*	Aipa30768_comp2_c0_seq3	Disease resistance protein (TIR-Nbs-LRR class); IPR000767 (Disease resistance protein), IPR027417 (P-loop containing nucleoside triphosphate hydrolase); GO:0006952 (defense response), GO:0043531 (ADP binding)
21	AhTE0504	Upstream	A03	*Aradu.LI04Q*	EZ735928.1	DCD (Development and Cell Death) domain protein; IPR013989 (Development/cell death domain)
22	AhTE0523	Exon	A05	*Aradu.22KJ4*	Adur16219_comp0_c0_seq1	Heavy metal transport/detoxification superfamily protein; IPR006121 (Heavy metal-associated domain, HMA); GO:0030001 (metal ion transport), GO:0046872 (metal ion binding)

Contd…

Sl. No.	Marker	Site of insertion	Chrom -osome	Gene	Transcript	Annotation (peanutbase.org)
23	AhTE0536	Intron	B01	*Araip.14380*	EZ737629.1, gi|372404186|gb|JR553639.1|	Ferredoxin 3; IPR012675 (Beta-grasp domain); GO:0009055 (electron carrier activity), GO:0051536 (iron-sulfur cluster binding)
24	AhTE0540	Downstream	A05	*Aradu.F5BID*	Adur13726_comp0_c0_seq7	Zinc finger MYND domain protein; IPR002893 (Zinc finger, MYND-type)
25	AhTE0547	Downstream	B06	*Araip.BUP6F*	GG10261|comp0_c0_seq1	Ethylene-responsive transcription factor 1B; IPR016177 (DNA-binding domain); GO:0003677 (DNA binding), GO:0003700 (sequence-specific DNA binding transcription factor activity)
26	AhTE0563	Exon	B07	*Araip.ISU30*	Aipa37662_comp0_c0_seq1	HXXXD-type acyl-transferase family protein; IPR003480 (Transferase), IPR023213 (Chloramphenicol acetyltransferase-like domain)
27	AhTE0572	Upstream	B09	*Araip.P20M1*	Aipa41497_comp0_c0_seq1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; IPR016140 (Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain)
28	AhTE0586	Upstream	A10	*Aradu.7EY7D*	gi|372416566|gb|JR564019.1|	U-box domain-containing protein 21-like [Glycine max]; IPR001752 (Kinesin, motor domain), IPR013083 (Zinc finger, RING/FYVE/PHD-type), IPR016024 (Armadillo-type fold), IPR027417 (P-loop containing nucleoside triphosphate hydrolase); GO:0000151 (ubiquitin ligase complex), GO:0003777 (microtubule motor activity), GO:0004842 (ubiquitin-protein ligase activity), GO:0005488 (binding), GO:0005524 (ATP binding), GO:0007018 (microtubule-based movement), GO:0008017 (microtubule binding), GO:0016567 (protein ubiquitination)
29	AhTE0599	Intron	A10	*Aradu.E2SFM*	Adur22652_comp0_c0_seq1	Protein YLS7-like [Glycine max]; IPR026057 (PC-Esterase)

AhTE0563, with *AhMITE1* transposition site at the exonic region of the gene *Araip.ISU30* on chromosome B07, was associated with disease (LLS) resistance and contents of fatty acids (oleic acid, linoleic acid and O/L ratio). The *Araip.ISU30* codes for HXXXD-type acyl-transferase family protein, involved in salicylic acid metabolism. The transcript, Aipa37662_comp0_c0_seq1 corresponding to this gene was expressed highly in reproductive and vegetative shoot tip followed by pod (Clevenger *et al.*, 2016). Similarly, at AhTE0572 locus, *AhMITE1* was inserted at 291 bp upstream region of the gene *Araip.P20M1* on chromosome B09. This gene codes for bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein, and AhTE0572 showed strong association with fatty acids like eicosenoic acid and lignoceric acid. The transcript, Aipa41497_comp0_c0_seq1 corresponding to this gene highly expressed in perianth followed by root and pod (Clevenger *et al.*, 2016). The marker AhTE0317 showed significant association with days to 50 per cent flowering, number of secondary branches, leaflet length, number of pods per plant and protein content. At AhTE0317 locus, *AhMITE1* was inserted at intronic region of the gene *Araip.AP706* on chromosome B05. The *Araip.AP706* encoded for MYB transcription factor. The transcript, Aipa895_comp1_c0_seq1 corresponding to this gene was highly expressed in perianth followed by gynoecium and androecium of the flower (Clevenger *et al.*, 2016).

Twenty-nine intergenic AhTE markers showed significant association with a few traits. Marker locus AhTE0674 corresponding to intergenic region (between *Araip.TF3HI* and *Araip.2JH4S*) on chromosome B01, showed significant association with LLS and rust resistance, sound mature kernel weight, palmitic acid, protein content, pod constriction, pod reticulation and pod beak. Similarly, AhTE0501 with intergenic position (*Araip.ZAK9V* and *Araip.D0TT7*) on chromosome B07 showed association with plant height and number of primary branches and LLS and rust resistance. AhTE0074 located between *Araip.5Q8JC* and *Araip.8Z50S* on chromosome B06 was associated with LLS resistance.

A detailed co-segregation between the allele at a marker locus and the phenotype for an associated trait was studied among the independent mutants. For this analysis, independent mutants of six parents (DER, VL 1, Spanish Improved (SI), TAG 24, TG 66 and TG 18A) were considered (Table 25). In most of the cases, contrasting

Table 25: Co-segregation of AhTE markers with selected traits

Phenotypic class	DER (25)*	VL 1 (24)*	SI (2)*	TAG 24 (18)*	TG 66 (11)*	TG 18A (4)*
AhTE0233-LLS score at 90 DAS						
Resistant	11/11 (100.00)	15/14 (93.3)	0/0	0/0	10/9 (90.0)	0/0
Susceptible	14/9 (64.3)	9/5 (55.5)	2/2 (100.0)	18/16 (88.9)	1/1 (100.0)	4/4 (100.0)
AhTE0233-Rust score at 90 DAS						
Resistant	19/13 (68.4)	23/23 (100.0)	0/0	1/0 (0.0)	10/10 (100.0)	0/0
Susceptible	6/6 (100.0)	1/1 (100.0)	2/2(100.0)	17/15 (88.2)	1/1 (100.0)	4/4 (100.0)
AhTE0563- Oleic acid						
High	5/1 (20.0)	3/1 (33.3)	1/1 (100.0)	1/1 (100.0)	4/0 (0.0)	0/0
Low	20/19 (95.0)	21/20 (95.2)	1/1 (100.0)	17/16 (94.1)	7/7 (100.0)	4/4 (100.0)
AhTE0317- Days to 50 per cent flowering						
Early	20/20 (100.0)	21/21 (100.0)	2/2 (100.0)	10/8 (80.0)	4/4 (100.0)	2/1 (50.0)
Late	5/1 (20.0)	3/1 (33.3)	0/0	8/6 (75.0)	7/1 (15.7)	2/1 (50.0)
AhTE0523-Pod size						
Small	7/4 (57.1)	3/1 (33.3)	1/0 (0.0)	3/0 (0.0)	2/0 (0.0)	0/0
Large	18/17 (94.4)	21/18 (85.7)	1/1 (100.0)	15/15 (100.0)	9/9 (100.0)	4/4 (100.0)

The values indicate the ratio of the number of genotypes with respective phenotype and allele
*The number indicates the total number of independent mutants from a parent
Parenthesis value indicates the percent co-segregation of marker with phenotype

phenotypic classes were observed among the independent mutants. For example, there were 11 resistant and 14 susceptible independent mutants for LLS reaction in the parent DER. Of the 11 resistant independent mutants, all 11 had resistant-type allele at AhTE0233 marker locus with a co-segregation of 100 per cent. Of the 14 susceptible independent mutants, nine had susceptible-type allele with a co-segregation of 64.3 per cent. Such a high rate of co-segregation was also observed among the mutants for AhTE0563-oleic acid, AhTE0317-days to 50 per cent flowering and AhTE0523-pod size.

Considering the importance of breeding for high productivity and nutritional traits in groundnut, an attempt was also made to identify the superior mutants that can be developed into varieties (Table 26). High h^2 and GAM were observed for LLS and rust score at 80 and 90 DAS, test weight, pod length, plant height, number of secondary branches, protein content, linoleic acid, behenic acid and seed dormancy (Table 18). Spanish Improved followed by 171-red recorded the highest pod yield (kg/ha) among the mutants. Spanish Improved was also comparable with the check varieties for days to 50 per cent flowering, number of pods per plant, shelling percentage, test weight, oil content and protein content. Similarly, VL 1 Dwarf, TGM 198 and 110(S) recorded 3.8 to 28.6 per cent increase over the checks for pod yield (kg/ha). SB 5 was also superior for important productivity and nutritional traits.

Table 26: Performance of superior mutants from mutant population of groundnut

Sl. No.	Genotype	Pod yield (kg/ha),	Number of pods per plant	Shelling percentage (%)	Test weight	Sound mature kernel weight	Late leaf spot at 90 DAS	Rust at 90 DAS	Days to 50 per cent flowering	Seed dormancy	Oil content	Protein content	Oleic acid	Oleic to linoleic acid ratio	Pod constriction	Pod reticulation	Pod beak and	Pod size
1	Spanish Improved	5,814.30	22.50	71.80	44.20	96.80	7.00	6.30	32.30	0.00	46.30	30.60	41.40	1.20	Medium	Medium	Slight	Medium
2	171-red	5,734.30	15.30	68.40	35.30	92.00	4.00	1.00	33.00	0.00	49.90	21.00	40.80	1.00	Slight	Very prominent	None	Large
3	TGM 117	5,038.60	17.10	72.40	55.90	99.40	6.80	6.00	33.50	0.00	42.80	24.90	49.60	1.60	Deep	Medium	Medium	Large
4	TGM 198	5,072.00	21.70	70.40	37.40	98.50	1.80	5.00	33.80	0.00	46.90	16.60	42.80	1.10	Medium	Slight	Slight	Medium
5	VL-1 Dwarf	5,077.10	18.30	69.70	40.20	98.00	3.50	4.80	33.80	0.00	46.60	30.60	48.00	1.50	Medium	Medium	Medium	Medium
6	SB 5	4,890.60	18.10	74.60	35.40	97.60	6.80	4.80	32.00	3.50	44.80	30.70	48.70	1.60	Medium	Medium	Medium	Medium
7	SB 3	4,217.10	23.20	74.30	30.20	98.70	5.50	5.00	33.30	0.00	44.50	29.40	45.70	1.30	Medium	Medium	Medium	Medium
8	SB 2	4,571.70	17.90	77.10	47.30	97.90	6.00	5.00	30.00	3.00	46.90	30.80	38.60	1.00	Medium	Slight	Slight	Medium
9	139-1 Viriscent	4,869.60	10.20	71.60	52.10	98.30	5.50	2.30	31.00	1.50	42.10	29.50	45.70	1.40	Slight	Slight	None	Large
10	110 (s)	5,086.30	17.50	67.70	45.80	95.50	4.30	3.30	32.50	0.50	45.00	31.40	50.10	1.70	Deep	Medium	Prominent	Large
11	VL 9	4,733.10	15.70	72.60	52.20	99.50	2.50	4.50	34.30	0.00	46.90	29.20	46.80	1.40	Medium	Slight	Slight	Medium
12	171-tan	5,251.20	11.90	67.90	43.00	96.90	5.00	2.30	32.50	2.00	44.70	30.00	45.70	1.40	Slight	Medium	None	Large
13	104-9 VL-1 type	4,474.40	9.50	69.10	51.40	98.20	6.00	1.30	31.80	3.00	43.10	29.90	44.90	1.30	Slight	Slight	None	Large
14	VL 13	4,547.70	12.50	67.50	47.10	98.60	4.80	4.50	32.30	0.50	51.10	22.20	41.40	1.10	Medium	Very prominent	Very prominent	Large
15	3-1	4,292.00	17.50	71.40	32.90	98.70	2.00	2.00	34.00	2.50	44.70	20.00	48.50	1.50	Slight	Very prominent	None	Slight
16	VR 5	4,274.70	15.30	71.20	49.60	97.60	6.00	5.00	33.00	0.00	45.80	32.80	44.40	1.30	Medium	Medium	Slight	Large
	28-2	4,427.80	12.10	70.80	53.30	99.10	3.30	4.50	33.80	0.50	47.90	31.20	44.40	1.30	Medium	Slight	Slight	Medium
	TAG 24	3,954.20	18.30	73.10	39.90	97.40	8.00	8.00	31.80	0.00	45.20	30.70	42.50	1.20	Medium	Medium	Medium	Medium
	TMV 2	4,883.50	24.60	74.10	36.30	95.80	7.10	6.30	32.50	2.80	46.60	32.10	42.50	1.20	Moderate	Slight	Slight	Medium
	GPBD 4	4,886.00	25.80	76.70	39.40	96.50	2.00	2.00	32.50	2.00	47.90	34.60	47.90	1.40	Moderate	Slight	Slight	Medium

5. DISCUSSION

Groundnut (*Arachis hypogaea* L. 2n=4x=40) is a legume crop mainly used for food, oil and fodder world-wide. With high nutritive values, groundnut is known as "Poor man's nut". Genetic improvement of groundnut for higher productivity and better quality is important. Breeding in groundnut mainly focusses on plant morphological traits, productivity traits, resistance to diseases and insects, tolerance to abiotic stress and nutritional quality traits, and the progress made with these objectives have been reviewed (Janila *et al.*, 2016). Several improved varieties have been developed with better phenotypes for these traits, and these improved varieties alone have contributed to 30 per cent yield increase in India since 1967 (Reddy and Basu, 1989).

Recently, the advances made in characterizing the plant genomes and their applications have been reviewed (Bevan *et al.*, 2017). These genomic innovations and molecular breeding methods can greatly help the crop improvement programmes and complement the conventional breeding methods to enhance the overall efficiency of plant breeding (Varshney, 2016). But the use of the molecular breeding methods requires the identification of genomic regions and genes responsible for the important traits so that the plant selection can be exercised based on the genotype rather than the phenotype. This can be best achieved when appropriate genotypes and a large number of molecular markers displaying high polymorphism are available.

Considerable efforts have been made to develop and employ various marker systems in groundnut. They include RFLP (Halward *et al.*, 1991, 1992), DAF and AFLP (He and Prakash, 1997) and SSR (Hopkins *et al.*, 1999; Palmieri *et al.*, 2002; He *et al.*, 2003; Ferguson *et al.*, 2004; Moretzsohn *et al.*, 2004; Moretzsohn *et al.*, 2005; Palmieri *et al.*, 2005; Hong *et al.*, 2008). Subsequently, a large number of SSR (Zhang *et al.*, 2012; Huang *et al.*, 2016; Peng *et al.*, 2016; Zhou *et al.*, 2016a), CAPS (Chu *et al.*, 2009), DArT (Kilian, 2008) and SNPs (Varshney *et al.*, 2009) (Alves *et al.*, 2008; Nagy *et al.*, 2012; Wang *et al.*, 2013a; Zhou *et al.*, 2014; Hong *et al.*, 2015; Shirasawa *et al.*, 2016c; Clevenger *et al.*, 2017) were developed and/or used in groundnut

Arachis hypogaea transposable element (AhTE) marker system was developed in groundnut (Bhat *et al.*, 2008). It showed as high as 22.0 per cent polymorphism in

groundnut (Shirasawa *et al.*, 2012a). In addition, AhTE marker system has been user-friendly (Kolekar *et al.*, 2016). TE markers were successfully used to construct linkage maps (Shirasawa *et al.*, 2013; Kolekar *et al.*, 2016) and to identify QTL for resistance to LLS and rust (Kolekar *et al.*, 2016). AhTE markers offer an advantage of identifying the gene governing a trait since the transposable element can act as a DNA tag. Using such TE markers, spikelet-tipped bristles1 (*stb1*) gene responsible for grain yield and grain number per panicle was identified in foxtail millet (Sato *et al.*, 2013). Lee *et al.* (2006) identified maize kernel starch biosynthesis genes on chromosome 3 in maize using *Isaac*-CACTA transposons. Monden *et al.* (2009) successfully mapped a locus involved in heading date on the short arm of chromosome 6 using *mPing* in rice.

Various mapping populations have been used in groundnut for mapping the traits. F_2 populations were used to construct the linkage maps in wild (Halward *et al.*, 1993; Milla, 2003) as well as cultivated groundnut (Herselman *et al.*, 2004). Backcross populations [*Arachis stenosperma* × (*Arachis stenosperma* × *A. cardenasii*)] were also used for mapping the agronomic traits (Garcia *et al.*, 2005). AB-QTL population, which facilitates simultaneous discovery of QTLs and development of elite genotypes, was developed for mapping the pod morphology, plant architecture, yield components and days to flowering (Fonceka *et al.*, 2012a). Chromosome segment substitution lines (CSSLs) were developed to facilitate characterization of different segments of wild species contributing for resistance to foliar diseases (Fonceka *et al.*, 2012b).

Considering the advantages of recombinant inbred lines (RILs), many such populations have been developed in groundnut. RIL populations were used to map plant morphological traits (Kayam *et al.*, 2017), productivity traits (Faye *et al.*, 2015; Huang *et al.*, 2015; Luo *et al.*, 2017a; Luo *et al.*, 2017b), resistance to diseases and insects (Khedikar *et al.*, 2010; Sarvamangala *et al.*, 2011; Shoba *et al.*, 2012; Sujay *et al.*, 2012; Shoba *et al.*, 2013; Kolekar *et al.*, 2016; Leal-Bertioli *et al.*, 2016; Zhou *et al.*, 2016b; Pandey *et al.*, 2017), tolerance to abiotic stress (Ravi *et al.*, 2011; Gautami *et al.*, 2012) and nutritional quality traits (Sarvamangala *et al.*, 2011; Pandey *et al.*, 2014b; Mondal *et al.*, 2015).

Only those genomic resources with significant contribution towards the trait can be employed for marker-assisted breeding. For example, the QTL and their flanking

markers were successfully identified (Khedikar *et al.*, 2010; Sarvamangala *et al.*, 2011; Sujay *et al.*, 2012; Kolekar *et al.*, 2016), validated (Yeri *et al.*, 2014; Sukruth *et al.*, 2015) and used to develop late leaf spot (LLS) and rust resistant genotypes in groundnut (Varshney *et al.*, 2014; Yeri and Bhat, 2016). Therefore, successful marker-assisted breeding requires identification and validation of strong markers, which in turn depends on the number and type of markers, and the mapping population employed for mapping.

RIL population derived from closely related genotypes (like parent and its mutant) offer an advantage of identifying the QTL/genes governing the traits by minimizing the background noise. Sequence differences between the mutant and its wild-type can provide strong evidence to identify a gene using map-based cloning strategies. The use of backcross lines from a recurrent parent provides an improvement since modifiers are removed and a small chromosomal region around the introgressed allele allows fine mapping using molecular markers (Koornneef *et al.*, 1994). In Arabidopsis, Hong and Vierling (2000) used backcross progenies of *mir159a* (parent) and its EMS derived mutant to map thermotolerence loci, *hot1*.

5.1 Mapping with RILs

In this study, TMV 2, a popular and elite variety of groundnut, and its EMS-derived mutant TMV 2-NLM (Prasad *et al.*, 1984) were used to identify the genomic regions contributing for the important taxonomic and productivity traits in groundnut by QTL mapping using a large number (432) of their RILs (Pattanashetti, 2005). TMV 2 and TMV 2-NLM differed significantly for the growth habit, number of branches (primary and secondary), productivity traits and quantity and quality of the oil. The RIL population showed considerably high variability not only for those traits for which the parents differed, but also for a few other traits (resistance to LLS and rust, pod and kernel features). ddRAD-Sequencing, which is a reduced representation of genome sequencing method evaluating ~1 per cent of the genome, revealed genetic differences in terms of SNPs and copy number variations (CNVs). Thirty-one SNPs spread over seven chromosomes with a density of ~1 per Mb were observed between TMV 2 and TMV 2-NLM. This SNP density was comparable to that found in tomato mutants (Shirasawa *et al.*, 2016b). Of the total 31 SNPs, only four were non-synonymous across

three genes leading to very few functional differences between TMV 2 and TMV 2-NLM. Likewise, only five significant CNVs were observed within 1 per cent of the genome, and only one CNV (121135001-121145000 bp region on A04) was statistically significant with $\log_2$ ratio of 5.27, indicating a gain of copies in TMV 2-NLM when compared to TMV 2. The polymorphism between TMV 2 and TMV 2-NLM for the transpositional activity of *AhMITE1* was also less (28.5 %). Of the 369 loci, only 105 showed differential activity of *AhMITE1*. Further, it was found that *AhMITE1* activity was restricted to exons of only six genes. Thus, TMV 2 and TMV 2-NLM showed very few genetic differences in terms of SNPs, CNVs and *AhMITE1* activity. In contrast, TMV 2 and TMV 2-NLM showed very high phenotypic differences, which could due to the fact that SNPs, CNVs and *AhMITE1* activity can have significant effect on phenotypes through expression variation (Patel *et al.*, 2004; Springer *et al.*, 2009; Gowda *et al.*, 2010; Hussein *et al.*, 2011; Bai *et al.*, 2016). Thus, the RILs derived from TMV 2 and TMV 2-NLM could constitute an ideal mapping population to map the important traits keeping the background noise to minimum.

Using 91 AhTE markers, a partial linkage map of 1,205.66 cM was constructed in a new RIL mapping population (TMV 2 × TMV 2-NLM) in groundnut. The marker order was grossly comparable to the maps for SKF2 (Satonoka × Kintoki) and NYF2 (YI-0311 × Nakateyutaka), which were also constructed with AhTE markers (Shirasawa *et al.*, 2012b). The markers mapped on A01, A02, A04, A05, B01, B03, B04 and B07 could be confirmed with BLAST. But other markers could not be confirmed since they mismatched partly (differing for homeologous chromosomes) or completely. Further, a QTL map was constructed using this linkage map along with the phenotypic data on taxonomic and productivity traits observed over two years (rainy season of 2014 and 2015). Major QTL regions were identified for days to 50 per cent flowering, number of branches, test weight, pod width, and contents of protein, oil, oleate, linoleate, O/L ratio and palmitate. A QTL region with AhTE0391 and AhTE0572 as the flanking markers (on A09) had PVE of 13.40, 15.42 and 20.53 per cent towards oleic acid (O) and linoleic acid (L) contents and O/L ratio, respectively. AhTE0391 and AhTE0572 marker loci had a distance of 0.50 Mb and 5.6 Mb, respectively from the *AhFAD2A* on chromosome A09. Though many genes contribute

to oleic acid, linoleic acid content and O/L in groundnut (Wang *et al.*, 2015), *AhFAD2A* and *AhFAD2B* (on B09) are the major genes (Jung *et al.*, 2000).

The markers flanking the QTL were found to be strongly associated with the same traits when checked with single marker analysis (SMA). AhTE0391, apart from being associated with the contents of oil, oleic acid, linoleic acid and palmitic acid, it also showed association with protein content. AhTE0391 locus was represented by the gene *Aradu.7N61X* coding for alpha-glucosidase. In germinating grains of barley, *HvAGL97* codes for α-glucosidase, which is a major endosperm enzyme. It catalyzes conversion of maltose to glucose, but is not required for starch degradation (Stanley *et al.*, 2010). The marker AhTE0357 with *AhMITE1* insertion polymorphism at 79 bp downstream of the gene *Araip.TG1BL* on chromosome B02, could differentiate the genotypes with sequential and alternate branching pattern to an extent of 32.8 per cent. AhTE0357 was also associated with days to 50 per cent flowering and number of primary and secondary branches. But selection for early maturing genotypes using AhTE0357 is not expected to bring in any yield advantage since days to 50 per cent flowering recorded negative and significant correlation with productivity and oil quality traits.

Test weight and pod width were positively and significantly correlated, and both showed strong association with AhTE0025, which corresponds to the gene *Aradu.7065G* (on A07 chromosome) coding for aldo/keto reductase family oxidoreductase. In *Digitalis purpurea*, aldo/keto reductase is known to take part in the biosynthesis of cardiac glycosides (Gavidia *et al.*, 2002). In the previous studies, Fonceka *et al.* (2012a) and Huang *et al.* (2015) identified QTL regions for test weight, which were located at a distance of 1.5 Mb and 29.1 Mb, respectively from the gene *Aradu.7065G* on A07 chromosome.

The genomic resources (QTL/genes/markers) developed in this study help in generating genetic resources to breed for improved groundnut varieties in future. But the recombinant inbred lines used in this study directly provided an opportunity to select the superior lines for productivity traits. RILs 2-14(a)(ii), 2-29(g), 2-33(a) and 2-23(c) were superior since they recorded 7-15, 35-50 and 1-4 per cent increase over TMV 2 for pod yield (kg/ha), test weight and oil content. They also had 12-21 per cent

higher oleate than TMV 2. They matured one to two days earlier than TMV 2. These superior RILs can be developed into commercial varieties.

5.2 Association studies in the mutant population

The independent mutants derived from several parents make a diverse association panel that can be used for genome-wide association studies. The mutant population showed significant phenotypic differences with moderate genetic diversity. Genotypes differing for a few genetic factors help in identifying the markers for traits by reducing the number of candidate genomic regions or genes (Andersen and Lubberstedt, 2003). Backcrossing of mutants to their non-mutagenized progenitor, and analyzing their isogenic lines could be one way of drastically reducing the background noise (Abe *et al.*, 2012). A large number of diverse independent mutants from common parents might also form an ideal population to identify MTAs by reducing the number of candidate mutations. Employing AhTE markers on such a mutant population can therefore assist in revealing useful MTAs and the key genes. A large collection (association panel) of independent mutants derived from physical and chemical mutagenesis of a few parental genotypes was evaluated in field for taxonomic, agronomic, productivity, nutritional traits along with foliar disease resistance during the rainy seasons of 2014 and 2015, and the association panel was genotyped with AhTE markers for identifying MTAs.

The genotypes showed significant differences for all the traits except for pod length, palmitic acid and seed dormancy. Environment and genotype × environment interactions were also significant for many traits, indicating the complexity of the traits and challenges in phenotypic selection. Genotypes followed normal distribution for all the traits except for the number of primary and secondary branches, and sound mature kernel weight. The traits like LLS and rust score at 70, 80 and 90 DAS, number of pods per plant, pod yield per plant, plant height, number of primary and secondary branches, O/L ratio and seed dormancy showed high PCV and GCV, indicating considerable variability for selection. In fact, the mutant population showed higher PCV and GCV for LLS score at 90 DAS, rust score at 70, 80 and 90 DAS, plant height, number of primary branches and O/L ratio when compared to the RIL population.

Genotyping of mutants and their parents with 110 AhTE markers showed the allele frequency of 0.50-1.00 with a mean of 0.73 across 110 marker loci, indicating that the mutants were heterozygous for many marker loci. Heterozygosity ranged from 0.00 to 0.68 with a mean of 0.02 across the genotypes. The ability of the markers to differentiate the genotypes (PIC) (Hildebrand *et al.*, 1994) ranged from 0.00 to 0.38 with a mean of 0.27, indicating low to moderate ability of the markers to differentiate the mutants. A total of 24 markers showed PIC value of ≥0.37, and AhTE0343 and AhTE0372 recorded the highest PIC (0.38). Fifty markers had a PIC of 0.26 to 0.36. However, none of the markers showed high PIC (≥0.50). The population showed low to moderate genetic diversity as measured by the gene diversity index, which ranged from 0.00 to 0.50 with an average of 0.35. In the past, Kottapalli *et al.* (2007) and Jiang *et al.* (2010) found high genetic diversity in groundnut minicore collection, while Ren *et al.* (2014) observed low genetic diversity (0.11) in case of cultivated Chinese groundnut varieties using SSR markers. Low to moderate PIC and genetic diversity observed in this study could be due to the biallelic nature of the AhTE markers, and also the type of population, which consisted of independent mutants from the common parents.

Association mapping is generally used to identify the loci involved in the inheritance of complex traits. But, the presence of population structure (based on allele frequency) can result in “spurious associations” (associations between a phenotype and markers that are not linked to any causative loci) (Lander and Schork, 1994). The panel of the genotypes showed structured population with three major groups and seven sub-groups since the highest ΔK value was obtained at K=3 followed by K=7. Presence of seven sub-clusters was further supported by principal co-ordinate analysis (PCoA) and by radial type of tree diagram generated by hierarchical clustering. It was interesting to note the grouping of independent mutants derived from each parent in respective subgroups. The independent mutants of VL 1 were grouped in the subgroups II and III, whereas the independent mutants of TG 66 were clustered in the subgroup VI. Eighteen independent mutants of TAG 24 were grouped in the subgroup VII. Most of the LLS resistant mutants derived from VL 1 were grouped in subgroup III, indicating their genetic relatedness. The Per cent polymorphism within the seven subgroups ranged from 1.8-17.1 per cent (subgroup V) to 4.5-66.1 per cent (subgroup I).

The mutant population, comprising of independent mutants derived from several parents, exhibited significant phenotypic differences despite low to moderate genetic diversity. When this association panel was subjected to genome-wide association studies using 110 markers and 40 traits, a total of 132 highly significant MTAs represented by 58 AhTE markers were identified for all the traits except test weight. Five traits showed 17 MTAs with PVE of more than 50 per cent. Thirty-seven MTAs had PVE of 30-50 per cent. The significant MTAs with high PVE indicated strong association of markers with the traits, which can be employed for selection.

A few markers were associated with multiple traits. This could be due to the pleiotropic nature of the marker, or the association among the traits. For example, AhTE0523 showed strong association with productivity traits like pod yield, pod size and sound mature kernel weight, and these traits were positively and significantly correlated. Similarly, AhTE0233 showed strong association with LLS and rust resistance, which were positively and significantly correlated.

Analysis of the genomic location of the markers showed that 29 out of 58 AhTE markers showing significant associations were genic with a distribution across 15 chromosomes. Structural analysis of these 29 genes indicated that 4, 7, 9, 5 and 4 genes had *AhMITE1* insertion in the exonic, intronic, upstream, downstream and UTR regions, respectively. Functions for these genes indicated that they were mainly involved in fatty acid metabolism, resistance to insect and diseases, amino acid synthesis, metabolism of starch, ion transportation, chromatin binding, signaling pathway etc.

Twenty-nine intergenic AhTE markers also showed significant association with a few traits. Transposon activity both in protein coding genes (Hoen *et al.*, 2006; Xiao *et al.*, 2008) and intergenic regions can bring in phenotypic changes (Piriyapongsa and Jordan, 2007). In rice, MITEs located in both the genic and intergenic regions were transcribed, and they contributed to the biogenesis of about one fourth of its total small RNAs (Lu *et al.*, 2012), which regulate several other genes. It was also evident in rice that the genes associated with MITEs were down-regulated.

At least 11 AhTE markers were found to be associated with LLS resistance, and they were distributed on 11 different chromosomes. Mapping studies till date have

identified major QTL for LLS resistance on four chromosomes (A03, B01, B03 and B06) (Kolekar *et al.*, 2016; Zhou *et al.*, 2016b). Same was the case with the contents of oleic acid and linoleic acid, for which five AhTE markers on five chromosomes showed strong association. This multigene control mechanism could be expected for the contents of oleic acid and linoleic acid considering the involvement of at least six gene members (Isleib *et al.*, 2006; Wang *et al.*, 2015), though it was earlier believed that only *AhFAD2A* and *AhFAD2B* controlled these traits (Jung *et al.*, 2000).

Since the association panel consisted of the independent mutants, it offered an opportunity to study the co-segregation between the allele and phenotype. Very strong co-segregation was observed between the resistant phenotype and the resistant-type of allele at AhTE0233. Similarly, the susceptible phenotype also co-segregated with the susceptible-type of allele. Such a strong co-segregation was also observed among the independent mutants for oleic acid-AhTE0563, days to 50 per cent flowering-AhTE0317, and pod size-AhTE0523. The markers showing very strong co-segregation with the phenotypes can be employed for marker-assisted selection in breeding programmes.

It was interesting to find that AhTE0050, an intergenic AhTE marker showed strong association with the number of primary branches in both the RIL population and mutant population. In TMV 2 × TMV 2-NLM RIL population, a QTL region flanked by AhTE0357 and AhTE0050 showed high PVE (19.9 %) for the number of primary branches. Upon single marker analysis in the RILs, AhTE0050 showed significant association with R^2 of 0.9 per cent. In the mutant population, AhTE0050 showed a significant association with the number of primary branches (R^2 of 10.7 %).

Presence of high variability, heritability and GAM for the traits allowed identification of a few superior mutants. Spanish Improved was superior for pod yield per plant (23.21-45.02 %), days to 50 per cent flowering, number of pods per plant, shelling percentage, test weight, oil content and protein content over the checks. Similarly, 171-red, VL 1 Dwarf, TGM 198 and 110(S) recorded 3.8 to 28.6 per cent higher yield over the checks. SB 5 was superior for important productivity and nutritional traits. These genotypes can be tested in larger plots to confirm their superior performance. Hitherto, many mutants have been developed into commercial varieties in

groundnut. 28-2, a secondary mutant of DER was released as a high yielding disease (LLS) resistant variety in Karnataka (Gowda *et al.*, 2002). Likewise, TLG 45 (TG 19 × TAG 24), a large-seeded, high yielding groundnut variety was released in Maharashtra (Kale *et al.*, 2008).

Overall, several AhTE markers strongly associated or linked with the important taxonomic, productivity and nutritional traits were identified in this study using two populations. These markers could be significant in molecular breeding in groundnut. For a few traits, the genes harbouring the AhTE marker locus were identified. Structure-function relation for these genes may be established in future by cloning these genes using *AhMITE1* as the DNA tag. Thus, the MTAs identified in this study could be significant for gene discovery as well as marker-assisted breeding. Further, the superior RILs and mutants identified for high productivity and foliar disease resistance form the novel genotypes for variety development and commercial release. The markers associated with the important traits are being validated for use in genomics-assisted breeding.

6. SUMMARY AND CONCLUSION

Considering the importance of marker-assisted breeding in groundnut, QTLs/ markers were identified for agronomic, productivity, resistance to diseases, nutritional and physiological traits using RIL population of TMV 2 × TMV 2-NLM and a population consisting of independent mutants by employing AhTE markers. The results of this study are summarized in this chapter.

- ddRAD-Seq analysis showed that TMV 2 and TMV 2-NLM shared a common genome except for a few SNPs and copy number variations. The polymorphism due to *AhMITE1* transposition as measured by AhTE markers was 28.5 per cent between TMV 2 and TMV 2-NLM.

- The RILs of TMV 2 × TMV 2-NLM differed significantly for agronomic, productivity, resistance to diseases, nutritional and physiological traits across the years. In general, a normal distribution of the RILs was observed for all the traits.

- Single marker analysis using the RIL population of TMV 2 × TMV 2-NLM detected three significant and major markers (AhTE0357, AhTE0391 and AhTE0523). AhTE0357 was associated with days to 50 per cent flowering, branching pattern and number of secondary branches. AhTE0391 was associated with oleic acid content, and AhTE0523 was associated with eicosenoic acid.

- A linkage map of 1,205.66 cM with 20 linkage groups was constructed from the RILs of TMV 2 × TMV 2-NLM using 91 mapped AhTE markers. Of these markers, 51 were genic and 40 were intergenic.

- QTL analysis in the RILs of TMV 2 × TMV 2-NLM detected seven major QTL regions for 22 traits across the years.

- QTL region flanked between AhTE0357 and AhTE0050 governed days to 50 per cent flowering (PVE 18.5-22.0 %) and the number of secondary branches (PVE 10.8-28.4 %). QTL region flanked by AhTE0391 and AhTE0572

governed oleic acid (PVE 12.4-15.1 %), linoleic acid, palmitic acid and O/L ratio.

- Gene prediction in the QTL region between AhTE0391 and AhTE0572 identified 256 genes, of which 14 were related to fatty acid metabolism.

- From the RILs of TMV 2 × TMV 2-NLM, 15 lines superior over TMV 2 for pod yield (kg/ha) were identified. Some of them were also superior for other productivity and nutritional traits.

- Genotyping of a population consisting of independent mutants and their parents with 110 AhTE markers identified three major groups and seven subgroups. Genotypes in four subgroups comprised of respective parents and mutants.

- Most of the mutants were homozygous at many loci, and the heterozygosity ranged from 0.00 to 0.68 with a mean of 0.02 across the genotypes. The PIC for the AhTE markers ranged from 0.00 to 0.38 with a mean of 0.27. Twenty-four markers recorded the PIC ≥0.37, and 50 markers had a PIC of 0.26 to 0.36. The gene diversity index ranged from 0.00 to 0.50 with an average of 0.35, indicating low to moderate genetic diversity in the population.

- In total, 132 highly significant MTAs were identified for 39 traits with 58 AhTE (29 genic and 29 intergenic) markers. Nutritional traits showed the highest number of MTAs (38) followed by agronomic traits (35), productivity traits (31), foliar disease resistance (23), and taxonomic traits (5). Seventeen MTAs with five traits showed phenotypic variance explained (PVE) of more than 50 per cent. AhTE0501-plant height recorded the highest PVE (69.66 %) followed by AhTE0233-LLS score at 90 DAS (59.39 %), AhTE0504-pod width (53.52 %), AhTE0233-rust score at 90 DAS (52.20 %) and AhTE0674-LLS score at 80 DAS (50.40 %). Further, thirty-seven MTAs with ten traits had a PVE of 30-50 per cent.

- Marker-trait association studies in the RIL population and the mutant population identified the markers for the new traits like days to 50 per cent flowering,

branching pattern, number of primary branches, number of secondary branches and leaflet shape in groundnut.

- A strong co-segregation of markers was observed in several groups of parent-independent mutants for LLS and rust resistance, pod size, days to 50 per cent flowering and oleic acid content.

- Since the RIL population used in this study is derived from a parent (TMV 2) and its mutant (TMV 2-NLM), and also association panel consisted of independent mutants from common parents, the AhTE markers and QTL identified in this study for taxonomic, agronomic and productivity traits will be of immense use for fine-mapping and identifying the candidate genes. Presence of *AhMITE1*, the basis of AhTE marker, both at genic and intergenic regions is known to influence the gene expressions. Thus, the AhTE markers governing important traits could help in gene discovery and functional analysis. Further, the superior RILs and mutants identified in this study form the novel genotypes, which could be developed into new commercial varieties.

REFERENCES

Abe, A., Kosugi, S., Yoshida, K., Natsume, S., Takagi, H., Kanzaki, H., Matsumura, H., Yoshida, K., Mitsuoka, C. and Tamiru, M., 2012, Genome sequencing reveals agronomically important loci in rice using MutMap. *Nat. Biotechnol.*, 30(2): 174-178.

Alves, D. M., Pereira, R. W., Leal-Bertioli, S. C., Moretzsohn, M. C., Guimaraes, P. M. and Bertioli, D. J., 2008, Development and use of single nucleotide polymorphism markers for candidate resistance genes in wild peanuts (*Arachis* spp.). *Genet. Mol. Res.*, 7(3): 631-642.

Andersen, J. R. and Lubberstedt, T., 2003, Functional markers in plants. *Trends Plant Sci.*, 8(11): 554-560.

Bai, Z., Chen, J., Liao, Y., Wang, M., Liu, R., Ge, S., Wing, R. A. and Chen, M., 2016, The impact and origin of copy number variations in the *Oryza* species. *BMC Genomics*, 17(261): 1-12.

Bamshad, M. J., Ng, S. B., Bigham, A. W., Tabor, H. K., Emond, M. J., Nickerson, D. A. and Shendure, J., 2011, Exome sequencing as a tool for Mendelian disease gene discovery. *Nat. Rev. Genet.*, 12(11): 745-755.

Belamkar, V., Selvaraj, M. G., Ayers, J. L., Payton, P. R., Puppala, N. and Burow, M. D., 2011, A first insight into population structure and linkage disequilibrium in the US peanut minicore collection. *Genetica*, 139(4): 411-429.

Bertioli, D. J., Cannon, S. B., Froenicke, L., Huang, G., Farmer, A. D., Cannon, E. K., Liu, X., Gao, D., Clevenger, J., Dash, S., Ren, L., Moretzsohn, M. C., Shirasawa, K., Huang, W., Vidigal, B., Abernathy, B., Chu, Y., Niederhuth, C. E., Umale, P., Araujo, A. C., Kozik, A., Do Kim, K., Burow, M. D., Varshney, R. K., Wang, X., Zhang, X., Barkley, N., Guimaraes, P. M., Isobe, S., Guo, B., Liao, B., Stalker, H. T., Schmitz, R. J., Scheffler, B. E., Leal-Bertioli, S. C., Xun, X., Jackson, S. A., Michelmore, R. and Ozias-Akins, P., 2016, The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut. *Nat. Genet.*, 48(4): 438-446.

Bevan, M. W., Uauy, C., Wulff, B. B., Zhou, J., Krasileva, K. and Clark, M. D., 2017, Genomic innovation for crop improvement. *Nature*, 543(7645): 346-354.

Bhat, R. S., Patil, V. U., Chandrashekar, T. M., Sujay, V., Gowda, M. V. C. and Kuruvinashetti, M. S., 2008, Recovering flanking sequence tags of miniature inverted-repeat transposable element by thermal asymmetric interlaced-PCR in peanut. *Curr. Sci.*, 95(4): 452-453.

Bhat, R. S., Upadhyaya, N. M., Chaudhury, A., Raghavan, C., Qiu, F., Wang, H., McNally, K., Leung, H. and Comai, L., 2007, Chemical and irradiation induced mutants and TILLING. In *Rice Functional Genomics- Challenges, Progress and Prospects*. Ed. Upadhyaya, N. M., Springer Life Sciences, New York, USA, pp. 149-180.

Bolon, Y., Haun, W. J., Xu, W. W., Grant, D., Stacey, M. G., Nelson, R. T., Gerhardt, D. J., Jeddeloh, J. A., Stacey, G. and Muehlbauer, G. J., 2011, Phenotypic and genomic analyses of a fast neutron mutant population resource in soybean. *Plant Physiol.*, 156(1): 240-253.

Burton, G. and De Vane, E., 1953, Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45(10): 478-481.

Chen, X., Li, H., Pandey, M. K., Yang, Q., Wang, X., Garg, V., Chi, X., Doddamani, D., Hong, Y., Upadhyaya, H., Guo, H., Khan, A. W., Zhu, F., Zhang, X., Pan, L., Pierce, G. J., Zhou, G., Krishnamohan, K. A., Chen, M., Zhong, N., Agarwal, G., Li, S., Chitikineni, A., Zhang, G. Q., Sharma, S., Chen, N., Liu, H., Janila, P., Wang, M., Wang, T., Sun, J., Li, X., Li, C., Yu, L., Wen, S., Singh, S., Yang, Z., Zhao, J., Zhang, C., Yu, Y., Bi, J., Liu, Z. J., Paterson, A. H., Wang, S., Liang, X., Varshney, R. K. and Yu, S., 2016, Draft genome of the peanut A-genome progenitor (*Arachis duranensis*) provides insights into geocarpy, oil biosynthesis and allergens. *Proc. Natl. Acad. Sci.*, 113(24): 6785-6790.

Chopra, R., Burow, G., Farmer, A., Mudge, J., Simpson, C. E., Wilkins, T. A., Baring, M. R., Puppala, N., Chamberlin, K. D. and Burow, M. D., 2015, Next-generation transcriptome sequencing, SNP discovery and validation in four market classes of peanut, *Arachis hypogaea* L. *Mol. Gen. Genet.*, 290(3): 1169-1180.

Chu, Y., Holbrook, C. C. and Ozias-Akins, P., 2009, Two alleles of *ahFAD2B* control the high oleic acid trait in cultivated peanut. *Crop Sci.*, 49(6): 2029-2036.

Clevenger, J., Chu, Y., Chavarro, C., Agarwal, G., Bertioli, D. J., Leal-Bertioli, S. C., Pandey, M. K., Vaughn, J., Abernathy, B., Barkley, N. A., Hovav, R., Burow, M., Nayak, S. N., Chitikineni, A., Isleib, T. G., Holbrook, C. C., Jackson, S. A., Varshney, R. K. and Ozias-Akins, P., 2017, Genome-wide SNP genotyping resolves signatures of selection and tetrasomic recombination in peanut. *Mol. Plant*, 10(2): 309-322.

Clevenger, J., Chu, Y., Scheffler, B. and Ozias-Akins, P., 2016, A developmental transcriptome map for allotetraploid *Arachis hypogaea*. *Front. Plant Sci.*, 7(1446): 1-18.

Cuc, L. M., Mace, E. S., Crouch, J. H., Quang, V. D., Long, T. D. and Varshney, R. K., 2008, Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (*Arachis hypogaea*). *BMC Plant Biol.*, 8(55): 1-11.

Dahmani-Mardas, F., Troadec, C., Boualem, A., Leveque, S., Alsadon, A. A., Aldoss, A. A., Dogimont, C. and Bendahmane, A., 2010, Engineering melon plants with improved fruit shelf life using the TILLING approach.*PLoS One*, 5(12): e15776.

Dhillon, S. S., Rake, A. V. and Miksche, J. P., 1980, Reassociation kinetics and cytophotometric characterization of peanut (*Arachis hypogaea* L.) DNA. *Plant Physiol.*, 65(6): 1121-1127.

Evanno, G., Regnaut, S. and Goudet, J., 2005, Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol. Ecol.*, 14(8): 2611-2620.

Falconer, D. S., 1975, Introduction to Quantitative Genetics. Longman Scientific and Technical, Essex, England, p. 22.

