

**Genetics of Drought Tolerance in bread wheat**  
**(*Triticum aestivum* L.)**

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**Genetics of Drought Tolerance in bread wheat  
(*Triticum aestivum* L.)**

By

**G. TRINADH KUMAR**

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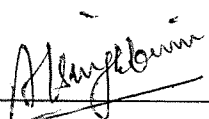
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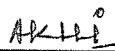
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I further certify that such help or information, as have been availed during the course of the investigation have been duly acknowledged.

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## LIST OF ABBREVIATIONS

|          |                                       |
|----------|---------------------------------------|
| 1. ABA   | Absciscic Acid                        |
| 2. ELWRC | Excised Leaf Water Retention Capacity |
| 3. EMSS  | Error Mean Sum of Squares             |
| 4. GCV   | Genotypic Coefficient of Variation    |
| 5. HI    | Harvest Index                         |
| 6. MSS   | Mean Sum of Squares                   |
| 7. PCV   | Phenotypic Coefficient of Variation   |
| 8. PEG   | Poly Ethylene Glycol                  |
| 9. RWC   | Relative Leaf Water Content           |
| 10. RWL  | Relative Water Loss                   |
| 11. SDS  | Sodium Dodesile Sulphate              |
| 12. WP   | Water potential                       |

# CHAPTER I

## INTRODUCTION

Wheat is the most widely cultivated cereal crop in the world and second most important cereal in the Indian subcontinent. The world food production is limited largely by environmental stresses. Yet a sufficient quantity of wheat comes from the area that is affected by stresses of various kinds. Dudal (1976) estimated that only ten per cent of the world's arable land may be categorized as free of stress, about twenty per cent of the land is under some kind of mineral stress, 26 per cent is affected by drought and 15 per cent by cold stress. Thus, various kinds of stresses cause significant reduction to wheat production. In India wheat is generally grown during October to April and the crop duration ranges from 90 to 155 days from the date of planting. The crop also experiences drought as well as high temperatures during germination and grain development. In whatsoever diverse agro-ecological condition wheat is cultivated, it has played a vital role in stabilizing the food grain production in the country over the past few decades. Only a meager share of total production has come from drought affected areas, where water is the major constraint. In India, wheat crop occupies an area of 25.5 m. ha (Anonymous 2002) of which less than 20 per cent is under some kind of stress particularly moisture stress (rainfed areas). The great fluctuations in production observed during the last five years are accounted for prevailing drought conditions as India produced less than 72 m. t of wheat in 2001-02 as compared to 76.4 m. t in 1999-2000.

Large area under wheat cultivation is continuously affected both by biotic and abiotic stresses. Biotic stresses have been managed to a greater extent by regularly

releasing the disease resistant cultivars. Whereas, large gaps in production are experienced under abiotic stress situations particularly due to moisture stress and terminal heat stress. Also progress in developing cultivars tolerant to abiotic stresses has been slow because of lack of knowledge of mechanism of tolerance, poor understanding of inheritance of tolerance, low heritability and lack of efficient techniques for screening the germplasm and breeding materials.

Soil moisture is the major limiting factor in dry farming and dryland farming areas. Development of cultivars tolerant to abiotic stresses like drought tolerance is one of the main objectives in breeding programmes of