FAO, 2016, FAO Statistical Database. http://faostat.fao.org.

Faye, I., Pandey, M. K., Hamidou, F., Rathore, A., Ndoye, O., Vadez, V. and Varshney, R. K., 2015, Identification of quantitative trait loci for yield and yield related traits in groundnut (*Arachis hypogaea* L.) under different water regimes in Niger and Senegal. *Euphytica*, 206(3): 631-647.

Ferguson, M., Burow, M., Schulze, S., Bramel, P., Paterson, A., Kresovich, S. and Mitchell, S., 2004, Microsatellite identification and characterization in peanut (*A. hypogaea* L.). *Theor. Appl. Genet.*, 108(6): 1064-1070.

Feschotte, C., Jiang, N. and Wessler, S. R., 2002a, Plant transposable elements: where genetics meets genomics. *Nat. Rev. Genet.*, 3(5): 329-341.

Feschotte, C. and Mouches, C., 2000, Evidence that a family of miniature inverted-repeat transposable elements (MITEs) from the *Arabidopsis thaliana* genome has arisen from a *pogo-like* DNA transposon. *Mol. Biol. Evol.*, 17: 730-737.

Feschotte, C. and Wessler, S. R., 2002, *Mariner*-like transposases are widespread and diverse in flowering plants. *Proc. Natl. Acad. Sci.*, 99(1): 280-285.

Feschotte, C., Zhang, X. and Wessler, S. R., 2002b, Miniature inverted-repeat transposable elements (MITEs) and their relationship with established DNA transposons. In *Mobile DNA II*. Eds. Craig, N. L., Craigie, R., Gellert, M. and Lambowitz, A. M., American Society for Microbiology Press, Washington DC, pp. 1147-1158.

Finnegan, D. J., 1989, Eukaryotic transposable elements and genome evolution. *Trends Genet.*, 5(4): 103-107.

Fisher, R. A. and Yates, F., 1963, Statistical Tables for Biological, Agricultural and Medical Research. Oliver and Boyd, Edinburgh, Scotland. p. 285.

Fonceka, D., Tossim, H. A., Rivallan, R., Vignes, H., Faye, I., Ndoye, O., Moretzsohn, M. C., Bertioli, D. J., Glaszmann, J. C. and Courtois, B., 2012a, Fostered and left behind alleles in peanut: interspecific QTL mapping reveals footprints of domestication and useful natural variation for breeding. *BMC Plant Biol.*, 12(26): 1-16.

Fonceka, D., Tossim, H. A., Rivallan, R., Vignes, H., Lacut, E., de Bellis, F., Faye, I., Ndoye, O., Leal-Bertioli, S. C. M. and Valls, J. F. M., 2012b, Construction of chromosome segment substitution lines in peanut (*Arachis hypogaea* L.) using a wild synthetic and QTL mapping for plant morphology. *PLoS One*, 7(11): e48642.

Fukai, E., Małolepszy, A., Sandal, N., Hayashi, M. and Andersen, S. U., 2014, Forward and reverse genetics: the *LORE1* retrotransposon insertion mutants. In *The Lotus japonicus Genome*. Eds. Tabata, S. and Stougaard, J., Springer, New York, pp. 221-227.

Garcia, G. M., Stalker, H. T., Schroeder, E., Lyerly, J., H. and Kochert, G., 2005, A RAPD-based linkage map of peanut based on a backcross population between the two diploid species *Arachis stenosperma* and *A. cardenasii*. *Peanut Sci.*, 32(1): 1-8.

Gautami, B., Pandey, M. K., Vadez, V., Nigam, S. N., Ratnakumar, P., Krishnamurthy, L., Radhakrishnan, T., Gowda, M. V. C., Narasu, M. L., Hoisington, D. A., Knapp, S. J. and Varshney, R. K., 2012, Quantitative trait locus analysis and construction of consensus genetic map for drought tolerance traits based on three recombinant inbred line populations in cultivated groundnut (*Arachis hypogaea* L.). *Mol. Breed.*, 30(2): 757-772.

Gavidia, I., Perez-Bermudez, P. and Seitz, H. U., 2002, Cloning and expression of two novel aldo/keto reductases from *Digitalis purpurea* leaves. *Eur. J. Biochem.*, 269(12): 2842-2850.

Gowda, M. V. C., Bhat, R. S., Motagi, B. N., Sujay, V., Varshakumari and Bhat, S., 2010, Association of high-frequency origin of late leaf spot resistant mutants with *AhMITE1* transposition in peanut. *Plant Breed.*, 129(5): 567-569.

Gowda, M. V. C., Bhat, R. S., Sujay, V., Kusuma, P., Varshakumari, Bhat, S. and Varshney, R. K., 2011, Characterization of *AhMITE1* transposition and its association with the mutational and evolutionary origin of botanical types in peanut (*Arachis* spp.). *Plant Syst. Evol.*, 291(3-4): 153-158.

Gowda, M. V. C., Motagi, B. N., Sheshagiri, R., Naidu, G. K. and Rajendraprasad M. N., 2002, Mutant 28-2: a bold-seeded disease and pest resistant groundnut genotype for Karnataka, India. *Int. Arachis Newslet.*, 22: 29-32.

Gowda, M. V. C., Nadaf, H. and Giriraj, K., 1989, A new growth habit variant of taxonomical importance in groundnut (*Arachis hypogaea* L.). *Int. Arachis Newslet.*, 6(6): 48-54.

Guo, B., Chen, X., Dang, P., Scully, B. T., Liang, X., Holbrook, C. C., Yu, J. and Culbreath, A. K., 2008, Peanut gene expression profiling in developing seeds at different reproduction stages during *Aspergillus parasiticus* infection. *BMC Dev. Biol.*, 8(12): 1-16.

Gupta, S. K., Baek, J., Carrasquilla-Garcia, N. and Penmetsa, R. V., 2015, Genome-wide polymorphism detection in peanut using next-generation restriction-site-associated DNA (RAD) sequencing. *Mol. Breed.*, 35(7): 1-10.

Haley, C. S. and Knott, S. A., 1992, A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity*, 69(4): 315-324.

Halward, T. M., Stalker, H. T. and Kochert, G., 1993, Development of an RFLP linkage map in diploid peanut species. *Theor. Appl. Genet.*, 87(3): 379-384.

Halward, T. M., Stalker, H. T., Larue, E. A. and Kochert, G., 1991, Genetic variation detectable with molecular markers among unadapted germplasm resources of cultivated peanut and related wild species. *Genome*, 34(6): 1013-1020.

Halward, T. M., Stalker, H. T., Larue, E. A. and Kochert, G., 1992, Use of single-primer DNA amplifications in genetic studies of peanut (*Arachis hypogaea* L.). *Plant Mol. Biol.*, 18(2): 315-325.

Hanson, C., Robinson, H. and Comstock, R., 1956, Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.*, 48(6): 268-272.

Hartwig, B., James, G. V., Konrad, K., Schneeberger, K. and Turck, F., 2012, Fast isogenic mapping-by-sequencing of ethyl methanesulfonate-induced mutant bulks. *Plant Physiol.*, 160(2): 591-600.

He, G., Meng, R., Newman, M., Gao, G., Pittman, R. N. and Prakash, C. S., 2003, Microsatellites as DNA markers in cultivated peanut (*Arachis hypogaea* L.). *BMC Plant Biol.*, 3(3): 1-6.

He, G. and Prakash, C., 1997, Identification of polymorphic DNA markers in cultivated peanut (*Arachis hypogaea* L.). *Euphytica*, 97(2): 143-149.

He, G., Woullard, F., Marong, I. and Guo, B., 2006, Transferability of soybean SSR markers in peanut (*Arachis hypogaea* L.). *Peanut Sci.*, 33(1): 22-28.

Henry, I. M., Nagalakshmi, U., Lieberman, M. C., Ngo, K. J., Krasileva, K. V., Vasquez-Gross, H., Akhunova, A., Akhunov, E., Dubcovsky, J. and Tai, T. H., 2014, Efficient genome-wide detection and cataloging of EMS-induced mutations using exome capture and next-generation sequencing. *Plant Cell*, 26(4): 1382-1397.

Herselman, L., 2003, Genetic variation among Southern African cultivated peanut (*Arachis hypogaea* L.) genotypes as revealed by AFLP analysis. *Euphytica*, 133(3): 319-327.

Herselman, L., Thwaites, R., Kimmins, F. M., Courtois, B., Van der Merwe, P. J. A. and Seal, S. E., 2004, Identification and mapping of AFLP markers linked to peanut (*Arachis hypogaea* L.) resistance to the aphid vector of groundnut rosette disease. *Theor. Appl. Genet.*, 109(7): 1426-1433.

Hildebrand, C. E., David, C., Torney, C. and Wagner, P., 1994, Informativeness of polymorphic DNA markers. In *The Human Genome Project: Deciphering the Blueprint of Heredity*. Ed. Cooper, N. C., University Science Books, Mill Valley, California, pp. 100-102.

Hirochika, H., 2001, Contribution of the *Tos17* retrotransposon to rice functional genomics. *Curr. Opin. Plant Biol.*, 4(2): 118-122.

Hirochika, H., Sugimoto, K., Otsuki, Y., Tsugawa, H. and Kanda, M., 1996, Retrotransposons of rice involved in mutations induced by tissue culture. *Proc. Natl. Acad. Sci.*, 93(15): 7783-7788.

Hoen, D. R., Park, K. C., Elrouby, N., Yu, Z., Mohabir, N., Cowan, R. K. and Bureau, T. E., 2006, Transposon-mediated expansion and diversification of a family of *ULP*-like genes. *Mol. Biol. Evol.*, 23(6): 1254-1268.

Hong, S. and Vierling, E., 2000, Mutants of *Arabidopsis thaliana* defective in the acquisition of tolerance to high temperature stress. *Proc. Natl. Acad. Sci*., 97(8): 4392-4397.

Hong, Y., Liang, X., Chen, X., Liu, H., Zhou, G., Li, S. and Wen, S., 2008, Construction of genetic linkage map based on SSR markers in peanut (*Arachis hypogaea* L.). *Agric. Sci. China*, 7(8): 915-921.

Hong, Y., Pandey, M. K., Liu, Y., Chen, X., Liu, H., Varshney, R. K., Liang, X. and Huang, S., 2015, Identification and evaluation of single-nucleotide polymorphisms in allotetraploid peanut (*Arachis hypogaea* L.) based on amplicon sequencing combined with high resolution melting (HRM) analysis. *Front. Plant Sci.*, 6(1068): 1-10.

Hopkins, M. S., Casa, A. M., Wang, T., Mitchell, S. E., Dean, R. E., Kochert, G. D. and Kresovich, S., 1999, Discovery and characterization of polymorphic simple sequence repeats (SSRs) in peanut. *Crop Sci.*, 39(4): 1243-1247.

Horst, I., Welham, T., Kelly, S., Kaneko, T., Sato, S., Tabata, S., Parniske, M. and Wang, T. L., 2007, TILLING mutants of *Lotus japonicus* reveal that nitrogen assimilation and fixation can occur in the absence of nodule-enhanced sucrose synthase. *Plant Physiol.*, 144(2): 806-820.

Huang, L., He, H., Chen, W., Ren, X., Chen, Y., Zhou, X., Xia, Y., Wang, X., Jiang, X., Liao, B. and Jiang, H., 2015, Quantitative trait locus analysis of agronomic and quality-related traits in cultivated peanut (*Arachis hypogaea* L.). *Theor. Appl. Genet.*, 128(6): 1103-1115.

Huang, L., Wu, B., Zhao, J., Li, H., Chen, W., Zheng, Y., Ren, X., Chen, Y., Zhou, X. and Lei, Y., 2016, Characterization and transferable utility of microsatellite markers in the wild and cultivated *Arachis* species. *PLoS One*, 111(5): e0156633.

Hui, W., ShuangLing, L., Yan, R., MengQi, X., YanMao, S., Mei, Y. and ChuanTang, W., 2013, Genetic relationship of peanut (*Arachis hypogaea* L.) varieties and advanced generation lines evaluated by *AhMITE* transposable markers. *J. Agric. Biotech.*, 21(10): 1176-1184.

Hussein, S. M., Batada, N. N., Vuoristo, S., Ching, R. W., Autio, R., Närvä, E., Ng, S., Sourour, M., Hamalainen, R. and Olsson, C., 2011, Copy number variation and selection during reprogramming to pluripotency. *Nature*, 471(7336): 58-62.

Husted, L., 1936, Cytological studies on the peanut, *Arachis*. II. *Cytologia*, 7(3): 396-423.

IBPGR/ICRISAT, 1992, Descriptors for groundnut. International Board of Plant Genetic Resources and International Crops Research Institute For the Semi-Arid Tropics, Rome, Italy and Patancheru, Andhra Pradesh, India, p. 51.

Isleib, T., Wilson, R. and Novitzky, W., 2006, Partial dominance, pleiotropism and epistasis in the inheritance of the high-oleate trait in peanut. *Crop Sci.*, 46(3): 1331-1335.

Janila, P., Variath, M. T., Pandey, M. K., Desmae, H., Motagi, B. N., Okori, P., Manohar, S. S., Rathnakumar, A. L., Radhakrishnan, T., Liao, B. and Varshney, R. K., 2016, Genomic tools in groundnut breeding program: status and perspectives. *Front. Plant Sci*., 7(289): 1-15.

Jansen, R. C. and Stam, P., 1994, High resolution of quantitative traits into multiple loci via interval mapping. *Genetics*, 136(4): 1447-1455.

Jiang, H., Huang, L., Ren, X., Chen, Y., Zhou, X., Xia, Y., Huang, J., Lei, Y., Yan, L., Wan, L. and Liao, B., 2014, Diversity characterization and association analysis of agronomic traits in a Chinese peanut (*Arachis hypogaea* L.) mini-core collection. *J. Integr. Plant Biol.*, 56(2): 159-169.

Jiang, H., Xiao-Ping, R., Zhang, X., Huang, J., Yong, L., Li-Ying, Y., Bo-Shou, L., Upadhyaya, H. D. and Holbrook, C. C., 2010, Comparison of genetic diversity based on SSR markers between peanut mini core collections from China and ICRISAT. *Acta Agron. Sin.*, 36(7): 1084-1091.

Johnson, H. W., Robinson, H. and Comstock, R., 1955, Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J.*, 47(10): 477-483.

Jung, S., Swift, D., Sengoku, E., Patel, M., Teulé, F., Powell, G., Moore, K. and Abbott, A., 2000, The high oleate trait in the cultivated peanut [*Arachis hypogaea* L.]. I. Isolation and characterization of two genes encoding microsomal oleoyl-PC desaturases. *Mol. Gen. Genet.*, 263(5): 796-805.

Kale, D. M., Murty, G. S. S., Badigannavar, A. M., Makane, V. G., Toprope, V. N., Shirshikar, S. P. and Jangawad, N. P., 2008, TLG 45, a large-seeded groundnut variety for Marathwada region of Maharashtra in India. *SAT eJournal*, 6: 1-2.

Kalendar, R., 2011, The use of retrotransposon-based molecular markers to analyze genetic diversity. *Ratar. Povrt.*, 48(2): 261-274.

Kalendar, R., Grob, T., Regina, M., Suoniemi, A. and Schulman, A., 1999, IRAP and REMAP: two new retrotransposon-based DNA fingerprinting techniques. *Theor. Appl. Genet.*, 98(5): 704-711.

Kayam, G., Brand, Y., Faigenboim-Doron, A., Patil, A., Hedvat, I. and Hovav, R., 2017, Fine-mapping the branching habit trait in cultivated peanut by combining bulked segregant analysis and high-throughput sequencing. *Front. Plant Sci*., 8(467): 1-11.

Kendall, M. and Stuart, A., 1961, The Advanced Theory of Statistics, Hafner Publishing Company, New York. p. 53.

Khedikar, Y., Gowda, M. V. C., Sarvamangala, C., Patgar, K., Upadhyaya, H. D. and Varshney, R. K., 2010, A QTL study on late leaf spot and rust revealed one major QTL for molecular breeding for rust resistance in groundnut (*Arachis hypogaea* L.). *Theor. Appl. Genet.*, 121(5): 971-984.

Khera, P., Upadhyaya, H. D., Pandey, M. K., Roorkiwal, M., Sriswathi, M., Janila, P., Guo, Y., McKain, M. R., Nagy, E. D. and Knapp, S. J., 2013, Single nucleotide polymorphism–based genetic diversity in the reference set of peanut (spp.) by developing and applying cost-effective Kompetitive Allele Specific Polymerase Chain Reaction genotyping assays. *Plant Genome*, 6(3): 1-11.

Kilian, A., 2008, DArT-based whole genome profiling and novel information technologies in support system of modern breeding of groundnut. *Proc. 3rd International Conference for Peanut Genomics and Biotechnology on "Advances in Arachis through Genomics and Biotechnology" (AAGB)*, 4-8, November 2008, ICRISAT, Patancheru, India, p. 2.

Kim, H., Terakami, S., Nishitani, C., Kurita, K., Kanamori, H., Katayose, Y., Sawamura, Y., Saito, T. and Yamamoto, T., 2012, Development of cultivar-specific DNA markers based on retrotransposon-based insertional polymorphism in Japanese pear. *Breed. Sci.*, 62(1): 53-62.

Kochert, G., Halward, T. M., Branch, W. D. and Simpson, C. E., 1991, RFLP variability in peanut (*Arachis hypogaea* L.) cultivars and wild species. *Theor. Appl. Genet.*, 81(5): 565-570.

Kochert, G., Stalker, H. T., Gimenes, M., Galgaro, L., Lopes, C. R. and Moore, K., 1996, RFLP and cytogenetic evidence on the origin and evolution of allotetraploid domesticated peanut, *Arachis hypogaea* (Leguminosae). *Am. J. Bot.*, 83(10): 1282-1291.

Kolekar, R. M., 2017, Transfer of resistance to late leaf spot and rust in groundnut through marker assisted backcrossing. *Ph. D. Thesis,* Univ. Agric. Sci., Dharwad (India).

Kolekar, R. M., Sujay, V., Shirasawa, K., Sukruth, M., Khedikar, Y. P., Gowda, M. V. C., Pandey, M. K., Varshney, R. K. and Bhat, R. S., 2016, QTL mapping for late leaf spot and rust resistance using an improved genetic map and extensive phenotypic data on a recombinant inbred line population in peanut (*Arachis hypogaea* L.). *Euphytica,* 209(1): 147-156.

Koornneef, M., Vries, H., Hanhart, C., Soppe, W. and Peeters, T., 1994, The phenotype of some late-flowering mutants is enhanced by a locus on chromosome 5 that is not effective in the Landsberg erecta wild-type. *Plant J.*, 6(6): 911-919.

Kosambi, D. D., 1943, The estimation of map distances from recombination values. *Ann. Eugenics,* 12(1): 172-175.

Kottapalli, K. R., Burow, M. D., Burow, G., Burke, J. and Puppala, N., 2007, Molecular Characterization of the U.S. Peanut mini core collection using microsatellite markers. *Crop Sci.*, 47(4): 1718-1727.

Krapovickas, A., 1969, The origin, variability and spread of the groundnut (*Arachis hypogaea*). In *The Domestication and Exploitation of Plant and Animals.* Eds. Ucko, R. J. and Dimbledy, W. C., Greald Duckworth Co. Ltd., London, pp. 427-441.

Krapovickas, A., 1973, Evolution of the genus *Arachis*. In *Agricultural Genetics-Selected Topics*. Ed. Moav, R., John Wiley and Sons, New York, USA, pp. 135-151.

Lander, E. S. and Schork, N. J., 1994, Genetic dissection of complex traits. *Science*, 265(5181): 2037-2048.

Landfort, W. R., Sowell, J. M. and Corely, W. L., 1965, Catalogue of peanuts. (Cited in: Faye, I., Ndoye, O. and Diop, T. A., 2009, Evaluation of fresh seed dormancy on seven peanut (*Arachis hypogaea* L.) lines derived from crosses between Spanish varieties: variability on intensity and duration. *J. Applied Sci. Res*., 5(7): 853-857.)

Le, Q. H., Wright, S., Yu, Z. and Bureau, T., 2000, Transposon diversity in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci.*, 97(13): 7376-7381.

Leal-Bertioli, S. C., Moretzsohn, M. C., Roberts, P. A., Ballén-Taborda, C., Borba, T. C., Valdisser, P. A., Vianello, R. P., Araújo, A. C. G., Guimarães, P. M. and Bertioli, D. J., 2016, Genetic mapping of resistance to *Meloidogyne arenaria* in *Arachis stenosperma*: a new source of nematode resistance for peanut. *G3(Bethesda)*, 6(2): 377-390.

Lee, J., Park, J., Kim, J., Kwon, S., Shin, J., Hong, S., Min, H. and Kim, N., 2006, Genetic mapping of the *Isaac*-CACTA transposon in maize. *Theor. Appl. Genet.*, 113(1): 16-22.

Lipka, A. E., Tian, F., Wang, Q., Peiffer, J., Li, M., Bradbury, P. J., Gore, M. A., Buckler, E. S. and Zhang, Z., 2012, GAPIT: genome association and prediction integrated tool. *Bioinformatics*, 28(18): 2397-2399.

Liu, K. and Muse, S. V., 2005, PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics*, 21(9): 2128-2129.

Liu, W., Fu, Y., Hu, G., Si, H., Zhu, L., Wu, C. and Sun, Z., 2007, Identification and fine mapping of a thermo-sensitive chlorophyll deficient mutant in rice (*Oryza sativa* L.). *Planta*, 226(3): 785-795.

Lu, C., Chen, J., Zhang, Y., Hu, Q., Su, W. and Kuang, H., 2012, Miniature inverted–repeat transposable elements (MITEs) have been accumulated through amplification bursts and play important roles in gene expression and species diversity in *Oryza sativa*. *Mol. Biol. Evol.*, 29(3): 1005-1017.

Luo, H., Ren, X., Li, Z., Xu, Z., Li, X., Huang, L., Zhou, X., Chen, Y., Chen, W., Lei, Y., Liao, B., Pandey, M. K., Varshney, R. K., Guo, B., Jiang, X., Liu, F. and Jiang, H., 2017, Co-localization of major quantitative trait loci for pod size and weight to a 3.7 cM interval on chromosome A05 in cultivated peanut (*Arachis hypogaea* L.). *BMC Genomics*, 18(58): 1-12.

Luo, Z., Yang, Z., Zhong, B., Li, Y., Xie, R., Zhao, F., Ling, Y. and He, G., 2007, Genetic analysis and fine mapping of a dynamic rolled leaf gene, *RL10(t)*, in rice (*Oryza sativa* L.). *Genome*, 50(9): 811-817.

Lush, J. L., 1940, Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *J. Anim. Sci.*, 1940(1): 293-301.

Mace, E. S., Buhariwalla, K. K., Buhariwalla, H. K. and Crouch, J. H., 2003, A high-throughput DNA extraction protocol for tropical molecular breeding programs. *Plant Mol. Biol. Rep.*, 21(4): 459-460.

Mace, E. S., Varshney, R. K., Mahalakshmi, V., Seetha, K., Gafoor, A., Leeladevi, Y. and Crouch, J. H., 2008, *In silico* development of simple sequence repeat markers within the aeschynomenoid/dalbergoid and genistoid clades of the Leguminosae family and their transferability to *Arachis hypogaea*, groundnut. *Plant Sci.*, 174(1): 51-60.

Manninen, O., Kalendar, R., Robinson, J. and Schulman, A., 2000, Application of *BARE-1* retrotransposon markers to the mapping of a major resistance gene for net blotch in barley. *Mol. Gen. Genet.*, 264(3): 325-334.

Milla, S. R., 2003, Relationships and utilization of *Arachis* germplasm in peanut improvement. *Ph. D. Thesis*, North Carolina State Uni., Raleigh (USA).

Mondal, S., Phadke, R. R. and Badigannavar, A. M., 2015, Genetic variability for total phenolics, flavonoids and antioxidant activity of testaless seeds of a peanut recombinant inbred line population and identification of their controlling QTLs. *Euphytica*, 204(2): 311-321.

Monden, Y., Hara, T., Okada, Y., Jahana, O., Kobayashi, A., Tabuchi, H., Onaga, S. and Tahara, M., 2015, Construction of a linkage map based on retrotransposon insertion polymorphisms in sweet potato via high-throughput sequencing. *Breed. Sci.*, 65(2): 145-153.

Monden, Y., Naito, K., Okumoto, Y., Saito, H., Oki, N., Tsukiyama, T., Ideta, O., Nakazaki, T., Wessler, S. R. and Tanisaka, T., 2009, High potential of a transposon *mPing* as a marker system in *japonica* × *japonica* cross in rice. *DNA Res.*, 16(2): 131-140.

Monden, Y., Takasaki, K., Futo, S., Niwa, K., Kawase, M., Akitake, H. and Tahara, M., 2014a, A rapid and enhanced DNA detection method for crop cultivar discrimination. *J. Biotechnol.*, 185: 57-62.

Monden, Y., Yamamoto, A., Shindo, A. and Tahara, M., 2014b, Efficient DNA fingerprinting based on the targeted sequencing of active retrotransposon insertion sites using a bench-top high-throughput sequencing platform. *DNA Res.*, 21(5): 491-498.

Moretzsohn, M. C., Gouvea, E. G., Inglis, P. W., Leal-Bertioli, S. C., Valls, J. F. M. and Bertioli, D. J., 2013, A study of the relationships of cultivated peanut (*Arachis hypogaea*) and its most closely related wild species using intron sequences and microsatellite markers. *Ann. Bot.*, 111(1): 113-126.

Moretzsohn, M. C., Hopkins, M., Mitchell, S., Kresovich, S., Valls, J. F. M. and Ferreira, M., 2004, Genetic diversity of peanut (*Arachis hypogaea* L.) and its wild relatives based on the analysis of hypervariable regions of the genome. *BMC Plant Biol.*, 4(11): 1-10.

Moretzsohn, M. C., Leoi, L., Proite, K., Guimaraes, P. M., Leal-Bertioli, S. C., Gimenes, M. A., Martins, W. S., Valls, J. F. M., Grattapaglia, D. and Bertioli, D. J., 2005, A microsatellite-based, gene-rich linkage map for the AA genome of *Arachis* (Fabaceae). *Theor. Appl. Genet.*, 111(6): 1060-1071.

Nadeau, J. H. and Frankel, W. N., 2000, The roads from phenotypic variation to gene discovery: mutagenesis versus QTLs. *Nat. Genet.*, 25(4): 381-384.

Nagy, E. D., Guo, Y., Tang, S., Bowers, J. E., Okashah, R. A., Taylor, C. A., Zhang, D., Khanal, S., Heesacker, A. F. and Khalilian, N., 2012, A high-density genetic map of *Arachis duranensis*, a diploid ancestor of cultivated peanut. *BMC Genomics*, 13(469): 1-11.

Nielen, S., Fonseca, F., Guimares, P., Leal-Bertioli, S. C. and Bertioli, D. J., 2009, Isolation and characterization of retrotransposons in wild and cultivated peanut species. In *Induced Plant Mutations in the Genomics Era.* Ed. Shu, Q. Y., Food and Agriculture Organization of the United Nations, Rome, pp. 499-502.

Palmieri, D. A., Bechara, M., Curi, R., Gimenes, M. and Lopes, C., 2005, Novel polymorphic microsatellite markers in section Caulorrhizae (*Arachis*, Fabaceae). *Mol. Ecol. Notes*, 5(1): 77-79.

Palmieri, D. A., Hoshino, A., Bravo, J., Lopes, C. and Gimenes, M., 2002, Isolation and characterization of microsatellite loci from the forage species *Arachis pintoi* (Genus *Arachis*). *Mol. Ecol. Notes*, 2(4): 551-553.

Pandey, M. K., Gautami, B., Jayakumar, T., Sriswathi, M., Upadhyaya, H. D., Gowda, M. V. C., Radhakrishnan, T., Bertioli, D. J., Knapp, S. J., Cook, D. R. and Varshney, R. K., 2012, Highly informative genic and genomic SSR markers to facilitate molecular breeding in cultivated groundnut (*Arachis hypogaea*). *Plant Breed.*, 131(1): 139-147.

Pandey, M. K., Upadhyaya, H. D., Rathore, A., Vadez, V., Sheshshaye, M. S., Sriswathi, M., Govil, M., Kumar, A., Gowda, M. V. C., Shivali, S., Hamidou, F., Anil Kumar, V., Khera, P., Bhat, R. S., Khan Amir, W., Sube, S., Hongjie, L., Emmanuel, M., Nadaf, H. L., Mukri, G., Liang, X., Jackson, S. and Varshney, R. K., 2014a, Genomewide association studies for 50 agronomic traits in peanut using the reference set comprising 300 genotypes from 48 countries of semi-arid tropics of the world. *PLoS One*, 9(8): e105228.

Pandey, M. K., Wang, H., Khera, P., Vishwakarma, M. K., Kale, S. M., Culbreath, A. K., Holbrook, C. C., Wang, X., Varshney, R. K. and Guo, B., 2017, Genetic dissection of novel QTLs for resistance to leaf spots and tomato spotted wilt virus in peanut (*Arachis hypogaea* L.). *Front. Plant Sci.*, 8(25): 1-12.

Pandey, M. K., Wang, M. L., Qiao, L., Feng, S., Khera, P., Wang, H., Tonnis, B., Barkley, N. A., Wang, J. and Holbrook, C. C., 2014b, Identification of QTLs associated with oil content and mapping *FAD2* genes and their relative contribution to oil quality in peanut (*Arachis hypogaea* L.). *BMC genetics*, 15(133): 1-14.

Panse, V. G. and Sukhatme, P. V., 1954, Statistical Methods for Agricultural Workers. 3rd Ed., ICAR, New Delhi. p. 58.

Patel, M., Jung, S., Moore, K., Powell, G., Ainsworth, C. and Abbott, A., 2004, High-oleate peanut mutants result from a MITE insertion into the *FAD2* gene. *Theor. Appl. Genet.*, 108(8): 1492-1502.

Paterson, A. H., 1997, Molecular Dissection of Complex Traits. CRC Press, New York, USA. p. 336.

Pattanashetti, S. K., 2005, Genetic analysis of mutational origin of diversity in groundnut (*Arachis hypogaea* L.). *Ph. D. Thesis,* Univ. Agric. Sci. Dharwad (India).

Peng, Z., Gallo, M., Tillman, B. L., Rowland, D. and Wang, J., 2016, Molecular marker development from transcript sequences and germplasm evaluation for

cultivated peanut (*Arachis hypogaea* L.). *Mol. Genet. Genomics*, 291(1): 363-381.

Perrier, X., Flori, A. and Bonnot, F., 2003. Data Analysis Methods. In *Genetic Diversity of Cultivated Tropical Plants*. Eds. Hamon, P., Seguin, M., Perrier, X., Glaszmann, J. C., Enfield, Science Publishers, Montpellier, pp. 43-76.

Piriyapongsa, J. and Jordan, I. K., 2007, A family of human microRNA genes from miniature inverted-repeat transposable elements. *PLoS ONE*, 2(2): e203.

Prasad, M. V. R., Kaul, S. and Jain, H. K., 1984, Induced mutants of peanut (*Arachis hypogaea* L.) for canopy and pod bearing characters. *Indian J. Genet. Plant Breed.*, 44(1): 25-34.

Pritchard, J. K., Stephens, M., Rosenberg, N. A. and Donnelly, P., 2000, Association mapping in structured populations. *Am. J. Hum. Genet.*, 67(1): 170-181.

Queen, R., Gribbon, B., James, C., Jack, P. and Flavell, A., 2004, Retrotransposon-based molecular markers for linkage and genetic diversity analysis in wheat. *Mol. Genet. Genomics*, 271(1): 91-97.

Ravi, K., Vadez, V., Isobe, S., Mir, R. R., Guo, Y., Nigam, S. N., Gowda, M. V. C., Radhakrishnan, T., Bertioli, D. J. and Knapp, S. J., 2011, Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). *Theor. Appl. Genet.*, 122(6): 1119-1132.

Reddy, P. S. and Basu, M. S., 1989, Groundnut Varieties of India. Tech. Bull. National Research Center for Groundnut, Junagadh. pp. 36-42.

Ren, X., Jiang, H., Yan, Z., Chen, Y., Zhou, X., Huang, L., Lei, Y., Huang, J., Yan, L. and Qi, Y., 2014, Genetic diversity and population structure of the major peanut (*Arachis hypogaea* L.) cultivars grown in China by SSR markers. *PloS one*, 9(2): e88091.

Robinson, H., Comstock, R. E. and Harvey, P., 1949, Estimates of heritability and the degree of dominance in corn. *Agron. J.*, 41(8): 353-359.

Sambrook, J. and Russell, D. W., 2001, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, New York, USA. pp. 434-445.

Samoluk, S. S., Robledo, G., Podio, M., Chalup, L., Ortiz, J. P. A., Pessino, S. C. and Seijo, J. G., 2015, First insight into divergence, representation and chromosome distribution of reverse transcriptase fragments from *L1* retrotransposons in peanut and wild relative species. *Genetica*, 143(1): 113-125.

Sarvamangala, C., Gowda, M. V. C. and Varshney, R. K., 2011, Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut (*Arachis hypogaea* L.). *Field Crops Res.*, 122(1): 49-59.

Sato, K., Mukainari, Y., Naito, K. and Fukunaga, K., 2013, Construction of a foxtail millet linkage map and mapping of spikelet-tipped bristles1 (*stb1*) by using transposon display markers and simple sequence repeat markers with genome sequence information. *Mol. Breed.*, 31(3): 675-684.

Savadi, S. B., Fakrudin, B., Nadaf, H. L. and Gowda, M. V. C., 2012, Transferability of sorghum genic microsatellite markers to peanut. *Am. J. Plant Sci.*, 3(9): 1169-1180.

Schneeberger, K., 2014, Using next-generation sequencing to isolate mutant genes from forward genetic screens. *Nat. Rev. Genet.*, 15(10): 662-676.

Shi, C., Ingvardsen, C., Thümmler, F., Melchinger, A. E., Wenzel, G. and Lübberstedt, T., 2005, Identification by suppression subtractive hybridization of genes that are differentially expressed between near-isogenic maize lines in association with sugarcane mosaic virus resistance. *Mol. Genet. Genomics*, 273(6): 450-461.

Shirasawa, K., Bertioli, D. J., Varshney, R. K., Moretzsohn, M. C., Leal-Bertioli, S. C., Thudi, M., Pandey, M. K., Rami, J. F., Fonceka, D., Gowda, M. V., Qin, H., Guo, B., Hong, Y., Liang, X., Hirakawa, H., Tabata, S. and Isobe, S., 2013, Integrated consensus map of cultivated peanut and wild relatives reveals

structures of the A and B genomes of *Arachis* and divergence of the legume genomes. *DNA Res.*, 20(2): 173-184.

Shirasawa, K., Hirakawa, H. and Isobe, S., 2016a, Analytical workflow of double-digest restriction site-associated DNA sequencing based on empirical and *in silico* optimization in tomato. *DNA Res.*, 23: 145-153.

Shirasawa, K., Hirakawa, H., Nunome, T., Tabata, S. and Isobe, S., 2016b, Genome-wide survey of artificial mutations induced by ethyl methanesulfonate and gamma rays in tomato. *Plant Biotechnol. J.*, 14(1): 51-60.

Shirasawa, K., Hirakawa, H., Tabata, S., Hasegawa, M., Kiyoshima, H., Suzuki, S., Sasamoto, S., Watanabe, A., Fujishiro, T. and Isobe, S., 2012a, Characterization of active miniature inverted-repeat transposable elements in the peanut genome. *Theor. Appl. Genet.*, 124(8): 1429-1438.

Shirasawa, K., Koilkonda, P., Aoki, K., Hirakawa, H., Tabata, S., Watanabe, M., Hasegawa, M., Kiyoshima, H., Suzuki, S., Kuwata, C., Naito, Y., Kuboyama, T., Nakaya, A., Sasamoto, S., Watanabe, A., Kato, M., Kawashima, K., Kishida, Y., Kohara, M., Kurabayashi, A., Takahashi, C., Tsuruoka, H., Wada, T. and Isobe, S., 2012b, *In silico* polymorphism analysis for the development of simple sequence repeat and transposon markers and construction of linkage map in cultivated peanut. *BMC Plant Biol.*, 12(80): 1-13.

Shirasawa, K., Kuwata, C., Watanabe, M., Fukami, M., Hirakawa, H. and Isobe, S., 2016c, Target amplicon sequencing for genotyping genome-wide single nucleotide polymorphisms identified by whole-genome resequencing in peanut. *Plant Genome*, 9(3): 1-11.

Shoba, D., Manivannan, N., Vindhiyavarman, P. and Nigam, S., 2012, SSR markers associated for late leaf spot disease resistance by bulked segregant analysis in groundnut (*Arachis hypogaea* L.). *Euphytica*, 188(2): 265-272.

Shoba, D., Manivannan, N., Vindhiyavarman, P. and Nigam, S. N., 2013, Identification of Quantitative Trait Loci (QTL) for late leaf spot disease resistance in groundnut (*Arachis hypogaea* L.). *Legume Res*., 36(5): 467-472.

Sikora, P., Chawade, A., Larsson, M., Olsson, J. and Olsson, O., 2012, Mutagenesis as a tool in plant genetics, functional genomics and breeding. *Int. J. Plant Genom.*, 2011: 48-51.

Singh, R. K. and Chaudhary, B., 1979, Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana, India. p. 58.

Sivasubramanian, S. and Menon, M., 1973, Heterosis and inbreeding depression in rice. *Madras Agric. J.*, 60: 1139.

Springer, N. M., Ying, K., Fu, Y., Ji, T., Yeh, C., Jia, Y., Wu, W., Richmond, T., Kitzman, J. and Rosenbaum, H., 2009, Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. *PLoS Genet.*, 5(11): e1000734.

Stanley, D., Rejzek, M., Naested, H., Smedley, M., Otero, S., Fahy, B., Thorpe, F., Nash, R. J., Harwood, W. and Svensson, B., 2011, The role of α-glucosidase in germinating barley grains. *Plant Physiol.*,155(2): 932-943.

Subbarao, P. V., Subramanyam, P. and Reddy, P. M., 1990, A modified nine points diseases scale for assessment of rust and late leaf spot of groundnut. *Proc. Second International Congress of French Phytopathological Society*, 28-30 November 1990, Montpellier, France, p 25.

Subrahmanyam, P., McDonald, D., Waliar, F., Reddy, L. J., Nigam, S. N., Gibbons, R. W., Rao, V. R., Singh, A. K., Pande, S., Reddy, P. M. and Rao, P. V. S., 1995, Screening methods and sources of resistance to rust and late leaf spot of groundnut. Inf. Bull. No.47, ICRISAT, Patancheru, Andhra Pradesh, p.33.

Sujay, V., Gowda, M. V. C., Pandey, M. K., Bhat, R. S., Khedikar, Y. P., Nadaf, H. L., Gautami, B., Sarvamangala, C., Lingaraju, S., Radhakrishan, T., Knapp, S. J. and Varshney, R. K., 2012, QTL analysis and construction of consensus

genetic map for foliar disease resistance based on two RIL populations in cultivated groundnut (*Arachis hypogaea* L.). *Mol. Breed.*, 30(2): 773-788.

Sukruth, M., Paratwagh, S. A., Sujay, V., Varshakumari, Gowda, M. V. C., Nadaf, H. L., Motagi, B. N., Lingaraju, S., Pandey, M. K., Varshney, R. K. and Bhat, R. S., 2015, Validation of markers linked to late leaf spot and rust resistance and selection of superior genotypes among diverse recombinant inbred lines and backcross lines in peanut (*Arachis hypogaea* L.). *Euphytica*, 204(2): 343-351.

Sundararaj, N., Nagaraju, S., Ramu, M. V. and Jagannath, M., 1972, Design and Analysis of Field Experiments. University of Agricultural Sciences, Bangalore, India, p. 419.

Till, B., Reynolds, S., Greene, E., Codomo, C., Enns, L., Johnson, J., Burtner, C., Odden, A., Young, K., Taylor, N., Henikoff, J., Comai, L. and Henikoff, S., 2003, Large-scale discovery of induced point mutations with high-throughput TILLING. *Genome Res.*, 13(3): 524-530.

Turcotte, K. and Bureau, T., 2002, Phylogenetic analysis reveals *Stowaway*-like elements may represent a fourth family of the IS*630*-Tc1-*mariner* superfamily. *Genome*, 45(1): 82-90.

Turcotte, K., Srinivasan, S. and Bureau, T., 2001, Survey of transposable elements from rice genomic sequences. *Plant J.*, 25(2): 169-179.

Van Ooijen, J., 2006, JoinMap® 4, Software for the calculation of genetic linkage maps in experimental populations. Kyazma BV, Wageningen, Netherlands. pp. 1-49.

Varshney, R. K., 2016, Exciting journey of 10 years from genomes to fields and markets: some success stories of genomics-assisted breeding in chickpea, pigeonpea and groundnut. *Plant Sci.*, 242: 98-107.

Varshney, R. K., Nayak, S. N., May, G. D. and Jackson, S. A., 2009, Next-generation sequencing technologies and their implications for crop genetics and breeding. *Trends Biotechnol.*, 27(9): 522-530.

Varshney, R. K., Pandey, M. K., Pasupuleti, J., Nigam, S. N., Sudini, H., Gowda, M. V. C., Sriswathi, M., Radhakrishan, T., Manohar, S. S. and Patne, N., 2014, Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.). *Theor. Appl. Genet.*, 127(8): 1771-1781.

Voorrips, R., 2002, MapChart: software for the graphical presentation of linkage maps and QTLs. *J. Hered.*, 93(1): 77-78.

Wang, M. L., Chen, C. Y., Tonnis, B., Barkley, N. A., Pinnow, D. L., Pittman, R. N., Davis, J., Holbrook, C. C., Stalker, H. T. and Pederson, G. A., 2013a, Oil, fatty acid, flavonoid and resveratrol content variability and *FAD2A* functional SNP genotypes in the U.S. peanut mini-core collection. *J. Agric. Food Chem.*, 61(11): 2875-2882.

Wang, M. L., Sukumaran, S., Barkley, N. A., Chen, Z., Chen, C. Y., Guo, B., Pittman, R. N., Stalker, H. T., Holbrook, C. C. and Pederson, G. A., 2011, Population structure and marker–trait association analysis of the US peanut (*Arachis hypogaea* L.) mini-core collection. *Theor. Appl. Genet.*, 123(8): 1307-1317.

Wang, N., Wang, Y., Tian, F., King, G. J., Zhang, C., Long, Y., Shi, L. and Meng, J., 2008, A functional genomics resource for *Brassica napus*: development of an EMS mutagenized population and discovery of *FAE1* point mutations by TILLING. *New Phytol.*, 180(4): 751-765.

Wang, S., Basten, C. and Zeng, Z., 2007, Windows QTL cartographer 2.5. *Thesis*, North Carolina State Uni., Raleigh, (USA).

Wang, X., Lin, Z., Gao, L., Wang, A., Wan, Z., Chen, W., Yang, Y. and Li, R., 2013b, Exome sequencing reveals a signal transducer and activator of transcription 1 (*STAT1*) mutation in a child with recalcitrant cutaneous fusariosis. *J. Allergy Clin. Immunol.*, 131(4): 1242.

Wang, Y., Zhang, X., Zhao, Y., Prakash, C., He, G. and Yin, D., 2015, Insights into the novel members of the *FAD2* gene family involved in high-oleate fluxes in peanut. *Genome*, 58(8): 375-383.

Weber, C. R. and Moorthy, B., 1952, Heritable and nonheritable relationships and variability of oil content and agronomic characters in the F_2 generation of soybean crosses. *Agron. J.*, 44(4): 202-209.

Wurschum, T., Liu, W., Gowda, M., Maurer, H., Fischer, S., Schechert, A. and Reif, J., 2012, Comparison of biometrical models for joint linkage association mapping. *Heredity*, 108(3): 332-340.

Xiao, H., Jiang, N., Schaffner, E., Stockinger, E. J. and van der Knaap, E., 2008, A retrotransposon-mediated gene duplication underlies morphological variation of tomato fruit. *Science*, 319(5869): 1527-1530.

Yeri, S. B. and Bhat, R. S., 2016, Development of late leaf spot and rust resistant backcross lines in JL 24 variety of groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.*, 7(1): 37-41.

Yeri, S. B., Shirasawa, K., Pandey, M. K., Gowda, M. V. C., Sujay, V., Shriswathi, M., Nadaf, H. L., Motagi, B. N., Lingaraju, S., Bhat, A. R. S., Varshney, R. K., Krishnaraj, P. U. and Bhat, R. S., 2014, Development of NILs from heterogeneous inbred families for validating the rust resistance QTLs in peanut (*Arachis hypogaea* L.). *Plant Breed.*, 133: 80-85.

Yu, Z., Wright, S. I. and Bureau, T. E., 2000, *Mutator*-like elements in *Arabidopsis thaliana*: structure, diversity and evolution. *Genetics*, 156(4): 2019-2031.

Zeng, Z. B., 1994, Precision mapping of quantitative trait loci. *Genetics*, 136(4): 1457-1468.

Zhang, J., Liang, S., Duan, J., Wang, J., Chen, S., Cheng, Z., Zhang, Q., Liang, X. and Li, Y., 2012, *De novo* assembly and characterisation of the transcriptome during seed development and generation of genic-SSR markers in peanut (*Arachis hypogaea* L.). *BMC Genomics*, 13(90): 1-6.

Zhang, X., Feschotte, C., Zhang, Q., Jiang, N., Eggleston, W. B. and Wessler, S. R., 2001, *P* instability factor: an active maize transposon system associated with the amplification of *Tourist*-like MITEs and a new superfamily of transposases. *Proc. Natl. Acad. Sci.*, 98(22): 12572-12577.

Zhang, Y., Luo, L., Xu, C., Zhang, Q. and Xing, Y., 2006, Quantitative trait loci for panicle size, heading date and plant height co-segregating in trait-performance derived near-isogenic lines of rice (*Oryza sativa*). *Theor. Appl. Genet.*, 113(2): 361-368.

Zhou, X., Dong, Y., Zhao, J., Huang, L., Ren, X., Chen, Y., Huang, S., Liao, B., Lei, Y. and Yan, L., 2016a, Genomic survey sequencing for development and validation of single-locus SSR markers in peanut (*Arachis hypogaea* L.). *BMC Genomics*, 17(420): 1-14.

Zhou, X., Xia, Y., Liao, J., Liu, K., Li, Q., Dong, Y., Ren, X., Chen, Y., Huang, L. and Liao, B., 2016b, Quantitative trait locus analysis of late leaf spot resistance and plant-type-related traits in cultivated peanut (*Arachis hypogaea* L.) under multi-environments. *PLoS One*, 11(11): e0166873.

Zhou, X., Xia, Y., Ren, X., Chen, Y., Huang, L., Huang, S., Liao, B., Lei, Y., Yan, L. and Jiang, H., 2014, Construction of a SNP-based genetic linkage map in cultivated peanut based on large scale marker development using next-generation double-digest restriction-site-associated DNA sequencing (ddRADseq). *BMC Genomics*, 15(351): 1-14.

Zou, J., Chen, Z., Zhang, S., Zhang, W., Jiang, G., Zhao, X., Zhai, W., Pan, X. and Zhu, L., 2005, Characterizations and fine mapping of a mutant gene for high tillering and dwarf in rice (*Oryza sativa* L.). *Planta*, 222(4): 604-612.

Appendix I: Taxonomic, agronomic and productivity traits among TMV 2, TMV 2-NLM and their RILs

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
1	TMV 2	S	E	W-E	LG	5	3	3	5	LT	F	2-1
2	TMV 2-NLM	A	D-3	L	DG	5	3	5	7	DT	F	2-1
3	1-2(a)	S	E	W-E	DG	5	3	5	5	LT	F	2-3-1
4	1-2(b)	S	E	W-E	DG	5	3	5	5	LT	F	2-3-1
5	1-2(d)	S	E	O-E	LG	5	3	3	5	LT	F	2-1
6	1-3	S	E	O-E	LG	5	3	3	5	LT	F	2-1
7	1-4(a)	A	D-3	W-E	DG	9	5	3	7	LT	C	2-3-1
8	1-5	A	D-3	W-E	DG	9	3	3	5	LT	F	2-1-3
9	1-6(a)	A	D-3	Ob	DG	5	3	3	5	LT	F	2-3-1
10	1-6(b)	A	D-3	W-E	DG	5	5	3	5	LT	F	2-1-3
11	1-7(a)	S	E	W-E	DG	5	3	7	3	LT	F	2-3-1
12	1-7(b)	S	E	W-E	DG	7	5	5	5	DT	C	2-1
13	1-7(c)	S	D-3	W-E	DG	5	5	3	5	LT	F	2-1-3
14	1-7(d)	A	E	O-L	DG	7	5	7	7	DT	F	2-1-3
15	1-7(9)	A	E	O-L	DG	7	5	9	7	DT	C	2-1-3
16	1-9	S	D-3	W-E	DG	3	3	3	5	DT	F	2-1
17	1-11(a)	A	E	W-E	DG	5	0	3	5	DT	C	2-1
18	1-11(b)	S	D-3	W-E	DG	5	5	3	5	LT	F	2-1
19	1-11(c)	A	D-3	W-E	DG	5	3	3	5	LT	F	2-1
20	1-11(g)	A	E	L	DG	7	7	0	5	LT	F	2-1
21	1-12 (a)	S	E	W-E	DG	5	3	3	5	DT	F	2-1-3
22	1-12 (c)	S	E	W-E	LG	5	3	3	5	LT	F	2-1-3
23	1-13 (c)	A	E	O-E	DG	5	0	0	5	LT	F	2-1-3
24	1-14 (a)	S	E	O-E	DG	5	3	0	5	LT	F	2-1-3
25	1-14 (b)	S	D-3	W-E	DG	5	3	0	5	DT	F	2-1
26	1-15	S	E	Ob	DG	5	3	0	5	LT	F	2-1-3
27	1-16(a)	S	D-3	W-E	DG	5	3	5	5	LT	F	2-3-1
28	1-16(b)	S	D-3	W-E	LG	5	3	0	5	LT	F	2-1-3
29	1-16(c)	A	E	O-E	LG	3	5	3	5	LT	F	2-1-3
30	1-16(d)	A	E	W-E	LG	5	3	3	5	LT	F	2-1
31	1-16(e)	S	E	W-E	DG	5	3	3	5	LT	F	2-1
32	1-16(f)	S	E	O-E	LG	5	3	3	5	LT	F	2-1
33	1-16(g)	A	E	W-E	LG	5	5	5	7	LT	F	2-1
34	1-16(h)	A	E	O-E	LG	5	5	5	7	LT	F	2-1
35	1-16(i)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
36	1-16(j)	A	E	W-E	DG	5	3	3	5	LT	F	2-1
37	1-16(k)	A	E	Ob	LG	7	3	5	5	LT	F	2-1
38	1-17	S	E	W-E	LG	3	5	3	5	DT	F	2-1-3
39	1-18(a)	A	E	W-E	DG	5	3	3	5	LT	F	2-1
40	1-18(c)	S	E	Ob	LG	5	0	0	3	LT	F	2-3-1

Contd…

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
41	1-18(e)	S	E	Ob	LG	5	3	0	3	LT	F	2-1
42	1-18(h)	A	E	W-E	LG	5	3	3	5	LT	F	2-1
43	1-18(i)	A	E	W-E	LG	5	3	3	5	LT	F	2-1
44	1-19	A	E	W-E	DG	5	3	3	5	LT	F	2-1
45	1-19(b)	A	E	W-E	DG	5	3	3	5	LT	F	2-1
46	1-19(c)	A	E	W-E	LG	5	3	5	7	LT	F	2-3-1
47	1-19(d)	A	E	O-L	DG	5	3	3	5	DT	F	2-1-3
48	1-19(e)	A	D-3	W-E	DG	9	3	5	5	DT	F	2-1
49	1-19(f)	S	E	W-E	LG	5	5	3	5	LT	F	2-3-1
50	1-20	A	E	W-E	DG	5	3	3	5	LT	F	2-1-3
51	1-21 (a)	A	E	W-E	DG	5	3	5	7	DT	F	2-1
52	1-21 (b)	A	D-3	W-E	DG	5	0	3	5	DT	F	2-1
53	1-21 (c)	A	E	O-L	DG	5	0	0	7	LT	F	2-3-1
54	1-22 (a)	S	D-3	O	LG	5	3	3	5	DT	F	2-3-1
55	1-22 (b)	S	E	Ob	DG	5	3	3	5	LT	F	2-3-1
56	1-22 (c)	S	E	W-E	LG	5	0	3	5	LT	F	2-1-3
57	1-22 (d)(i)	A	E	Ob	DG	5	3	3	5	LT	F	2-1-3
58	1-22 (d)(ii)	S	E	W-E	DG	5	3	3	5	LT	F	2-1
59	1-22 (f)	S	D-3	W-E	DG	5	3	0	5	LT	F	2-1-3
60	1-22 (g)	A	D-3	O-E	DG	5	3	3	5	LT	F	2-3-1
61	1-24(a)	S	E	L-L	LG	3	3	3	3	LT	F	2-1
62	1-24 (b)	A	E	O-L	DG	7	3	3	7	LT	C	2-3-1
63	1-25(a)	A	E	L	DG	5	3	3	5	LT	F	2-1-3
64	1-25(b)	S	D-3	W-E	DG	3	3	3	3	LT	F	2-1
65	1-25(c)	S	E	W-E	DG	5	3	5	5	DT	F	2-1
66	1-25(e)	A	E	S-O	DG	5	3	3	5	LT	F	2-1
67	1-25(f)	S	E	O-E	DG	5	5	3	7	LT	F	2-1-3
68	1-25(h)	S	D-3	W-E	DG	3	3	0	3	LT	F	2-1
69	1-25(i)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1-3
70	1-25(k)	S	D-3	Ob	LG	5	3	3	5	LT	F	2-1
71	1-25(l)	A	D-3	O-L	DG	7	0	3	5	DT	F	2-1
72	1-26(a)	S	D-3	O-L	DG	5	3	3	5	LT	F	2-1
73	1-26(b)	S	D-3	W-E	DG	5	3	0	5	LT	F	2-1-3
74	1-28(a)	S	D-3	O	DG	5	3	5	5	DT	F	2-1-3
75	1-28(b)	A	D-3	L	DG	7	3	0	5	DT	F	2-1
76	1-28(c)	A	E	O-L	DG	7	3	0	5	DT	F	2-1
77	1-29(b)	A	E	W-E	DG	5	5	3	5	DT	F	2-1-3
78	1-30(a)	S	E	W-E	LG	5	3	3	7	DT	F	2-1
79	1-30(c)	S	E	W-E	DG	5	3	3	5	DT	F	2-1-3
80	1-30(d)	S	E	O-E	LG	5	3	3	5	LT	F	2-1-3
81	1-30(i)	S	E	W-E	LG	5	5	5	7	DT	F	2-1-3
82	1-30(j)	S	E	O-E	YG	5	5	3	7	DT	F	2-1-3
83	1-31(a)	S	E	W-E	YG	5	3	3	5	LT	F	2-1-3

Contd…

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
84	1-31(b)	S	E	O-E	YG	7	5	3	7	LT	F	2-1-3
85	1-31(c)	S	E	W-E	LG	7	7	5	7	LT	C	2-3-4-1
86	1-31(e)	A	E	Ob	YG	3	0	0	5	LT	F	2-1
87	1-31(f)	S	E	W-E	DG	5	3	3	5	LT	F	2-1-3
88	1-33	S	E	W-E	LG	5	3	3	5	LT	F	2-1
89	1-34(a)	S	E	W-E	LG	5	3	3	5	LT	F	2-1-3
90	1-35(a)	S	E	W-E	DG	5	0	3	5	LT	F	2-3-1
91	1-35(b)	A	E	O-L	LG	5	5	5	5	DT	F	2-3-1
92	1-35(c)	S	E	Ob	YG	5	5	3	5	LT	F	2-1-3
93	1-35(e)	S	E	W-E	YG	5	5	3	5	LT	F	2-1-3
94	1-36(a)	S	E	Ob	YG	5	3	3	7	DT	F	2-1
95	1-36(e)	S	E	Ob	YG	5	5	3	5	DT	F	2-1-3
96	1-37(a)	S	E	Ob	LG	5	5	3	5	LT	F	2-1
97	1-37(b)	A	E	W-E	DG	7	3	5	7	LT	F	2-3-1
98	1-37(c)	S	E	W-E	LG	5	3	3	5	LT	F	2-1-3
99	1-37(d)(i)	S	E	W-E	DG	5	0	0	5	DT	F	2-1-3
100	1-37(d)(ii)	S	E	O-E	DG	5	3	3	5	DT	F	2-3-1
101	1-37(e)	S	E	W-E	DG	5	3	3	5	DT	F	2-1-3
102	1-37(f)	S	D-3	O-E	DG	5	3	3	5	DT	F	2-3-1
103	1-37(g)	A	E	L	LG	5	7	5	3	DT	F	2-3-1
104	1-37(h)	S	E	W-E	LG	7	3	5	7	LT	F	2-1-3
105	1-37(i)	S	D-3	W-E	DG	5	3	3	5	LT	F	2-1
106	2-1(b)(i)	S	E	W-E	LG	5	5	3	5	LT	F	2-1
107	2-2(b)	A	E	L-L	DG	9	0	3	7	LT	F	2-1
108	2-3(a)(i)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
109	2-3(a)(ii)	A	E	W-E	LG	5	5	3	5	DT	F	2-1
110	2-3(b)	A	D-3	W-E	LG	5	5	3	7	DT	C	2-1-3
111	2-5(a)	S	D-3	W-E	LG	5	5	3	7	DT	F	2-1
112	2-5(b)	S	D-3	W-E	LG	5	3	3	7	DT	F	2-1
113	2-5(c)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
114	2-5(d)	A	E	O-L	DG	5	3	3	5	LT	F	2-1-3
115	2-6(b)	S	D-3	W-E	DG	5	5	3	5	LT	F	2-1
116	2-6(c)	A	D-3	Ob	YG	7	5	3	7	DT	C	2-1
117	2-6(d)	S	D-3	Ob	LG	7	3	3	5	DT	C	2-1
118	2-6(e)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
119	2-7(b)	S	E	Ob	DG	7	5	5	7	LT	F	2-1
120	2-7(c)	S	E	W-E	DG	7	3	5	7	LT	F	2-1-3
121	2-7(d)(i)	A	E	W-E	DG	7	5	5	7	DT	C	2-1
122	2-7(d)(ii)	A	E	W-E	LG	7	3	7	7	LT	F	2-1
123	2-8(a)	S	E	Ob	DG	7	3	3	7	LT	F	2-1
124	2-8(b)	A	E	Ob	DG	7	3	3	7	DT	C	2-1
125	2-10(a)	A	E	Ob	DG	7	5	3	5	DT	F	2-1
126	2-11(a)	A	E	Ob	DG	5	3	3	7	LT	C	2-3-1

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Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
127	2-12(a)(ii)	A	E	Ob	DG	9	3	3	7	DT	C	2-1
128	2-12(b)	A	D-3	Ob	DG	5	3	3	7	DT	F	2-1
129	2-13(a)	A	E	Ob	LG	5	3	3	5	LT	F	2-1-3
130	2-13(b)	S	E	W-E	LG	5	5	3	5	LT	F	2-1
131	2-13(d)(i)	A	D-3	O-L	DG	7	3	3	5	LT	F	2-1
132	2-13(f)	A	D-3	O-L	DG	7	3	3	7	LT	F	2-1
133	2-14(a)(i)	S	E	W-E	LG	0	5	0	7	DT	F	3-4-2-7
134	2-14(a)(ii)	S	E	W-E	DG	5	5	3	7	DT	C	2-1
135	2-14(b)(i)	S	E	Ob	DG	5	3	3	5	DT	C	2-1-3
136	2-14(b)(ii)	S	E	W-E	LG	5	5	3	5	DT	F	2-1-3
137	2-14(c)	A	E	L	DG	7	5	3	5	DT	C	2-1
138	2-14(d)	S	E	W-E	LG	7	5	3	7	DT	**C**	2-1
139	2-14(e)	A	E	L	DG	5	5	3	7	DT	F	2-1
140	2-14(f)	A	E	L	DG	5	5	3	7	DT	C	2-1-3
141	2-14(g)	A	E	L	DG	5	3	3	7	LT	F	2-1-3
142	2-15(a)	S	E	Ob	DG	7	5	3	5	DT	F	2-1-3
143	2-15(c)	S	E	O-E	DG	5	3	3	5	LT	F	2-1
144	2-15(e)	S	D-3	Ob	DG	5	3	3	5	LT	F	2-1
145	2-15(f)	S	D-3	Ob	LG	5	3	3	5	DT	F	2-3-1-4
146	2-15(h)(i)	A	D-3	Ob	LG	5	3	3	5	LT	F	2-1-3
147	2-15(h)(ii)	S	D-3	W-E	DG	5	3	3	7	LT	F	2-1
148	2-15(i)(a)	S	D-3	W-E	DG	5	3	3	7	DT	C	2-1
149	2-15(i)(b)	S	D-3	Ob	LG	7	3	5	7	DT	F	2-1
150	2-16(a)	A	D-3	L-L	YG	7	7	5	7	DT	F	2-1
151	2-16(b)	S	E	Ob	YG	5	5	3	5	LT	F	2-1-3
152	2-17(a)	S	E	W-E	YG	7	3	3	5	DT	C	2-1-3
153	2-17(b)	A	D-3	O-E	LG	5	3	5	7	LT	F	2-1-3
154	2-17(c)	A	D-3	L-L	LG	5	5	5	7	DT	F	2-1-3
155	2-17(d)	S	E	O-L	LG	5	5	3	7	DT	F	2-1
156	2-17(e)	S	D-3	W-E	LG	5	5	3	5	LT	F	2-1-3
157	2-17(f)	A	D-3	L	LG	5	7	5	7	DT	F	2-1-3
158	2-17(g)	A	E	Ob	LG	5	5	3	5	DT	F	2-1
159	2-18(a)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1
160	2-18(b)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1
161	2-18(c)	S	D-3	W-E	LG	5	3	3	3	LT	F	2-1-3
162	2-18(d)	S	D-3	W-E	LG	5	3	3	3	DT	F	2-1-3
163	2-19(a)	S	D-3	W-E	YG	5	3	3	3	LT	F	2-1-3
164	2-19(c)	S	D-3	W-E	YG	5	3	3	3	LT	F	2-1-3
165	2-19(d)	S	E	L	DG	5	3	0	7	DT	F	2-1
166	2-19(f)	S	D-3	W-E	LG	5	7	3	5	DT	F	2-1-3
167	2-19(g)	S	D-3	W-E	LG	3	3	0	3	LT	S	2-1
168	2-19(h)	S	D-3	W-E	DG	3	3	0	3	LT	F	2-1-3
169	2-20(a)	S	D-3	W-E	LG	7	3	3	5	LT	F	2-1-3

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Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
170	2-20(b)	S	E	Ob	LG	5	3	3	3	LT	F	2-1
171	2-20(c)	A	E	W-E	LG	5	3	3	5	DT	C	2-1
172	2-20(d)	A	E	W-E	LG	7	3	3	5	DT	C	2-1
173	2-20(e)	A	E	W-E	LG	5	3	3	7	LT	**F**	2-1-3
174	2-21(a)	A	E	W-E	LG	0	3	0	3	DT	F	2-1-3
175	2-21(c)	S	E	W-E	LG	3	3	0	3	LT	F	2-1
176	2-21(d)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
177	2-21(e)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1
178	2-21(f)	A	D-3	W-E	LG	5	3	3	5	LT	F	2-1-3
179	2-22(a)	S	E	W-E	YG	5	3	3	5	DT	C	2-1-3
180	2-23(a)	A	E	W-E	YG	3	5	0	7	DT	F	2-3-1
181	2-23(b)	S	D-3	W-E	LG	7	7	7	7	LT	C	2-1
182	2-23(c)	S	E	W-E	DG	5	3	3	5	DT	F	2-1-3
183	2-23(d)	A	D-3	W-E	DG	5	5	3	3	LT	F	2-1-3
184	2-23(e)	S	E	Ob	YG	5	3	3	5	DT	F	2-1
185	2-23(f)	S	E	W-E	LG	5	3	3	5	DT	F	2-1
186	2-23(g)	S	E	W-E	LG	5	3	3	5	DT	F	2-1-3
187	2-24(a)	S	E	W-E	LG	5	3	5	5	DT	F	2-1-3
188	2-24(b)	S	D-3	W-E	LG	5	3	5	5	DT	F	2-1
189	2-24(c)	A	D-3	W-E	DG	5	5	5	7	DT	F	2-1
190	2-25(a)	A	D-3	W-E	DG	5	3	5	7	DT	C	2-1
191	2-25(b)	S	D-3	W-E	LG	7	3	3	5	DT	C	2-1
192	2-26	A	D-3	W-E	LG	9	3	3	5	DT	C	2-13
193	2-27(c)	A	D-3	W-E	LG	9	3	3	7	DT	F	2-1
194	2-27(d)	A	D-3	Ob	DG	5	3	3	7	DT	F	2-3-1-4
195	2-27(e)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
196	2-27(f)	A	D-3	Ob	LG	5	3	3	3	LT	F	2-1-3
197	2-28(a)	S	D-3	W-E	DG	5	3	3	5	DT	F	2-1
198	2-28(b)	A	D-3	W-E	DG	7	5	3	5	DT	C	2-1
199	2-29(a)(i)	S	D-3	W-E	DG	7	5	3	5	DT	F	2-1
200	2-29(a)(ii)	S	E	W-E	LG	5	7	5	5	DT	F	2-1
201	2-29(a)	S	E	W-E	LG	5	7	5	7	DT	F	2-1
202	2-29(c)	S	D-3	W-E	DG	7	3	3	3	DT	F	2-1
203	2-29(e)	S	E	W-E	LG	5	5	3	5	LT	F	2-1-3
204	2-29(f)	S	E	W-E	LG	5	3	3	5	DT	F	2-1
205	2-29(g)	S	D-3	W-E	LG	5	3	3	7	LT	F	2-1
206	2-30(a)	S	D-3	W-E	LG	5	3	3	7	LT	F	2-1-3
207	2-30(b)	S	E	W-E	LG	5	3	5	7	DT	F	2-1-3
208	2-30(c)(i)	S	D-3	W-E	LG	3	3	0	3	LT	**F**	2-1
209	2-30(d)	S	D-3	W-E	LG	5	3	0	5	LT	F	2-1
210	2-30(e)	S	E	W-E	LG	5	3	3	5	LT	C	2-1
211	2-30(f)	S	D-3	W-E	LG	7	3	0	3	DT	F	2-1
212	2-30(g)	S	D-3	W-E	LG	5	3	3	7	DT	F	2-1

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Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
213	2-32(a)	A	D-3	W-E	LG	5	3	3	7	LT	C	2-1
214	2-32(c)	S	D-3	W-E	DG	5	3	3	5	LT	F	2-1-3
215	2-32(e)	S	D-3	W-E	DG	7	3	3	5	DT	F	2-1
216	2-32(g)	A	D-3	W-E	DG	5	5	0	5	LT	F	2-1-3
217	2-32(b)	A	D-3	W-E	DG	3	3	0	7	DT	F	3-2-1
218	2-33(a)	S	E	W-E	DG	5	3	3	5	LT	F	2-1-3
219	2-33(d)	A	D-3	W-E	LG	5	3	3	7	LT	F	2-1
220	2-33(e)	S	E	W-E	DG	5	5	3	7	DT	C	2-1
221	2-34(a)	A	D-3	W-E	DG	7	3	3	7	DT	C	2-1
222	2-35(a)	A	E	Ob	DG	5	5	0	5	LT	F	2-1
223	2-35(b)	A	E	L	DG	5	3	3	7	LT	C	2-1-3
224	2-35(d)	A	D-3	W-E	DG	7	3	3	7	DT	C	2-1
225	2-35(e)	S	D-3	L	DG	5	5	3	5	LT	F	2-1-3
226	2-36(a)(i)	A	E	L	DG	5	3	3	7	LT	C	2-1-3
227	2-36(a)(ii)	S	D-3	W-E	DG	5	3	5	7	DT	F	2-1
228	2-36(b)	A	E	W-E	LG	5	7	3	7	DT	F	2-1
229	2-36(c)	A	D-3	W-E	LG	5	7	3	7	DT	F	2-1
230	2-37(a)	S	D-3	W-E	LG	5	7	0	7	LT	F	2-1
231	2-38(b)(i)	A	D-3	Ob	DG	5	5	3	7	LT	F	2-1
232	2-38(b)(ii)	A	D-3	W-E	DG	5	5	3	5	DT	F	2-1
233	2-38(d)	A	D-3	W-E	DG	5	5	3	7	DT	F	2-1
234	2-39(a)	A	D-3	W-E	LG	5	5	0	5	LT	F	2-1
235	2-39(b)	S	E	W-E	LG	5	5	3	5	DT	F	2-1
236	2-39(c)	S	E	Ob	LG	5	5	3	5	LT	F	2-1
237	2-39(d)	A	E	L	DG	5	3	3	7	DT	F	2-1
238	2-39(e)	S	E	W-E	LG	7	3	3	7	LT	F	2-1-3
239	2-39(f)	A	D-3	W-E	LG	7	3	0	7	DT	F	2-1
240	2-39(g)	S	E	Ob	DG	5	5	5	7	LT	F	2-1-3
241	2-39(i)	S	E	W-E	LG	5	3	3	7	LT	F	2-1-3
242	2-40(b)	S	E	W-E	LG	5	5	3	5	LT	F	2-1
243	2-40(c)	S	E	W-E	DG	5	5	3	7	LT	**F**	2-1-3
244	2-40(d)	S	E	W-E	LG	5	3	3	3	LT	F	2-1
245	2-41(a)	A	E	W-E	DG	5	3	3	5	DT	F	2-1
246	2-41(b)	S	D-3	W-E	LG	9	3	3	5	DT	F	2-1
247	2-41(c)	A	E	W-E	DG	5	3	3	5	DT	F	2-1
248	2-41(d)	A	E	Ob	LG	5	5	3	7	DT	F	2-1
249	2-41(e)	A	E	L-L	DG	5	3	3	5	LT	F	2-1
250	2-42(b)	A	D-3	W-E	LG	5	3	3	5	LT	F	2-1
251	2-42(c)	S	D-3	W-E	LG	5	3	3	5	DT	F	2-1
252	2-42(e)	S	D-3	W-E	LG	5	3	3	5	DT	F	2-1
253	2-42(f)	S	E	W-E	LG	7	3	3	7	DT	C	2-1-3
254	2-42(g)	S	E	W-E	LG	3	3	0	7	DT	F	4-3-2-1
255	2-43(b)	S	E	W-E	LG	7	3	5	7	DT	C	2-1-3

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Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
256	2-43(c)	A	E	W-E	DG	7	3	5	5	DT	F	2-1-3
257	2-44(d)	S	E	O	LG	5	3	3	7	DT	C	2-1-3
258	2-44(e)	A	E	O-L	DG	7	3	3	7	DT	C	2-1
259	2-45(a)	S	E	W-E	LG	5	3	3	7	LT	C	2-1
260	2-45(b)	S	E	W-E	YG	5	3	0	3	LT	F	2-1
261	2-45(c)	A	E	O-L	LG	7	3	3	5	DT	F	2-1
262	2-45(d)	A	D-3	Ob	YG	7	5	3	5	DT	C	2-1
263	2-45(e)	A	E	O-L	DG	5	5	5	7	DT	C	2-1-3
264	2-45(f)	S	E	O-L	DG	5	5	5	7	DT	F	2-1
265	2-45(g)	A	E	O-L	LG	5	3	3	3	DT	F	2-1-3
266	2-46(a)	A	E	O-L	DG	5	3	3	3	LT	F	2-1
267	2-46(b)	A	E	O-L	LG	7	5	3	7	DT	F	2-1
268	2-46(c)	A	D-3	O-L	LG	7	5	3	7	DT	C	2-1-3
269	2-47(a)	A	D-3	O-L	LG	5	3	3	5	LT	F	2-1
270	2-48(a)	A	D-3	L	LG	5	3	3	5	LT	F	2-1
271	2-48(b)	A	D-3	L	LG	7	3	3	5	DT	F	2-1-3
272	2-48(c)	A	E	L	LG	7	0	3	7	DT	C	2-1
273	2-48(f)	A	E	L	LG	7	0	0	7	DT	F	2-1
274	2-48(i)	S	E	W-E	LG	5	3	3	5	LT	F	2-1-3
275	2-49	S	E	W-E	YG	3	3	0	5	DT	F	2-1-3
276	2-50(a)	S	E	O-L	DG	5	5	5	5	DT	F	2-1-3
277	2-50(b)	S	E	W-E	YG	5	3	3	3	LT	F	2-1
278	2-50(c)	S	E	O-E	LG	5	3	3	3	LT	**F**	2-1
279	2-50(e)	S	E	O-E	LG	5	5	3	3	DT	F	2-1
280	2-50(f)	S	D-3	W-E	LG	5	5	3	3	DT	F	2-1-3
281	2-50(g)	S	D-3	W-E	LG	7	3	3	5	LT	C	2-1-3
282	2-50(i)	A	E	L-L	LG	5	5	5	5	DT	F	2-1-3
283	2-51(a)	S	E	W-E	LG	5	3	3	7	DT	F	2-1
284	2-51(b)	S	D-3	W-E	LG	7	0	0	5	LT	F	2-1-3
285	2-51(c)	S	E	W-E	YG	5	3	3	5	LT	F	2-1
286	2-51(d)	S	E	W-E	LG	5	3	3	7	DT	F	2-1-3
287	2-51(e)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1
288	2-51(f)	S	E	W-E	LG	5	3	3	7	DT	F	2-1
289	2-52(a)	S	E	W-E	LG	5	3	3	5	DT	F	2-1
290	2-52(c)	A	E	W-E	DG	5	3	3	7	DT	F	2-1
291	2-52(d)	S	E	W-E	DG	5	3	3	7	DT	F	2-1
292	2-52(e)	S	E	W-E	LG	5	3	3	5	DT	F	2-1-3
293	2-54(a)	A	E	W-E	LG	7	3	5	7	DT	F	2-1
294	2-54(b)	A	E	W-E	LG	7	3	5	7	DT	F	2-1
295	2-55(a)	S	E	W-E	YG	7	3	5	5	LT	F	2-1
296	2-55(b)	S	E	W-E	LG	7	0	5	5	DT	F	2-1
297	2-55(d)	S	E	W-E	YG	5	3	3	7	DT	F	2-1
298	2-55(e)	S	E	W-E	YG	7	3	3	7	DT	F	2-1

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Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
299	2-55(f)	A	D-3	L	YG	5	3	3	7	DT	F	2-1
300	2-56	A	D-3	L	YG	7	3	3	5	LT	F	2-1
301	2-57(b)	A	D-3	L	YG	5	3	3	7	LT	F	2-1
302	2-57(c)	A	E	W-E	YG	7	3	3	7	DT	C	2-1-3
303	2-57(d)	A	E	O-L	LG	7	0	3	7	DT	C	2-1-3
304	2-58	A	D-3	W-E	LG	7	3	3	7	DT	C	2-1-3
305	2-59(a)	S	E	W-E	DG	7	3	3	3	DT	C	2-1
306	2-59(b)	A	D-3	W-E	LG	5	5	3	5	DT	F	2-3-1
307	2-59(c)	S	E	W-E	YG	5	3	3	5	DT	F	2-1-3
308	2-59(d)	S	E	W-E	LG	5	3	3	5	DT	F	2-1
309	2-59(g)	A	E	W-E	LG	7	5	3	7	DT	C	2-1
310	2-59(j)	A	D-3	W-E	LG	7	3	5	7	LT	C	2-1-3
311	2-59(k)	A	E	O-L	LG	7	3	5	7	DT	C	2-1
312	2-59(l)	S	E	W-E	YG	5	5	3	5	LT	F	2-1
313	2-60(a)	A	E	W-E	YG	5	5	3	5	DT	**F**	2-1
314	2-60(c)	A	E	W-E	DG	5	7	5	7	DT	C	2-1-3
315	2-60(d)	A	E	W-E	DG	5	5	3	5	DT	F	2-1
316	2-60(e)	A	E	W-E	DG	5	3	3	7	DT	F	2-1
317	2-60(f)	S	E	W-E	DG	5	3	3	7	DT	C	2-1
318	2-61(a)	A	E	W-E	LG	7	3	3	5	DT	F	2-1
319	2-61(b)	A	E	W-E	LG	7	3	3	5	DT	F	2-1
320	2-61(d)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
321	2-62	S	D-3	W-E	DG	5	3	3	5	LT	F	2-1
322	2-63(a)	A	D-3	W-E	LG	5	7	3	5	DT	F	2-1-3
323	2-63(b)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
324	2-63(c)	A	E	W-E	DG	5	5	3	5	LT	F	2-1
325	2-63(d)	S	E	W-E	LG	3	3	0	3	DT	F	2-3-1
326	2-64(a)	A	E	L	LG	5	3	3	5	LT	F	2-1
327	2-64(b)	A	E	W-E	LG	5	3	3	5	DT	F	2-1
328	2-64(c)	A	D-3	W-E	LG	5	5	3	5	LT	F	2-1
329	2-65(a)	S	D-3	W-E	YG	5	3	0	7	LT	F	2-1
330	2-65(b)	S	D-3	W-E	DG	5	3	3	7	LT	F	2-1
331	2-65(c)	A	D-3	L	LG	5	5	3	5	DT	F	2-1
332	2-66(a)(i)	A	D-3	W-E	LG	5	7	5	7	LT	F	2-3-1
333	2-66(a)(ii)	S	D-3	W-E	LG	5	5	3	7	LT	F	2-1
334	2-66(b)	S	D-3	W-E	LG	5	3	3	5	DT	F	2-1
335	2-66(d)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1
336	2-67(a)	A	D-3	W-E	LG	5	5	3	5	DT	F	2-1
337	2-67(b)	A	E	O-L	LG	5	3	3	5	DT	F	2-1-3
338	2-68(a)	A	E	W-E	LG	5	5	3	5	DT	F	2-1-3
339	2-68(b)	A	E	O-L	DG	7	5	3	5	LT	F	2-1-3
340	2-70(a)	A	D-3	W-E	DG	5	5	3	7	DT	F	2-1
341	2-70(c)	S	E	W-E	LG	5	3	3	7	LT	F	2-1

Contd…

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
342	2-71(a)	S	E	Ob	YG	5	5	3	5	DT	F	2-1-3
343	2-71(d)	S	E	Ob	YG	5	5	3	5	DT	F	2-1
344	2-72(a)	S	E	W-E	YG	7	5	3	5	LT	C	2-1-3
345	2-72(b)	S	E	W-E	YG	5	3	3	5	DT	F	2-1-3
346	2-72(c)	A	E	L-L	LG	5	0	3	5	DT	F	2-1-3
347	2-72(d)	S	E	W-E	YG	5	5	3	5	LT	F	2-1
348	2-72(f)	S	E	W-E	YG	5	3	3	5	LT	**F**	2-1-3
349	2-73(b)	A	E	W-E	YG	5	3	3	7	DT	F	2-1-3
350	2-73(c)	A	E	W-E	LG	5	3	3	7	DT	F	2-1-3
351	2-73(d)	S	E	W-E	LG	5	5	3	5	DT	F	2-1-3
352	2-74(b)	S	E	W-E	LG	5	7	3	7	LT	F	2-1-3
353	2-74(c)	A	E	W-E	LG	7	5	5	7	LT	F	2-1-3
354	2-74(d)	S	E	W-E	LG	5	3	3	5	LT	F	2-1-3
355	2-74(e)	S	D-3	W-E	LG	5	3	3	5	LT	F	2-1-3
356	2-74(f)(i)	A	D-3	W-E	LG	5	3	3	5	LT	F	2-1
357	2-74(f)(ii)	S	D-3	W-E	LG	7	3	3	3	LT	F	2-1-3
358	2-75	A	E	W-E	DG	5	3	0	5	DT	F	2-1
359	2-76(a)	S	E	W-E	DG	5	3	0	5	LT	F	2-1
360	2-76(b)	A	D-3	W-E	LG	3	3	0	7	DT	F	2-3-1
361	2-76(d)	S	D-3	W-E	YG	7	3	3	5	LT	C	2-1-3
362	2-76(e)	A	D-3	W-E	LG	5	3	3	5	DT	F	2-1
363	2-76(f)	A	E	Ob	LG	5	3	3	5	DT	F	2-1
364	2-76(g)	A	E	W-E	LG	5	5	3	7	DT	F	2-1-3
365	2-77(a)	A	E	W-E	LG	7	3	5	7	LT	C	2-1
366	2-77(c)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
367	2-78(a)	S	E	W-E	DG	7	3	3	5	DT	F	2-1-3
368	2-78(c)	S	E	Ob	DG	7	5	3	5	LT	C	2-1-3
369	2-79(b)	S	E	Ob	LG	5	5	5	7	DT	F	2-3-1
370	2-79(c)	S	E	Ob	LG	5	5	5	7	DT	F	2-1-3
371	2-79(e)	S	E	W-E	DG	5	3	3	7	LT	C	2-1-3
372	2-80(a)	S	D-3	O-E	DG	5	3	3	7	DT	F	2-3-1
373	2-80(b)	S	E	W-E	DG	7	0	0	5	DT	F	2-1
374	2-80(d)	A	E	O-L	LG	7	3	0	5	DT	F	2-1
375	2-81(a)	S	E	Ob	LG	7	5	5	7	DT	F	2-1
376	2-81(a)(ii)	S	D-3	W-E	LG	7	5	3	7	DT	F	2-1
377	2-81(c)	S	E	W-E	DG	7	3	5	7	DT	F	2-1
378	2-81(e)	S	E	W-E	DG	7	3	5	7	LT	C	2-1-3
379	2-81(f)	A	E	Ob	DG	5	3	5	7	DT	F	2-1
380	2-81(h)	A	E	Ob	DG	5	3	5	7	DT	F	2-1
381	2-81(i)	A	E	Ob	DG	5	3	5	7	DT	F	2-1
382	2-82(a)	S	E	W-E	DG	5	3	3	7	DT	F	2-3-1
383	2-82(b)	S	E	O-E	DG	7	0	0	5	DT	**F**	2-1
384	2-83(a)	A	E	W-E	DG	7	5	5	5	DT	F	2-1

Contd…

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
385	2-83(b)	S	E	O	LG	7	3	5	5	DT	C	2-1-3
386	2-83(d)	S	E	Ob	LG	7	5	3	7	LT	C	2-1
387	2-84(a)	S	E	O-E	DG	7	5	5	7	LT	C	2-1-3
388	2-84(b)	S	E	W-E	LG	5	5	3	7	LT	F	2-1-3
389	2-85(a)	A	E	O-E	DG	7	3	5	7	DT	C	2-1
390	2-85(c)	A	E	O	LG	7	3	5	5	DT	C	2-1
391	2-86(c)	S	E	O-E	LG	5	0	3	3	DT	F	2-1-3
392	2-86(d)	S	D-3	W-E	LG	7	3	3	5	DT	F	2-1
393	2-86(e)	S	E	W-E	LG	5	3	3	5	LT	F	2-1
394	2-86(f)	A	E	W-E	DG	5	5	3	5	DT	F	2-1
395	2-87(a)	A	E	O-L	LG	5	5	5	5	DT	F	2-1
396	2-87(b)	A	E	L	DG	7	3	5	7	DT	C	2-1
397	2-87(d)	A	E	L	DG	7	3	5	7	DT	C	2-1
398	2-87(e)	A	E	W-E	DG	7	3	5	7	LT	C	2-1
399	2-87(f)	A	E	W-E	LG	5	5	3	7	DT	F	2-1-3
400	2-87(g)	A	D-3	O	LG	7	3	3	7	DT	C	2-1
401	2-87(h)	A	E	W-E	LG	7	5	3	7	DT	C	2-1-3
402	2-88(a)	A	E	O-E	LG	7	0	5	7	DT	C	2-1
403	2-88(b)	S	D-3	W-E	LG	5	3	0	5	LT	F	2-1-3
404	2-88(c)	A	E	O-E	LG	7	5	3	7	DT	F	2-1
405	2-88(d)	A	E	W-E	LG	7	5	3	7	DT	C	2-1
406	2-89	S	E	W-E	LG	3	3	3	5	DT	F	2-1
407	2-90(a)	S	E	Ob	LG	5	3	5	5	DT	F	2-1
408	2-90(b)	S	E	O-L	DG	5	5	3	3	LT	F	2-1
409	2-91(a)	A	D-3	O-E	LG	5	3	3	3	DT	F	2-1
410	2-91(b)	S	E	W-E	LG	3	3	3	5	LT	F	2-1
411	2-91(c)	S	E	W-E	LG	5	3	3	7	DT	F	2-1-3
412	2-91(d)	S	E	W-E	YG	5	3	3	7	DT	F	2-1-3
413	2-91(f)	S	E	W-E	LG	5	3	5	7	LT	F	2-1
414	2-91(g)	S	D-3	W-E	LG	5	3	5	7	LT	F	2-1
415	2-92(a)	S	D-3	Ob	LG	5	3	5	5	DT	F	2-1
416	2-92(b)	S	E	W-E	LG	5	3	3	5	DT	F	2-1
417	2-92(c)	A	E	W-E	LG	5	3	3	3	DT	F	2-1
418	2-92(d)	S	E	O-L	LG	5	7	5	7	LT	F	2-3-1
419	2-92(e)	S	E	W-E	YG	7	3	5	7	DT	C	2-1
420	2-92(f)	S	E	W-E	LG	5	5	3	5	DT	F	2-3-1
421	2-93(a)	S	E	W-E	DG	5	3	5	7	DT	F	2-1
422	2-94(c)	S	E	W-E	DG	5	3	3	7	DT	F	2-1-3
423	2-94(d)	S	E	Ob	DG	5	3	3	3	LT	F	2-1
424	2-95(a)	A	E	W-E	LG	5	3	3	3	LT	F	2-1
425	2-95(b)	A	E	W-E	DG	5	3	3	3	LT	F	2-1
426	2-95(c)	A	E	W-E	LG	5	3	3	5	LT	F	2-1
427	2-95(d)	A	E	O	DG	3	3	0	5	DT	F	2-3-1

Contd…

Sl. No.	Genotype /trait	BP	GH	LS	LC	PC	PR	PB	PS	KC	SS	SPP
428	2-95(e)	A	E	O	YG	5	3	3	5	LT	F	2-1
429	2-96	A	E	O-L	LG	7	3	5	7	LT	F	2-1
430	2-96(c)	S	E	O-E	LG	5	3	5	5	LT	F	2-3-1
431	2-97	S	E	W-E	LG	7	3	5	5	LT	F	2-1-3
432	2-98(a)	S	E	W-E	LG	7	3	3	5	DT	F	2-1
433	2-98(b)	S	E	W-E	LG	7	3	3	5	DT	F	2-1
434	2-98(c)	S	E	W-E	LG	5	3	3	5	LT	F	2-1

BP	Branching pattern	S: Sequential, A: Alternate
GH	Growth habit	E: Erect, D-3: Decumbent-3, D-2: Decumbent-2
LS	Leaflet shape	W-E: Wide-elliptic, O-E: Oblong elliptic, L: Lanceolate, L-L:Linear lanceolate, O-L: Oblong lanceolate O: Ovate, Ob: Obovate, S-O:Suborbicular
LC	Leaflet colour	G: Green, DG: Dark green, LG: Light green, YG: Yellow green
SS	Seed shape	F: Fusiform, C: Cylindrical, S: Spherical
KC	Kernel colour	DT: Dark tan, LT: Light tan
PC	Pod constriction	0:None, 3: Slight, 5: Moderate, 7: Deep, 9: Very deep
PR	Pod reticulation	0:Absent, 3: Slight, 5: Moderate, 7: Prominent, 9: Very prominent
PB	Pod beak:	0: Absent, 3: Slight, 5: Moderate, 7: Prominent, 9: Very prominent
SPP	Seeds per pod	

Appendix II: Mean performance of the RILs of TMV 2 × TMV 2-NLM for disease resistance, agronomic and physiological traits

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
1	TMV 2	2.75	5.00	7.13	2.75	4.63	6.25	32.50	35.58	5.73	0.75	5.57	2.66	2.75	23.20
2	TMV 2-NLM	2.50	5.00	7.00	2.63	4.25	6.25	37.00	28.69	9.00	10.92	4.76	1.18	5.50	41.10
3	1-2(a)	2.75	5.00	7.25	2.75	4.75	6.25	31.25	38.25	4.50	0.00	4.49	2.30	0.00	34.65
4	1-2(b)	3.00	5.25	7.75	3.00	5.00	6.50	31.25	38.58	4.92	0.00	4.30	2.43	0.00	44.35
5	1-2(d)	3.00	5.25	8.25	3.00	5.00	7.00	31.50	32.42	5.08	0.00	4.24	2.41	5.50	35.15
6	1-3	3.00	5.25	7.50	3.00	5.00	6.50	31.00	37.25	4.58	2.17	4.14	2.23	3.00	30.70
7	1-4(a)	3.00	4.75	6.75	3.00	4.50	5.50	35.75	35.50	5.25	6.75	4.68	2.74	1.00	30.15
8	1-5	2.50	4.00	6.50	2.50	4.00	5.25	34.75	31.00	5.42	3.00	5.31	2.53	0.50	28.15
9	1-6(a)	2.50	3.50	6.50	2.00	3.00	5.75	33.50	23.75	4.92	0.67	4.20	2.13	0.00	34.25
10	1-6(b)	2.50	3.50	6.50	2.25	3.25	5.75	33.00	22.08	4.25	1.00	3.58	2.24	0.50	32.15
11	1-7(a)	3.00	5.25	7.25	2.50	4.25	5.75	31.50	44.92	5.00	1.42	4.65	2.42	0.00	37.25
12	1-7(b)	3.50	5.50	7.75	2.75	4.75	6.50	32.50	26.00	5.42	1.08	5.18	2.24	1.00	36.70
13	1-7(c)	4.00	6.00	8.00	3.50	6.00	7.25	32.00	28.83	5.50	2.25	4.06	2.24	0.50	32.00
14	1-7(d)	4.00	6.00	7.75	4.00	6.00	6.50	34.50	29.50	9.17	7.50	3.49	1.64	0.00	46.40
15	1-7(9)	4.00	6.00	7.75	4.00	6.00	6.50	34.25	30.33	8.50	5.25	3.43	1.26	0.00	45.40
16	1-9	3.75	5.75	8.25	3.75	5.75	7.75	33.00	26.83	4.83	0.17	4.60	2.18	0.00	38.15
17	1-11(a)	2.75	3.75	7.25	3.00	4.50	5.75	33.75	28.67	5.00	0.00	4.29	2.13	0.00	28.15
18	1-11(b)	2.50	3.50	7.00	2.75	4.25	5.75	31.25	22.92	4.08	1.50	4.93	2.56	4.00	36.95
19	1-11(c)	2.50	4.00	6.75	2.75	4.25	5.50	33.25	23.33	5.33	3.92	3.77	2.34	0.00	39.10
20	1-11(g)	2.25	4.25	6.75	2.50	4.50	6.50	34.50	29.25	7.50	8.08	4.16	1.59	0.00	46.05
21	1-12 (a)	2.00	3.00	6.75	2.50	4.50	6.00	34.00	25.25	5.00	0.00	4.34	2.11	1.00	25.75
22	1-12 (c)	1.75	2.75	6.75	2.75	4.25	5.75	33.50	24.83	6.25	0.00	4.80	2.48	3.00	25.40
23	1-13 (c)	2.75	4.75	6.50	2.25	4.25	6.00	38.50	28.75	5.58	3.75	4.49	2.23	0.00	28.05
24	1-14 (a)	2.50	4.00	6.75	2.50	4.50	6.00	33.75	26.75	6.00	0.83	4.40	2.18	0.00	32.70
25	1-14 (b)	2.75	4.25	7.25	2.75	4.50	6.25	34.00	27.58	5.75	0.17	4.40	2.02	0.50	23.85
26	1-15	2.75	4.25	7.00	2.50	4.00	6.00	33.50	33.08	5.42	2.58	5.08	2.01	1.00	27.45

Contd…

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
27	1-16(a)	2.00	3.00	6.75	2.50	4.00	5.50	33.75	27.42	5.75	0.00	4.23	2.28	0.00	37.50
28	1-16(b)	1.50	2.50	6.75	2.25	4.25	6.25	33.25	26.33	6.08	0.00	4.30	2.02	0.00	33.05
29	1-16(c)	1.00	1.50	7.25	2.25	3.50	6.00	34.25	28.33	6.50	5.50	4.29	2.04	0.00	34.55
30	1-16(d)	1.50	2.25	6.75	2.25	3.50	5.50	33.75	32.42	6.92	3.25	3.79	2.09	0.00	33.45
31	1-16(e)	1.50	2.25	6.50	2.25	3.50	5.25	33.50	30.58	6.00	2.58	4.18	2.43	0.00	26.50
32	1-16(f)	1.50	2.75	6.25	2.00	3.50	5.25	33.75	31.33	7.33	8.17	4.53	2.57	0.00	31.90
33	1-16(g)	1.50	2.50	5.75	1.50	3.00	5.00	36.25	32.92	6.58	3.75	4.37	2.03	0.00	33.20
34	1-16(h)	1.00	1.50	6.50	2.25	3.75	5.50	35.75	33.08	6.58	3.92	4.01	2.06	0.00	25.30
35	1-16(i)	2.00	3.50	5.75	2.25	3.75	5.00	37.00	36.75	7.33	2.83	4.11	1.93	0.50	36.05
36	1-16(j)	2.00	3.00	5.00	2.75	4.50	5.50	37.50	37.83	7.42	5.75	5.31	2.74	2.00	33.80
37	1-16(k)	3.50	5.50	7.75	3.50	5.50	7.00	34.75	27.25	7.08	3.33	3.35	1.72	0.00	32.10
38	1-17	1.00	1.50	3.50	1.00	1.75	1.75	33.50	39.08	7.33	0.83	4.53	2.28	2.50	28.40
39	1-18(a)	2.25	4.25	6.75	2.25	4.00	5.50	34.00	36.00	7.00	7.75	4.65	2.08	0.00	38.30
40	1-18(c)	2.75	4.75	7.75	2.00	3.50	6.75	32.00	26.08	5.75	1.25	3.63	2.01	2.50	34.90
41	1-18(e)	3.25	5.25	7.50	2.25	4.25	6.75	33.00	26.17	5.50	0.00	3.51	1.65	0.00	31.20
42	1-18(h)	2.75	4.75	6.75	2.50	4.00	5.00	35.50	32.17	5.67	6.58	4.18	2.26	0.00	38.70
43	1-18(i)	2.50	4.00	6.00	2.00	3.50	5.00	36.75	37.83	6.42	2.33	4.36	2.01	0.00	28.00
44	1-19	2.75	4.75	6.75	2.25	4.00	5.50	36.00	33.92	6.58	7.33	4.30	1.86	0.00	36.35
45	1-19(b)	3.00	5.00	7.00	2.00	3.75	5.50	37.75	32.58	6.50	5.25	4.36	2.29	0.50	40.50
46	1-19(c)	2.00	3.00	6.50	1.75	2.50	5.50	31.00	27.67	4.42	0.92	4.67	2.17	3.00	32.20
47	1-19(d)	2.75	4.75	6.50	2.25	4.00	5.25	36.00	41.92	7.50	11.67	4.87	1.55	1.00	45.15
48	1-19(e)	2.50	4.50	6.00	2.25	4.25	5.25	38.25	27.42	8.58	13.25	4.23	2.31	1.50	34.55
49	1-19(f)	2.25	3.25	5.25	2.50	4.00	5.25	33.50	34.92	5.33	3.08	3.97	1.83	0.00	34.70
50	1-20	2.00	3.00	6.25	2.25	3.50	6.00	35.00	30.17	7.08	4.83	4.59	2.23	0.50	34.00
51	1-21 (a)	2.75	4.75	7.25	3.00	4.75	6.50	37.50	31.75	7.17	4.75	4.44	2.48	0.50	28.85
52	1-21 (b)	1.75	3.00	5.75	2.50	3.75	5.50	34.50	32.25	6.17	4.17	4.35	2.11	0.00	33.05
53	1-21 (c)	2.75	4.00	6.25	2.00	3.25	5.50	35.50	25.08	6.67	7.08	4.08	1.83	3.00	37.10
54	1-22 (a)	1.50	2.50	6.00	1.75	3.00	4.75	32.50	29.33	4.58	1.25	4.36	1.98	0.00	30.65

Contd…

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
55	1-22 (b)	2.25	3.50	6.50	1.50	2.75	5.00	33.75	30.50	6.67	7.25	4.33	2.03	0.00	24.80
56	1-22 (c)	2.00	3.25	6.00	1.50	2.50	5.00	34.00	29.92	6.17	2.17	4.30	1.99	0.00	38.95
57	1-22 (d)(i)	1.75	3.00	6.25	1.25	2.50	5.25	34.00	30.83	8.33	9.08	4.13	2.06	0.00	26.80
58	1-22 (d)(ii)	2.00	3.50	6.25	2.00	3.25	5.25	31.75	29.58	6.17	4.67	4.28	2.38	0.00	31.40
59	1-22 (f)	2.25	3.75	6.75	2.00	3.25	5.75	33.25	30.50	6.33	5.17	5.04	2.33	0.00	32.25
60	1-22 (g)	2.25	3.75	6.25	2.00	3.25	5.25	36.00	28.17	6.75	7.42	5.02	2.34	0.00	40.95
61	1-24(a)	2.75	4.00	6.25	1.75	3.50	5.50	33.25	31.58	4.75	1.50	4.54	1.13	0.00	36.15
62	1-24 (b)	2.50	3.25	6.00	1.25	2.50	5.25	38.50	29.42	8.33	6.58	3.68	1.52	2.00	35.05
63	1-25(a)	2.00	3.50	6.00	1.75	3.25	5.25	35.50	31.33	7.17	7.42	4.15	1.83	0.00	36.85
64	1-25(b)	2.00	3.50	6.50	2.00	3.75	6.00	34.25	17.50	4.75	0.17	4.10	2.20	3.50	25.35
65	1-25(c)	1.50	2.50	6.50	2.00	3.00	5.50	33.75	34.67	5.00	0.00	4.80	2.57	2.00	31.10
66	1-25(f)	1.50	2.75	6.00	2.25	3.75	5.50	32.50	30.42	4.75	0.00	4.01	2.40	1.50	38.25
67	1-25(f)	1.50	2.50	6.25	2.00	3.50	5.50	32.25	37.33	5.25	0.00	5.38	2.84	2.50	30.40
68	1-25(h)	1.50	2.00	5.50	2.00	3.25	5.00	33.75	20.58	4.92	0.00	3.58	1.94	0.00	32.05
69	1-25(i)	2.00	3.00	7.00	2.00	3.50	5.50	32.00	29.42	5.67	2.42	4.20	2.18	1.50	37.05
70	1-25(k)	1.50	2.75	7.00	1.50	3.00	5.75	32.25	22.58	5.67	2.42	4.06	2.36	1.00	31.65
71	1-25(l)	2.50	4.25	8.00	2.25	3.75	6.75	35.00	23.83	5.58	7.75	4.23	1.18	0.50	35.25
72	1-26(a)	1.75	3.50	7.25	2.00	3.50	7.00	31.50	24.58	4.92	0.00	5.01	2.48	3.00	33.10
73	1-26(b)	2.50	4.25	7.25	2.00	3.75	5.25	32.00	26.75	5.58	0.75	4.46	2.46	0.50	28.80
74	1-28(a)	2.00	3.25	6.50	2.00	3.75	5.50	32.00	27.33	5.00	0.00	4.73	2.25	1.00	31.60
75	1-28(b)	2.50	3.75	6.50	2.25	4.00	6.00	37.75	32.25	6.75	6.17	3.70	1.13	7.00	46.95
76	1-28(c)	2.50	3.75	8.00	2.00	3.75	7.50	38.00	31.58	7.92	7.42	4.08	1.28	7.00	36.50
77	1-29(b)	2.50	4.25	7.25	2.25	3.75	6.50	30.50	35.58	4.92	1.67	4.57	2.47	0.00	35.05
78	1-30(a)	2.00	4.00	7.00	2.25	4.00	6.00	31.00	34.50	5.33	1.08	4.43	2.45	0.50	38.35
79	1-30(c)	2.50	4.50	7.25	2.25	4.00	6.50	32.75	34.50	5.00	0.50	4.63	2.64	2.50	26.80
80	1-30(d)	2.50	4.00	7.25	2.00	3.50	6.50	30.50	25.75	4.50	0.00	4.98	2.43	2.50	33.65
81	1-30(i)	2.50	4.50	7.25	2.00	3.50	6.25	31.50	29.75	5.33	1.08	4.67	2.15	0.00	33.55
82	1-30(j)	2.00	3.50	6.25	1.50	2.75	5.25	31.50	38.08	4.92	0.00	6.05	2.47	0.50	23.50

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
83	1-31(a)	2.50	3.75	7.00	2.00	3.25	6.00	31.75	30.00	6.67	0.67	4.80	2.13	0.50	40.00
84	1-31(b)	2.25	3.50	6.25	1.50	2.00	5.50	32.25	36.92	6.33	0.50	5.89	2.47	0.00	20.00
85	1-31(c)	2.25	3.50	6.25	1.50	2.50	5.50	31.50	42.25	6.58	0.25	5.45	2.39	0.50	23.60
86	1-31(e)	1.75	3.25	6.75	1.50	2.25	5.50	34.50	33.67	6.00	3.83	4.96	2.46	0.00	29.20
87	1-31(f)	3.00	5.00	7.00	2.25	4.00	5.50	33.50	33.33	6.00	1.17	4.42	2.37	3.50	43.45
88	1-33	1.00	1.00	1.00	1.50	2.50	5.75	32.00	35.42	6.00	0.00	3.73	2.09	0.00	40.35
89	1-34(a)	1.00	1.00	2.00	1.50	2.00	5.00	33.50	29.25	6.17	1.75	4.63	2.27	0.50	39.15
90	1-35(a)	2.50	4.50	7.00	2.75	4.50	6.75	32.50	35.92	4.92	0.00	4.70	2.38	0.00	33.45
91	1-35(b)	3.25	5.50	8.00	2.25	4.25	7.50	35.25	28.83	8.42	8.75	3.97	1.11	0.00	38.65
92	1-35(c)	3.75	6.00	7.75	2.75	4.75	7.50	35.00	33.67	6.50	0.92	3.75	1.90	3.00	35.15
93	1-35(e)	3.00	4.50	7.50	2.25	4.00	7.50	33.75	32.42	6.25	1.67	3.95	2.09	3.50	29.70
94	1-36(a)	3.00	5.00	6.75	2.25	4.00	7.00	33.00	31.50	6.00	0.92	4.05	2.10	0.50	29.20
95	1-36(e)	2.75	4.75	7.00	1.50	3.75	7.00	33.00	33.92	7.42	0.42	4.08	2.14	5.00	31.90
96	1-37(a)	3.00	5.00	6.75	1.50	3.25	6.50	33.25	34.67	6.08	0.50	3.97	2.12	4.50	29.00
97	1-37(b)	1.00	1.50	3.25	1.00	2.00	4.00	33.50	36.83	7.08	4.92	3.93	2.14	1.00	41.80
98	1-37(c)	1.00	1.00	2.50	1.00	2.00	4.50	33.25	32.75	7.75	3.08	4.10	2.02	0.00	39.65
99	1-37(d)(i)	1.25	2.75	5.25	1.50	3.25	5.50	33.25	33.92	6.00	1.00	4.92	2.56	2.00	39.50
100	1-37(d)(ii)	1.00	1.00	1.75	2.50	4.25	6.00	33.75	30.92	6.58	1.42	4.69	2.28	1.00	32.05
101	1-37(e)	1.50	2.25	3.75	2.50	4.50	6.00	33.25	31.33	5.92	0.58	4.77	2.56	0.50	28.25
102	1-37(f)	1.00	1.25	1.00	2.00	4.00	5.75	34.50	28.33	6.50	1.00	4.78	2.29	1.00	32.00
103	1-37(g)	2.50	4.50	7.25	2.25	4.25	6.25	34.50	33.42	6.58	4.42	4.46	1.43	0.00	26.50
104	1-37(h)	2.25	3.50	7.00	2.00	4.00	6.25	34.75	28.08	5.33	1.92	4.23	1.95	0.00	21.45
105	1-37(i)	2.75	4.50	6.50	2.25	4.00	6.25	33.50	29.42	7.67	4.17	3.81	1.78	0.00	23.20
106	2-1(b)(i)	3.00	5.00	7.25	2.50	4.50	7.00	32.50	29.13	6.13	0.00	4.04	2.25	1.00	24.35
107	2-2(b)	3.50	5.50	7.50	2.50	5.00	6.75	36.75	37.00	7.83	3.83	3.44	1.27	0.00	31.05
108	2-3(a)(i)	3.50	5.00	7.50	2.50	4.00	7.00	33.00	31.75	6.96	1.46	3.99	2.20	1.00	25.15
109	2-3(a)(ii)	3.50	5.00	7.75	3.00	5.00	7.50	35.50	31.88	6.63	3.63	3.76	1.90	0.50	25.15
110	2-3(b)	1.75	5.00	8.00	2.50	4.50	7.50	37.25	28.50	6.75	6.42	3.89	2.01	0.00	32.00

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
111	2-5(a)	2.00	5.00	8.00	2.50	4.50	7.25	34.75	34.56	6.21	3.58	4.06	2.03	0.00	31.05
112	2-5(b)	2.00	5.00	8.00	2.50	4.50	7.50	32.25	34.75	5.08	0.00	4.08	2.20	0.00	26.40
113	2-5(c)	2.50	5.00	7.50	2.50	5.00	6.75	32.50	41.06	5.54	2.58	4.38	2.12	0.00	35.95
114	2-5(d)	1.50	4.00	7.00	1.75	4.00	6.75	34.50	37.69	7.42	5.83	3.32	1.56	0.00	36.65
115	2-6(b)	2.00	5.00	7.75	2.50	4.50	7.50	33.00	29.25	4.67	1.00	3.82	2.04	4.00	44.55
116	2-6(c)	2.00	5.00	7.75	2.00	4.50	7.50	33.75	34.88	5.38	7.33	3.70	2.04	1.00	27.00
117	2-6(d)	2.00	5.00	7.50	2.00	4.50	6.75	33.25	37.00	7.08	3.17	3.90	1.87	0.00	19.55
118	2-6(e)	3.50	6.00	7.75	2.75	4.75	6.75	32.50	32.31	4.83	1.46	4.31	2.09	4.50	30.30
119	2-7(b)	3.00	5.50	7.50	2.50	4.25	6.50	31.50	34.50	5.21	5.13	4.87	1.80	0.00	23.60
120	2-7(c)	2.75	4.75	7.00	2.50	4.00	6.50	31.50	36.69	5.04	2.33	5.65	2.42	0.00	21.25
121	2-7(d)(i)	2.50	4.50	6.50	2.75	4.75	7.00	32.50	41.88	8.83	5.13	4.56	1.88	2.00	28.95
122	2-7(d)(ii)	3.00	4.75	6.50	2.00	4.75	7.00	33.50	37.81	10.29	9.50	3.95	2.02	0.00	33.75
123	2-8(a)	3.00	4.50	7.50	1.75	4.00	6.50	31.50	36.19	6.25	1.54	3.44	1.83	0.00	24.45
124	2-8(b)	2.50	5.00	6.75	2.25	4.75	6.25	33.00	38.56	6.96	6.17	3.68	1.81	2.00	32.40
125	2-10(a)	2.00	4.50	7.00	2.00	4.25	6.50	32.50	38.56	10.46	8.17	3.98	2.26	1.00	26.50
126	2-11(a)	3.00	5.00	6.50	2.00	4.50	6.50	33.50	37.50	8.75	9.88	4.21	2.31	0.00	31.80
127	2-12(a)(ii)	2.50	4.50	7.25	2.00	4.00	6.25	32.50	48.75	7.96	3.79	4.25	2.40	0.00	30.25
128	2-12(b)	2.00	4.00	7.00	2.00	4.00	6.25	37.25	39.69	6.96	3.54	4.16	2.27	2.00	29.25
129	2-13(a)	3.00	4.50	7.00	2.50	4.50	6.50	33.00	31.75	6.67	1.75	3.49	2.09	3.50	29.75
130	2-13(b)	3.00	4.50	7.50	2.50	4.50	6.50	31.50	31.94	4.88	0.00	4.25	2.15	3.50	29.75
131	2-13(d)(i)	4.00	5.25	8.50	2.50	4.50	7.50	34.75	40.13	5.50	3.13	3.28	1.19	0.00	36.55
132	2-13(f)	3.50	5.50	8.00	2.00	5.00	7.50	32.50	29.50	5.83	3.21	2.51	1.05	0.50	34.50
133	2-14(a)(i)	4.00	5.50	7.25	2.50	3.00	4.50	31.00	39.50	4.54	0.00	4.80	1.99	1.00	33.05
134	2-14(a)(ii)	2.50	4.50	7.00	2.00	2.50	5.25	31.00	37.69	6.67	0.75	4.67	2.68	1.50	35.85
135	2-14(b)(i)	2.00	4.00	6.75	2.00	3.00	5.75	33.50	35.88	4.88	0.00	4.70	2.40	1.50	27.00
136	2-14(b)(ii)	2.50	4.00	7.25	2.50	3.50	6.25	31.00	36.56	5.13	0.00	4.10	2.06	0.00	28.20
137	2-14(c)	2.50	4.50	7.50	2.00	3.50	6.00	32.75	40.38	7.38	8.54	4.70	1.49	0.00	32.20
138	2-14(d)	3.50	5.00	7.25	2.50	3.75	6.50	30.50	43.44	6.13	0.50	3.97	1.66	0.50	24.65

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
139	2-14(e)	3.25	5.00	7.25	2.50	4.00	6.50	34.25	49.38	8.54	0.50	3.73	1.26	0.00	29.90
140	2-14(f)	3.50	5.50	7.50	2.50	4.00	7.00	34.00	46.94	8.58	7.08	3.44	1.32	0.00	35.70
141	2-14(g)	3.00	5.50	8.00	2.50	4.00	7.00	34.25	38.81	7.79	6.38	4.16	1.18	0.50	49.25
142	2-15(a)	3.00	5.00	7.25	2.00	3.50	6.50	30.50	39.88	5.29	0.00	4.08	1.81	0.00	32.00
143	2-15(c)	3.50	5.00	7.00	2.50	4.00	6.50	34.50	44.13	7.71	5.88	4.29	2.11	1.50	32.60
144	2-15(e)	3.00	5.00	8.00	2.50	4.00	7.50	33.00	35.25	6.29	2.38	3.78	2.24	0.00	30.25
145	2-15(f)	4.50	6.00	8.00	2.00	2.50	5.00	31.25	32.63	4.88	0.00	3.62	1.81	1.00	32.00
146	2-15(h)(i)	3.50	5.00	7.00	2.50	3.50	5.50	35.75	38.13	7.38	10.50	3.16	2.24	0.00	29.10
147	2-15(h)(ii)	3.50	5.00	7.25	2.50	3.50	6.25	31.50	45.25	6.00	1.13	3.95	2.11	0.00	39.45
148	2-15(i)(a)	3.50	5.50	7.25	3.00	4.50	6.75	33.00	34.63	5.25	2.25	4.23	1.87	2.50	32.80
149	2-15(i)(b)	4.00	6.00	7.75	2.50	4.50	7.00	32.50	37.13	5.00	1.38	3.64	1.80	2.00	40.10
150	2-16(a)	4.00	6.25	8.00	2.50	4.50	7.25	33.25	29.88	5.50	4.25	4.05	1.83	0.00	29.55
151	2-16(b)	4.00	6.00	8.00	2.50	4.50	7.50	32.00	37.63	5.38	0.00	4.51	2.26	2.00	27.65
152	2-17(a)	3.00	6.00	8.00	2.50	4.50	7.00	32.50	39.25	5.38	0.00	3.99	1.60	0.50	23.55
153	2-17(b)	3.50	6.00	8.00	2.50	4.25	7.00	33.00	37.25	7.25	6.50	3.53	1.39	0.00	33.30
154	2-17(c)	2.50	5.50	7.50	3.00	4.25	6.50	32.50	35.25	6.50	11.25	3.44	1.28	1.00	33.05
155	2-17(d)	2.75	5.25	7.00	3.00	4.50	7.00	36.00	32.13	7.63	1.63	3.41	1.30	0.50	31.40
156	2-17(e)	2.50	5.00	7.50	3.00	4.50	7.00	34.00	37.75	6.50	0.00	4.47	2.23	1.50	37.20
157	2-17(f)	2.50	5.00	7.75	2.50	4.50	7.25	34.00	29.75	6.13	3.75	4.50	1.40	0.00	31.30
158	2-17(g)	2.50	4.50	7.25	2.50	4.50	7.00	34.50	31.75	6.00	3.88	3.35	1.77	3.50	28.00
159	2-18(a)	2.25	4.25	7.00	2.00	4.00	6.50	33.50	40.75	7.13	1.00	3.80	2.31	6.00	29.10
160	2-18(b)	1.75	3.75	6.50	2.00	4.00	6.50	33.50	34.00	4.50	0.00	3.76	2.10	4.50	27.00
161	2-18(c)	3.00	5.00	7.00	2.00	4.50	6.50	32.50	36.88	6.38	1.63	3.33	1.95	0.00	39.40
162	2-18(d)	3.25	5.25	6.25	2.50	4.50	6.75	34.00	33.00	6.13	4.38	3.64	2.02	6.00	32.10
163	2-19(a)	4.00	5.75	7.75	2.50	4.50	7.25	34.50	28.50	4.50	0.00	3.78	2.02	3.00	28.60
164	2-19(c)	3.00	6.00	8.00	3.00	5.00	7.75	32.50	34.13	4.38	0.00	4.28	2.15	2.00	24.70
165	2-19(d)	2.50	5.50	8.00	2.50	4.50	7.25	36.25	34.50	6.38	0.00	3.30	1.42	1.00	17.35
166	2-19(f)	2.00	5.00	7.50	2.50	4.50	7.00	33.25	37.38	5.00	3.00	3.85	1.69	3.00	30.60

Contd…

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
167	2-19(g)	3.00	5.50	8.00	2.00	4.00	7.50	32.00	36.25	4.63	0.00	4.21	2.04	1.00	37.25
168	2-19(h)	3.00	5.50	7.75	2.50	4.50	7.25	33.00	22.69	5.00	1.88	3.38	1.94	0.50	34.40
169	2-20(a)	3.00	6.00	8.00	2.50	4.50	7.00	33.75	19.38	4.50	0.00	2.93	1.63	2.00	31.60
170	2-20(b)	4.00	5.50	7.50	2.00	4.50	7.00	31.75	29.13	4.75	1.63	4.00	2.11	4.00	33.85
171	2-20(c)	3.50	5.50	7.50	2.50	4.50	6.75	33.25	37.50	4.75	0.00	3.51	1.70	0.00	30.40
172	2-20(d)	3.50	5.50	7.50	2.50	4.50	7.00	34.50	41.50	5.50	1.25	4.01	2.23	0.00	31.25
173	2-20(e)	4.00	5.00	6.50	3.75	5.50	7.50	33.50	54.75	6.75	7.50	4.96	2.32	0.50	37.50
174	2-21(a)	3.50	5.00	6.50	3.25	5.00	7.00	35.00	53.63	6.38	1.88	3.54	2.08	0.50	26.40
175	2-21(c)	2.00	3.50	7.00	3.00	4.50	7.00	32.50	39.63	6.38	0.00	4.18	2.02	1.50	33.65
176	2-21(d)	3.50	5.00	7.50	3.00	4.50	7.50	32.50	41.00	5.00	0.00	4.65	2.29	4.50	32.95
177	2-21(e)	2.50	4.00	7.75	2.50	4.00	7.75	33.50	41.13	5.13	2.75	4.10	2.26	4.00	35.45
178	2-21(f)	2.00	3.00	6.50	2.00	3.00	7.00	33.00	30.75	4.88	0.38	3.68	1.86	8.00	36.05
179	2-22(a)	1.50	2.50	6.00	1.50	2.50	6.50	31.00	37.25	5.38	0.00	4.54	2.04	0.00	23.95
180	2-23(a)	1.50	2.50	6.00	1.50	2.50	5.50	34.00	39.75	6.00	1.75	4.53	2.10	0.00	27.20
181	2-23(b)	2.50	4.00	7.00	2.50	4.00	6.50	36.25	37.13	5.88	1.25	4.06	1.93	6.00	32.55
182	2-23(c)	2.50	4.00	7.25	2.00	3.50	7.00	35.00	46.25	5.75	0.00	4.35	2.29	3.00	34.50
183	2-23(d)	2.00	3.50	7.25	2.00	3.50	6.75	33.00	44.00	4.63	2.25	4.45	2.39	0.50	34.40
184	2-23(e)	2.00	3.50	7.25	2.00	3.50	7.00	32.50	36.63	5.50	2.88	4.90	2.10	0.50	38.25
185	2-23(f)	2.50	4.00	7.75	2.50	4.00	7.00	32.50	39.88	5.38	0.00	4.22	1.96	0.50	39.70
186	2-23(g)	3.00	4.50	7.50	2.00	3.50	6.25	31.50	31.13	5.63	0.00	3.77	1.95	0.00	34.05
187	2-24(a)	3.00	4.50	6.25	2.50	4.00	6.75	34.50	33.00	6.00	0.00	3.90	2.07	2.50	38.20
188	2-24(b)	3.00	4.50	7.00	2.50	4.00	6.50	35.50	37.88	6.13	0.00	4.02	1.75	2.00	38.15
189	2-24(c)	1.00	1.00	3.50	1.50	2.50	4.00	35.00	36.13	6.50	5.63	3.28	1.77	0.00	24.15
190	2-25(a)	1.00	1.00	3.50	1.00	1.00	4.00	35.00	33.00	7.25	10.38	3.69	2.12	0.00	23.20
191	2-25(b)	3.00	4.50	7.50	3.00	4.50	6.50	35.25	41.88	7.25	2.88	4.35	2.06	0.00	30.65
192	2-26	3.00	4.50	7.75	3.00	4.50	6.75	35.00	40.13	6.63	9.00	4.19	2.01	0.00	28.80
193	2-27(c)	2.75	4.50	6.75	3.00	4.50	7.25	36.00	38.88	7.75	2.75	3.59	1.69	0.00	31.25
194	2-27(d)	3.75	5.50	8.50	3.00	4.50	6.25	33.50	38.88	5.88	2.38	3.81	1.92	0.50	32.80

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
195	2-27(e)	3.75	5.50	8.00	3.00	4.50	6.25	34.50	38.00	4.88	0.00	4.04	2.21	3.00	34.70
196	2-27(f)	3.50	5.00	6.75	2.00	3.50	6.50	36.00	35.75	5.63	3.88	4.00	2.10	0.00	39.50
197	2-28(a)	3.00	4.50	7.00	2.50	4.00	6.25	34.00	34.25	5.50	0.00	3.81	2.08	3.50	25.50
198	2-28(b)	3.00	4.50	7.00	2.50	4.00	6.25	34.50	39.38	7.00	5.88	3.88	2.16	4.50	30.50
199	2-29(a)(i)	3.25	5.00	6.75	2.50	4.00	6.75	34.50	49.50	6.88	5.88	4.64	2.35	7.00	34.20
200	2-29(a)(ii)	3.50	5.00	7.50	2.50	4.00	7.00	34.50	34.75	5.13	0.00	3.20	1.69	0.00	33.65
201	2-29(a)	3.50	5.00	7.50	2.50	4.00	7.25	31.50	33.38	4.38	0.00	2.84	1.57	0.00	33.05
202	2-29(c)	4.50	6.00	8.25	3.50	5.00	7.75	31.50	30.00	4.88	0.00	3.09	1.68	0.00	33.15
203	2-29(e)	2.00	4.50	7.25	2.00	3.50	7.00	30.50	28.50	4.50	0.00	4.30	1.80	0.50	35.50
204	2-29(f)	3.00	4.50	6.75	2.00	3.50	6.75	30.50	24.25	4.50	0.00	3.90	1.85	3.00	37.25
205	2-29(g)	2.50	4.00	6.75	2.00	3.50	6.75	31.00	23.25	6.13	0.00	4.15	2.06	3.00	42.35
206	2-30(a)	3.00	5.00	7.25	2.50	4.00	6.75	31.00	26.13	5.75	0.00	3.94	2.11	0.00	35.05
207	2-30(b)	3.00	5.00	7.25	2.50	4.00	6.75	32.00	33.50	5.13	0.25	5.09	2.35	2.50	37.65
208	2-30(c)(i)	3.50	5.50	8.00	3.00	5.00	7.00	32.50	35.00	5.13	0.25	4.88	2.36	0.50	32.95
209	2-30(d)	3.00	4.75	8.00	3.00	4.50	7.50	33.75	44.88	5.38	0.63	4.98	2.50	8.00	34.75
210	2-30(e)	3.00	5.00	8.50	3.00	4.50	7.50	32.00	33.50	6.00	0.50	4.53	2.22	7.00	41.90
211	2-30(f)	3.00	5.00	8.00	2.50	4.00	7.50	32.50	32.75	5.13	1.75	4.86	2.39	2.50	35.35
212	2-30(g)	3.00	5.00	7.75	2.50	4.00	7.00	33.50	32.75	5.13	0.38	3.68	2.00	5.00	34.90
213	2-32(a)	2.50	4.00	7.25	1.50	3.00	6.50	37.00	33.25	6.13	4.38	4.14	2.13	1.00	28.90
214	2-32(c)	3.00	4.50	7.25	2.50	3.50	6.50	32.00	33.75	5.13	1.38	3.63	1.76	0.00	42.75
215	2-32(e)	3.00	5.00	7.25	2.50	4.50	6.00	34.00	33.50	6.50	6.50	3.59	1.92	0.00	29.80
216	2-32(g)	2.50	4.00	7.50	2.00	3.50	6.50	34.00	32.75	8.25	5.25	3.38	1.78	0.00	41.55
217	2-32(b)	3.00	4.50	6.25	2.50	4.00	6.25	33.00	33.38	5.50	2.13	4.33	1.94	2.00	40.15
218	2-33(a)	2.00	3.00	5.00	1.50	3.00	5.50	31.50	30.75	6.50	0.00	4.31	2.25	0.00	36.90
219	2-33(d)	1.50	2.50	6.75	2.00	3.50	6.50	36.00	28.13	7.50	4.13	3.64	2.03	2.50	37.05
220	2-33(e)	3.00	4.50	7.50	2.50	4.00	6.75	31.00	30.25	5.38	0.00	4.35	2.18	7.50	43.50
221	2-34(a)	3.00	4.50	7.75	2.00	3.50	7.75	36.50	34.38	5.63	0.50	4.12	2.12	0.00	37.00
222	2-35(a)	3.00	4.50	7.50	2.00	3.50	7.25	34.00	35.75	6.88	2.38	3.65	2.00	2.00	36.60

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
223	2-35(b)	2.00	3.00	7.25	1.50	2.50	7.25	35.50	35.00	8.75	12.00	3.67	1.84	0.50	42.45
224	2-35(d)	2.25	4.00	6.00	2.00	3.50	6.00	37.50	33.88	8.88	19.88	4.95	2.34	4.00	35.95
225	2-35(e)	2.00	3.50	6.75	2.00	3.00	6.75	31.00	34.75	5.50	1.13	4.09	1.97	4.00	41.70
226	2-36(a)(i)	2.00	3.50	6.50	1.50	3.00	7.00	36.25	34.25	8.75	5.63	4.02	1.37	0.00	41.20
227	2-36(a)(ii)	1.50	3.00	6.25	1.50	3.00	6.25	35.00	39.50	6.75	4.13	4.44	2.42	3.50	40.05
228	2-36(b)	2.50	4.00	6.25	2.00	3.50	6.25	34.50	32.88	9.50	4.38	4.62	2.40	0.00	35.30
229	2-36(c)	2.50	4.00	6.50	2.50	4.00	6.50	33.00	28.88	8.63	5.25	4.06	2.35	0.00	35.05
230	2-37(a)	2.00	3.00	5.50	2.00	4.00	5.25	35.50	29.38	7.00	4.63	4.12	2.16	1.00	34.05
231	2-38(b)(i)	2.00	3.00	6.50	2.50	4.00	5.75	34.50	32.75	5.13	4.88	4.95	2.60	0.00	33.90
232	2-38(b)(ii)	2.00	3.00	6.50	2.00	3.50	5.25	38.00	31.75	6.50	4.88	4.48	2.27	0.00	31.15
233	2-38(d)	2.00	3.00	5.50	1.50	3.00	5.25	35.00	31.38	6.63	5.75	4.77	2.63	1.00	38.40
234	2-39(a)	2.00	3.50	6.75	1.50	3.00	6.50	33.50	33.31	6.38	2.88	4.14	2.14	1.00	34.10
235	2-39(b)	2.50	4.00	7.00	1.50	2.50	6.50	34.75	30.13	6.88	5.75	3.63	1.40	3.50	46.70
236	2-39(c)	2.00	3.00	6.75	2.00	3.50	7.00	33.00	30.00	6.00	1.00	3.67	1.98	2.00	32.75
237	2-39(d)	2.00	3.50	6.75	1.50	3.00	6.50	37.00	32.31	5.83	3.63	3.84	1.44	0.50	38.65
238	2-39(e)	2.00	3.00	7.00	1.50	3.00	6.25	32.50	26.56	4.88	2.13	4.28	1.70	0.00	35.20
239	2-39(f)	2.00	3.50	6.25	2.50	4.00	6.25	36.50	32.38	5.17	1.96	4.05	2.41	2.00	30.55
240	2-39(g)	2.00	3.50	6.25	2.50	4.00	6.75	34.00	36.25	6.25	2.21	4.37	2.02	4.00	28.85
241	2-39(i)	2.50	4.00	6.50	2.00	3.50	6.00	32.00	36.31	5.38	0.38	4.33	2.55	1.00	31.00
242	2-40(b)	2.50	4.00	6.25	2.00	4.00	6.00	32.50	33.88	5.79	0.33	4.93	2.72	1.50	28.70
243	2-40(c)	2.50	3.50	6.50	2.50	4.00	6.00	31.00	32.88	6.08	0.00	4.71	2.85	0.50	28.30
244	2-40(d)	2.00	3.00	6.25	1.50	2.50	5.50	31.00	32.63	4.58	0.00	3.73	2.42	0.50	33.55
245	2-41(a)	2.50	4.00	6.25	1.50	2.50	5.50	36.50	39.19	9.00	10.58	4.43	2.40	5.00	37.05
246	2-41(b)	3.00	5.00	7.25	2.00	3.50	6.25	32.00	31.50	4.50	0.00	4.13	2.31	4.50	31.80
247	2-41(c)	2.50	4.00	6.50	2.00	3.50	5.75	34.50	40.81	8.38	8.71	4.32	2.23	5.50	34.65
248	2-41(d)	2.50	4.00	7.25	2.50	4.00	6.50	34.25	32.44	8.29	7.00	4.38	2.21	6.50	38.40
249	2-41(e)	3.00	5.00	7.00	2.00	4.00	6.00	34.50	39.31	10.38	11.25	3.98	1.03	0.00	46.25
250	2-42(b)	2.50	4.50	7.50	2.50	4.50	7.50	34.00	38.44	6.92	6.63	4.10	1.97	2.50	39.10

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
251	2-42(c)	2.00	3.50	7.00	2.00	3.50	6.50	32.00	34.38	6.25	3.08	4.28	2.33	0.00	32.10
252	2-42(e)	2.00	3.00	7.75	2.00	3.50	7.00	32.00	37.38	5.38	2.38	4.43	2.21	0.00	33.30
253	2-42(f)	3.00	4.50	6.75	2.00	4.00	6.00	30.50	36.13	5.75	0.00	3.87	1.86	0.00	38.50
254	2-42(g)	3.00	5.00	7.00	2.00	3.00	4.00	32.50	34.00	5.46	0.25	4.05	1.71	0.00	31.65
255	2-43(b)	2.50	4.50	7.25	2.00	3.50	6.50	30.50	32.00	5.38	0.00	3.96	2.00	4.50	241.00
256	2-43(c)	2.50	4.00	6.50	2.00	3.50	6.00	37.00	36.13	6.63	4.63	4.40	2.45	1.00	39.20
257	2-44(d)	2.50	4.00	6.50	2.00	3.50	6.00	33.00	44.13	6.63	2.00	4.48	2.39	0.50	44.50
258	2-44(e)	3.00	4.50	7.25	2.50	4.00	6.50	35.00	33.00	6.88	9.00	4.18	1.26	0.00	45.80
259	2-45(a)	1.00	1.00	1.75	2.00	3.00	4.75	31.00	34.63	5.50	1.25	4.72	2.20	0.00	32.40
260	2-45(b)	3.00	4.50	7.50	2.00	3.00	6.00	31.50	31.25	6.00	4.00	3.96	2.05	0.00	35.85
261	2-45(c)	2.00	3.50	7.00	2.00	3.50	6.50	37.50	35.00	8.75	8.88	3.78	1.85	1.00	45.85
262	2-45(d)	3.00	4.50	7.00	2.00	3.50	6.50	36.75	30.25	9.00	8.25	4.03	2.07	0.00	34.55
263	2-45(e)	3.00	4.50	7.50	3.00	4.50	7.00	32.00	46.88	7.63	5.50	4.20	1.58	2.50	44.95
264	2-45(f)	3.25	5.50	6.75	2.50	4.50	6.00	30.75	44.75	5.63	0.75	3.65	2.03	2.00	46.25
265	2-45(g)	3.00	5.25	7.25	2.50	4.50	6.75	34.00	31.88	9.75	10.38	3.80	1.62	0.00	47.90
266	2-46(a)	3.00	5.00	6.50	2.50	4.50	6.25	33.50	35.00	7.75	5.75	3.68	1.45	0.00	43.95
267	2-46(b)	3.00	5.00	7.75	2.50	4.00	7.75	35.00	41.75	8.63	5.13	3.70	1.50	1.50	41.65
268	2-46(c)	3.50	6.00	8.00	3.50	5.50	8.00	34.50	31.63	7.00	7.50	3.46	1.37	1.50	37.65
269	2-47(a)	3.50	6.00	8.25	3.00	5.00	7.50	35.00	33.50	8.38	5.50	3.55	1.83	0.50	44.75
270	2-48(a)	4.00	6.50	8.75	3.00	5.00	8.25	35.00	34.75	5.38	4.25	3.78	1.63	0.00	41.70
271	2-48(b)	3.50	6.00	8.75	3.00	5.50	8.00	33.50	32.88	6.25	4.88	3.17	1.55	0.00	43.25
272	2-48(c)	3.00	5.00	8.00	3.00	5.00	7.75	36.25	31.50	6.63	6.63	3.79	1.28	5.50	44.80
273	2-48(f)	3.00	5.00	8.50	3.00	4.50	7.75	37.00	31.63	7.13	7.63	4.25	1.40	0.00	22.70
274	2-48(i)	3.00	5.00	8.50	2.50	4.00	8.25	31.50	25.50	6.13	1.50	3.40	1.91	1.50	36.45
275	2-49	2.50	4.00	8.50	2.50	4.50	7.00	33.00	38.38	4.63	0.00	3.86	1.80	0.00	39.60
276	2-50(a)	2.50	4.50	8.00	3.00	5.50	6.75	31.00	32.50	5.13	0.50	3.78	1.16	0.00	39.85
277	2-50(b)	3.00	5.00	7.50	2.50	4.50	6.75	32.00	35.38	5.88	2.38	3.95	2.03	1.50	36.10
278	2-50(c)	2.50	4.00	8.00	2.50	4.00	7.50	32.50	31.13	6.00	2.13	3.86	1.62	0.50	24.65

Contd…

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
279	2-50(e)	2.50	4.25	6.50	3.00	5.00	6.50	33.00	36.75	6.25	5.63	4.60	2.15	0.00	37.50
280	2-50(f)	2.50	3.75	6.50	2.00	3.50	7.00	31.50	33.88	5.75	5.38	4.80	2.14	0.50	36.25
281	2-50(g)	2.00	3.00	6.75	2.00	3.50	6.75	32.50	26.00	6.13	2.13	4.02	2.25	0.00	25.20
282	2-50(i)	3.00	4.50	7.25	2.00	4.00	6.75	33.00	29.13	8.63	9.00	4.25	1.27	1.00	32.40
283	2-51(a)	3.00	4.75	7.75	2.50	4.25	7.00	31.50	33.25	4.75	0.00	4.90	2.12	3.00	26.65
284	2-51(b)	3.00	4.75	7.50	3.00	4.75	6.75	31.00	31.50	5.75	1.50	4.08	1.83	0.00	27.15
285	2-51(c)	3.00	4.75	8.00	3.00	4.50	7.50	32.50	29.00	5.88	0.00	4.04	1.88	0.00	25.50
286	2-51(d)	2.50	4.00	7.75	2.50	4.50	7.25	32.00	31.50	5.38	0.88	4.07	2.03	0.00	32.00
287	2-51(e)	2.00	3.00	5.50	2.00	3.00	6.00	32.50	28.63	6.25	0.00	3.96	2.23	0.00	33.35
288	2-51(f)	2.50	4.00	5.50	2.50	4.25	6.00	33.00	34.13	5.50	0.00	4.76	2.26	2.00	29.40
289	2-52(a)	3.00	4.50	6.50	3.00	5.00	6.50	31.50	32.50	5.38	0.00	4.55	2.24	0.00	29.60
290	2-52(c)	2.50	4.00	6.00	2.50	4.00	5.50	36.00	36.25	5.38	4.63	4.48	2.19	1.00	34.05
291	2-52(d)	3.00	4.50	6.50	2.50	5.00	6.50	32.00	34.88	5.25	0.00	4.68	2.32	0.00	33.05
292	2-52(e)	3.00	5.00	6.75	2.50	4.50	6.00	32.50	36.00	6.50	3.50	5.04	2.56	0.50	31.15
293	2-54(a)	2.50	4.00	6.50	2.50	4.00	5.50	36.50	32.38	6.88	4.88	5.33	2.70	2.00	28.25
294	2-54(b)	2.00	3.00	6.50	2.00	3.50	6.25	36.00	32.88	8.63	3.75	4.37	2.37	3.50	32.50
295	2-55(a)	3.00	4.50	7.00	2.50	4.00	6.50	33.50	31.50	4.88	1.38	4.15	2.21	0.00	26.30
296	2-55(b)	3.00	5.00	7.00	3.00	4.50	7.25	32.00	32.88	4.88	0.00	3.83	1.93	2.00	34.35
297	2-55(d)	3.50	5.25	7.50	3.00	5.00	7.00	31.50	32.88	5.25	0.00	3.70	1.87	1.50	32.00
298	2-55(e)	3.50	5.50	8.50	3.00	5.25	8.00	30.50	31.25	5.00	0.00	3.48	1.97	5.50	28.65
299	2-55(f)	3.00	5.00	7.75	3.50	5.50	7.75	34.00	27.13	6.38	3.75	3.44	1.49	0.00	38.50
300	2-56	2.50	4.00	7.75	3.00	5.00	7.25	35.00	23.25	7.88	6.63	3.45	1.34	0.00	27.20
301	2-57(b)	3.00	4.50	7.50	2.00	3.50	7.00	34.00	26.38	5.88	3.25	3.44	1.49	1.00	33.80
302	2-57(c)	3.00	4.50	8.00	3.00	4.50	7.50	35.50	34.25	6.25	2.63	4.50	2.28	5.00	28.00
303	2-57(d)	3.00	5.00	7.00	3.00	4.75	7.50	35.50	33.63	7.25	9.00	4.36	1.38	5.50	44.05
304	2-58	3.00	5.50	7.75	3.00	5.00	7.50	35.50	31.00	7.38	6.13	4.58	2.10	2.50	29.55
305	2-59(a)	3.00	5.00	7.75	3.00	5.00	7.75	33.50	32.63	5.38	2.75	4.71	2.08	3.50	27.90
306	2-59(b)	3.00	5.00	7.75	2.50	4.00	7.75	31.00	28.38	4.38	0.25	3.54	1.87	0.50	35.35

Contd…

Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
307	2-59(c)	3.00	5.00	7.75	3.00	4.50	7.50	31.50	32.75	5.88	1.75	3.19	1.84	0.00	38.10
308	2-59(d)	3.00	5.00	7.50	3.00	4.50	6.75	33.50	32.63	4.88	2.63	4.10	1.97	0.50	35.30
309	2-59(g)	2.50	3.50	6.00	2.50	3.50	5.75	35.00	32.63	6.88	6.88	3.96	2.16	0.00	34.90
310	2-59(j)	2.50	3.50	6.50	2.50	4.00	6.00	34.00	32.50	5.38	1.50	4.37	2.04	0.00	30.10
311	2-59(k)	3.00	5.00	6.50	3.00	4.50	6.50	34.50	44.50	10.88	14.63	3.44	1.37	0.50	44.60
312	2-59(l)	3.00	5.00	7.25	2.50	4.50	6.50	32.50	27.13	6.75	3.50	3.92	2.02	0.00	30.95
313	2-60(a)	2.00	3.50	6.25	2.00	3.50	5.75	34.50	29.38	5.13	0.00	4.17	2.15	2.00	38.65
314	2-60(c)	2.00	3.00	5.75	2.50	4.25	5.75	36.75	43.38	9.63	11.63	4.70	2.44	0.50	38.45
315	2-60(d)	2.00	3.00	5.75	2.00	3.75	5.75	35.00	35.63	8.25	9.63	4.18	2.35	0.00	38.20
316	2-60(e)	2.50	4.00	6.25	2.00	3.50	5.75	35.50	50.25	10.63	11.88	5.00	2.42	0.00	31.05
317	2-60(f)	10.00	4.00	6.75	2.00	3.50	6.75	34.00	36.38	7.75	6.75	4.35	2.29	0.00	30.20
318	2-61(a)	2.50	4.50	7.00	2.50	4.50	6.50	37.25	37.00	9.75	5.63	3.94	1.91	2.00	35.15
319	2-61(b)	2.50	4.00	7.50	2.50	4.00	6.50	36.50	32.50	7.38	8.88	4.65	2.17	1.50	33.20
320	2-61(d)	2.75	4.25	6.75	2.50	4.00	6.25	32.50	34.00	5.63	0.25	4.67	2.27	1.50	25.20
321	2-62	2.50	3.50	7.00	2.25	3.75	5.50	32.00	34.75	5.00	0.00	4.09	2.30	1.50	34.80
322	2-63(a)	3.00	5.00	7.00	2.75	4.25	6.50	34.00	34.13	9.50	9.63	4.51	2.44	0.00	26.05
323	2-63(b)	2.00	3.00	6.50	2.50	3.75	6.00	35.00	38.25	4.88	6.75	3.65	2.28	1.50	18.85
324	2-63(c)	2.00	3.50	6.50	1.50	3.00	6.00	35.00	37.50	8.75	10.88	4.83	2.61	2.50	31.60
325	2-63(d)	2.00	3.00	6.50	2.00	3.25	5.50	33.00	36.13	6.13	0.00	4.44	2.21	0.00	36.40
326	2-64(a)	2.50	4.00	6.75	2.50	4.00	6.25	36.50	34.13	7.38	8.63	4.32	1.12	3.50	47.05
327	2-64(b)	3.00	5.00	7.25	3.00	5.00	6.75	33.00	38.13	5.50	3.38	4.25	2.30	4.00	33.70
328	2-64(c)	2.75	4.25	6.75	2.50	4.00	6.25	32.50	31.25	6.38	5.63	4.55	2.30	2.00	31.00
329	2-65(a)	3.00	4.50	7.25	2.75	4.25	6.75	32.00	26.50	6.38	0.00	4.07	2.23	2.00	30.65
330	2-65(b)	3.00	4.50	7.50	3.00	4.50	7.50	32.00	38.38	4.75	14.75	5.50	2.40	2.50	35.10
331	2-65(c)	2.75	5.00	7.50	2.75	5.00	7.50	36.50	32.38	8.38	10.88	3.14	1.02	0.00	39.10
332	2-66(a)(i)	3.00	5.25	6.50	3.00	5.25	7.50	32.50	33.25	4.88	0.50	4.67	2.31	1.50	29.30
333	2-66(a)(ii)	3.00	5.00	7.75	3.00	5.00	7.75	32.50	29.13	4.88	0.00	3.86	2.05	6.00	27.10
334	2-66(b)	2.75	5.00	7.00	3.00	5.00	7.50	31.50	30.25	5.00	0.00	4.83	2.35	0.00	27.90

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
335	2-66(d)	3.00	5.00	7.50	2.75	4.50	7.00	33.50	29.13	4.88	0.00	4.45	2.22	0.00	26.95
336	2-67(a)	3.50	5.25	7.50	2.50	4.50	6.50	37.75	34.88	7.13	9.00	3.86	1.93	0.00	27.20
337	2-67(b)	2.50	4.75	7.75	2.75	4.25	7.25	36.00	31.63	7.13	7.25	3.58	1.18	3.00	36.80
338	2-68(a)	3.50	5.75	7.75	3.50	5.75	7.75	34.50	32.63	6.38	4.25	3.07	1.65	6.00	26.45
339	2-68(b)	3.00	4.75	7.50	2.75	4.75	7.50	37.25	44.63	6.63	5.50	3.99	1.37	3.00	34.05
340	2-70(a)	3.00	5.25	7.75	3.00	5.50	7.75	37.00	31.75	7.75	8.63	3.85	1.85	0.00	27.30
341	2-70(c)	3.00	5.50	8.25	3.00	5.25	7.75	32.50	29.13	5.63	0.00	3.38	1.48	4.50	30.95
342	2-71(a)	3.00	5.50	8.25	3.00	4.50	7.50	34.00	24.50	6.63	2.25	2.73	1.76	4.00	29.55
343	2-71(d)	3.00	4.75	8.25	2.50	4.25	7.50	35.00	26.63	4.00	1.63	3.21	1.56	0.50	35.30
344	2-72(a)	3.00	4.75	8.25	2.50	4.25	7.25	31.50	43.88	5.63	0.25	3.85	1.70	0.50	40.00
345	2-72(b)	2.50	4.25	7.50	2.00	3.50	7.00	35.00	20.00	5.50	0.63	3.57	1.93	0.00	34.60
346	2-72(c)	3.00	5.00	6.75	3.00	4.75	7.25	34.50	25.13	9.13	7.38	3.15	1.13	3.50	37.45
347	2-72(d)	3.00	4.75	7.50	2.50	3.75	6.50	38.50	31.38	7.38	1.50	3.93	1.88	0.00	17.70
348	2-72(f)	1.00	1.75	8.00	1.50	2.75	7.00	32.00	38.13	5.75	0.63	3.67	1.81	0.00	30.05
349	2-73(b)	1.00	1.00	7.25	2.00	2.50	6.25	34.50	30.38	7.50	6.25	3.97	2.08	0.00	37.85
350	2-73(c)	1.00	1.00	6.50	2.50	3.25	6.00	36.50	32.75	8.00	4.50	3.43	1.87	1.00	34.55
351	2-73(d)	3.00	5.00	6.50	2.50	4.25	6.00	34.00	35.38	7.38	2.38	4.22	2.24	3.00	31.10
352	2-74(b)	3.00	5.50	7.50	3.00	4.75	7.00	31.50	31.75	8.13	4.13	3.79	1.76	2.50	29.15
353	2-74(c)	3.00	5.00	7.50	3.00	5.00	7.00	36.25	33.38	7.50	1.75	4.06	2.07	0.00	42.65
354	2-74(d)	3.00	5.00	7.50	3.00	4.75	7.00	32.50	30.00	5.38	1.13	4.45	2.32	1.00	32.80
355	2-74(e)	3.00	5.50	7.50	2.50	4.75	7.00	32.00	36.63	5.63	0.00	4.53	2.33	2.00	32.35
356	2-74(f)(i)	2.50	3.50	6.25	2.75	4.25	6.25	33.00	30.38	6.75	9.75	3.98	2.08	0.00	25.10
357	2-74(f)(ii)	2.00	3.00	6.25	2.00	3.50	5.50	33.00	29.63	5.50	0.63	3.41	1.84	1.50	38.55
358	2-75	2.50	3.50	6.00	2.00	3.50	5.50	36.50	42.13	6.63	3.50	4.28	2.01	3.00	35.15
359	2-76(a)	2.50	3.50	6.25	3.00	4.50	6.00	32.00	32.13	5.00	1.38	3.96	1.91	3.00	33.00
360	2-76(b)	1.00	1.00	4.75	1.00	1.00	3.50	35.25	26.88	7.00	0.38	3.84	1.87	0.00	38.10
361	2-76(d)	1.00	1.00	6.50	1.00	1.00	6.00	32.00	36.38	5.13	2.63	3.35	1.63	2.00	40.95
362	2-76(e)	2.00	3.00	6.50	1.50	3.00	5.25	33.50	28.38	5.13	0.00	4.20	1.96	0.00	37.10

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
363	2-76(f)	2.50	4.00	6.25	2.00	3.50	5.50	35.50	31.00	8.88	6.63	3.17	1.85	0.00	25.70
364	2-76(g)	3.00	4.50	6.75	2.00	3.50	6.00	36.75	29.00	8.25	3.75	4.28	2.06	0.00	22.55
365	2-77(a)	3.50	5.50	8.50	2.50	4.50	6.50	35.50	29.75	7.13	4.38	3.69	2.15	5.50	39.80
366	2-77(c)	3.50	5.50	8.50	2.50	4.00	7.00	32.00	33.63	5.50	0.00	3.60	2.00	0.00	33.60
367	2-78(a)	3.50	5.50	7.75	3.00	5.00	7.00	33.00	34.63	5.50	0.00	4.80	2.11	2.00	27.45
368	2-78(c)	3.00	4.50	8.25	2.50	4.00	7.00	30.50	37.50	4.75	2.38	3.99	2.00	3.50	34.60
369	2-79(b)	3.00	4.50	7.75	2.50	4.00	6.50	33.00	33.50	7.00	0.00	3.63	2.05	5.50	30.35
370	2-79(c)	3.00	4.50	7.25	2.50	4.00	6.25	33.50	33.63	8.25	4.50	4.06	2.02	3.50	26.65
371	2-79(e)	3.00	5.00	7.25	3.00	4.50	7.00	32.50	32.25	6.50	1.00	3.48	1.90	1.50	24.85
372	2-80(a)	1.00	1.00	2.00	2.50	4.00	6.25	35.00	28.75	5.88	1.00	4.61	2.20	0.00	24.40
373	2-80(b)	2.00	3.00	4.75	3.00	5.00	6.75	34.50	36.25	5.75	3.00	6.02	2.52	0.50	40.25
374	2-80(d)	2.00	3.50	6.75	2.50	4.00	6.25	35.50	35.00	8.00	6.38	4.00	1.41	3.00	37.35
375	2-81(a)	2.50	4.50	8.50	2.50	4.50	8.00	32.50	35.88	5.25	0.63	3.33	1.86	0.00	30.80
376	2-81(a)(ii)	3.00	5.00	8.00	2.50	4.50	7.50	32.00	33.13	6.88	2.25	3.00	2.03	0.50	24.05
377	2-81(c)	3.00	4.50	7.25	2.50	4.00	6.00	32.50	36.00	5.75	2.25	3.15	2.00	0.50	30.70
378	2-81(e)	2.50	4.00	7.00	2.00	3.50	6.00	32.50	40.63	6.13	1.00	3.65	2.23	5.00	32.25
379	2-81(f)	2.50	4.00	7.00	2.50	4.00	6.00	33.00	42.88	7.38	5.63	4.16	1.95	0.00	30.00
380	2-81(h)	3.00	4.50	7.00	2.50	3.75	6.00	33.50	42.75	7.38	3.38	4.30	2.16	0.50	31.60
381	2-81(i)	2.50	4.50	7.00	2.50	4.00	6.00	33.00	37.75	7.38	6.75	4.11	2.05	0.00	33.40
382	2-82(a)	2.50	4.50	6.50	2.00	3.50	5.50	34.50	38.88	6.25	0.88	4.25	2.51	0.50	28.95
383	2-82(b)	2.50	4.00	6.50	1.50	3.00	5.50	33.50	41.13	6.00	0.00	4.27	2.35	0.00	36.70
384	2-83(a)	2.75	4.25	6.50	2.50	4.00	6.00	33.50	37.38	8.63	9.75	3.66	2.38	0.00	34.40
385	2-83(b)	2.50	4.75	7.50	2.00	3.50	6.50	31.50	38.38	6.13	1.00	4.50	2.13	0.00	27.95
386	2-83(d)	2.50	4.50	7.50	2.00	4.00	6.50	32.50	38.13	4.75	0.00	3.77	2.24	0.50	23.15
387	2-84(a)	2.50	4.50	7.50	2.50	4.50	6.50	32.50	43.25	5.63	1.25	4.21	2.39	0.00	33.35
388	2-84(b)	3.00	5.00	7.50	2.50	4.50	6.25	32.00	39.75	6.75	1.25	3.90	2.56	1.50	24.65
389	2-85(a)	3.50	5.50	8.00	2.50	5.00	6.75	32.50	37.00	6.00	3.38	3.68	1.63	0.00	31.20
390	2-85(c)	3.50	5.50	7.75	3.00	5.25	7.50	33.00	40.75	8.25	4.92	3.80	2.37	0.00	32.10

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
391	2-86(c)	3.50	5.50	8.00	3.00	5.50	7.00	30.50	34.50	5.63	0.25	4.15	2.61	0.00	35.90
392	2-86(d)	2.50	4.50	7.50	2.50	4.50	7.00	31.50	36.63	4.00	0.63	3.80	2.13	0.00	36.50
393	2-86(e)	3.00	5.00	8.50	2.75	5.00	7.50	33.00	35.50	6.25	1.50	3.94	2.02	2.00	32.30
394	2-87(f)	2.00	3.00	7.25	2.50	4.00	6.50	38.50	41.13	7.38	5.29	3.68	2.05	0.00	35.25
395	2-87(a)	2.50	4.50	7.75	3.00	4.50	7.00	36.50	34.88	6.50	5.63	3.37	1.28	3.50	42.90
396	2-87(b)	3.00	4.50	7.50	2.50	4.00	6.75	37.00	46.00	8.88	13.92	5.68	1.84	1.00	44.40
397	2-87(d)	2.50	4.50	7.25	2.50	4.50	6.50	37.00	44.50	11.13	11.96	4.08	1.86	0.50	43.65
398	2-87(e)	3.00	5.00	6.75	3.25	5.25	7.25	35.50	40.38	8.88	6.63	5.52	1.94	3.00	36.70
399	2-87(f)	2.50	4.50	7.50	3.25	5.25	7.50	38.00	33.13	9.75	6.33	3.73	2.16	4.00	28.90
400	2-87(g)	3.00	5.00	7.50	3.25	5.25	7.50	35.00	39.25	8.63	3.38	5.60	2.25	0.00	31.50
401	2-87(h)	2.00	4.00	7.00	3.50	5.50	7.25	37.25	37.38	10.75	8.63	3.76	1.88	2.50	35.15
402	2-88(a)	2.00	4.00	6.75	3.00	5.00	6.75	36.00	40.75	9.00	3.88	3.70	2.00	4.00	35.80
403	2-88(b)	1.50	2.00	6.75	2.75	4.75	7.00	34.00	34.63	5.75	3.38	4.51	1.90	1.50	29.25
404	2-88(c)	1.50	2.00	6.75	2.75	4.75	7.00	35.00	38.25	9.50	2.88	3.68	2.01	2.00	31.10
405	2-88(d)	1.50	2.00	6.50	2.50	4.50	6.75	35.50	32.88	12.00	5.63	4.85	2.18	0.00	34.40
406	2-89	2.00	3.75	6.50	2.00	3.75	6.00	35.50	39.75	4.50	1.13	4.55	2.08	7.00	45.00
407	2-90(a)	3.00	4.75	7.25	2.50	4.75	6.75	31.50	40.38	6.00	0.00	4.05	2.08	0.50	34.45
408	2-90(b)	2.50	4.00	6.00	2.50	4.75	6.50	35.00	29.63	6.50	3.25	3.51	2.20	1.00	38.10
409	2-91(a)	2.00	3.00	7.00	2.75	4.75	6.50	34.50	31.63	7.38	4.00	3.89	2.21	0.00	45.70
410	2-91(b)	2.75	4.00	7.00	2.75	4.50	6.50	34.00	30.75	6.88	0.00	3.60	2.25	5.00	37.70
411	2-91(c)	3.00	4.50	7.50	2.75	4.75	7.00	32.50	41.38	5.00	1.25	3.76	2.40	2.00	37.80
412	2-91(d)	3.00	5.00	7.75	3.00	5.00	7.75	32.00	34.75	4.50	0.88	3.59	2.25	0.00	38.90
413	2-91(f)	3.00	5.25	8.00	3.00	4.50	7.75	31.00	36.25	6.13	0.00	3.81	2.43	0.00	38.10
414	2-91(g)	3.00	5.25	8.00	3.00	4.50	7.75	31.50	29.13	5.50	0.63	3.69	2.05	0.00	32.20
415	2-92(a)	3.00	5.25	8.00	3.00	4.50	7.25	31.00	28.50	5.50	3.00	3.43	2.01	1.00	33.20
416	2-92(b)	2.75	5.00	6.75	2.50	4.00	6.25	33.50	34.88	5.13	0.63	3.34	2.16	0.00	39.15
417	2-92(c)	2.00	3.00	6.50	2.75	4.25	6.50	35.00	27.50	7.50	2.75	4.00	2.13	0.00	34.70
418	2-92(d)	3.00	5.75	7.50	2.75	4.75	7.00	32.00	37.63	5.00	2.50	4.72	1.50	2.00	42.00
419	2-92(e)	3.00	5.00	7.75	2.75	4.25	7.25	33.50	33.25	5.63	0.50	3.68	2.05	0.50	36.10
420	2-92(f)	2.50	4.50	7.50	2.00	3.50	6.25	34.00	31.50	6.75	0.63	3.76	2.30	4.00	35.55
421	2-93(a)	3.50	5.50	7.50	2.50	4.50	6.50	32.00	43.00	3.88	0.88	4.24	2.50	0.50	37.45

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Sl. No.	Genotype/trait	LLS 70	LLS 80	LLS 90	R 70	R 80	R 90	50% F	PH	NPB	NSB	LL	LW	DORM	SCMR
422	2-94(c)	3.50	6.00	8.00	3.50	5.75	8.00	31.50	30.25	5.25	2.38	4.10	2.25	0.00	31.05
423	2-94(d)	3.00	5.50	7.75	3.00	5.25	7.75	32.00	35.38	5.63	0.38	3.98	2.43	0.00	40.45
424	2-95(a)	2.00	3.00	7.25	2.00	3.00	6.25	34.00	30.63	7.88	7.00	3.90	2.09	0.00	41.55
425	2-95(b)	2.50	3.50	6.50	2.00	3.50	5.75	34.75	32.75	8.50	5.13	3.76	1.94	2.00	29.10
426	2-95(c)	2.25	3.25	6.50	2.50	4.00	6.00	33.50	30.88	8.00	4.38	4.06	2.03	3.00	32.80
427	2-95(d)	2.00	3.00	5.75	2.00	3.50	5.50	34.00	31.25	5.13	2.25	3.55	2.14	0.50	40.25
428	2-95(e)	3.00	5.00	8.25	3.00	4.75	7.75	33.00	31.25	5.75	0.00	3.73	2.18	3.50	38.55
429	2-96	3.00	4.75	8.25	3.00	4.50	7.75	35.50	27.50	6.50	6.13	3.57	1.37	1.00	39.95
430	2-96(c)	3.50	5.75	8.00	3.00	5.00	7.25	30.50	36.38	5.13	0.63	3.58	1.83	0.00	34.40
431	2-97	3.50	5.75	8.00	3.00	5.00	7.25	30.00	36.75	5.13	0.00	3.84	2.19	0.00	33.05
432	2-98(a)	4.00	6.25	8.00	3.50	5.50	7.25	31.00	38.50	6.00	2.00	3.51	1.76	1.50	45.85
433	2-98(b)	3.50	5.75	8.00	3.00	5.25	8.00	32.00	43.25	5.88	0.00	3.78	2.23	0.50	40.10
434	2-98(c)	3.00	5.00	8.50	3.50	5.75	8.00	32.50	41.13	5.75	2.75	3.15	1.76	0.00	43.25

LLS 70: Late leaf spot score at 70 days after sowing (DAS), **LLS 80:** Late leaf spot score at 80 DAS, **LLS 90:** Late leaf spot score at 90 DAS,**R 70:** Rust score at 70 DAS, **R 80:** Rust score at 80 DAS, **R 90:** Rust score at 90 DAS, **50%F**: Days to 50% flowering, **PH**: Plant height (cm), **NPB**: Number of primary branches (cm), **NSB**: Number of secondary branches (cm), **LL**: Leaflet length (cm), **LW**: Leaflet width (cm), **DORM**: Seed dormancy and **SCMR**: SPAD chlorophyll meter reading (µg/cm^2)

Appendix III: Mean performance of the RILs of TMV 2 × TMV 2-NLM for productivity and nutritional traits

Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
1	TMV 2	24.59	16.83	4883.52	74.12	36.25	95.84	2.69	1.12	46.58	32.13	1.99	3.48	0.93	1.23	35.38	42.48	12.37	4.00	1.20
2	TMV 2-NLM	10.28	7.06	2043.86	68.40	44.40	94.83	3.08	1.14	43.94	27.95	1.56	2.75	0.93	1.24	27.38	54.87	11.47	3.15	2.00
3	1-2(a)	11.92	10.90	3148.28	72.27	32.31	95.67	2.72	0.97	45.04	30.32	1.80	3.23	0.86	1.15	32.76	48.55	12.06	3.73	1.48
4	1-2(b)	11.75	12.00	3341.34	76.20	35.06	96.04	2.62	0.89	46.80	29.60	1.76	3.17	0.90	1.19	32.34	48.77	12.12	3.45	1.51
5	1-2(d)	12.00	11.46	3346.60	69.92	35.99	97.86	2.34	1.05	48.05	35.78	2.12	3.88	0.84	1.19	39.82	37.48	12.69	4.29	0.94
6	1-3	12.75	9.10	2639.05	70.77	31.78	97.59	2.59	0.94	48.36	34.68	2.06	4.24	0.91	1.25	42.58	34.06	13.14	3.95	0.80
7	1-4(a)	8.50	12.78	3808.54	55.90	55.84	96.14	3.53	1.52	49.11	31.24	1.86	3.47	0.85	1.16	37.44	37.94	13.52	3.35	1.01
8	1-5	9.50	14.45	4313.46	61.31	61.66	97.38	3.45	1.34	47.56	31.20	1.77	3.35	0.87	1.23	34.02	43.27	13.17	3.45	1.27
9	1-6(a)	6.75	13.01	3722.74	68.35	41.28	97.22	2.52	1.18	46.00	30.90	1.73	3.49	0.94	1.26	37.12	42.98	12.44	2.93	1.16
10	1-6(b)	9.84	12.38	3463.81	70.20	43.94	98.42	2.62	1.20	45.48	30.53	1.80	3.74	0.90	1.28	41.02	37.61	13.03	3.23	0.92
11	1-7(a)	16.92	15.02	4262.29	75.73	38.54	98.07	2.90	0.97	46.26	30.02	1.87	3.60	0.92	1.22	35.88	44.22	12.10	3.73	1.23
12	1-7(b)	12.42	9.35	2814.14	58.84	36.75	96.14	3.05	0.89	41.76	30.96	1.79	3.09	0.90	1.18	29.91	51.53	11.59	3.51	1.72
13	1-7(c)	7.42	8.43	2646.57	49.45	27.95	95.71	2.27	0.98	43.75	29.85	2.03	3.85	0.80	1.06	36.81	42.67	11.70	3.81	1.16
14	1-7(d)	14.17	7.89	2218.03	60.74	40.75	96.97	3.42	1.06	43.98	32.01	1.80	3.15	0.97	1.21	28.78	52.34	11.43	3.81	1.82
15	1-7(9)	8.84	11.38	3556.90	58.13	42.42	95.06	3.80	1.03	43.37	31.61	1.80	3.27	0.94	1.27	27.51	53.38	10.95	3.59	1.94
16	1-9	10.34	12.31	3722.87	65.53	47.96	96.89	2.94	1.17	46.21	32.96	1.93	3.38	0.89	1.15	36.34	42.68	11.78	3.15	1.17
17	1-11(a)	12.92	10.63	3092.83	68.75	33.48	96.41	2.60	0.98	46.16	29.08	1.63	3.17	1.02	1.36	33.83	46.51	12.30	3.18	1.37
18	1-11(b)	10.17	16.68	5027.00	75.71	52.89	99.11	2.81	1.11	44.96	31.94	1.85	3.10	0.86	1.12	30.16	49.08	11.75	3.61	1.63
19	1-11(c)	9.59	11.99	3468.42	68.94	46.58	97.86	2.92	1.02	47.09	31.85	1.88	3.34	0.87	1.19	33.70	45.38	12.59	3.73	1.35
20	1-11(g)	17.09	12.91	3947.16	66.82	54.00	97.46	3.23	1.08	46.63	26.92	1.60	3.15	0.90	1.25	34.02	45.47	12.61	3.30	1.34
21	1-12 (a)	10.09	14.49	4240.34	71.58	43.60	96.81	2.73	1.19	43.59	28.67	1.67	3.15	0.79	1.08	36.11	44.90	12.48	3.72	1.24
22	1-12 (c)	15.00	13.92	3928.05	71.78	42.72	96.66	2.59	1.15	42.84	30.73	1.70	3.41	0.82	1.11	35.21	44.56	12.32	3.97	1.27
23	1-13 (c)	12.75	18.18	5638.76	68.16	51.53	97.39	2.92	1.35	43.32	29.54	1.68	3.40	0.81	1.11	38.75	39.77	12.95	3.55	1.03
24	1-14 (a)	16.50	12.49	3863.43	64.64	39.34	96.06	2.89	1.23	43.20	31.60	1.75	3.22	0.86	1.10	34.63	46.59	12.19	3.82	1.35
25	1-14 (b)	12.67	12.72	3841.51	63.79	41.78	96.30	2.87	1.24	43.18	35.47	1.64	3.05	0.87	1.13	33.70	48.12	12.30	3.71	1.43

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
26	1-15	11.67	11.57	3297.22	69.41	33.28	95.57	2.54	0.94	44.62	31.13	1.60	2.93	0.94	1.23	30.49	51.98	11.91	3.29	1.71
27	1-16(a)	7.92	8.60	2506.06	68.49	40.20	98.02	2.83	1.09	44.42	31.54	1.64	3.40	0.94	1.24	37.08	42.82	12.68	3.64	1.15
28	1-16(b)	13.00	14.60	4218.93	72.39	37.87	97.93	3.15	1.08	44.76	30.99	1.69	3.28	0.88	1.17	33.21	47.23	12.09	3.93	1.42
29	1-16(c)	9.84	11.86	3454.66	69.17	41.32	96.27	2.75	1.20	46.58	30.46	1.72	3.33	0.88	1.21	34.67	45.16	12.20	3.45	1.30
30	1-16(d)	15.17	11.82	3397.69	66.84	42.75	96.05	2.74	1.20	45.55	29.85	1.67	3.21	0.87	1.21	35.97	44.16	12.49	3.27	1.23
31	1-16(e)	11.50	11.80	3400.59	70.24	35.27	95.77	2.53	0.94	42.78	31.46	1.87	3.49	0.88	1.18	34.02	46.07	12.00	4.00	1.35
32	1-16(f)	9.59	11.53	3313.47	69.26	39.97	96.66	2.59	1.09	44.97	29.87	1.63	3.23	0.94	1.29	33.72	46.93	12.05	3.07	1.39
33	1-16(g)	12.00	13.50	3940.49	67.97	52.48	97.81	3.31	1.54	44.96	33.40	1.82	3.32	0.88	1.19	33.23	46.36	11.81	3.58	1.40
34	1-16(h)	9.84	10.80	3167.95	63.78	51.62	97.55	2.97	1.15	45.44	34.27	1.77	3.29	0.96	1.22	35.56	42.88	12.37	3.42	1.21
35	1-16(i)	10.92	7.37	2132.14	65.97	35.22	103.89	2.70	1.10	43.16	31.57	1.90	3.49	0.86	1.17	31.57	49.59	11.26	3.92	1.57
36	1-16(j)	11.67	7.73	2208.40	74.54	37.93	94.85	2.63	1.09	44.63	31.61	1.81	3.23	0.88	1.19	30.28	51.06	11.41	3.95	1.69
37	1-16(k)	11.25	7.19	2143.67	59.10	35.31	95.61	3.19	0.92	44.97	32.50	1.90	3.47	0.88	1.15	34.05	46.38	11.62	3.82	1.36
38	1-17	12.09	9.47	2720.61	70.64	36.27	97.14	2.37	1.14	46.12	31.48	1.60	3.46	0.98	1.37	36.36	43.58	12.71	3.22	1.20
39	1-18(a)	9.75	7.89	2287.25	74.03	36.02	96.37	2.63	1.18	44.29	31.70	1.83	3.38	0.82	1.11	35.46	44.39	12.15	3.93	1.25
40	1-18(c)	10.75	9.24	2730.54	65.99	25.01	96.80	2.13	0.94	41.03	29.52	2.21	4.20	0.73	0.98	40.10	38.32	11.60	4.31	0.96
41	1-18(e)	9.92	5.92	1787.48	70.85	31.02	96.77	2.36	1.01	42.97	30.37	1.58	3.00	0.91	1.14	33.30	48.73	12.13	3.66	1.46
42	1-18(h)	13.42	8.89	2615.30	75.76	40.79	96.11	2.59	1.05	43.95	31.84	1.93	3.27	0.78	1.02	33.80	46.86	11.69	4.24	1.39
43	1-18(i)	8.09	8.22	2348.57	68.30	39.22	97.16	2.69	1.08	44.45	33.81	1.81	3.32	0.82	1.07	34.40	45.97	11.85	4.15	1.34
44	1-19	10.00	5.87	1769.50	65.79	35.99	95.61	2.68	1.25	45.09	32.25	1.75	3.27	0.88	1.21	32.61	47.93	12.07	3.77	1.47
45	1-19(b)	7.75	6.21	1849.35	67.29	37.53	91.66	2.67	1.12	44.54	31.79	1.89	3.40	0.84	1.15	33.25	47.63	11.90	3.72	1.43
46	1-19(c)	9.09	9.60	2801.46	67.31	48.86	97.77	3.24	1.13	46.30	33.10	1.54	3.02	1.00	1.34	35.12	45.37	12.55	3.11	1.29
47	1-19(d)	10.92	6.50	1825.48	68.28	38.56	95.27	2.67	1.06	46.00	28.67	1.58	3.47	0.86	1.22	37.22	42.27	12.82	3.43	1.14
48	1-19(e)	9.42	4.56	1273.83	59.86	44.17	94.82	2.88	1.09	43.66	32.53	1.63	2.73	0.95	1.21	26.45	56.00	11.70	3.58	2.12
49	1-19(f)	7.92	13.46	3974.33	65.24	49.49	98.44	2.84	1.18	46.13	30.79	1.39	2.70	0.96	1.31	31.48	50.84	12.46	3.00	1.62
50	1-20	12.92	9.59	2778.59	71.26	37.87	94.75	2.65	1.05	42.76	31.23	1.84	3.20	0.82	1.10	34.60	46.36	11.93	3.95	1.34
51	1-21 (a)	10.92	9.32	2698.54	72.20	45.55	94.30	3.28	1.10	43.76	31.22	1.71	3.35	0.86	1.14	37.71	42.38	12.56	3.81	1.12
52	1-21 (b)	14.59	16.01	4482.29	67.71	35.78	97.47	2.74	1.18	43.47	28.20	1.89	3.62	0.84	1.12	38.50	41.45	12.27	3.92	1.08

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
53	1-21 (c)	16.75	11.21	3164.23	64.89	47.17	96.42	3.28	1.24	47.12	33.99	1.84	3.65	0.92	1.21	37.99	40.03	12.20	3.27	1.05
54	1-22 (a)	12.75	9.79	2845.67	71.84	51.75	97.68	3.04	1.10	44.76	30.69	1.73	3.26	0.97	1.28	30.81	49.69	11.73	3.26	1.61
55	1-22 (b)	12.00	10.92	3130.62	69.95	38.12	96.84	2.68	1.09	44.65	29.27	1.77	3.34	0.90	1.25	36.39	43.15	12.48	3.33	1.19
56	1-22 (c)	19.09	10.30	2878.40	69.83	40.18	97.91	2.82	0.98	45.87	27.24	1.62	3.27	0.99	1.36	34.02	45.88	12.51	2.96	1.35
57	1-22 (d)(i)	12.17	8.33	2396.50	73.47	39.90	97.83	2.51	1.02	44.08	29.56	1.85	3.64	0.90	1.27	38.48	41.49	12.27	3.44	1.08
58	1-22 (d)(ii)	17.17	11.37	3203.35	70.38	32.10	95.49	2.61	1.06	43.08	29.17	1.88	3.38	0.78	1.04	39.21	40.43	12.49	4.19	1.03
59	1-22 (f)	9.09	11.27	3128.02	67.93	37.96	96.06	2.62	1.03	46.08	31.31	1.81	3.23	0.87	1.17	35.15	44.95	12.28	3.52	1.28
60	1-22 (g)	24.00	15.31	4297.32	66.49	40.66	96.04	2.48	1.20	46.41	31.35	1.91	3.46	0.88	1.26	37.50	41.49	12.57	3.60	1.11
61	1-24(a)	10.84	8.01	2305.22	64.02	43.16	98.33	2.33	1.29	43.91	33.65	1.60	3.44	1.02	1.37	37.28	43.21	12.32	3.29	1.16
62	1-24 (b)	20.87	10.24	2827.78	62.14	29.42	94.59	2.88	1.05	43.71	28.40	1.75	3.47	0.82	1.11	39.99	39.15	12.98	3.79	0.98
63	1-25(a)	11.59	9.29	2658.18	63.49	36.70	95.67	2.93	1.06	41.72	28.85	1.60	3.27	0.92	1.24	39.93	40.46	13.24	3.44	1.01
64	1-25(b)	8.25	7.35	2080.93	71.86	35.60	97.43	2.15	1.01	46.05	32.60	1.88	3.99	0.94	1.24	37.32	41.38	12.22	3.67	1.11
65	1-25(c)	12.67	13.08	3720.60	70.00	49.22	97.81	2.68	1.16	44.95	31.98	1.74	3.53	0.97	1.29	35.64	43.56	12.32	3.30	1.22
66	1-25(f)	13.42	13.39	3779.94	69.87	48.78	97.85	2.61	1.15	46.52	32.99	1.70	3.59	1.01	1.35	34.95	44.22	12.22	3.29	1.27
67	1-25(f)	15.09	13.35	3700.02	69.28	48.16	97.19	2.99	1.14	47.68	33.88	1.81	3.79	1.01	1.34	39.23	40.09	12.65	3.41	1.02
68	1-25(h)	8.84	8.07	2274.75	73.89	33.99	96.86	2.35	1.13	50.25	29.78	1.88	3.69	0.83	1.16	37.77	40.91	12.61	4.06	1.08
69	1-25(i)	11.42	12.76	3659.20	73.24	30.99	97.32	2.26	0.98	43.54	28.01	1.85	3.29	0.81	1.12	37.53	42.28	12.70	4.09	1.13
70	1-25(k)	16.75	13.39	3775.80	70.69	32.16	97.68	2.39	0.93	44.34	28.16	1.86	3.34	0.82	1.12	39.70	39.81	13.06	4.08	1.00
71	1-25(l)	6.09	4.77	1236.70	60.38	34.59	88.50	2.75	0.99	45.55	33.64	1.91	3.42	0.86	1.16	31.97	47.13	12.23	3.64	1.47
72	1-26(a)	14.50	12.59	3624.82	75.26	41.48	94.86	2.45	1.05	45.84	34.43	1.92	3.66	0.93	1.21	36.04	42.08	12.52	3.99	1.17
73	1-26(b)	8.09	7.54	2205.22	69.81	36.26	96.79	2.36	0.98	42.45	31.02	1.96	3.69	0.83	1.11	40.89	37.19	13.11	4.32	0.91
74	1-28(a)	13.34	12.82	3711.80	73.07	41.81	96.79	2.87	1.02	44.91	31.88	1.75	3.07	0.81	1.12	30.37	50.39	12.13	4.01	1.66
75	1-28(b)	13.34	8.53	2476.96	71.03	43.94	91.53	3.15	1.23	45.97	30.74	1.59	3.15	1.00	1.33	31.44	48.26	12.24	3.31	1.54
76	1-28(c)	14.09	11.82	3407.63	69.48	46.24	93.84	3.07	1.28	48.10	29.88	1.69	3.24	0.96	1.29	32.66	46.71	12.20	3.32	1.43
77	1-29(b)	14.09	14.03	4042.73	69.92	49.80	97.78	2.78	1.26	46.66	29.94	1.77	3.37	0.94	1.20	33.92	46.33	11.98	3.60	1.37
78	1-30(a)	14.00	16.05	4633.97	67.54	51.37	98.19	2.74	1.30	45.35	29.67	1.72	3.26	1.02	1.35	29.74	51.29	11.20	3.34	1.72
79	1-30(c)	12.67	14.31	4144.82	72.96	48.63	98.03	2.63	1.27	45.65	31.41	1.67	3.53	1.03	1.41	35.58	44.22	12.43	3.34	1.24

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
80	1-30(d)	9.67	11.70	3355.06	76.68	41.62	97.98	2.42	1.02	45.87	34.13	1.85	3.47	0.88	1.15	36.42	42.05	12.73	3.99	1.15
81	1-30(i)	12.67	12.29	3660.79	68.80	52.83	98.03	3.15	1.25	44.57	27.66	1.63	3.18	0.86	1.15	33.89	46.46	12.25	3.64	1.37
82	1-30(j)	12.59	14.69	4237.07	65.77	54.98	96.39	3.22	1.27	48.20	32.92	1.79	3.48	0.86	1.15	35.73	41.39	13.04	3.90	1.16
84	1-31(b)	9.92	13.14	3655.52	64.62	53.88	87.46	3.19	1.30	47.86	31.67	1.70	3.10	1.02	1.35	28.82	50.41	12.32	3.37	1.75
85	1-31(c)	11.84	10.97	3227.18	66.04	44.52	98.60	3.32	1.14	47.51	32.54	1.81	3.44	0.92	1.22	35.08	42.70	12.81	3.67	1.22
86	1-31(e)	18.59	10.31	2971.82	70.04	34.79	94.20	2.44	1.11	44.64	31.63	1.76	3.29	0.97	1.23	34.49	45.28	11.68	3.61	1.31
87	1-31(f)	14.00	20.28	5849.89	72.18	46.38	97.42	2.62	1.14	45.20	31.80	1.58	3.11	1.04	1.41	33.66	45.75	12.43	2.81	1.36
88	1-33	27.09	16.04	4535.18	75.20	39.25	92.83	2.41	1.03	46.72	34.12	1.85	3.48	1.07	1.39	30.95	48.79	11.59	3.83	1.58
89	1-34(a)	18.42	14.92	4353.55	75.12	36.96	97.66	2.41	1.01	46.94	35.85	1.87	3.67	1.04	1.37	34.37	43.69	12.22	3.74	1.27
90	1-35(a)	20.17	14.67	3937.59	66.64	44.05	96.00	2.94	1.23	45.04	29.39	1.58	3.27	0.87	1.13	38.26	41.91	13.04	3.31	1.10
91	1-35(b)	11.17	4.93	1384.66	60.22	30.91	94.21	2.50	1.05	43.26	28.19	1.77	3.12	0.86	1.19	35.26	45.05	12.64	3.85	1.28
92	1-35(c)	15.75	12.02	3354.74	70.05	32.53	93.98	2.64	1.10	44.59	31.90	1.80	3.20	0.94	1.24	31.50	49.31	12.03	3.80	1.57
93	1-35(e)	14.09	9.50	2731.34	67.45	32.26	93.24	2.72	1.08	45.11	31.16	1.87	3.21	1.02	1.31	29.56	51.64	11.65	3.39	1.75
94	1-36(a)	12.75	14.56	4175.19	73.43	56.88	97.92	3.06	1.33	44.07	31.14	1.73	3.32	0.92	1.21	36.65	42.44	12.64	3.65	1.16
95	1-36(e)	18.34	12.33	3784.01	68.98	33.22	96.52	2.57	1.06	43.91	31.53	1.81	3.17	0.91	1.21	30.84	50.05	11.74	3.75	1.62
96	1-37(a)	16.25	7.11	2084.05	64.88	32.01	96.56	2.65	1.08	44.17	31.58	1.81	3.24	0.88	1.17	31.51	48.99	11.98	3.77	1.55
97	1-37(b)	12.00	10.23	2881.75	67.30	45.70	97.24	2.97	1.15	49.18	34.90	2.06	3.76	0.97	1.30	33.09	43.97	11.73	3.57	1.33
98	1-37(c)	12.17	13.54	3744.51	71.10	42.81	96.23	2.77	1.15	48.41	31.15	1.88	3.21	0.96	1.31	30.44	49.26	11.99	3.39	1.62
99	1-37(d)(i)	13.50	14.51	4260.02	65.72	41.65	96.39	2.50	1.23	43.90	29.91	1.62	2.95	0.94	1.25	32.32	48.97	12.16	3.53	1.52
100	1-37(d)(ii)	14.09	8.91	2607.91	69.49	48.99	97.51	2.85	1.22	47.03	32.44	1.50	2.98	1.03	1.43	35.62	44.72	13.08	3.10	1.26
101	1-37(e)	11.75	13.36	4089.38	73.67	49.02	98.33	2.70	1.18	47.80	32.63	1.63	3.14	0.99	1.35	37.46	42.85	13.24	3.25	1.14
102	1-37(f)	17.00	15.46	4358.60	72.22	49.44	96.81	2.70	1.20	47.73	32.23	1.51	2.98	1.00	1.38	33.50	47.59	12.57	2.83	1.42
103	1-37(g)	16.09	16.70	5132.37	69.78	31.45	96.06	2.44	0.99	46.45	28.64	1.66	3.04	0.94	1.31	30.42	51.90	12.02	2.94	1.71
104	1-37(h)	18.84	8.47	2397.81	62.83	44.97	93.67	3.21	1.26	44.75	33.32	1.79	3.31	0.98	1.25	32.67	47.87	11.50	3.47	1.47
105	1-37(i)	18.25	14.82	4383.71	74.47	37.70	97.23	2.68	1.14	49.19	32.65	1.89	3.63	1.02	1.41	30.44	49.66	11.61	3.42	1.63
106	2-1(b)(i)	13.29	16.58	4649.74	75.03	38.43	97.17	2.40	1.08	46.77	33.20	2.02	3.49	0.79	1.15	36.08	45.10	12.04	3.97	1.25
107	2-2(b)	7.24	7.51	2074.78	69.08	49.57	93.74	3.10	1.24	45.19	25.67	1.67	2.83	0.93	1.19	26.50	54.13	11.21	3.61	2.04

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
108	2-3(a)(i)	14.80	11.66	3167.18	71.95	40.06	97.48	2.66	1.15	46.83	29.89	1.76	3.43	0.95	1.25	33.34	43.68	12.50	3.53	1.31
109	2-3(a)(ii)	9.24	10.80	2803.67	67.58	39.26	97.05	2.78	1.23	43.57	29.28	1.61	3.02	0.82	1.04	35.20	43.69	12.26	3.73	1.24
110	2-3(b)	7.81	9.80	2628.94	72.43	52.82	96.57	3.33	1.30	44.66	26.92	1.55	2.96	0.95	1.25	28.88	51.42	11.47	3.04	1.78
111	2-5(a)	10.23	10.37	2990.80	71.82	49.24	97.84	3.34	1.31	45.23	28.79	1.74	2.75	0.90	1.31	25.04	58.24	10.32	3.46	2.33
112	2-5(b)	8.37	9.30	2568.97	69.34	48.16	95.80	3.08	1.35	43.20	28.15	1.71	2.92	0.88	1.11	31.78	49.05	11.61	4.06	1.54
113	2-5(c)	18.98	17.42	5033.05	73.45	31.30	96.31	2.48	1.04	49.60	31.36	1.89	3.17	1.01	1.39	29.12	53.39	10.73	3.77	1.83
114	2-5(d)	9.29	8.00	2158.08	68.05	30.87	95.85	2.75	1.05	46.01	30.29	2.01	3.09	0.83	1.14	32.44	48.41	11.34	4.20	1.49
115	2-6(b)	12.25	12.02	3453.21	76.03	43.70	97.69	2.46	1.11	47.18	31.66	1.99	3.57	0.85	1.14	34.53	41.81	11.98	3.89	1.21
116	2-6(c)	11.79	12.28	3489.71	71.77	41.74	97.25	2.90	1.21	44.04	27.74	1.75	3.11	0.87	1.11	28.89	49.95	11.27	3.79	1.73
117	2-6(d)	10.28	7.97	2581.71	66.63	38.91	97.13	3.10	1.24	44.16	27.36	1.89	3.46	0.92	1.09	31.02	49.05	11.02	3.78	1.58
118	2-6(e)	14.08	11.68	3322.26	72.77	39.28	97.52	2.51	1.23	46.50	31.54	1.97	3.63	0.92	1.16	34.84	42.49	11.89	3.45	1.22
119	2-7(b)	14.58	11.54	3237.47	66.29	46.77	93.84	2.99	1.29	41.47	26.10	1.84	3.22	0.86	1.11	30.73	48.15	11.24	3.66	1.57
120	2-7(c)	10.19	13.03	3503.07	66.27	51.28	96.33	3.33	1.38	46.70	30.93	1.92	3.50	0.85	1.15	37.55	38.67	12.36	3.73	1.03
121	2-7(d)(i)	14.01	14.71	4265.15	70.01	48.36	95.55	3.25	1.29	45.64	29.45	1.80	3.68	0.99	1.27	33.58	42.94	11.82	3.42	1.28
122	2-7(d)(ii)	11.92	8.34	2339.37	75.39	39.51	95.72	3.13	1.03	47.37	28.17	1.67	2.99	0.91	1.21	30.02	49.20	11.86	3.41	1.64
123	2-8(a)	10.40	9.03	2610.87	67.85	52.93	97.64	3.30	1.36	42.56	29.18	1.51	2.96	0.90	1.23	32.58	46.84	12.28	3.05	1.44
124	2-8(b)	13.57	7.75	2214.05	69.42	37.75	97.70	3.00	1.13	42.08	26.74	1.76	3.25	0.97	1.25	29.16	49.96	11.15	3.17	1.71
125	2-10(a)	12.40	8.89	2497.51	73.08	38.91	96.81	2.60	1.05	42.19	26.49	1.75	3.13	0.92	1.24	30.03	49.02	11.38	3.35	1.63
126	2-11(a)	11.28	8.08	2235.49	72.52	40.73	94.45	3.08	1.19	43.27	27.12	1.57	3.21	1.06	1.36	30.43	49.51	11.44	2.95	1.63
127	2-12(a)(ii)	11.97	14.38	4076.12	66.98	55.82	96.22	4.04	1.59	44.24	27.87	1.58	3.10	0.99	1.21	28.68	51.67	11.13	3.50	1.80
128	2-12(b)	10.39	10.15	2870.35	70.12	42.01	95.89	2.99	1.38	48.36	28.15	1.82	3.13	0.94	1.20	28.76	51.37	10.43	3.49	1.79
129	2-13(a)	17.88	19.13	5851.11	66.09	39.82	98.78	2.63	1.20	47.62	33.56	1.86	3.56	1.03	1.29	36.85	40.65	12.25	3.47	1.10
130	2-13(b)	16.76	17.93	4909.74	73.70	41.07	98.52	2.60	1.10	46.47	32.96	1.85	3.62	0.95	1.23	37.36	39.21	12.58	3.72	1.05
131	2-13(d)(i)	9.17	5.50	1962.68	70.66	52.10	71.12	3.10	1.20	41.87	30.74	1.77	3.32	0.90	1.11	33.80	43.40	11.52	3.71	1.28
132	2-13(f)	7.50	7.40	2068.54	70.33	51.71	89.90	3.08	1.28	40.66	28.59	1.90	3.62	0.85	1.12	34.23	45.19	11.02	3.82	1.32
133	2-14(a)(i)	13.58	20.93	5471.71	71.84	49.53	97.47	3.53	1.53	43.35	28.59	1.51	2.97	0.95	1.23	32.94	46.49	12.17	2.99	1.41
134	2-14(a)(ii)	20.28	20.55	5597.27	70.02	42.73	107.56	3.10	1.28	46.08	28.25	1.56	3.03	0.94	1.17	32.00	47.80	11.84	3.44	1.49

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
135	2-14(b)(i)	15.43	9.66	2782.79	70.65	36.16	95.69	3.10	1.15	45.79	27.42	1.57	2.97	1.05	1.37	27.45	53.43	11.38	3.06	1.95
136	2-14(b)(ii)	17.07	14.01	3883.27	71.48	39.93	96.77	2.94	1.04	45.27	28.86	1.45	2.78	1.07	1.41	26.33	54.94	11.21	2.52	2.09
137	2-14(c)	14.33	12.62	3448.09	69.18	38.56	95.51	3.00	1.13	47.26	26.30	1.64	2.84	0.98	1.32	27.89	53.21	11.74	3.62	1.91
138	2-14(d)	14.43	14.01	3823.54	64.11	40.37	94.98	3.14	1.34	45.45	22.93	1.38	2.78	0.94	1.28	28.15	53.56	11.24	2.72	1.90
139	2-14(e)	13.81	11.07	3027.72	65.79	36.44	95.95	2.79	1.06	46.93	28.54	1.73	3.32	1.01	1.26	35.04	42.62	12.24	3.52	1.22
140	2-14(f)	15.42	11.13	3062.59	70.29	34.72	94.63	2.94	1.10	45.23	24.94	1.53	2.80	0.92	1.18	27.18	53.61	11.35	3.16	1.97
141	2-14(g)	12.26	12.95	3581.17	72.14	51.43	97.29	3.21	1.34	42.96	25.93	1.45	2.66	1.02	1.26	25.42	55.51	11.43	3.15	2.18
142	2-15(a)	15.42	13.48	3802.08	69.75	32.86	95.63	2.68	1.08	44.44	24.54	1.67	2.98	1.00	1.30	27.34	54.16	10.74	3.41	1.98
143	2-15(c)	12.47	11.18	3171.01	74.19	41.70	97.36	2.69	1.13	44.37	30.65	1.77	3.12	0.85	1.14	25.52	56.41	10.58	3.98	2.21
144	2-15(e)	15.88	12.87	3691.59	72.39	30.46	97.50	2.36	1.10	43.94	28.77	1.79	3.25	0.86	1.11	36.92	42.42	12.06	4.04	1.15
145	2-15(f)	9.84	10.93	3483.43	61.30	37.67	94.20	3.48	1.10	45.24	34.28	1.91	3.83	0.95	1.33	35.80	43.31	11.35	3.88	1.21
146	2-15(h)(i)	13.29	11.15	3000.50	64.52	33.58	95.29	2.61	1.21	46.48	27.32	1.80	3.15	0.86	1.20	31.62	47.98	11.70	4.25	1.52
147	2-15(h)(ii)	12.44	16.36	4651.38	70.87	54.22	97.88	3.15	1.35	45.64	30.53	1.53	2.86	0.95	1.23	30.60	49.67	12.05	3.49	1.62
148	2-15(i)(a)	13.50	12.32	3672.60	69.63	44.86	97.44	3.08	1.26	45.83	29.49	1.73	3.20	0.91	1.26	27.21	53.40	11.36	3.93	1.96
149	2-15(i)(b)	8.73	6.91	1828.60	74.05	54.65	95.89	3.13	1.39	45.32	28.09	1.79	3.58	0.89	1.24	34.97	43.30	12.05	3.71	1.24
150	2-16(a)	10.99	10.36	3177.92	70.09	57.38	94.45	3.24	1.41	44.37	28.90	1.58	3.18	0.87	1.14	28.98	49.35	11.58	3.55	1.70
151	2-16(b)	17.23	13.34	4047.31	72.76	39.37	97.95	2.50	1.19	48.51	33.13	1.98	3.86	0.98	1.27	34.04	43.69	11.44	4.16	1.28
152	2-17(a)	9.23	9.16	2349.83	73.61	48.22	96.60	2.86	1.31	45.73	29.31	1.42	2.94	1.05	1.49	27.52	54.12	11.45	3.05	1.97
153	2-17(b)	14.77	13.70	3979.82	72.14	51.85	95.21	3.15	1.36	44.70	30.67	1.83	3.26	0.86	1.15	30.55	47.13	11.48	3.43	1.54
154	2-17(c)	11.10	15.91	4533.19	74.53	51.21	96.98	3.10	1.33	47.73	31.48	1.87	3.42	0.90	1.21	32.67	44.84	12.11	3.85	1.37
155	2-17(d)	15.13	13.58	4195.56	67.37	40.80	90.80	3.11	1.21	41.28	27.29	1.78	3.35	0.90	1.13	22.46	54.28	8.94	3.51	2.42
156	2-17(e)	19.98	15.31	4368.26	71.75	30.74	96.87	2.64	1.18	44.88	29.50	1.85	3.09	0.86	1.25	28.25	55.06	10.46	3.48	1.95
157	2-17(f)	7.99	11.04	3088.21	65.47	61.85	96.61	3.19	1.38	45.66	30.14	1.56	2.80	0.92	1.21	25.61	54.15	11.53	3.61	2.11
158	2-17(g)	17.13	13.75	3936.13	70.26	35.80	97.35	2.58	1.23	45.42	22.90	1.58	3.33	0.95	1.29	35.95	42.58	12.19	3.15	1.18
159	2-18(a)	12.20	7.63	2292.44	69.94	35.52	97.04	2.70	1.13	44.67	29.79	1.87	3.40	0.94	1.18	31.90	46.88	11.30	3.68	1.47
160	2-18(b)	16.01	7.71	2337.65	70.90	35.70	96.97	2.50	1.08	43.93	30.17	1.80	3.45	0.87	1.19	37.22	42.72	11.73	3.23	1.15
161	2-18(c)	21.88	18.13	4792.67	73.82	32.23	97.72	2.43	1.09	43.62	28.31	2.05	3.30	0.75	1.16	33.11	48.55	10.87	4.03	1.47

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
162	2-18(d)	12.14	8.41	2923.35	69.47	36.70	98.22	2.56	1.20	45.14	30.00	1.79	3.53	1.03	1.30	34.78	42.50	11.96	3.85	1.22
163	2-19(a)	10.02	10.33	2949.06	75.25	37.87	99.36	2.74	1.11	44.75	32.70	1.68	3.61	0.91	1.21	39.67	37.77	13.09	4.02	0.95
164	2-19(c)	13.15	12.44	3401.56	76.30	40.31	97.88	2.63	1.13	45.13	30.80	1.77	3.41	0.91	1.15	35.03	41.88	12.37	3.96	1.20
165	2-19(d)	14.51	9.51	2815.73	65.59	43.51	94.71	3.28	1.30	43.26	27.15	1.63	3.12	0.88	1.18	29.06	49.68	11.70	3.35	1.71
166	2-19(f)	22.39	22.01	6508.52	69.42	48.02	98.23	2.91	1.23	44.99	29.14	1.57	2.93	0.93	1.22	27.48	54.64	11.17	3.24	1.99
167	2-19(g)	10.10	7.17	1839.25	69.96	26.37	96.34	1.80	1.06	44.46	35.13	1.90	3.51	1.00	1.30	32.37	48.86	10.67	4.12	1.51
168	2-19(h)	11.49	7.72	2194.31	73.43	29.86	98.13	2.13	1.15	47.91	31.22	1.77	3.90	1.00	1.31	40.71	37.55	12.52	3.67	0.92
169	2-20(a)	14.35	9.80	2681.18	76.04	35.68	97.09	2.83	1.10	43.66	25.81	1.72	3.62	0.95	1.27	31.97	47.02	11.42	3.41	1.47
170	2-20(b)	13.61	8.01	2031.35	75.69	24.59	97.78	2.34	0.88	45.12	28.44	1.93	3.53	0.92	1.19	33.30	46.80	10.95	4.02	1.41
171	2-20(c)	12.43	11.09	3030.38	71.48	36.55	98.24	2.75	1.11	46.71	29.86	1.58	3.13	0.91	1.19	33.42	44.38	12.51	3.61	1.33
172	2-20(d)	17.85	17.59	4840.24	71.58	46.59	96.71	2.85	1.16	45.89	29.56	1.61	3.22	0.93	1.24	35.26	42.80	12.55	3.74	1.21
173	2-20(e)	9.41	15.31	4102.06	70.99	60.74	97.15	3.53	1.33	45.33	29.24	1.63	3.48	0.87	1.20	32.06	45.31	11.96	3.44	1.41
174	2-21(a)	17.20	12.20	3559.27	68.93	36.09	98.44	2.38	1.45	46.57	28.67	1.52	3.09	1.06	1.44	27.94	53.23	11.08	3.16	1.90
175	2-21(c)	14.25	13.29	3933.69	69.96	40.80	97.54	2.58	1.41	46.03	28.98	1.62	3.07	0.93	1.34	31.85	49.76	11.50	3.36	1.56
176	2-21(d)	21.45	12.88	4178.49	73.55	35.50	95.64	2.48	1.15	46.50	34.25	1.95	3.79	0.91	1.13	38.79	35.44	12.96	4.24	0.91
177	2-21(e)	8.98	7.24	2173.33	70.57	37.74	98.79	2.70	1.19	44.54	30.56	1.94	3.43	0.85	1.21	30.90	47.79	11.01	4.27	1.55
178	2-21(f)	18.19	10.31	2839.29	67.72	33.72	94.69	3.00	1.06	46.11	29.55	1.62	3.27	0.93	1.22	30.52	47.08	11.91	3.64	1.54
179	2-22(a)	11.56	10.74	3016.05	69.50	45.05	97.17	3.10	1.21	43.58	29.91	1.65	3.12	0.98	1.24	27.68	52.14	11.36	3.74	1.88
180	2-23(a)	14.35	17.71	5062.69	75.04	53.39	98.36	2.88	1.46	44.03	28.79	1.48	3.06	0.96	1.24	28.25	52.14	11.30	3.21	1.85
181	2-23(b)	11.62	9.35	2637.18	68.72	42.30	97.24	3.10	1.11	46.06	28.69	1.58	2.97	0.96	1.27	30.18	48.50	11.64	2.95	1.61
182	2-23(c)	20.13	20.48	5309.72	68.89	45.37	98.67	2.58	1.16	46.60	32.05	1.59	3.21	1.02	1.36	29.34	51.26	11.26	3.54	1.75
183	2-23(d)	11.35	8.35	2382.94	70.82	37.52	98.47	2.44	1.26	46.14	33.55	1.52	3.05	1.09	1.39	32.38	48.55	11.55	3.50	1.50
184	2-23(e)	20.24	17.02	4975.38	72.84	44.46	96.64	2.89	1.14	45.28	29.70	1.54	3.20	0.88	1.15	31.92	46.57	11.85	3.51	1.46
185	2-23(f)	12.08	9.43	2777.80	74.47	43.59	97.92	2.53	1.20	47.75	30.15	1.59	3.32	1.03	1.35	32.30	46.71	11.71	3.22	1.45
186	2-23(g)	14.21	9.91	2920.56	72.09	41.89	98.47	2.79	1.20	47.49	31.93	1.61	3.30	1.02	1.30	31.09	48.15	11.51	3.49	1.55
187	2-24(a)	14.89	14.53	4116.55	71.14	42.05	97.60	2.64	1.28	44.54	29.67	1.58	3.14	0.95	1.16	33.95	44.63	11.96	3.48	1.31
188	2-24(b)	16.60	13.81	4249.69	68.88	40.59	98.47	2.60	1.29	47.96	31.08	1.64	3.30	0.95	1.25	31.65	46.91	12.14	3.57	1.48

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
189	2-24(c)	18.80	20.32	5561.45	70.63	55.44	97.93	3.30	1.31	46.09	31.10	1.65	3.09	1.00	1.30	23.41	57.14	10.68	3.17	2.44
190	2-25(a)	12.30	14.59	4532.88	71.65	46.47	95.50	3.15	1.33	46.56	30.60	1.55	3.00	0.96	1.25	28.04	52.10	11.41	3.40	1.86
191	2-25(b)	18.17	14.19	4384.87	65.41	38.15	95.84	2.93	1.26	43.46	27.06	1.57	3.24	1.04	1.31	31.19	48.67	11.80	3.42	1.56
192	2-26	11.90	10.51	2852.92	45.45	37.84	96.27	2.91	1.36	43.05	24.81	1.51	3.05	0.90	1.25	29.79	51.13	11.26	3.27	1.72
193	2-27(c)	18.71	14.95	4580.01	64.27	44.25	96.02	2.96	1.34	43.14	27.45	1.43	3.14	0.92	1.23	31.81	47.72	12.16	3.33	1.50
194	2-27(d)	5.33	13.09	3218.75	64.96	29.30	96.24	3.34	1.14	45.53	33.77	1.76	3.59	1.01	1.27	35.96	40.48	12.54	3.93	1.13
195	2-27(e)	17.02	13.99	4201.90	66.75	36.85	98.49	2.60	1.20	46.92	32.47	2.01	3.95	0.97	1.27	35.85	39.38	12.14	4.23	1.10
196	2-27(f)	11.25	9.17	2502.56	69.89	31.26	106.81	2.45	0.98	45.65	26.68	1.78	3.55	0.97	1.25	35.96	43.51	12.12	4.30	1.21
197	2-28(a)	11.07	10.20	2951.54	66.25	40.47	96.49	2.51	1.11	43.33	29.38	1.66	3.02	0.81	1.16	31.32	51.13	11.40	3.71	1.63
198	2-28(b)	9.05	7.24	1966.08	65.02	41.47	93.42	3.04	1.18	46.18	27.98	1.53	3.37	1.04	1.37	36.10	42.33	12.54	3.51	1.17
199	2-29(a)(i)	7.27	8.64	2230.82	61.67	35.91	93.25	2.73	1.18	45.42	27.45	1.52	2.96	0.92	1.20	30.21	48.61	11.92	3.62	1.61
200	2-29(a)(ii)	14.89	12.29	3430.37	65.68	37.59	95.77	2.90	1.14	44.73	29.98	1.84	3.28	0.95	1.21	33.55	45.64	11.56	4.12	1.36
201	2-29(a)	16.45	15.53	4691.30	66.49	38.42	96.15	2.96	1.16	43.15	30.27	1.67	3.10	0.93	1.17	32.49	46.46	11.69	3.59	1.43
202	2-29(c)	9.89	6.49	1774.18	68.58	31.84	96.18	2.55	0.99	43.29	29.88	1.87	3.72	0.97	1.23	36.46	40.83	11.84	3.95	1.12
203	2-29(e)	13.86	14.48	4221.06	73.35	47.09	97.33	3.04	1.25	46.37	28.42	1.67	3.41	0.90	1.19	33.55	43.67	12.35	3.45	1.30
204	2-29(f)	12.84	12.39	3396.63	68.83	44.49	96.36	2.86	1.14	47.51	28.42	1.61	3.38	0.95	1.27	31.51	46.71	11.85	3.45	1.48
205	2-29(g)	22.08	20.40	5234.94	73.14	50.08	98.14	3.05	1.26	47.65	30.44	1.58	3.28	0.97	1.34	30.95	48.52	11.66	3.22	1.57
206	2-30(a)	13.81	16.84	4656.96	72.17	46.93	97.12	2.81	1.21	46.90	30.74	1.75	3.42	0.96	1.30	34.28	43.67	12.45	3.28	1.27
207	2-30(b)	13.12	17.00	4582.89	74.33	54.71	97.90	3.16	1.31	43.72	30.33	1.81	3.36	0.97	1.30	33.03	44.88	12.04	3.11	1.36
208	2-30(c)(i)	11.38	10.84	2883.17	74.19	49.42	97.32	2.78	1.24	47.72	29.32	1.85	3.25	0.94	1.27	34.49	44.73	12.01	3.57	1.30
209	2-30(d)	14.43	13.38	3923.34	74.50	37.98	96.98	2.66	1.26	47.99	30.35	1.83	3.40	0.96	1.25	33.83	43.20	12.28	3.41	1.28
210	2-30(e)	12.12	10.55	3014.00	61.30	34.86	96.94	3.16	1.03	46.74	30.66	1.79	3.19	0.99	1.26	32.33	46.45	11.93	3.36	1.44
211	2-30(f)	12.96	10.71	3374.31	74.49	35.30	97.15	2.74	1.10	43.71	26.53	1.83	3.28	1.00	1.31	30.70	50.42	10.98	3.56	1.64
212	2-30(g)	12.65	12.28	3415.27	71.97	52.32	95.94	2.81	1.30	46.52	30.83	1.82	3.58	0.97	1.36	38.53	39.82	12.48	3.49	1.03
213	2-32(a)	9.07	8.98	2598.47	51.10	43.19	97.13	3.11	1.36	46.29	26.81	1.72	3.14	0.91	1.22	33.44	45.40	12.37	3.35	1.36
214	2-32(c)	23.08	18.17	4930.82	69.45	30.72	96.18	2.53	1.11	48.85	30.58	1.82	3.42	1.11	1.43	32.01	47.67	11.30	3.32	1.49
215	2-32(e)	12.03	10.37	2955.76	68.68	43.57	96.92	3.05	1.23	42.25	29.11	1.61	3.10	0.97	1.21	32.45	46.34	12.09	3.69	1.43

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
216	2-32(g)	14.75	10.48	2991.36	72.53	36.92	99.21	2.61	1.16	45.51	28.23	1.66	3.17	0.97	1.24	32.67	46.83	11.87	3.56	1.43
217	2-32(b)	10.81	12.81	3475.11	74.08	42.56	98.10	2.76	1.45	41.34	29.88	1.60	3.01	0.98	1.20	31.82	48.01	11.94	3.75	1.51
218	2-33(a)	22.68	19.63	5387.88	72.56	35.38	98.97	2.53	1.19	48.45	29.40	1.91	3.24	0.93	1.30	32.75	47.58	11.38	3.78	1.45
219	2-33(d)	8.93	9.89	2863.04	72.41	54.82	98.41	2.98	1.51	47.18	29.68	1.73	3.19	0.94	1.25	34.18	42.88	12.11	3.05	1.25
220	2-33(e)	14.50	11.55	3514.56	72.20	35.62	97.88	2.71	1.08	47.03	30.83	1.69	3.28	1.06	1.40	35.70	43.67	12.34	3.41	1.22
221	2-34(a)	10.03	8.23	2336.02	71.02	45.32	96.40	3.20	1.14	45.22	28.62	1.82	3.17	0.89	1.07	32.99	45.55	11.91	4.03	1.38
222	2-35(a)	18.19	13.48	3907.26	72.79	38.11	98.86	2.43	1.13	44.77	27.37	1.97	3.18	0.99	1.32	30.84	49.04	11.38	4.51	1.59
223	2-35(b)	9.44	8.17	2282.54	70.39	35.87	96.57	3.08	1.25	46.78	30.12	1.75	3.35	1.04	1.29	34.34	44.27	11.99	3.50	1.29
224	2-35(d)	11.15	8.94	2497.90	71.11	43.70	94.09	3.00	1.21	46.45	28.44	1.57	2.83	0.94	1.22	29.02	52.14	11.33	3.23	1.80
225	2-35(e)	7.93	6.93	1658.80	61.36	38.25	96.32	2.48	1.13	47.13	32.19	1.87	3.75	0.98	1.21	39.46	36.74	12.54	3.79	0.93
226	2-36(a)(i)	15.69	12.95	3817.68	72.80	42.34	96.37	3.21	1.16	44.47	27.82	1.66	2.88	0.99	1.34	27.84	54.46	11.36	3.59	1.96
227	2-36(a)(ii)	7.21	9.05	2500.35	67.00	36.96	91.12	3.35	1.40	42.74	30.81	1.58	2.92	1.00	1.31	26.74	53.91	11.28	3.13	2.02
228	2-36(b)	12.48	11.63	3340.59	71.11	49.96	94.41	2.95	1.35	44.76	29.83	1.64	3.10	0.96	1.26	33.90	44.31	12.62	3.50	1.31
229	2-36(c)	12.57	8.15	2328.40	71.22	49.37	96.54	3.13	1.34	46.05	29.37	1.73	3.46	0.95	1.26	33.26	44.22	12.05	3.41	1.33
230	2-37(a)	14.31	13.58	3789.29	66.89	48.50	97.19	3.21	1.44	44.24	28.47	1.61	3.29	1.00	1.38	33.56	44.32	12.73	3.17	1.32
231	2-38(b)(i)	12.05	11.00	3141.93	68.00	58.46	97.41	3.23	1.56	46.03	27.82	1.73	3.48	1.00	1.32	33.46	44.74	11.80	3.40	1.34
232	2-38(b)(ii)	13.44	9.63	2855.50	72.53	39.69	96.77	2.54	1.23	48.20	26.90	1.82	3.77	0.85	1.32	38.90	41.09	12.21	3.32	1.06
233	2-38(d)	11.80	13.34	3665.33	67.92	57.38	96.94	3.33	1.56	47.21	28.42	1.62	3.47	0.98	1.29	34.51	42.83	12.28	3.47	1.24
234	2-39(a)	11.34	14.92	4119.17	74.49	35.81	97.36	2.53	1.25	44.23	29.61	1.83	3.98	0.97	1.33	38.10	38.91	12.54	3.84	1.02
235	2-39(b)	11.31	9.85	2695.02	74.14	39.87	112.87	2.75	1.13	48.48	30.54	1.76	3.47	0.97	1.33	34.49	44.10	11.82	3.51	1.28
236	2-39(c)	23.27	19.03	4793.40	75.51	37.48	98.57	2.45	1.15	45.44	28.23	1.71	3.24	0.97	1.30	32.88	45.91	12.17	3.43	1.40
237	2-39(d)	12.68	12.99	3417.42	73.77	43.91	98.10	2.83	1.36	44.43	30.59	1.66	3.07	1.02	1.43	26.14	56.63	11.16	3.30	2.17
238	2-39(e)	15.26	14.95	4417.23	72.00	48.43	96.71	3.33	1.30	45.84	33.87	1.66	3.26	1.04	1.34	31.16	47.69	11.56	3.10	1.53
239	2-39(f)	9.78	10.16	2471.89	64.13	51.94	90.88	3.14	1.43	43.86	24.71	1.64	3.02	1.02	1.29	28.45	51.10	11.50	3.43	1.80
240	2-39(g)	17.82	13.88	4292.53	66.92	39.53	92.41	3.11	1.14	46.83	25.57	1.73	3.06	1.04	1.35	27.90	52.17	11.70	3.29	1.87
241	2-39(i)	14.23	11.18	3596.04	65.58	45.80	96.46	2.80	1.43	44.44	29.33	1.72	3.29	1.07	1.37	32.27	48.71	11.71	3.76	1.51
242	2-40(b)	11.37	12.09	3584.60	65.93	39.27	98.06	3.06	1.19	44.48	28.02	1.67	3.16	1.00	1.46	26.08	56.61	10.72	2.94	2.17

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
243	2-40(c)	16.84	12.48	3788.48	64.78	39.33	102.55	2.76	1.40	43.80	29.94	1.75	3.38	1.03	1.32	32.68	45.97	12.01	3.93	1.41
244	2-40(d)	16.48	15.88	4645.55	69.31	39.43	96.80	2.83	1.24	46.87	32.92	1.85	3.64	1.13	1.42	34.89	43.76	11.72	3.99	1.25
245	2-41(a)	15.32	10.66	3327.98	65.08	43.79	97.79	2.84	1.15	45.54	27.81	1.75	3.29	1.03	1.30	33.85	44.76	11.88	3.69	1.32
246	2-41(b)	9.71	8.21	2650.74	75.81	50.82	95.94	2.89	1.40	42.22	28.51	1.58	3.11	0.93	1.23	33.27	45.77	11.92	2.88	1.38
247	2-41(c)	16.04	11.15	3121.47	71.98	46.95	97.78	2.98	1.33	45.37	30.38	1.71	3.60	1.10	1.49	31.97	48.66	10.99	2.94	1.52
248	2-41(d)	10.21	10.07	2778.01	76.85	46.58	96.52	2.99	1.16	42.69	25.02	1.70	3.24	0.87	1.18	31.77	47.18	11.77	3.08	1.49
249	2-41(e)	16.63	8.14	2337.80	70.77	34.51	97.95	2.89	1.16	43.12	28.71	1.77	3.46	0.92	1.20	35.82	42.33	11.92	3.54	1.18
250	2-42(b)	12.21	7.93	2298.84	73.24	39.39	97.41	2.54	1.01	44.85	25.10	1.69	3.68	0.88	1.23	38.69	38.79	12.56	3.18	1.00
251	2-42(c)	13.91	11.54	3070.15	66.39	37.09	98.44	2.40	1.20	46.01	26.23	1.65	3.11	1.02	1.39	32.74	47.62	12.04	3.56	1.45
252	2-42(e)	7.86	9.04	2325.46	66.56	37.34	96.90	2.45	1.13	46.36	26.25	1.53	3.08	0.98	1.39	33.17	46.13	12.42	3.05	1.39
253	2-42(f)	12.42	19.81	4862.90	74.25	61.08	98.02	3.41	1.36	42.97	26.18	1.34	2.73	0.98	1.33	28.62	52.02	11.76	2.95	1.82
254	2-42(g)	8.18	11.89	3385.05	70.75	45.26	98.62	3.49	1.56	43.21	27.11	1.68	3.15	0.90	1.33	31.72	50.68	11.40	3.57	1.60
255	2-43(b)	13.63	17.33	4883.91	72.99	56.99	95.68	3.38	1.33	42.76	26.18	1.47	2.78	1.00	1.34	27.31	53.77	11.58	3.05	1.97
256	2-43(c)	8.17	9.91	2699.36	66.93	45.85	96.67	3.26	1.35	46.24	26.09	1.42	3.11	0.97	1.31	34.99	44.63	12.68	3.04	1.28
257	2-44(d)	12.50	16.31	4499.99	71.59	61.35	98.67	3.70	1.59	45.72	29.20	1.55	3.23	0.98	1.26	33.02	46.51	12.09	2.96	1.41
258	2-44(e)	14.68	11.73	3054.21	71.45	51.26	97.99	3.24	1.40	46.78	30.61	1.55	3.04	0.96	1.27	32.50	45.93	12.41	3.18	1.41
259	2-45(a)	18.80	19.51	5209.09	73.09	58.25	99.06	3.35	1.34	46.67	32.79	1.76	3.26	1.07	1.35	30.39	47.90	11.55	3.07	1.58
260	2-45(b)	9.41	9.75	2604.43	73.52	34.43	96.82	2.35	1.08	42.94	30.10	1.65	3.54	0.99	1.35	34.39	45.51	11.70	3.74	1.32
261	2-45(c)	11.93	8.40	2321.01	73.22	37.66	97.66	3.23	1.06	44.58	27.22	1.63	3.18	0.93	1.33	28.55	54.14	11.08	3.30	1.90
262	2-45(d)	18.12	11.68	2998.36	66.23	39.85	95.95	3.25	1.21	44.18	27.13	1.59	3.14	0.89	1.22	32.37	48.24	11.93	3.67	1.49
263	2-45(e)	6.82	4.16	1114.00	71.41	43.10	92.31	3.35	1.14	44.48	27.28	1.53	3.02	0.96	1.24	28.51	51.29	11.80	3.17	1.80
264	2-45(f)	11.06	10.22	2665.55	72.12	49.81	96.15	3.26	1.23	45.16	28.00	1.42	2.75	0.94	1.22	29.17	51.69	11.91	3.04	1.77
265	2-45(g)	13.55	7.01	2019.06	68.09	26.95	96.90	2.39	1.14	43.77	29.52	1.91	3.40	0.95	1.27	31.36	49.82	10.78	3.61	1.59
266	2-46(a)	8.60	5.78	1593.03	73.70	31.11	96.07	2.48	1.08	43.97	31.22	1.79	3.53	1.08	1.38	31.00	50.10	11.36	3.65	1.62
267	2-46(b)	9.91	13.23	3374.22	73.69	51.80	95.87	3.65	1.40	44.07	29.74	1.53	3.25	0.92	1.24	34.63	43.12	12.61	3.39	1.25
268	2-46(c)	8.73	9.39	2570.13	71.41	52.88	97.78	3.48	1.43	44.72	28.97	1.59	3.26	0.94	1.27	32.65	44.95	12.48	3.42	1.38
269	2-47(a)	11.62	9.95	2826.74	71.71	46.19	96.14	2.88	1.21	44.90	28.93	1.68	3.36	1.01	1.35	29.21	48.38	11.79	3.07	1.66

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
270	2-48(a)	12.15	9.36	2635.06	73.99	38.41	98.18	3.09	1.29	44.18	28.83	1.74	3.41	1.03	1.26	33.11	43.97	11.87	3.53	1.33
271	2-48(b)	8.81	9.04	2407.18	72.82	41.32	94.43	3.14	1.14	44.18	29.29	1.65	3.41	1.02	1.32	31.51	47.13	11.51	3.27	1.50
272	2-48(c)	10.76	11.39	3185.29	67.74	54.04	88.99	3.35	1.49	43.96	30.39	1.44	2.85	0.90	1.14	31.85	48.03	11.94	3.32	1.51
273	2-48(f)	10.21	9.54	2746.68	65.77	53.81	93.50	3.35	1.41	46.98	27.33	1.55	3.06	0.87	1.14	31.66	48.22	12.13	3.61	1.52
274	2-48(i)	10.13	14.31	3318.83	71.03	37.42	96.90	2.93	1.14	45.56	32.46	2.03	3.65	1.00	1.41	31.39	47.82	11.14	3.76	1.52
275	2-49	15.15	14.46	4125.71	75.55	46.24	98.85	2.69	1.56	47.27	28.40	1.70	3.41	1.04	1.34	32.75	45.20	11.52	2.94	1.38
276	2-50(a)	11.05	9.12	2472.30	63.99	42.98	93.90	2.88	1.33	45.96	28.64	1.56	3.07	1.12	1.37	31.59	46.48	12.10	3.09	1.47
277	2-50(b)	14.40	11.35	3198.48	73.04	35.04	97.00	2.51	1.11	48.09	32.94	2.10	4.10	0.96	1.21	38.61	38.20	12.31	4.23	0.99
278	2-50(c)	10.66	8.49	2465.34	73.61	33.12	95.48	2.61	1.08	45.62	30.28	1.85	3.44	0.90	1.25	29.98	48.38	11.59	4.03	1.61
279	2-50(e)	17.87	8.17	2150.84	72.06	27.68	96.00	2.53	1.03	42.99	28.57	1.94	3.64	0.90	1.14	31.72	48.37	10.97	4.43	1.52
280	2-50(f)	16.47	7.66	2393.05	54.39	26.11	96.11	2.73	1.03	43.26	27.73	2.02	3.51	0.94	1.17	30.00	50.74	10.55	4.41	1.69
281	2-50(g)	13.56	10.12	2755.60	66.97	33.96	96.49	2.86	1.21	46.36	31.23	1.85	3.60	0.83	1.07	37.94	39.35	12.62	4.47	1.04
282	2-50(i)	11.01	10.18	2868.51	65.76	37.72	96.33	3.01	1.29	44.62	29.47	1.72	3.26	0.96	1.25	28.65	49.70	11.83	3.22	1.73
283	2-51(a)	15.79	21.05	5587.69	65.22	47.64	97.25	2.90	1.43	45.51	29.17	1.49	3.18	1.05	1.34	33.05	46.33	12.11	3.11	1.40
284	2-51(b)	12.39	7.32	2052.28	64.55	30.57	97.34	2.60	1.09	46.27	31.27	2.10	3.64	0.84	1.10	35.32	44.03	11.51	4.57	1.25
285	2-51(c)	15.34	12.25	3436.56	70.25	35.14	97.59	2.50	1.13	47.42	33.69	1.99	3.93	0.96	1.16	40.64	34.44	12.86	4.17	0.85
286	2-51(d)	15.33	16.08	4407.35	68.18	44.29	95.91	3.03	1.26	43.83	30.04	1.53	3.20	1.00	1.25	32.28	46.96	11.73	3.36	1.45
287	2-51(e)	22.43	17.38	4844.06	74.27	36.87	98.40	2.46	1.04	48.31	35.29	1.92	3.56	1.01	1.29	33.93	45.55	11.55	3.81	1.34
288	2-51(f)	9.58	12.65	3375.21	69.15	47.13	97.45	2.96	1.30	45.54	29.08	1.50	3.18	0.99	1.25	34.06	45.28	12.35	3.29	1.33
289	2-52(a)	17.26	12.69	3631.72	69.22	42.64	98.44	2.83	1.30	44.24	28.32	1.60	3.16	0.95	1.30	27.74	53.83	10.84	3.12	1.94
290	2-52(c)	9.80	13.41	3769.13	65.35	50.42	97.81	3.43	1.38	43.75	27.71	1.33	2.98	1.06	1.33	28.05	52.73	11.50	2.83	1.88
291	2-52(d)	14.32	14.47	3993.24	64.41	47.66	98.42	2.80	1.39	44.79	28.51	1.42	3.04	1.01	1.27	29.61	50.57	11.73	3.04	1.71
292	2-52(e)	10.31	9.86	3051.39	67.49	42.98	97.31	2.98	1.28	46.80	28.94	1.65	3.31	0.92	1.26	33.63	44.28	12.37	3.07	1.32
293	2-54(a)	8.65	7.13	2018.38	67.21	55.60	94.68	3.39	1.39	45.43	27.67	1.64	3.38	0.95	1.25	32.11	45.93	12.11	3.44	1.43
294	2-54(b)	7.16	14.55	3496.06	65.59	45.97	95.92	3.60	1.43	43.82	28.52	1.54	3.06	1.03	1.35	25.81	54.16	11.24	2.96	2.10
295	2-55(a)	19.65	14.83	4169.10	70.28	42.55	98.19	2.86	1.23	48.13	32.76	1.74	3.83	1.00	1.25	39.45	37.02	13.12	3.77	0.94
296	2-55(b)	17.75	14.16	3678.53	70.82	35.58	95.95	2.76	1.14	42.39	27.75	1.65	3.37	0.94	1.23	30.45	50.42	11.12	3.86	1.66

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
297	2-55(d)	13.57	12.89	3778.26	68.14	47.08	96.60	3.19	1.33	43.37	28.87	1.51	3.18	0.98	1.26	30.59	48.16	11.60	3.17	1.57
298	2-55(e)	13.73	15.08	4572.73	67.45	42.71	96.92	3.25	1.23	44.03	27.82	1.60	3.19	1.00	1.29	29.22	50.06	11.34	3.17	1.71
299	2-55(f)	9.13	9.12	2535.50	72.68	44.19	96.37	3.24	1.23	43.36	29.24	1.65	3.41	0.95	1.33	31.28	48.69	11.27	3.26	1.56
300	2-56	14.56	15.17	4130.24	71.87	51.35	98.19	2.98	1.28	43.48	29.61	1.71	3.25	0.98	1.24	29.36	48.26	11.55	3.43	1.64
301	2-57(b)	10.75	10.45	2971.35	72.59	50.11	97.50	2.96	1.23	43.79	29.06	1.67	3.35	0.95	1.23	29.04	49.20	11.65	3.51	1.69
302	2-57(c)	11.05	11.15	3108.90	73.39	56.93	97.43	3.58	1.26	45.14	28.94	1.57	3.07	0.95	1.25	27.68	51.76	11.41	3.34	1.87
303	2-57(d)	8.65	11.32	2776.56	67.60	50.06	94.61	3.58	1.26	45.30	27.83	1.68	3.20	0.89	1.14	30.68	49.62	11.19	4.13	1.62
304	2-58	11.83	12.82	3424.37	73.19	51.17	98.22	3.48	1.21	45.58	29.67	1.48	2.89	1.09	1.32	27.60	53.04	11.21	3.28	1.92
305	2-59(a)	13.08	12.40	3670.79	75.56	32.74	97.59	2.48	0.90	44.21	26.17	1.75	2.94	0.95	1.19	28.85	52.76	11.09	3.91	1.83
306	2-59(b)	14.73	13.21	3865.03	65.95	33.36	96.56	2.84	1.18	47.07	33.54	2.17	3.65	1.01	1.28	32.11	48.50	10.89	3.52	1.51
307	2-59(c)	18.74	14.72	4769.39	69.87	49.84	97.83	2.89	1.19	45.56	26.00	1.83	3.54	0.88	1.23	36.34	40.86	12.40	3.18	1.12
308	2-59(d)	17.28	16.27	3889.44	70.14	36.82	99.50	2.66	1.14	45.57	28.37	1.75	2.92	0.97	1.29	30.66	49.75	11.56	3.25	1.62
309	2-59(g)	15.48	17.07	4643.84	73.76	51.27	97.20	3.15	1.24	46.61	30.64	1.64	2.91	1.01	1.31	29.03	51.77	11.50	3.11	1.78
310	2-59(j)	8.30	7.83	2289.61	71.87	57.12	96.11	3.54	1.35	46.20	28.79	1.90	3.73	0.92	1.23	38.20	37.93	12.70	3.30	0.99
311	2-59(k)	11.47	10.13	2857.61	64.91	39.36	96.69	3.49	1.18	44.67	28.14	1.58	3.23	0.97	1.30	36.88	42.48	12.52	3.45	1.15
312	2-59(l)	13.99	7.53	2176.84	66.17	27.84	96.85	2.41	1.19	45.77	28.73	2.00	3.56	0.91	1.17	39.75	39.82	12.37	4.04	1.00
313	2-60(a)	15.69	13.67	3902.02	68.86	38.31	95.19	2.78	1.15	45.14	25.99	1.67	3.10	0.92	1.24	34.09	45.88	11.78	3.69	1.35
314	2-60(c)	17.23	12.35	4151.68	73.51	45.73	96.12	3.11	1.15	47.56	29.62	1.67	3.37	0.99	1.35	32.64	46.71	12.09	3.16	1.43
315	2-60(d)	12.82	17.46	4463.79	72.74	43.19	95.77	3.26	1.20	47.27	28.02	1.72	3.29	0.97	1.31	32.84	47.02	12.06	3.43	1.43
316	2-60(e)	13.16	12.08	3657.04	72.18	51.99	97.54	3.36	1.23	42.57	24.89	1.66	2.69	0.87	1.10	24.19	60.62	10.40	3.38	2.51
317	2-60(f)	22.30	19.39	5573.46	68.11	47.34	95.04	3.44	1.33	45.93	30.63	1.68	3.03	1.00	1.29	30.03	50.26	11.47	3.04	1.67
318	2-61(a)	18.01	10.99	3404.89	71.17	33.54	97.69	2.60	1.11	44.43	25.83	1.76	3.40	1.09	1.40	31.34	50.03	11.26	3.27	1.60
319	2-61(b)	13.89	9.92	3059.91	53.92	33.83	97.38	2.50	1.15	42.65	26.88	1.80	3.12	1.02	1.34	28.87	53.15	10.71	3.39	1.84
320	2-61(d)	17.98	10.83	3178.46	70.49	37.31	97.49	2.73	1.21	44.58	28.91	1.97	3.69	0.99	1.28	36.66	40.07	12.03	3.46	1.09
321	2-62	14.03	10.81	3275.83	66.90	37.12	97.39	2.63	1.18	45.05	29.35	1.67	3.08	0.99	1.25	32.01	47.51	11.90	3.36	1.48
322	2-63(a)	11.98	14.34	4026.78	71.20	53.80	98.27	3.21	1.30	44.73	28.58	1.67	3.11	0.97	1.33	32.39	46.95	12.20	3.00	1.45
323	2-63(b)	10.25	7.49	2152.37	72.79	44.92	95.71	2.65	1.23	44.44	31.20	1.80	3.52	0.96	1.29	35.49	42.97	12.17	3.62	1.21

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
324	2-63(c)	17.53	11.49	3368.46	69.79	30.43	96.88	2.59	1.14	46.88	28.46	1.77	3.22	0.99	1.33	35.07	44.45	12.10	3.69	1.27
325	2-63(d)	12.63	13.70	4105.56	73.41	47.62	98.61	3.00	1.60	45.38	28.97	1.77	3.28	1.04	1.44	34.37	46.36	11.89	3.69	1.35
326	2-64(a)	12.77	9.46	2869.56	69.23	38.33	96.50	2.85	1.11	44.29	30.24	1.80	3.21	0.92	1.22	35.85	44.23	12.10	3.82	1.23
327	2-64(b)	17.41	13.22	3855.12	72.63	33.53	97.79	2.50	1.11	48.43	28.55	1.90	3.38	0.98	1.26	34.79	46.23	11.60	3.82	1.33
328	2-64(c)	13.57	12.10	3459.68	59.66	51.11	97.86	3.16	1.55	44.30	28.37	1.81	3.33	0.88	1.15	33.35	45.19	12.04	3.70	1.36
329	2-65(a)	10.83	13.26	3627.01	69.87	48.28	97.88	3.29	1.26	45.43	29.35	1.77	3.46	0.95	1.23	33.51	43.70	12.09	3.46	1.30
330	2-65(b)	18.14	12.69	4080.77	69.83	38.53	97.12	3.00	1.11	45.56	30.79	1.85	3.43	0.99	1.26	35.46	41.25	12.49	3.42	1.16
331	2-65(c)	9.80	6.98	1883.05	70.60	40.38	94.79	2.88	1.20	43.07	29.78	1.52	2.84	0.99	1.26	30.46	49.93	11.78	3.28	1.64
332	2-66(a)(i)	16.06	18.94	5249.85	64.16	57.68	97.66	3.16	1.40	44.64	30.41	1.77	3.41	0.86	1.10	33.91	44.22	12.04	3.81	1.30
333	2-66(a)(ii)	8.35	8.99	2505.54	67.77	49.71	96.08	3.28	1.36	46.82	30.13	1.71	3.38	0.89	1.15	34.43	42.76	11.98	3.24	1.24
334	2-66(b)	13.17	10.84	3337.48	73.46	35.04	97.28	3.28	1.19	43.03	30.58	1.90	3.28	1.00	1.30	29.34	50.49	11.02	3.66	1.72
335	2-66(d)	10.12	5.80	1702.06	73.86	32.32	96.89	2.53	1.10	44.55	30.47	1.81	3.66	0.90	1.14	37.81	39.98	12.15	3.90	1.06
336	2-67(a)	12.84	9.71	2688.03	69.61	37.99	94.82	2.64	1.16	47.03	28.61	1.86	3.41	0.85	1.22	29.84	49.70	11.17	4.06	1.67
337	2-67(b)	10.74	8.66	2415.13	75.13	37.45	97.86	2.74	1.11	42.55	28.47	1.76	3.34	1.01	1.26	30.20	50.09	10.96	3.54	1.66
338	2-68(a)	20.58	12.19	3972.70	69.33	31.42	96.97	2.50	1.18	46.04	23.89	1.67	3.29	0.90	1.23	32.33	47.57	11.66	3.39	1.47
339	2-68(b)	10.36	7.82	2234.27	72.92	37.74	97.13	2.71	1.15	43.11	29.39	1.87	3.27	0.87	1.15	29.50	52.14	10.29	3.66	1.77
340	2-70(a)	13.72	9.50	3184.01	70.43	39.71	98.08	2.55	1.21	46.22	25.19	1.76	3.45	0.91	1.25	38.91	37.74	12.90	3.80	0.97
341	2-70(c)	10.07	9.03	2580.98	74.49	42.54	96.29	3.33	1.33	44.13	29.24	2.01	3.98	0.75	1.04	34.50	42.29	11.91	3.74	1.23
342	2-71(a)	18.18	14.48	4536.71	68.93	36.66	96.86	2.40	1.18	45.93	22.70	1.66	3.29	1.05	1.35	34.71	45.25	12.08	3.23	1.30
343	2-71(d)	14.64	9.25	2536.32	73.42	35.69	94.95	2.81	1.19	44.12	27.86	1.57	3.17	0.92	1.19	33.73	46.23	11.87	3.78	1.37
344	2-72(a)	22.63	17.28	5073.45	71.45	37.27	97.99	2.88	1.18	44.38	29.68	2.04	3.52	0.92	1.16	36.44	42.95	11.67	4.06	1.18
345	2-72(b)	12.49	10.28	2810.61	70.23	33.21	96.45	2.81	1.13	43.53	25.21	1.62	2.96	0.97	1.26	29.25	51.94	11.09	3.38	1.78
346	2-72(c)	16.96	8.35	3024.07	66.09	25.25	94.56	3.03	1.00	41.02	26.58	2.08	3.36	0.94	1.28	24.78	57.68	9.93	4.00	2.33
347	2-72(d)	12.78	14.05	3956.21	71.56	35.86	97.22	2.51	1.13	47.29	33.38	1.97	4.05	0.92	1.26	39.80	37.76	12.15	3.87	0.95
348	2-72(f)	19.20	15.65	4925.06	75.01	41.01	97.72	2.58	1.15	47.45	34.83	2.05	3.74	1.00	1.32	37.22	37.84	12.34	3.25	1.02
349	2-73(b)	8.77	7.16	2348.19	70.49	46.85	95.99	3.20	1.24	45.21	26.72	1.70	3.26	0.93	1.23	30.39	48.13	11.58	2.98	1.58
350	2-73(c)	12.59	9.71	3043.56	68.89	43.58	95.52	3.06	1.23	45.13	25.17	1.72	3.20	0.85	1.13	29.39	49.59	11.40	3.22	1.69

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
351	2-73(d)	13.17	9.15	2756.24	73.32	39.62	98.34	2.76	1.10	46.37	27.86	1.83	2.74	0.95	1.33	26.60	54.97	10.80	3.84	2.07
352	2-74(b)	15.91	10.99	3378.56	73.16	40.54	97.05	3.13	1.28	46.88	30.94	1.73	3.50	0.92	1.20	38.70	38.40	12.79	3.62	0.99
353	2-74(c)	8.44	9.24	2962.32	72.57	54.28	96.06	3.44	1.48	47.34	30.66	1.81	3.61	0.84	1.16	33.66	42.60	12.34	3.60	1.27
354	2-74(d)	14.52	12.30	3246.05	72.05	39.70	97.37	2.61	1.18	48.20	32.79	1.86	3.68	0.89	1.16	37.89	37.55	13.02	3.57	0.99
355	2-74(e)	17.29	12.66	4362.32	76.02	40.32	97.38	2.69	1.23	48.41	33.33	1.85	3.41	0.94	1.24	37.01	39.08	12.71	3.78	1.06
356	2-74(f)(i)	13.21	13.27	3787.76	67.22	43.43	98.57	2.69	1.25	44.66	30.39	1.63	3.28	0.90	1.22	37.64	40.96	12.82	3.46	1.09
357	2-74(f)(ii)	10.62	7.07	1939.12	77.67	28.17	97.95	2.78	0.88	44.99	28.67	2.00	3.39	0.87	1.15	30.24	51.36	10.83	3.87	1.70
358	2-75	15.90	14.62	4781.89	67.67	44.64	98.06	2.58	1.24	46.64	27.83	1.81	3.56	0.87	1.30	36.76	41.73	12.18	2.47	1.14
359	2-76(a)	9.92	9.15	2549.91	69.54	42.00	97.64	2.75	1.20	45.40	26.65	1.63	3.35	0.93	1.25	37.96	39.97	12.53	3.89	1.05
360	2-76(b)	15.65	18.98	5364.43	70.99	56.54	98.92	2.96	1.61	44.12	28.08	1.51	3.29	0.99	1.33	33.77	46.25	12.15	3.50	1.37
361	2-76(d)	19.04	15.51	4425.07	72.11	37.36	98.51	2.96	1.08	45.03	28.84	1.83	3.45	0.84	1.14	37.21	41.83	11.96	4.10	1.12
362	2-76(e)	5.85	5.84	1583.10	69.97	37.04	96.47	3.20	1.30	44.71	25.77	1.84	3.55	0.96	1.26	32.64	45.67	11.59	3.59	1.40
363	2-76(f)	16.09	11.47	3212.70	65.57	30.97	95.87	2.56	1.18	46.38	28.20	1.85	3.42	0.86	1.22	35.83	44.52	11.88	3.96	1.24
364	2-76(g)	9.18	11.20	3048.42	64.61	51.18	96.32	3.13	1.40	43.58	28.28	1.52	2.89	0.91	1.18	26.81	53.51	11.20	3.34	2.00
365	2-77(a)	10.10	11.83	3176.77	72.38	50.98	97.53	3.48	1.30	45.46	28.77	1.51	3.05	0.93	1.23	33.54	44.92	12.43	3.09	1.34
366	2-77(c)	16.49	12.67	4174.26	71.02	40.37	97.43	2.71	1.24	46.60	32.80	1.85	3.39	0.92	1.18	31.22	49.81	11.22	3.99	1.60
367	2-78(a)	12.98	8.61	2329.52	73.53	33.37	98.38	2.48	0.98	43.72	26.38	1.65	3.00	0.97	1.26	29.06	54.53	10.45	3.72	1.88
368	2-78(c)	17.20	12.83	4219.54	72.94	39.06	96.64	3.19	1.10	45.16	30.02	1.87	3.67	0.94	1.22	37.75	40.61	12.04	3.86	1.08
369	2-79(b)	17.85	16.44	4196.39	71.06	38.29	94.24	3.09	1.11	46.22	25.48	1.55	3.37	1.02	1.35	33.22	45.02	12.26	3.16	1.36
370	2-79(c)	18.47	14.52	4096.37	70.07	36.27	95.90	2.93	1.18	47.46	25.37	1.72	3.16	1.00	1.32	28.60	50.59	11.76	3.32	1.77
371	2-79(e)	15.86	15.11	5002.88	71.97	41.03	98.16	2.93	1.23	46.11	31.39	1.80	3.53	0.91	1.15	38.58	37.59	12.73	3.86	0.97
372	2-80(a)	15.11	13.60	4304.72	72.45	48.45	99.43	2.96	1.20	45.41	30.37	1.41	3.11	1.04	1.37	33.83	45.57	12.45	2.85	1.35
373	2-80(b)	12.22	10.64	2896.58	65.24	38.81	95.04	2.53	1.14	44.36	29.91	1.56	3.18	0.89	1.15	35.40	44.00	12.36	3.78	1.24
374	2-80(d)	10.07	8.20	2437.71	68.51	38.96	95.70	2.84	1.16	43.30	31.35	1.62	2.93	0.99	1.28	27.65	52.13	11.20	3.17	1.89
375	2-81(a)	11.54	12.21	3358.19	65.81	44.64	96.96	3.25	1.35	41.56	25.11	1.49	2.63	0.80	1.07	27.88	53.57	11.18	3.75	1.92
376	2-81(a)(ii)	21.13	7.77	2788.91	65.06	34.18	94.03	2.96	1.20	43.13	30.57	1.66	3.23	0.91	1.18	31.21	48.87	11.15	3.52	1.57
377	2-81(c)	10.13	13.88	3800.92	66.15	52.78	96.79	3.24	1.28	43.82	26.82	1.53	3.01	0.94	1.26	30.17	48.73	11.86	2.95	1.62

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
378	2-81(e)	11.75	14.63	4180.43	65.77	47.54	95.97	3.06	1.33	41.69	27.31	1.63	3.23	0.90	1.17	32.13	46.30	12.05	3.53	1.44
379	2-81(f)	12.29	11.96	3142.09	73.95	36.37	93.13	3.09	1.15	44.94	26.62	1.53	3.37	0.93	1.22	35.82	42.19	12.27	2.87	1.18
380	2-81(h)	10.87	8.74	2382.63	75.75	39.62	95.51	2.88	1.08	45.38	26.68	1.50	3.07	0.94	1.25	31.35	48.88	11.47	2.85	1.56
381	2-81(i)	10.55	7.32	1795.67	73.10	39.14	95.64	3.00	1.10	45.44	28.08	1.46	3.29	1.02	1.34	32.41	47.55	11.60	2.72	1.47
382	2-82(a)	12.69	13.82	4156.46	69.70	50.50	98.91	3.20	1.45	44.63	29.43	1.52	2.96	0.89	1.19	32.42	48.20	12.09	3.40	1.49
383	2-82(b)	12.50	9.06	2662.23	68.97	41.19	97.29	2.69	1.26	43.57	29.80	1.57	3.21	0.94	1.17	32.51	46.20	11.86	3.29	1.42
384	2-83(a)	13.54	7.92	2226.16	74.38	43.86	97.44	2.94	1.20	43.29	28.16	1.67	3.02	0.93	1.21	29.33	50.41	11.67	3.73	1.72
385	2-83(b)	16.95	13.46	3711.51	61.85	40.91	97.35	2.96	1.25	43.83	24.98	1.52	3.03	0.89	1.15	33.57	45.19	12.19	3.48	1.35
386	2-83(d)	15.47	10.61	3110.92	65.26	36.68	95.17	3.01	1.21	45.01	28.59	1.65	3.29	0.98	1.18	35.70	42.19	12.20	3.77	1.18
387	2-84(a)	14.48	19.02	5365.38	66.11	52.86	97.02	3.48	1.49	42.66	26.75	1.41	2.96	0.86	1.14	31.68	47.52	12.36	3.40	1.50
388	2-84(b)	15.91	12.66	3680.67	63.70	44.81	97.52	2.93	1.38	42.98	27.56	1.67	3.35	0.97	1.29	36.77	40.04	12.47	3.06	1.09
389	2-85(a)	14.25	12.76	3416.79	62.03	38.29	94.33	3.06	1.14	43.02	25.67	1.69	3.20	1.01	1.26	30.95	49.16	11.25	3.63	1.59
390	2-85(c)	14.83	13.25	3520.62	67.67	38.86	96.13	3.00	1.11	42.54	28.84	1.52	3.01	0.99	1.27	27.31	52.75	11.29	3.33	1.93
391	2-86(c)	19.26	14.51	3947.23	65.93	33.37	97.33	2.41	1.18	44.02	27.64	1.76	3.21	0.91	1.16	31.23	50.69	10.98	4.15	1.62
392	2-86(d)	10.83	10.71	2948.36	73.36	45.63	97.05	3.06	1.21	46.54	28.61	1.58	3.07	0.99	1.32	27.71	51.90	11.37	3.28	1.87
393	2-86(e)	14.94	12.40	3342.30	72.59	38.03	97.37	2.54	1.11	44.69	30.70	1.78	3.50	0.94	1.25	36.61	41.84	12.46	3.70	1.14
394	2-87(f)	12.21	10.26	2872.53	53.25	43.38	97.21	2.79	1.26	41.23	18.55	1.32	2.56	0.94	1.20	29.38	51.71	11.43	3.11	1.76
395	2-87(a)	13.97	7.88	2616.43	63.16	32.40	97.13	2.76	1.00	41.93	24.15	1.71	3.24	0.92	1.22	35.00	46.25	11.71	3.61	1.32
396	2-87(b)	7.78	10.08	2423.43	59.86	48.72	89.16	3.91	1.41	45.41	26.10	1.64	2.66	0.98	1.22	22.28	59.59	10.78	3.06	2.67
397	2-87(d)	11.84	9.15	2493.83	64.14	52.60	95.03	3.89	1.38	46.65	25.12	1.44	2.75	0.94	1.25	26.69	53.40	11.95	3.08	2.00
398	2-87(e)	12.71	13.21	3711.06	64.60	54.57	89.07	4.00	1.55	44.30	25.97	1.62	3.08	0.94	1.23	27.24	52.91	11.01	3.46	1.94
399	2-87(f)	16.22	14.56	4155.44	62.03	45.75	96.97	3.14	1.39	45.36	27.62	1.57	2.95	0.94	1.22	28.63	50.55	11.71	3.41	1.77
400	2-87(g)	6.77	5.27	1440.69	55.49	37.49	79.18	3.88	1.39	43.58	22.93	1.23	2.75	0.99	1.25	29.54	51.58	11.91	2.99	1.75
401	2-87(h)	11.57	10.38	2797.41	62.11	40.84	87.84	3.54	1.30	43.38	28.19	1.51	3.01	1.02	1.33	35.25	44.33	12.52	3.45	1.26
402	2-88(a)	12.83	12.49	3547.10	68.91	69.04	95.41	3.98	1.48	44.39	30.21	1.69	3.14	0.95	1.24	28.87	50.05	11.16	2.97	1.73
403	2-88(b)	18.51	10.22	3725.11	71.92	34.10	97.00	2.39	1.06	42.58	26.13	1.78	3.59	0.84	1.06	41.70	35.13	12.95	4.44	0.84
404	2-88(c)	12.28	15.96	4146.11	66.95	44.91	97.42	3.29	1.25	41.62	27.34	1.54	3.04	0.95	1.24	30.51	49.31	11.68	3.47	1.62

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
405	2-88(d)	13.99	16.06	4487.62	65.49	45.50	96.72	2.98	1.25	42.77	28.36	1.53	2.92	0.95	1.25	28.50	51.26	11.65	3.20	1.80
406	2-89	17.61	17.64	4859.32	71.99	42.93	97.28	2.60	1.34	46.51	27.36	1.50	2.26	1.18	1.43	36.61	43.91	11.22	2.23	1.20
407	2-90(a)	11.93	9.65	2732.42	73.14	46.11	96.94	2.90	1.39	43.64	28.00	1.60	3.24	0.89	1.18	34.72	43.03	12.05	3.29	1.24
408	2-90(b)	15.38	9.79	2828.33	70.95	36.96	98.00	2.81	1.24	45.87	28.39	1.85	3.44	0.96	1.27	33.87	44.12	11.97	4.14	1.30
409	2-91(a)	10.98	5.36	1359.57	67.98	30.50	96.15	2.34	1.04	48.16	33.31	2.06	3.80	0.98	1.28	31.60	48.17	10.98	4.17	1.52
410	2-91(b)	17.74	16.39	4676.84	73.42	42.07	98.19	2.63	1.31	47.15	27.48	1.74	3.39	0.92	1.18	37.94	39.09	12.08	3.30	1.03
411	2-91(c)	12.63	12.23	3441.62	71.09	49.85	97.63	3.00	1.28	42.61	26.82	1.48	2.92	0.96	1.20	30.52	49.59	11.71	3.23	1.62
412	2-91(d)	14.07	12.02	3291.08	71.07	44.46	97.95	3.13	1.36	43.27	28.63	1.49	3.11	1.03	1.32	29.00	49.92	11.76	3.11	1.72
413	2-91(f)	11.28	8.14	2157.33	73.63	42.02	96.36	2.88	1.24	43.01	27.97	1.62	3.24	0.90	1.18	32.35	45.92	11.86	3.77	1.42
414	2-91(g)	16.67	15.91	4487.59	71.45	45.69	95.78	2.94	1.28	41.72	28.81	1.66	3.29	1.05	1.37	31.78	46.63	11.86	3.58	1.47
415	2-92(a)	14.02	10.31	2955.37	70.78	44.27	96.55	2.90	1.33	42.02	29.97	1.61	3.29	0.92	1.24	31.90	46.77	11.48	3.88	1.47
416	2-92(b)	14.27	11.48	3196.12	65.38	33.71	97.13	3.03	1.33	44.42	25.10	1.46	2.76	1.01	1.34	30.82	49.76	11.99	3.19	1.61
417	2-92(c)	13.48	9.17	2624.68	71.08	33.55	95.41	2.15	1.06	47.61	31.88	1.64	3.63	1.06	1.44	37.11	42.60	12.22	3.91	1.15
418	2-92(d)	10.89	9.15	2821.53	64.36	42.87	95.93	3.14	1.30	44.13	27.33	1.46	2.90	1.03	1.30	26.25	54.07	11.35	3.10	2.06
419	2-92(e)	15.41	12.14	3373.53	65.09	38.45	96.01	3.26	1.21	42.56	25.24	1.44	2.84	0.94	1.24	27.68	53.07	11.49	3.38	1.92
420	2-92(f)	12.50	13.64	3791.09	68.34	32.73	96.29	2.75	1.06	46.84	25.75	1.60	3.10	1.01	1.35	30.32	51.16	11.15	3.44	1.69
421	2-93(a)	11.41	7.63	2160.31	63.85	40.31	93.85	3.25	1.24	45.12	28.44	1.50	3.29	0.89	1.17	35.66	42.64	12.39	3.33	1.20
422	2-94(c)	13.56	10.97	3090.90	65.00	45.39	94.04	3.05	1.24	45.08	29.22	1.67	3.42	0.93	1.19	34.70	42.76	12.06	3.47	1.23
423	2-94(d)	9.08	6.54	1893.63	66.60	37.50	94.29	3.10	1.29	44.72	29.18	1.61	3.49	1.00	1.27	36.81	41.79	12.36	3.61	1.14
424	2-95(a)	16.10	10.82	3080.63	72.32	31.33	97.87	2.30	1.05	47.87	33.65	1.74	3.31	1.09	1.39	35.51	44.12	12.10	4.05	1.24
425	2-95(b)	17.27	12.95	3636.46	73.80	32.29	98.14	2.16	1.09	47.82	33.86	1.70	3.57	0.95	1.35	37.22	42.25	12.22	3.89	1.14
426	2-95(c)	17.51	12.11	3421.66	73.21	30.82	96.68	2.29	1.06	47.93	33.07	1.89	3.81	1.03	1.33	30.74	47.96	11.34	4.12	1.56
427	2-95(d)	13.83	14.83	4232.47	70.45	49.33	96.75	2.93	1.48	44.41	27.53	1.52	3.14	1.02	1.36	30.46	48.97	11.72	2.97	1.61
428	2-95(e)	19.86	12.63	3814.26	73.42	31.07	97.63	2.34	1.11	46.82	33.51	2.07	3.83	0.97	1.21	38.49	38.00	12.26	4.33	0.99
429	2-96	11.73	9.43	2860.70	66.02	39.65	94.21	3.58	1.29	45.55	27.47	1.91	3.12	0.86	1.14	31.12	47.31	11.37	4.17	1.52
430	2-96(c)	16.27	13.50	3772.00	76.10	51.76	98.29	2.64	1.08	44.75	28.05	1.69	3.16	0.90	1.15	32.57	47.15	11.82	4.14	1.45
431	2-97	15.08	14.23	3686.75	71.80	36.58	96.05	2.83	1.13	43.09	28.99	1.85	3.12	0.80	1.19	31.09	50.66	11.30	4.30	1.63
432	2-98(a)	14.90	12.73	3597.35	68.07	42.99	94.75	2.76	1.30	42.19	29.40	1.83	3.48	1.01	1.23	32.42	45.83	10.96	3.92	1.41
433	2-98(b)	13.94	11.18	3485.89	70.18	43.69	96.69	2.85	1.26	41.90	27.05	1.60	3.17	0.89	1.19	32.69	45.98	11.73	3.32	1.41
434	2-98(c)	18.20	15.17	4081.34	74.80	38.48	98.25	2.48	1.20	45.18	32.89	1.76	3.45	0.86	1.14	35.96	41.27	12.11	3.68	1.15

NPPP: Number of pods per plant, **PYPP**: Pod yield per plant, **PY**: Pod yield, **SP**: Shelling percentage, **TW**: Test weight, **SMKW**: Sound mature kernel weight, **PL**: Pod length, **PW**: Pod width, **OIL:** Oil content, **PROT:** Protein content, **ARA:** Arachidic acid, **BEH:** Behenic acid, **ECO:** Eicosanoic acid, **LIG:** Lignoseric acid, **LIN:** Linoleic acid, **OLE:** Oleic acid, **PAL:** Palmitic acid, **STE:** Stearic acid and **O/L**: Oleic to linoleic acid ratio

Appendix IV: AhTE markers used for genotyping the RILs of TMV 2 × TMV 2-NLM

Sl. No.	Marker	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)
1	AhTE0001	AATGTCCATGGCTCCTTGTC	ACCCCATCCTTTCAGACACA
2	AhTE0005	ACAGTACGAACGGTCCCAAG	TGGTGCATGTTGTTGTTGTG
3	AhTE0006	AATACCCGAAGCACCTGAAA	CCAACAACCCAAGGATGAAG
4	AhTE0010	GCCGTGTCATTCCACAAAG	TGGACAATGCTGTTTGTCGT
5	AhTE0025	TTCTCCCTGCTCTCCGTAAA	CGAATCTTCATTTTATTAGGTGTATGG
6	AhTE0032	CATGGTGCCGAGTAATTCAA	GGGGATTAGTGTTTTTAGCATGA
7	AhTE0045	TTTTCTGGAGAAGCACAAACA	CACTGCTGCCAAGCAAAAT
8	AhTE0050	TTGAATGGGCTCAATTCCTT	CAAATGTTTCAAGTTCTCTCCTCA
9	AhTE0074	GCAATCACATTGGCTAACTCC	GGCCAGCATGCAACTAGTAA
10	AhTE0101	GGGGATGAATTCTCCTACCA	AAAATTTCTTTTATGGTAACCTATGC
11	AhTE0107	CACTCGGAAAACCAAACTCC	CAAGAAGCCTACAAAAATGGTG
12	AhTE0113	TTATGGCATCCAAGGGTCAT	TCCCTAGTACCCGGATGATT
13	AhTE0119	AAGCTAGCGATGGCGATAAC	TTTATGCCCGCAAACTTTTT
14	AhTE0121	CTGGCAATACGCCCCAAG	AAAACTGCATTGTTGAAATTGG
15	AhTE0129	GCATGCAATCGAAAGATGAC	TGGAAGCAATAAGGACTTCG
16	AhTE0130	TGGCTTGTCTCACTTATCCTCA	TGAAAAATTCATTAACTTAACACCTT
17	AhTE0143	CTGCTTTCCTATGTCCACCAG	CCTCACTTTTCTTCTTAGTGAGCA
18	AhTE0148	GAATCCAGAGCTGCCATTGT	ATTTTTGCCTCTCAGCCTCA
19	AhTE0163	TAGAAGCCATGCTTGTATGTGG	CCACCTTCCAAATTCATATTGC
20	AhTE0164	AACCACCACCATTCTTTTAAGG	TCGTCTCCTCTAAGGTTTGCTT
21	AhTE0189	CAAGCAAGTTGTGAAGTGGTGT	CGCTGACGAGAAAAAGTCTCAT
22	AhTE0191	ACATGATGTTTCTGCCTTCCTT	CAAGTACAGTGGTGGTCTTCCA
23	AhTE0212	TGGTAGCCTGAAAATGAGGTTT	GCATTGTGCCGATCAGTTAATA
24	AhTE0218	ATGGAGTTTCAGCAAATGAGGT	GAAAATCAAAACTGGCTGCAT
25	AhTE0222	ATTCACACCCAAAACAAAACAT	ACGAGGATCGATCGTTATACAT
26	AhTE0232	CGTTAAAAACTGAAGGGAAAAA	CATTCACCTTCCGCCATATTTA
27	AhTE0233	CAGCATATTGGCTGATCAACTT	CTGATGCCATATGTGTGAAGGT
28	AhTE0237	AAAAATAGTGATGAGCTTGATTGA	AATAAAAACCCCAAAGCCACATA
29	AhTE0245	GCATGTTTTCAATCATAGCACAA	CATAAGCTAATGAAATGGAGAATTT
30	AhTE0249	TGTCTTTGATGTGTGTTTCTTGTTT	TAAAAGTTTGTTTAGATGTATGTTGTT
31	AhTE0251	GCGTCGTCTTCAATTAGGTTACT	AAAGATCAACAAAGAGCAATGAAA
32	AhTE0254	CTTTCTTTCTATTCGTGCCAAAA	TTAAAGATCTGTAGCTGGCCAAA
33	AhTE0261	ATATAACAAACTCCCCTCCTCCA	TCACCACAAAACAACTCAAAGAA
34	AhTE0278	CTTTTCTTTTGTAATGAATCTGTTTTT	GCAATGCTAATATGCTAAATCGTT
35	AhTE0283	TCGGACACTTCATTATTTTCGAC	TGTGTTTGTGGTTACGTCTGTTC
36	AhTE0296	ACTTCAAATCTGACGCACCTACT	CAATTCATGTTCTAGCAAGGGTTA
37	AhTE0303	AAGATGCATACCTTTGGTTTTCT	CTGCACTTAAGCCAACTTCTCAT

Contd…

Sl. No.	Marker	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)
38	AhTE0305	CTCATTGACCATGACTATCACGA	CGAAACGTTCTCCTATTTGAATG
39	AhTE0317	AGTTGATGATGATGTTTGGTGTT	CCATCCAGCCACTAAAAATAAAA
40	AhTE0324	TTTCAACAATGCAAACCCAA	GTGGATGTGGGAGTTTGTGA
41	AhTE0328	CAGTGGATGCATTCTACTCCAG	AATTCGTGCCCAAATTGAGT
42	AhTE0332	TGGGACCAATGGTTTCCTAA	CCAGCATGTCCTTGCATTAC
43	AhTE0335	GACAAAGGTAGAGGTTAATCCCA	CCTAACATTGGGTTGGAGGA
44	AhTE0357	GCCTCCCCCAGAAAGTTATC	CACATGCTTGCATCTCCAAC
45	AhTE0359	ATCGTTGCTTGTTAGCACGG	AAAAGCGCAAAGAAATGGGT
46	AhTE0369	TGAGGCGAGTTGTTGAGATG	TGTTGAACGATTTGCGCTAC
47	AhTE0373	TGGTGTTGGAGATGGAGACA	CACGTGAACAGCTTCCAAAA
48	AhTE0381	TGCTTTTCCGGAGTCACAAT	TGCATGTAGCAGAAAGCCAG
49	AhTE0391	TTCCTTTTTCTGATGAAATATGAGAT	GCCTTTGAAGATCTTTCACCC
50	AhTE0416	GAGTTACATCGGTATTGAATATGTGA	CTCCGTGATTGAGGCGTTA
51	AhTE0433	TTGAGAATAATCGCGTGTGG	CAAACTGTGATGTTGCGTTT
52	AhTE0437	TGGCTTTTGGGTGTGTATGA	GCCACGAGAGAATCCAAAAA
53	AhTE0465	TGCTGGAGATTCGTACATGC	TTCGAGAAAGCCTAAGCAAGA
54	AhTE0470	AACTGTTGGATGCAGTGTGC	CCCCACTCCCATTATTCCTT
55	AhTE0477	GGTGGTGGCCATTTCTCTT	TTTGCCCATTTTTGGTTCTG
56	AhTE0482	GCCAACCGTACAAGAAATCC	GAAATGCAGCCATCAATGAA
57	AhTE0483	CCACAAAAGAAAGTATTATTA	AAGAGGTATAGCAAATTGCTG
58	AhTE0486	TGATTGGATCTCAATTCCCA	TTTGATCGCTCTCTCTTTCTTTC
59	AhTE0487	GATTCTACAATGAGTGGAATGA	TCCTGCCTCAACCAATTTTC
60	AhTE0491	ATTATAACAGTATACAATTTCTAT	GAAGTTTTATTTGGTTCAGAATT
61	AhTE0498	ATGACTTACATGTAGCAATTG	TGAAAGGAGTCAAAGGTCATG
62	AhTE0501	GAAGCAGGGAACACCCACTA	TCTCATGCCCTTAATTAACTACAAA
63	AhTE0517	ATGCGAAAAAGGTAGTTGGAGTT	AAACCTACCCATTCACCAACTTT
64	AhTE0523	AAAATTGAGCGGTATTAGACATCA	GTGAGCACCTATCATCCACAAATA
65	AhTE0524	GTATGGGCCACTAATAAGCTATGG	GGAATTCGGATGCTCAAAGTATAA
66	AhTE0536	ATTTGGGGTTTGATGACAGG	TCACACATGGACATCTTGCTT
67	AhTE0540	CCACTAGACTGAAGGTTGGTTG	AGTTCGATGGTAGTGACCCG
68	AhTE0550	CTGGCATGTCGGTGTCTCTA	CAATGGTGGGGTTTTTGACT
69	AhTE0552	GCAACAAAAATTCTCGAAAGC	TCTGCTTATGCTTCCTCCTACC
70	AhTE0563	TGAGAAGTAACCCCACAAGG	GAGGATTTCAAGACGATGGC
71	AhTE0571	TTACATAAGGCATTAACGAGTGTT	AACAGCTTTGCAGGAGATGG
72	AhTE0572	GAAGCGTGTTGGATCGGTAT	TGCAAAAGTGGATAACCCAA
73	AhTE0586	CATTGTCTCGTTCGCGTTTA	GAACGTGGGGAAAGTCAAAA
74	AhTE0590	CATTAAGCAAATCGGACCCT	CAAGTTGCTCAGCCTATATCCA
75	AhTE0599	AGAAAATGCACGAGAGCCAT	CGATGAGCACAATCGCTTTA
76	AhTE0607	CCTGTTTTCTATGGCTGGCT	GGGAAGCATTACGAATTTACAA
77	AhTE0630	CAGCTCCCAACCTACCAAAA	TCTCTCACCCTCAAGCACCT
78	AhTE0661	CAAGCCTGTGACTAGAACGGA	GGCGAATGTCCAACTCATTT

Contd…

Sl. No.	Marker	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)
79	AhTE0674	AATCCACTTACTCCCTTGCG	CATCGTTATCTGCATGGTGG
80	AhTE0003	GCCCAGCTTATTAGCAAAGG	CCTTCCACTTTGATGGTTGC
81	AhTE0055	AAATTACATGGAAGACCATAATTGC	AGAATCATATTCATATGTGAGCAAA
82	AhTE0162	CTTGCGATCAATGAGGTTATCA	CCACCTTCCAAATTCATATTGC
83	AhTE0167	GGCTGAACAAATGAATCACAAA	CCACTGTCGGTTAATGTATTGC
84	AhTE0178	GGTCCAGTCCATAGTTTGAAGC	TCCAGCTCACAGACAGAAACAT
85	AhTE0200	AGTAGTGGACCAATTTCGCACT	CTAGGCTAACAGCCTCGAGAAA
86	AhTE0294	TTATCTGTGCCGAAATGAAAACT	AGCGAAAATGCAACAAAATAAAA
87	AhTE0295	GACAATTTTAATGGCAGAAGCAG	TGTTGATCAAAATCCCAGAAAGT
88	AhTE0300	GGTTGTGTAATCCAATTTCCACT	TCGTCCCATTCATAGTTCTTTTG
89	AhTE0313	TGCAGTTATAGTTTGTGCAGTTTC	AGGTTGAATGACTGAGGCATATT
90	AhTE0389	TAGCACCGAGTCTGAACCCT	AGAGGGAGAGAAAAGAGGGG
91	AhTE0457	TTGCGCAATTTAGCAGAGATT	CCACCTTTCATTATCCCCTC
92	AhTE0478	TGAAGCAGCCACACCATACT	GACGGTTGACTAAAAATGTTGG
93	AhTE0499	TTTTCTTCCTCCCCCAATTC	AAAGAATGAGTAAAATATATTCAGA
94	AhTE0508	TGGCCAACTTATTCTTGTGATTT	CTGTTCAAAGCACTTTGGAGTTT
95	AhTE0549	TGGTTACCGAAAGATCAGAAAAA	AATGCACGTCGACACTCAAA
96	AhTE0556	GATAGATGGTTTGACAAGTGGG	CATAGGCCTCATCCCATGTAA
97	AhTE0566	ATGCTATTCGCCATCCCTAA	CTTTATACACCGCCGCATTT
98	AhTE0573	TTGGAATCATGGCTCCTATTG	AGCATACTGCGAAGAGCACA
99	AhTE0584	ATCGCATATGATGTCACCCA	GTGGTGGCATACAGGAATCA
100	AhTE0615	TGTCCTCCCAAGTTTTCGTT	CCCGTTCCCAACCTTAAAAT
101	AhTE0641	TGTTTAACATTGATCCCCAATAAA	TCTTTTCCTTTTCCCTTTTGC
102	AhTE0678	CATTTTCTTTTTCTTTATGACCG	AGGGAGCATACCCACATACA
103	AhTE0893	CCATGAAGGAGAAGACGAGC	TCCATCATCCAAAGGTCAAA
104	AhTE0913	GGTAAAAGCTAAGACAGGCTCAA	TGAAGTGTGGCCAAATCAAT
105	AhTE1016	CAGCCTTTTACTTTGTTAGCCA	TGATTTGGCCACACTTCAAA

Appendix V: Taxonomic, agronomic and productivity features of genotypes in the mutant population

Sl. No.	Genotype	MSF	Pedigree	BG	INF	GH	LS	LC	FC	SS	KC	PC	PR	PB	PS	SPP
1	DER	P	Dh 3-20 × CGC -1	*	Com	P-1	W-E	G	O	F	T	7	5	5	3	2-1
2	SB 1	P	Mutant of DER	SB	Com	E	O-E	LG	O	F	T	5	5	7	3	2-1
3	SB 2	P	Mutant of DER	SB	Com	E	W-E	LG	O	F	T	5	3	3	5	2-1
4	SB 3	P	Mutant of DER	SB	Com	E	W-E	LG	O	F	T	5	5	5	5	2-1
5	SB 4	P	Mutant of DER	SB	Com	E	W-E	LG	O	F	T	5	3	3	5	2-1-3
6	SB 5	P	Mutant of DER	SB	Com	E	W-E	LG	O	F	T	5	5	5	5	2-1-3
7	SB 6	P	Mutant of DER	SB	Com	E	W-E	LG	O	F	T	5	5	3	5	2-1
8	SB 9	P	Mutant of DER	SB	Com	E	N-E	G	O	F	T	0	3	0	7	2-3-1
9	VL 1	P	Mutant of DER	VL	Com	E	N-E	G	O	F	T	0	7	7	7	3-4-2-1
10	VL 2	P	Mutant of DER	VL	Com	E	O-E	G	O	S	PR	3	7	0	3	2-1
11	VL 3	P	Mutant of DER	VL	Com	D-3	O-E	G	O	S	W	3	9	3	5	3-2-4-1
12	VL 6	P	Mutant of DER	VL	Com	D-3	O-E	G	O	S	T	3	3	0	3	2-1-3
13	VL 7	P	Mutant of DER	VL	Com	D-2	O-E	G	O	F	T	3	9	3	7	3-2-4-1
14	VL 9	P	Mutant of DER	VL	Com	D-2	O-E	G	O	F	Ro	5	3	3	5	2-3-1
15	VL 10	P	Mutant of DER	VL	Com	D-2	O-E	G	O	F	T	5	3	3	5	2-1
16	VL 12	P	Mutant of DER	VL	Com	D-2	W-E	G	O	F	T	5	7	3	7	3-2-1-4
17	VL 13	P	Mutant of DER	VL	Com	D-2	O-E	LG	O	C	LP	5	9	9	7	3-2-1
18	VB 2	Ab	Mutant of DER	VB	Com	D-3	W-E	LG	O	F	T	5	3	3	5	2-1
19	VB 7	Ab	Mutant of DER	VB	Com	E	W-E	G	O	F	T	5	7	3	7	2-1-3
20	VB 8a	P	Mutant of DER	SB	Com	E	N-E	G	O	F	T	5	3	3	5	2-1
21	VB 9	Ab	Mutant of DER	VB	Com	D-3	W-E	G	O	F	T	5	5	3	5	2-1
22	VR1{a}	Ab	Mutant of DER	VR	Com	D-3	W-E	DG	O	F	LR	3	3	3	7	3-2-1
23	VR 3	P	Mutant of DER	SB	Com	D-3	W-E	G	O	F	LT	5	3	0	3	2-1
24	VR 5	P	Mutant of DER	SB	Com	D-3	W-E	LG	O	F	LT	5	5	3	7	2-1
25	VR 8	P	Mutant of DER	VR	Com	D-3	W-E	LG	O	S	RP	3	7	0	3	2-1

Contd…

Sl. No.	Genotype	MSF	Pedigree	BG	INF	GH	LS	LC	FC	SS	KC	PC	PR	PB	PS	SPP
26	DER VL PURPLE	P	Mutant of DER	VL	Com	E	W-E	G	O	S	DP	5	5	3	3	2-1
27	1-1	P	Mutant of VL1	VL	Com	E	O-E	G	O	F	DT	0	3	0	7	3-4-2-1
28	2-1	P	Mutant of VL1	VL	Com	E	W-E	LG	O	F	DT	5	7	3	7	3-4-2-1
29	2-2	P	Mutant of VL1	VL	Com	E	N-E	G	O	F	DT	0	3	0	7	2-3-1
30	3-1	P	Mutant of VL1	VL	Com	E	O-E	G	O	S	P	3	9	0	3	2-1-3
31	28-2	P	Mutant of VL1	SB	Com	E	W-E	G	O	F	T	5	3	3	5	2-1
32	28-2 (S)	P	Mutant of 28-2	SB	Com	E	W-E	LG	O	F	T	5	5	3	5	2-1
33	45	P	Mutant of VL1	SB	Com	D-3	W-E	DG	O	F	T	5	3	0	5	2-1-3
34	45 (S-7)	P	Mutant of 45	SB	Com	E	O-E	G	O	F	P	3	7	3	5	2-3-1
35	45 (M3)	P	Mutant of 45	VL	Com	E	W-E	G	O	F	P	3	7	3	5	2-3-1
36	98	P	Mutant of VL1	SB	Com	E	W-E	LG	O	F	T	3	3	0	7	3-2-4-1
37	98 (S)	Ab	Mutant of 98	VB	Com	D-3	O	DG	O	F	T	5	3	3	3	2-1
38	110	P	Mutant of VL1	SB	Com	D-3	S-O	G	O	C	Ro	7	3	3	5	2-1
39	110 (S)	P	Mutant of 110	SB	Com	E	O-E	LG	O	C	Ro	7	5	9	7	2-1-3
40	110(8)	Ab	Mutant of 110	SB	Com	E	W-E	DG	O	F	T	5	7	5	5	2-1-3
41	29-1	P	Mutant of VL1	VL	Com	E	W-E	G	O	F	T	3	5	0	5	2-3-1
42	78-1	P	Mutant of VL1	VL	Com	E	W-E	G	O	F	T	3	5	0	5	2-3-1
43	78-2	P	Mutant of VL1	VL	Com	E	Obl	LG	O	F	T	3	3	0	7	3-2-4-1
44	104-9VL-1 type	P	Mutant of VL1	VL	Com	E	O-E	G	O	F	T	3	3	0	7	3-4-2-1
45	121- purple seeded	P	Mutant of VL1	VL	Com	E	O-E	LG	O	F	P	3	7	3	3	2-1-3
46	139-1 Viriscent	P	Mutant of VL1	VL	Com	E	W-E	LG	O	F	T	3	3	0	7	3-4-2-1
47	161- reticulated pods	P	Mutant of VL1	VL	Com	E	W-E	G	O	F	T	5	7	3	5	2-3-1
48	171-tan	P	Mutant of VL1	VL	Com	E	W-E	G	O	F	T	3	5	0	7	3-4-2-1
49	171-red	P	Mutant of VL1	VL	Com	E	W-E	LG	O	F	LR	3	9	0	7	3-4-2-1
50	VL-1 Dwarf	P	Mutant of VL1	VL	Com	E	W-E	G	O	C	T	5	5	5	5	2-1-3
51	Spanish Improved	P	Selection from Spanish peanut	SB	Com	E	W-E	G	O	F	T	5	5	3	5	2-1

Contd…

Sl. No.	Genotype	MSF	Pedigree	BG	INF	GH	LS	LC	FC	SS	KC	PC	PR	PB	PS	SPP
52	TG 2	P	Spanish Improved	SB	Com	E	W-E	DG	O	F	T	3	5	5	3	2-1
53	TGM 8	P	Spanish Improved	SB	Com	E	W-E	Y	Y-W	C	LR	7	5	3	7	2-1
54	TGM 16	P	TAG-24	SB	Com	E	W-E	G	O	C	DT	5	5	5	5	2-1-3
55	TGM 17	P	TAG-24	SB	Com	E	W-E	G	O	F	LT	5	5	5	7	2-1
56	TGM 19	P	TAG-24	SB	Com	E	W-E	G	O	F	T	5	5	5	7	2-1-3
57	TGM 44	P	TAG-24	SB	Com	E	W-E	G	O	C	RP	7	5	5	7	2-1-3
58	TGM 46	P	TG-18 A	SB	Com	E	S-O	G	O	F	RP	5	5	3	5	2-1
59	TGM 47	P	TAG-24	SB	Com	E	W-E	G	O	C	PR	7	5	3	7	2-1
60	TGM 49	P	TAG-24	SB	Com	E	W-E	G	O	F	DP	5	5	5	7	2-3-1
61	TGM 50	P	TAG-24	SB	Com	E	W-E	G	O	F	W	3	5	3	5	2-3-1
62	TGM 51	P	TAG-24	SB	Com	D-3	W-E	G	O	C	OW	5	7	7	7	2-3-1
63	TGM 54	P	TG18-A	SB	Com	D-3	W-E	G	O	C	DT	5	5	5	7	2-1-3
64	TGM 20	P	TAG-24	SB	Com	E	Ob	LG	O	F	T	3	3	3	3	2-1
65	TGM 25	P	TAG-24	SB	Com	E	W-E	DG	O	F	LT	3	3	3	3	2-1
66	TGM 101	P	TG-18 A	SB	Com	E	Cu	DG	O	F	LT	5	5	3	5	2-1-3
67	TGM 111	P	TAG-24	SB	Com	E	Ob	DG	O	F	T	5	3	3	3	2-1
68	TGM 112	P	TAG-24	SB	Com	E	W-E	G	W	F	T	7	5	5	7	2-1
69	TGM 36	P	TAG-24	SB	Com	E	Cu	DG	O	F	T	5	3	3	5	2-1-3
70	TGM 37	P	TG18-A	SB	Com	E	W-E	G	W	F	T	5	5	5	7	2-1-3
71	TGM 113	P	TAG-24	SB	Com	E	W-E	Y	O	F	LT	3	3	3	5	2-1-3
72	TGM 117	P	TAG-24	SB	Com	D-3	W-E	G	O	F	Ro	7	5	5	7	2-1-3
73	TGM 119	P	TAG-24	SB	Com	E	Cu	G	O	F	Ro	5	3	5	7	2-1-3
74	TGM 136	P	TAG-24	SB	Com	E	Ob	G	O	F	RP	5	3	5	7	2-1-3
75	TGM 138	P	TAG-24	SB	Com	E	Ob	G	O	F	RP	5	3	3	7	2-1-3
76	TGM 165	P	TG-66	SB	Com	E	Ob	G	O	F	R	5	3	3	3	2-1-3
77	TGM 167	P	TG-66	SB	Com	E	Ob	DG	O	F	R	3	0	3	3	2-1-3

Contd…

Sl. No.	Genotype	MSF	Pedigree	BG	INF	GH	LS	LC	FC	SS	KC	PC	PR	PB	PS	SPP
78	TGM 178	P	TG-66	SB	Com	E	Ob	G	O	F	R	5	5	5	5	2-3-1
79	TGM 189	P	TG-66	SB	Com	E	Ob	Y	O	F	R	5	5	5	5	2-1-3
80	TGM 193	P	TG-66	SB	Com	E	O-E	G	O	F	R	5	5	3	5	2-3-1
81	TGM 196	P	TG-66	SB	Com	E	O-E	G	O	F	RP	5	3	3	5	2-1
82	TGM 198	Ab	TG-66	VB	Com	E	W-E	G	O	F	RP	5	3	3	5	2-3-1
83	TGM 213	P	TG-66	SB	Com	E	W-E	G	O	F	T	7	5	5	7	2-3-4-1
84	TGM 214	P	TG-66	SB	Com	D-3	W-E	G	O	F	R	5	3	3	5	2-3-1
85	TGM 215	P	TG-66	SB	Com	E	O-E	G	O	F	R	5	5	5	7	2-3-1
86	TGM 218	P	TG-66	SB	Com	E	W-E	LG	O	F	R	5	3	3	5	2-3-1
87	TGM 219	P	TPG 41	SB	Com	E	W-E	LG	O	C	T	7	3	9	7	2-1
88	TGM 220	P	TPG 41	SB	Com	E	W-E	LG	O	C	P T	7	3	5	7	2-1
89	TGM 221	P	GFDS-272	SB	Com	E	O-E	G	W	F	T	5	3	3	5	2-1-3
90	TGM 223	P	TG-51	SB	Com	D-3	W-E	LG	O	F	DT	3	3	0	7	2-3-1
91	TGM 225	Ab	TG-51	VB	Com	D-3	L	G	O	F	T	3	3	3	5	2-3-1
92	TAG 24	P	(TG-18A × M-13) × (TGE-1) (Tall mutant × TG-9)	SB	Com	E	W-E	LG	O	F	T	5	5	5	5	2-3-1
93	TG 16	P	Viriscent / TG-1	SB	Com	E	W-E	LG	O	C	T	7	7	5	7	2-1-3
94	SOMNATH	P	TG-18 A × M-13	SB	Com	D-2	W-E	LG	O	C	Ro	7	5	7	7	2-1-3
95	TG 18 A	P	TG-18	SB	Com	D-3	W-E	LG	O	C	T	7	5	5	7	2-1-3
96	TG 9	P	TG-1 × Viriscent	SB	Com	D-3	W-E	LG	O	C	DT	7	0	0	5	2-1
97	TG 66	P	TAG-24 X VG 9514	SB	Com	E	W-E	G	O	F	R	3	3	3	5	2-3-1
98	TMV 10	Ab	Natutal mutant from Argentina 1	VB	Com	D-3	W-E	DG	O	F	RW	5	3	5	5	2-1

MSF	Main stem flower	P: Present, Ab: Absent
BG	Botanical group	SB: Spanish bunch, VL: Valencia, VB: Virginia bunch, VR: Virginia runner
INF	Inflorescence	Com: Compound
GH	Growth habit	E: Erect, D-3: Decumbent-3, D-2: Decumbent-2, P-1: Proumbent-1
LS	Leaflet shape	W-E: Wide-elliptic, O-E: Oblong elliptic, N-E: Narrow elliptic, L: Lanceolate, O: Ovate, Ob: Obovate, S-O:Suborbicular, Obl: Oblong, Cu: Cuneate
LC	Leaflet colour	G: Green, DG: Dark green, LG: Light green, Y: Yellow
FC	Flower colour	O: Orange, W: White, Y-W: Yellowish white
SS	Seed shape	F: Fusiform, C: Cylindrical, S: Spherical
KC	Kernel colour	T: Tan, DT: Dark tan, LT: Light tan, W: White, OW: Off white, Ro: Rose, R: Red, LR: Light red, DR: Dark red, P: Purple, PR: Purplish red, RP: Reddish purple, RW: Reddish white, PT: Pale tan
PC	Pod constriction	0: None, 3: Slight, 5: Moderate, 7: Deep, 9: Very deep
PR	Pod reticulation	0: Absent, 3: Slight, 5: Moderate, 7: Prominent, 9: Very prominent
PB	Pod beak:	0: Absent, 3: Slight, 5: Moderate, 7: Prominent, 9: Very prominent
SPP	Seeds per pod	

Appendix VI: Mean performance of genotypes for disease resistance and agronomic traits in the mutant population

Sl. No.	Genotype/trait	R70	R80	R90	LLS70	LLS80	LLS90	50% F	PH	NPB	NSB	LL	LW	DORM
1	DER	2.00	4.50	5.50	3.00	4.50	6.00	32.50	17.63	4.25	0.00	3.84	2.25	4.00
2	SB 1	2.50	4.00	5.00	2.75	4.50	5.50	30.75	37.38	8.00	0.17	4.63	2.16	1.00
3	SB 2	3.00	4.00	5.00	2.50	4.75	6.00	30.00	25.67	5.50	0.00	4.23	2.18	3.00
4	SB 3	1.50	4.00	5.00	2.00	3.50	5.50	33.25	31.00	6.50	0.00	4.51	2.34	0.00
5	SB 4	1.75	3.75	5.00	2.50	4.50	6.25	31.50	26.42	4.33	0.00	4.38	2.36	7.50
6	SB 5	2.00	3.50	4.75	1.75	4.50	6.75	32.00	30.42	5.50	0.00	4.43	2.36	3.50
7	SB 6	2.75	4.00	6.50	3.50	5.00	6.75	31.00	25.42	6.42	0.00	4.43	2.28	2.50
8	SB 9	2.50	4.50	5.25	2.75	5.00	5.50	35.25	33.42	14.67	8.33	4.70	2.04	1.00
9	VL 1	1.25	2.50	3.25	2.75	5.00	5.75	32.00	31.46	4.75	0.67	5.28	2.65	1.00
10	VL 2	1.00	1.00	2.00	1.00	1.00	1.00	32.25	32.46	4.75	5.58	4.56	2.08	3.00
11	VL 3	2.75	3.75	4.75	2.75	2.75	6.25	32.50	20.17	6.25	0.00	4.81	2.32	2.00
12	VL 6	3.25	5.00	5.50	4.00	5.50	6.25	32.00	19.63	4.17	0.00	4.03	2.23	0.00
13	VL 7	1.50	2.75	3.75	3.75	6.00	6.75	32.50	29.58	5.42	0.00	5.23	2.49	0.50
14	VL 9	1.00	1.50	4.50	1.00	3.00	2.50	34.25	22.00	9.00	0.00	4.58	2.21	0.00
15	VL 10	2.50	2.00	4.50	1.00	1.00	1.25	34.75	23.33	7.25	0.00	4.72	2.43	1.50
16	VL 12	2.25	4.00	5.50	1.50	3.00	6.25	34.75	32.75	5.42	0.00	5.22	2.52	1.50
17	VL 13	2.25	3.00	4.50	2.00	4.25	4.75	32.25	38.25	4.75	0.92	4.87	2.43	0.50
18	VB 2	2.50	3.50	5.50	2.25	4.00	6.75	31.75	28.50	6.08	0.00	4.50	2.51	0.00
19	VB 7	1.50	4.00	5.00	1.75	4.50	5.50	37.25	34.00	7.75	8.83	4.28	2.20	0.00
20	VB 8a	2.25	3.50	6.25	2.50	4.50	6.75	31.75	29.83	5.58	0.00	4.32	2.27	3.00
21	VB 9	3.00	4.00	5.50	2.50	4.25	5.75	35.50	28.83	8.33	8.83	4.48	2.38	0.00
22	VR1{a}	2.25	4.25	5.00	1.25	4.25	4.75	36.25	24.92	7.08	9.17	4.00	2.31	3.50

Contd…

Sl. No.	Genotype/trait	R70	R80	R90	LLS70	LLS80	LLS90	50% F	PH	NPB	NSB	LL	LW	DORM
23	VR 3	1.00	2.50	3.25	1.00	2.00	2.50	33.25	33.42	6.83	0.33	4.47	2.13	0.50
24	VR 5	1.50	4.00	5.00	2.00	5.00	6.00	33.00	33.67	4.75	1.00	4.25	2.27	0.00
25	VR 8	1.00	2.00	2.50	1.00	2.00	2.50	31.75	33.42	4.50	7.92	4.30	2.01	3.00
26	DER VL PURPLE	1.75	2.50	5.25	3.50	5.00	6.50	30.75	31.33	4.58	0.00	4.43	2.15	1.50
27	1-1	1.00	1.25	2.00	3.50	5.00	6.50	31.50	32.00	4.58	0.25	4.98	2.33	1.00
28	2-1	1.50	2.25	4.00	3.00	5.00	7.00	32.00	32.58	4.50	0.00	4.16	2.05	4.00
29	2-2	2.25	2.50	2.75	1.50	3.00	5.00	33.00	35.25	4.92	0.00	4.85	2.29	1.50
30	3-1	1.50	1.50	2.00	1.00	1.00	2.00	34.00	34.50	5.92	1.33	4.82	2.34	2.50
31	28-2	1.50	4.50	4.50	1.50	2.50	3.25	33.75	28.67	5.92	0.00	4.28	2.27	0.50
32	28-2 (S)	2.75	3.50	5.25	3.75	5.00	6.25	31.75	33.75	6.75	0.92	4.60	2.38	3.00
33	45	1.00	1.00	3.25	1.00	1.50	2.75	32.75	33.33	7.42	0.00	4.72	2.38	0.50
34	45 (S-7)	1.00	1.50	3.25	1.50	2.25	2.50	33.25	40.75	7.08	1.67	4.78	2.51	2.50
35	45 (M3)	1.00	1.00	1.25	2.75	3.50	3.75	34.50	36.33	5.67	3.67	5.13	2.46	0.50
36	98	1.00	1.00	1.50	2.00	3.00	3.50	33.25	28.67	5.33	1.75	4.46	2.40	1.50
37	98 (S)	2.25	2.75	4.25	2.50	4.00	5.75	35.50	29.25	8.75	6.33	3.51	2.08	2.50
38	110	2.00	2.50	4.25	1.00	1.00	2.00	34.75	27.75	6.67	0.00	4.36	2.31	1.00
39	110 (S)	1.25	1.75	3.25	1.50	2.50	4.25	32.50	43.42	5.50	0.08	5.55	2.72	0.50
40	110(8)	1.00	2.50	3.75	1.00	1.00	2.75	34.75	28.75	8.33	4.50	3.97	2.22	0.00
41	29-1	1.00	1.00	3.25	1.00	1.00	3.25	35.00	38.58	5.25	0.00	5.22	2.49	0.00
42	78-1	1.00	1.00	1.00	4.00	5.50	6.75	31.75	34.08	5.58	0.92	5.13	2.63	0.00
43	78-2	2.00	1.00	1.00	4.00	5.50	6.75	31.50	29.58	4.83	0.00	4.93	2.53	2.50
44	104-9VL-1 type	1.50	1.00	1.25	4.00	5.00	6.00	31.75	34.42	4.33	0.00	5.08	2.40	3.00
45	121- purple seeded	1.50	1.00	1.00	1.00	1.00	1.50	31.75	34.33	5.75	6.50	4.21	1.89	3.50

Contd…

Sl. No.	Genotype/trait	R70	R80	R90	LLS70	LLS80	LLS90	50% F	PH	NPB	NSB	LL	LW	DORM
46	139-1 Viriscent	1.00	2.00	2.25	1.50	3.50	5.50	31.00	36.83	4.50	0.00	5.08	2.32	1.50
47	161- reticulated pods	1.75	2.00	3.50	3.50	5.00	6.00	32.75	34.08	5.50	0.08	4.05	2.12	5.00
48	171-tan	1.25	1.75	2.25	2.50	4.00	5.00	32.50	40.50	4.42	0.00	4.71	2.62	2.00
49	171-red	1.00	1.00	1.00	1.75	2.50	4.00	33.00	43.25	5.42	0.00	5.23	2.83	0.00
50	VL-1 Dwarf	2.00	3.25	4.75	1.50	2.50	3.50	33.75	37.33	8.00	2.75	4.36	2.41	0.00
51	Spanish Improved	4.00	4.75	6.25	3.75	5.25	7.00	32.25	28.83	7.42	1.00	4.53	2.47	0.00
52	TG 2	1.75	3.25	4.00	3.25	5.50	7.00	30.75	23.08	8.75	5.08	2.45	1.53	0.00
53	TGM 8	1.75	3.50	5.00	4.25	5.25	6.75	32.25	22.92	5.17	1.67	4.37	2.18	4.00
54	TGM 16	2.50	4.25	5.75	4.25	6.25	7.75	33.00	21.17	6.42	1.75	3.78	2.11	0.00
55	TGM 17	2.25	4.25	6.25	3.75	5.75	7.50	32.25	21.25	5.33	0.00	3.83	2.16	0.00
56	TGM 19	2.25	3.75	6.00	3.00	5.25	7.50	31.75	20.83	4.83	0.00	3.67	2.44	0.00
57	TGM 44	2.25	4.50	6.50	3.50	5.75	7.75	33.50	21.83	6.42	0.00	3.98	2.28	0.00
58	TGM 46	2.25	3.75	6.00	4.75	6.50	8.00	32.50	19.83	6.42	0.00	3.73	2.25	0.00
59	TGM 47	2.75	4.00	6.25	4.50	6.00	7.75	33.00	21.42	5.92	0.00	4.08	2.14	0.00
60	TGM 49	3.25	4.00	5.75	4.25	5.00	6.75	32.25	26.00	5.42	0.00	4.56	2.18	0.00
61	TGM 50	2.75	4.00	5.75	4.50	6.00	7.50	30.75	25.00	4.92	0.00	4.75	2.39	2.50
62	TGM 51	3.00	4.75	6.00	5.25	6.50	8.25	31.50	22.63	4.08	0.00	4.60	2.41	3.50
63	TGM 54	3.50	4.25	6.00	4.00	6.25	8.00	31.25	23.42	5.92	0.00	3.77	1.89	0.00
64	TGM 20	2.75	3.75	5.50	3.25	5.75	7.50	30.50	22.75	6.25	1.17	3.68	2.13	0.00
65	TGM 25	1.75	3.00	5.00	3.00	5.50	7.50	30.50	10.52	6.58	0.50	3.24	1.93	0.00
66	TGM 101	3.00	4.25	7.00	4.50	5.50	8.25	31.50	9.63	6.25	1.08	2.63	1.85	0.00
67	TGM 111	2.25	4.25	6.00	2.50	5.75	7.25	34.25	9.29	5.75	0.25	2.86	1.55	0.00
68	TGM 112	4.00	5.75	6.75	4.00	6.00	7.25	32.25	13.25	8.42	0.17	3.08	2.02	0.00

Contd…

Sl. No.	Genotype/trait	R70	R80	R90	LLS70	LLS80	LLS90	50% F	PH	NPB	NSB	LL	LW	DORM
69	TGM 36	3.25	5.75	6.75	3.50	6.25	7.50	34.00	9.67	5.33	0.00	3.02	1.97	0.00
70	TGM 37	2.75	4.75	5.75	2.50	5.50	6.75	34.25	10.58	6.50	0.00	3.33	1.83	0.00
71	TGM 113	2.75	3.00	3.75	1.75	6.00	7.25	33.25	9.88	5.25	0.00	2.92	1.77	0.00
72	TGM 117	3.25	5.00	6.00	1.00	5.00	6.75	33.50	20.46	6.33	0.00	3.75	2.13	0.00
73	TGM 119	3.75	5.00	6.25	2.75	4.75	6.75	32.25	21.00	6.50	0.00	4.58	2.36	0.00
74	TGM 136	3.75	4.50	6.25	3.00	5.25	6.75	33.50	12.46	5.50	0.00	3.67	2.08	0.00
75	TGM 138	2.50	4.00	5.75	3.25	5.00	6.75	33.75	12.75	5.17	0.00	3.80	1.95	0.00
76	TGM 165	1.00	1.50	2.50	1.25	1.25	2.00	35.50	10.67	5.92	0.00	3.31	1.82	1.50
77	TGM 167	1.00	2.00	2.50	1.75	3.50	5.00	35.75	9.08	4.42	0.25	3.65	1.93	0.00
78	TGM 178	1.00	1.25	2.00	1.25	2.00	4.50	33.00	10.17	6.17	0.00	3.75	1.92	0.00
79	TGM 189	1.00	1.00	1.50	1.75	3.75	5.50	34.75	9.33	6.25	0.00	3.44	1.72	0.00
80	TGM 193	1.50	1.25	2.75	2.00	3.00	5.25	32.75	11.63	6.58	0.00	3.68	1.95	0.00
81	TGM 196	1.50	1.50	2.00	2.00	3.00	5.00	32.25	9.54	5.25	0.00	3.03	1.60	0.00
82	TGM 198	3.00	3.75	5.00	1.00	1.00	1.75	33.75	17.58	9.58	1.33	3.81	2.20	0.00
83	TGM 213	1.00	1.75	3.00	3.50	5.00	6.00	31.25	17.96	6.83	0.00	3.91	2.21	0.00
84	TGM 214	1.00	1.75	3.00	1.50	1.50	3.75	34.50	13.38	7.33	1.00	3.73	1.90	0.50
85	TGM 215	1.00	2.50	3.25	1.50	2.50	3.75	33.75	13.46	5.08	0.00	3.92	2.13	0.00
86	TGM 218	1.00	1.75	2.50	1.00	1.25	3.25	32.25	13.25	5.83	0.00	3.78	2.03	0.00
87	TGM 219	2.75	5.00	6.50	1.00	4.25	6.75	33.75	12.79	6.00	0.00	3.93	1.86	0.50
88	TGM 220	3.75	6.00	7.50	2.50	5.75	7.25	32.75	17.08	6.17	0.00	3.74	1.77	0.00
89	TGM 221	2.50	3.50	5.00	1.00	1.00	1.00	34.50	22.75	5.50	0.00	5.19	2.28	0.00
90	TGM 223	3.00	4.75	6.75	1.00	4.25	6.25	35.50	16.13	4.83	0.00	3.93	1.91	0.00
91	TGM 225	3.00	5.50	7.00	1.00	3.25	6.00	35.25	18.92	10.00	6.25	5.29	1.45	0.00
92	TAG 24	3.00	6.00	8.00	3.75	6.75	8.00	31.75	21.42	6.92	0.25	3.87	1.90	0.00
93	TG 16	2.75	5.25	6.25	5.00	6.50	8.00	31.75	22.54	5.58	0.00	4.03	2.08	3.50

Contd…

Sl. No.	Genotype/trait	R70	R80	R90	LLS70	LLS80	LLS90	50% F	PH	NPB	NSB	LL	LW	DORM
94	SOMNATH	3.25	4.75	6.00	1.00	5.00	7.25	32.75	24.75	5.67	0.17	3.99	2.12	0.00
95	TG 18 A	3.50	5.25	7.00	4.50	6.00	8.25	33.50	23.17	5.00	0.25	3.96	2.23	1.00
96	TG 9	3.50	5.25	6.75	3.25	6.00	7.75	34.75	25.00	4.92	0.33	4.32	2.36	1.50
97	TG 66	1.00	3.50	4.75	1.00	4.00	5.50	34.25	17.96	5.33	0.33	3.72	2.01	1.00
98	TMV 10	1.75	2.75	5.00	1.00	2.25	4.00	35.00	21.92	10.17	11.33	4.28	2.07	0.00

LLS 70: Late leaf spot score at 70 days after sowing (DAS), **LLS 80:** Late leaf spot score at 80 DAS, **LLS 90:** Late leaf spot score at 90 DAS,**R 70:** Rust score at 70 DAS, **R 80:** Rust score at 80 DAS, **R 90:** Rust score at 90 DAS, **50%F**: Days to 50% flowering, **PH**: Plant height (cm), **NPB**: Number of primary branches (cm), **NSB**: Number of secondary branches (cm), **LL**: Leaflet length (cm), **LW**: Leaflet width (cm) and **DORM**: Seed dormancy

Appendix VII: Mean performance of genotypes for productivity and nutritional traits in the mutant population

Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
1	DER	10.86	4.71	941.99	68.60	21.44	88.59	2.40	0.95	45.25	30.96	1.78	3.65	1.04	1.40	32.27	48.44	10.88	3.49	1.53
2	SB 1	17.22	8.65	2538.67	73.62	25.28	95.47	2.54	0.98	47.46	29.52	1.77	3.81	0.91	1.23	34.99	44.69	11.13	3.72	1.29
3	SB 2	17.94	16.70	4499.10	77.09	47.25	97.85	2.79	1.16	46.93	30.84	1.70	3.69	0.88	1.17	37.72	38.61	12.64	3.91	1.03
4	SB 3	23.18	15.40	4175.40	74.34	30.18	98.70	2.30	1.03	44.46	29.37	1.54	3.54	0.99	1.32	34.33	45.65	11.73	3.61	1.34
5	SB 4	12.77	10.80	3041.45	70.51	40.61	98.35	2.55	1.24	48.71	34.07	1.70	3.88	0.93	1.20	41.10	34.86	12.94	3.77	0.86
6	SB 5	18.07	17.86	4697.64	74.56	35.36	97.61	2.49	1.09	44.84	30.66	1.59	3.59	1.00	1.33	31.61	48.67	11.01	3.54	1.57
7	SB 6	15.29	10.30	2805.92	74.92	40.66	97.99	2.80	1.09	45.41	32.77	1.56	3.78	0.91	1.21	39.81	37.03	12.89	3.58	0.94
8	SB 9	10.38	12.22	3224.87	64.53	48.62	95.17	3.00	1.44	43.19	30.81	1.50	3.09	0.91	1.13	27.99	53.87	11.05	3.61	1.97
9	VL 1	11.11	11.63	3285.15	71.76	46.58	98.28	3.25	1.44	45.53	29.37	1.46	3.30	0.95	1.19	33.93	45.49	11.99	3.30	1.35
10	VL 2	14.93	12.67	3425.92	69.88	28.56	96.65	2.13	1.20	46.21	19.19	1.77	3.71	1.03	1.15	30.57	49.99	10.05	3.63	1.66
11	VL 3	11.28	10.59	2840.49	71.43	37.03	99.10	2.69	1.21	45.00	25.68	2.05	4.24	0.78	0.99	43.39	34.62	12.33	4.84	0.84
12	VL 6	9.14	5.11	1465.12	74.33	31.59	94.74	1.81	1.05	43.96	32.00	1.71	3.52	1.05	1.39	31.26	50.99	10.71	3.60	1.74
13	VL 7	12.44	15.56	4418.68	66.90	42.04	97.56	3.45	1.36	43.18	30.04	1.32	2.90	0.95	1.20	31.58	49.05	12.10	3.52	1.57
14	VL 9	15.73	17.29	4741.50	72.64	52.16	99.53	2.76	1.31	46.94	29.21	1.25	2.98	0.97	1.30	33.11	46.84	12.51	3.02	1.42
15	VL 10	11.65	14.20	3956.83	70.18	45.92	97.92	2.85	1.30	46.42	29.28	1.34	3.31	0.94	1.29	34.37	45.22	12.49	3.24	1.32
16	VL 12	11.65	7.30	1906.03	69.11	40.13	97.74	3.13	1.14	40.40	30.17	1.65	3.32	0.90	1.15	34.61	44.39	11.96	3.83	1.29
17	VL 13	12.45	16.61	4435.47	67.54	47.11	98.57	3.19	1.21	51.05	22.15	1.14	3.20	1.11	1.49	37.50	41.35	12.30	1.77	1.11
18	VB 2	16.06	12.37	3411.85	74.95	39.92	100.10	2.78	1.06	46.94	32.32	1.67	3.85	0.88	1.17	38.31	37.82	12.74	3.89	1.00
19	VB 7	10.83	11.29	3024.40	70.38	50.49	96.85	3.11	1.26	47.71	33.63	1.63	3.48	0.99	1.27	33.70	43.27	12.20	3.53	1.30

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
20	VB 8a	16.16	14.84	4076.00	70.36	43.45	98.80	2.78	1.19	46.94	32.46	1.69	3.82	0.94	1.24	39.23	36.77	12.87	3.80	0.94
21	VB 9	11.87	7.75	2138.32	68.43	38.98	92.58	2.73	1.18	43.97	30.08	1.58	3.31	0.93	1.20	33.38	45.45	11.98	3.82	1.36
22	VR1{a}	11.19	11.00	2946.36	69.86	39.16	98.67	3.38	1.23	43.76	29.46	1.44	3.22	0.98	1.30	29.75	50.89	11.49	3.38	1.72
23	VR 3	13.60	11.33	3142.83	66.22	31.11	97.72	2.29	1.04	46.59	30.41	1.55	3.52	0.97	1.30	33.73	46.32	11.66	3.53	1.39
24	VR 5	15.34	15.61	4290.96	71.17	49.63	97.58	3.05	1.19	45.78	32.78	1.58	3.35	0.98	1.21	33.47	44.42	12.09	3.59	1.33
25	VR 8	15.52	11.60	3269.60	70.56	31.64	97.61	2.13	1.21	44.93	21.20	1.77	3.88	1.07	1.20	28.82	51.86	9.75	3.79	1.82
26	DER VL PURPLE	12.23	7.55	2159.12	72.26	26.35	94.85	1.89	1.01	43.19	23.77	1.88	4.21	1.08	1.28	24.79	56.22	8.59	3.26	2.39
27	1-1	10.23	16.30	4441.56	66.69	50.54	97.82	3.43	1.53	43.51	29.26	1.29	3.01	0.95	1.20	32.91	47.13	11.88	3.24	1.46
28	2-1	15.23	12.75	3793.10	76.02	40.65	98.03	3.40	1.24	44.80	27.80	1.32	3.31	0.93	1.19	36.51	41.82	12.26	2.83	1.15
29	2-2	11.18	14.44	3962.69	70.39	45.79	96.98	3.10	1.46	44.12	29.27	1.37	3.30	0.95	1.20	31.94	47.51	11.77	3.06	1.53
30	3-1	17.47	15.68	4247.45	71.40	32.93	98.69	2.09	1.28	44.71	20.04	1.73	4.10	1.06	1.16	32.03	48.46	9.86	3.42	1.51
31	28-2	12.09	16.17	4409.05	70.82	53.29	99.13	2.98	1.81	47.92	31.20	1.43	3.30	1.01	1.28	34.47	44.42	11.82	2.82	1.30
32	28-2 (S)	16.22	14.30	3952.55	71.87	48.21	95.95	2.86	1.24	46.03	29.70	1.33	3.27	0.96	1.27	36.37	43.06	12.83	3.27	1.19
33	45	11.56	10.67	3200.34	68.89	44.37	97.95	2.60	1.33	44.60	29.87	1.29	3.28	1.00	1.28	33.92	44.65	12.13	3.15	1.32
34	45 (S-7)	12.08	12.08	3471.90	66.76	41.34	97.46	2.43	1.24	46.68	18.91	1.88	4.12	1.02	1.14	29.26	49.90	9.52	4.05	1.72
35	45 (M3)	13.48	12.73	3561.34	71.50	39.16	96.82	2.79	1.38	45.07	21.50	1.75	3.77	1.08	1.20	23.77	56.55	8.69	3.69	2.40
36	98	10.86	13.05	3328.07	70.06	41.45	97.41	3.10	1.49	42.31	29.16	1.39	3.12	0.94	1.15	30.85	48.99	11.75	3.54	1.61
37	98 (S)	12.26	10.06	2883.10	69.60	45.28	97.22	2.21	1.24	44.08	31.80	1.39	3.16	1.02	1.34	31.89	48.48	11.47	3.59	1.55
38	110	12.66	14.36	3974.48	70.04	50.84	98.75	2.76	1.35	46.02	29.83	1.27	3.26	1.00	1.29	32.50	47.71	11.73	3.02	1.52
39	110 (S)	17.52	18.58	5019.43	67.67	45.83	95.51	3.06	1.30	44.96	31.39	1.31	3.08	1.00	1.28	29.94	50.05	11.57	3.19	1.70
40	110(8)	9.44	11.20	3565.84	71.38	56.12	96.96	2.70	1.29	42.10	30.60	1.43	3.26	0.96	1.16	29.16	51.51	11.07	3.39	1.77

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
41	29-1	13.98	14.67	4068.20	70.10	45.67	98.02	2.41	1.40	44.04	30.41	1.36	3.33	1.03	1.31	33.09	46.51	11.93	3.10	1.41
42	78-1	9.28	9.53	2739.17	66.31	47.40	97.25	2.38	1.48	44.58	30.57	1.47	3.71	1.05	1.44	39.36	41.00	12.21	3.15	1.06
43	78-2	10.40	12.83	3589.76	65.95	48.61	98.74	2.94	1.53	42.85	28.33	1.37	3.31	0.90	1.11	35.22	44.78	11.91	3.53	1.30
44	104-9VL-1 type	9.53	16.34	4572.47	69.05	51.40	98.15	3.13	1.56	43.13	29.94	1.37	3.36	0.93	1.19	34.90	44.89	11.76	3.10	1.32
45	121- purple seeded	17.80	13.07	3742.59	71.61	31.17	97.41	2.04	1.23	44.61	19.69	1.80	4.06	1.03	1.16	30.66	49.43	9.53	3.76	1.65
46	139-1 Viriscent	10.17	17.79	5083.11	71.60	52.09	98.33	2.80	1.46	42.06	29.45	1.39	3.40	0.95	1.17	33.84	45.66	11.81	3.41	1.36
47	161- reticulated pods	12.24	10.26	2891.38	65.72	37.16	90.41	2.78	1.19	42.75	29.14	1.26	3.27	1.03	1.33	32.65	47.58	11.56	2.92	1.48
48	171-tan	11.89	19.18	5052.31	59.93	43.02	96.85	3.35	1.49	44.69	30.04	1.33	3.42	1.04	1.30	34.38	45.71	11.53	3.01	1.36
49	171-red	15.34	21.67	5814.25	63.43	35.25	91.98	2.83	1.39	49.85	20.96	1.05	3.39	1.12	1.48	40.19	40.75	12.14	2.14	1.03
50	VL-1 Dwarf	18.32	18.54	5277.04	69.70	40.21	97.99	3.03	1.30	46.57	30.56	1.36	3.35	1.02	1.28	32.54	47.97	11.27	3.16	1.50
51	Spanish Improved	22.53	20.95	6112.11	71.80	44.18	96.81	3.00	1.09	46.31	30.58	1.66	3.45	0.90	1.20	35.99	41.35	12.65	3.33	1.15
52	TG 2	17.00	7.96	2413.56	73.20	27.86	95.67	2.42	0.93	41.62	27.83	1.75	3.59	0.90	1.19	37.41	41.06	12.09	3.39	1.10
53	TGM 8	7.57	6.99	1895.53	59.52	46.34	95.00	3.39	1.22	45.52	25.53	1.32	2.68	0.97	1.31	25.54	56.09	11.23	2.58	2.32
54	TGM 16	14.57	13.70	3886.28	69.76	51.62	95.90	3.49	1.15	42.18	28.56	1.50	2.85	0.88	1.10	31.98	47.16	11.94	3.35	1.50
55	TGM 17	13.87	13.25	3925.54	68.74	55.86	98.18	3.37	1.34	42.45	29.30	1.52	3.22	0.89	1.16	34.09	44.14	12.18	3.28	1.30
56	TGM 19	13.63	13.66	4162.45	67.96	51.51	96.24	3.18	1.35	42.39	29.29	1.62	3.31	0.89	1.12	34.36	43.49	11.79	3.33	1.27
57	TGM 44	13.69	14.76	4330.21	66.15	51.86	97.62	3.40	1.33	42.25	17.94	1.26	2.57	1.15	1.37	32.87	48.62	11.29	1.61	1.51
58	TGM 46	13.00	11.43	3173.28	67.59	39.85	95.81	3.12	1.18	42.09	18.30	1.51	3.11	1.03	1.23	34.07	46.13	11.18	2.50	1.36

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
59	TGM 47	11.35	12.23	3551.89	67.38	54.40	98.40	3.61	1.40	39.86	18.43	1.27	2.50	1.13	1.31	33.31	47.79	11.13	1.74	1.44
60	TGM 49	13.52	14.13	4080.12	67.19	47.96	97.74	3.26	1.33	44.41	26.95	1.98	3.89	1.02	1.06	26.30	51.33	9.86	3.54	1.95
61	TGM 50	18.39	15.64	4555.10	70.73	34.68	98.07	2.89	1.13	45.02	25.91	2.19	4.16	0.91	1.13	42.00	34.73	12.54	4.51	0.85
62	TGM 51	9.26	7.72	2317.31	70.22	42.22	99.04	3.27	1.17	47.70	29.22	2.04	3.71	0.95	1.11	38.34	36.27	12.49	3.46	0.95
63	TGM 54	17.22	15.86	4720.77	65.89	51.23	97.97	3.59	1.30	37.81	29.53	1.94	3.53	0.97	1.18	32.12	45.10	10.30	3.73	1.41
64	TGM 20	17.70	7.72	2294.72	71.99	24.41	95.82	2.16	0.86	45.27	28.51	1.80	3.74	0.91	1.27	38.78	39.91	12.25	3.70	1.03
65	TGM 25	15.25	8.07	2384.89	72.07	30.12	96.91	2.37	1.01	43.17	30.62	1.86	3.56	0.88	1.22	33.17	44.84	11.72	3.50	1.39
66	TGM 101	9.81	5.31	1471.09	70.62	31.86	94.49	2.50	1.16	43.51	31.61	1.80	3.47	0.88	1.13	34.71	43.06	11.91	3.58	1.25
67	TGM 111	13.97	6.16	1838.40	64.75	31.34	94.20	2.53	1.01	42.59	30.40	1.87	3.42	0.78	1.06	34.01	45.42	11.59	3.97	1.37
68	TGM 112	13.87	12.07	3554.92	74.77	43.34	97.05	2.97	1.16	45.59	31.59	1.72	3.28	0.84	1.06	35.84	41.78	12.50	3.82	1.17
69	TGM 36	11.65	7.94	2345.92	68.20	39.77	95.98	2.95	1.15	43.68	29.98	1.75	3.34	0.78	1.02	36.79	41.72	12.27	4.08	1.13
70	TGM 37	14.50	11.76	3403.32	72.30	42.97	96.47	3.15	1.23	45.54	30.09	1.78	3.44	0.79	1.09	36.28	41.69	12.34	4.11	1.16
71	TGM 113	15.08	7.33	2172.33	65.82	28.22	93.09	2.72	1.05	44.33	32.33	2.22	3.74	0.82	1.19	43.43	34.44	13.65	3.44	0.85
72	TGM 117	17.14	18.40	5306.79	72.41	55.93	99.38	3.42	1.37	42.77	24.92	1.50	2.90	0.83	1.10	30.65	49.58	12.08	3.35	1.63
73	TGM 119	10.26	8.63	2501.19	66.22	51.02	94.62	3.49	1.38	43.15	29.53	1.71	3.30	0.82	1.11	31.97	46.24	12.09	3.55	1.47
74	TGM 136	11.70	11.39	3437.58	70.46	40.50	94.80	3.07	1.18	44.07	20.29	1.53	3.20	0.97	1.21	33.63	45.83	11.34	2.81	1.37
75	TGM 138	13.70	11.67	3459.07	74.00	44.13	96.92	3.04	1.17	45.97	19.37	1.66	3.32	1.08	1.33	34.03	45.45	10.90	2.39	1.34
76	TGM 165	14.60	8.08	2393.87	69.07	32.27	97.54	2.87	0.95	47.58	20.03	1.44	3.17	1.10	1.39	35.15	47.84	11.24	2.35	1.36
77	TGM 167	13.95	8.52	2585.78	75.24	33.73	98.57	2.50	1.10	45.79	18.20	1.45	3.04	1.07	1.46	29.38	54.14	10.25	2.47	1.85
78	TGM 178	17.70	12.05	3479.00	74.62	34.81	95.38	2.96	0.95	45.21	19.19	1.35	2.95	1.08	1.36	33.15	49.22	11.21	2.40	1.49
79	TGM 189	13.07	8.34	2518.47	74.84	38.67	98.39	2.93	1.08	46.20	18.56	1.24	2.86	1.08	1.43	32.60	50.58	11.31	2.17	1.55
80	TGM 193	19.99	12.94	3814.65	75.65	36.83	98.02	2.89	1.13	48.31	18.88	1.38	3.04	1.07	1.36	33.52	48.80	11.08	2.35	1.47

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Sl. No.	Genotype /trait	NPPP	PYPP	PY	SP	TW	SMKW	PL	PW	OIL	PROT	ARA	BEH	ECO	LIG	LIN	OLE	PAL	STE	O/L
81	TGM 196	12.70	6.93	1999.86	76.52	36.57	97.37	2.55	1.11	46.10	18.52	1.47	3.09	1.03	1.37	32.00	51.00	10.53	2.50	1.62
82	TGM 198	21.71	18.53	5434.43	70.36	37.35	98.51	2.86	1.12	46.91	16.55	1.20	3.09	1.01	1.40	37.80	42.83	12.24	2.18	1.14
83	TGM 213	16.77	14.53	4261.29	71.98	49.61	98.36	3.02	1.08	45.86	32.44	1.64	3.47	0.84	1.14	38.57	39.03	12.87	3.64	1.02
84	TGM 214	19.22	13.47	3656.51	68.04	34.43	97.73	3.20	1.15	45.55	18.98	1.17	2.98	1.04	1.40	35.25	46.17	11.94	2.13	1.31
85	TGM 215	17.24	9.34	2821.85	71.75	38.10	94.94	3.18	1.11	47.54	20.75	1.26	2.91	1.11	1.44	31.07	51.62	11.12	1.92	1.68
86	TGM 218	15.17	9.57	2855.62	72.66	36.54	96.61	2.87	1.01	47.78	18.44	1.44	3.05	1.03	1.33	35.69	46.23	11.43	2.45	1.30
87	TGM 219	18.13	11.60	3316.88	70.63	52.53	93.93	3.68	1.38	43.39	28.39	1.43	2.83	0.98	1.24	27.24	52.93	11.45	2.85	2.06
88	TGM 220	11.88	10.55	2989.62	67.62	49.45	96.81	3.40	1.25	37.44	32.31	1.79	3.30	1.05	1.26	25.62	54.89	9.19	3.30	2.18
89	TGM 221	17.49	11.01	3248.19	70.43	47.39	99.04	2.85	1.22	45.89	30.43	1.55	3.36	0.95	1.26	32.17	46.83	11.98	3.44	1.47
90	TGM 223	14.02	9.93	2933.26	68.12	37.72	95.92	3.31	1.18	41.84	31.64	1.96	3.97	0.91	1.17	35.70	41.01	10.74	3.90	1.18
91	TGM 225	10.83	9.59	2603.60	72.53	46.87	96.92	2.89	1.23	43.96	29.48	1.62	3.45	0.89	1.16	35.10	42.52	12.16	3.55	1.22
92	TAG 24	18.28	14.44	4242.76	73.06	39.89	97.36	2.68	1.13	45.21	30.69	1.74	3.51	0.86	1.15	35.06	42.50	12.22	3.76	1.24
93	TG 16	12.72	9.33	2790.40	66.59	51.77	98.50	3.70	1.33	43.84	28.47	1.53	3.23	0.89	1.20	31.84	45.83	12.33	3.31	1.48
94	SOMNATH	13.38	12.32	3544.47	71.85	52.58	97.17	3.70	1.36	41.10	25.06	1.52	3.00	0.86	1.09	29.16	50.59	11.45	3.68	1.76
95	TG 18 A	12.36	14.19	4078.10	66.36	48.06	97.96	3.43	1.35	44.63	30.49	1.51	3.24	0.88	1.15	33.62	43.88	12.55	3.59	1.33
96	TG 9	14.76	10.57	3154.63	65.60	44.47	96.77	2.98	1.31	45.14	26.00	1.57	3.38	0.89	1.21	33.67	44.01	12.20	3.32	1.32
97	TG 66	13.92	8.31	2404.99	74.09	34.73	96.20	2.77	1.01	46.72	20.33	1.45	3.24	0.97	1.29	34.96	46.98	11.22	2.68	1.36
98	TMV 10	14.43	12.63	3743.24	68.19	45.55	97.94	3.04	1.39	44.51	21.14	1.32	2.60	1.15	1.34	23.98	60.59	9.81	2.29	2.57

NPPP: Number of pods per plant, **PYPP**: Pod yield per plant, **PY**: Pod yield, **SP**: Shelling percentage, **TW**: Test weight, **SMKW**: Sound mature kernel weight, **PL**: Pod length, **PW**: Pod width, **OIL:** Oil content, **PROT:** Protein content, **ARA:** Arachidic acid, **BEH:** Behenic acid, **ECO:** Eicosanoic acid, **LIG:** Lignoseric acid, **LIN:** Linoleic acid, **OLE:** Oleic acid, **PAL:** Palmitic acid, **STE:** Stearic acid and **O/L**: Oleic to linoleic acid ratio

Appendix VIII: AhTE primers used for genotyping the mutant population

Sl. No.	Marker	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)
1	AhTE0012	GTTTCCTGCATGCGGTATCT	TTGCTTGGGATCTGCTTTCT
2	AhTE0029	GGTAAAATGTTTTTATTCGTTTGG	TTGCTTGCGACTAAGCATCA
3	AhTE0060	GGGTGTTATGCTGCATGGTT	TCAGCTCAAATCGTGGAATG
4	AhTE0159	CGCCATGACCACCTCTAAGT	GCAAAGAAATGCCTGCAAAC
5	AhTE0180	GAAAGAATCCGTGGGATATTCA	TTCACAATGAAAGAGGAGAATCAA
6	AhTE0181	GAAAGTACGCCATGTTGTGGTA	TTTAAGTCGAGTTTTCCGCTAA
7	AhTE0190	AAATTTATCTGTTTCGATCGAGTG	TCGAACCGACTCTGGTTTTAAT
8	AhTE0202	GAGAGCGGTAATTTTTATGATTTG	TACTTTTGCGACTTTGTCTCCA
9	AhTE0205	TTCATTTCCATCTGTCTCATGC	TCGTCTCCTCTAAGGTTTGCTT
10	AhTE0227	CAAACAGTTATCCACGTGCTGT	CAACTCATGCAGCGCTAACTAC
11	AhTE0248	CAGCCTTAACCCTAGCACTTTTT	TTAGAATTGTAGGTGGTGGGTTG
12	AhTE0268	GAAGGCCTATCTCATTTTGTTTG	CGCCGTTACCTAGGTTTTAGAAT
13	AhTE0333	TTGTGCTTTTGGGATGTTCA	ATGTCGGTAATTGATTCGGC
14	AhTE0343	CGATCGCTACTTGCTACCAC	GGACATCAATCAAGAGGCGT
15	AhTE0360	GGATATGATGCCCATAGCTGA	TGCTGACTACTTGCAATGCC
16	AhTE0361	TTGGAGTTTATCTCAAACTCTGAAG	CCGGTAGTCCGGTAAATTAAA
17	AhTE0372	GCAATTTGGCATAGCCTCTC	CGTATTGACAAGGGTTCCGT
18	AhTE0378	ATTCAACTAGGCTCGCCATT	GCATGGTTCGGTAGATTTGG
19	AhTE0398	TCAGCCCAACAGAATACACAA	GGACTTTGTTGGGGTGGTAG
20	AhTE0417	CGAACGCACGACAATTCTAA	TGATTGCGCTACAAGAATCG
21	AhTE0422	TGGCGTAATCTTTTAAGAACCAA	AGAATTAATGTCATCAAACGAATG
22	AhTE0426	CAACCCATGATTTGTGAATTAAG	TGACTACAATGTTTGGTCATTTTG
23	AhTE0429	ACGAGGTATATGCGTCAGGG	GGAGCTAATACATACTACAACTCCACC
24	AhTE0442	TTGTCTTTTTCCCCTCCCTT	AAAGATGGTCAATGATTCTTTTGTT
25	AhTE0445	ACACTGCTCGCAGTTTGAGA	AAAGCAGGTGATTAGTGTTACCTT
26	AhTE0446	GTGCCACGAGGTACACGATA	AGACACACACCACACGCATT
27	AhTE0459	CATCCGATTCCTTCTTGCAT	TGGAGGACCTTTTTCATTGC
28	AhTE0467	AGGTTCCCGTTGAATGAAAT	TTCGCGAGCGTAAGGTTAGT
29	AhTE0489	TGACTACAATGTTTGGTCATTTTG	GAACCACCCATGATTTGTGA
30	AhTE0504	CTTCACAAGTCCAACGCAGA	TTCCACGAAGGTTCATTTCA
31	AhTE0547	TTTGAGTGTTTAGATGACAAATTGC	CCAACCTTACCCAGACATTCA

(The remaining 79 AhTE markers have been listed in Appendix IV [Sl No. 1 to 79])

ANALYSIS OF TAXONOMIC, AGRONOMIC, PRODUCTIVITY AND NUTRITIONAL TRAITS, AND RESISTANCE TO FOLIAR DISEASES FOR THEIR ASSOCIATION WITH TE MARKERS IN GROUNDNUT

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ABSTRACT

An attempt was made to identify the marker-trait associations for taxonomic, agronomic, productivity, resistance to foliar diseases and nutritional traits in groundnut using AhTE marker data and two season (*kharif*-2014 and 2015) phenotypic data generated at IABT garden at UAS Dharwad using 432 RILs derived from a biparental cross (TMV 2 × TMV 2-NLM) and 98 independent mutants.

Though the RAD-Sequencing data showed very high genome similarity between TMV 2 and TMV 2-NLM in terms of SNPs and CNVs, they differed significantly for taxonomic, agronomic, and productivity traits. A genetic linkage map of 1,205.66 cM was constructed from the RILs using 91 markers. Single marker analysis detected major markers for 18 traits across the years. AhTE0357, AhTE0391 and AhTE0523 were associated with days to 50 per cent flowering, oleic acid, and eicosenoic acid, respectively. QTL analysis detected seven major QTL regions for 22 traits across the years. The QTL AhTE0357-AhTE0050 governed days to 50 per cent flowering (R^2 22.0 %) while AhTE0391-AhTE0572 governed oleic acid (R^2 15.1 %). Two genic markers (AhTE0357 and AhTE0391) with *AhMITE1* activity in the genes *Araip.TG1BL* (B02 chromosome) and *Aradu.7N61X* (A09 chromosome) respectively showed strong linkage with taxonomic, agronomic and nutritional traits.

Using the mutant population, 132 highly significant marker-trait associations (MTAs) represented by 58 AhTE markers were identified for 39 traits. Nutritional traits recorded the highest number of MTAs (38), followed by agronomic (35), productivity (31), foliar disease resistance (23) and taxonomic traits (5). AhTE0050 showed strong association with the number of primary branches in both the RIL and mutant population, indicating the scope of its application in selections. The AhTE markers linked/associated with the important traits could help in gene discovery and functional analysis. Thirty one superior RILs (15) and mutants (16) identified in this study could be developed into new commercial varieties.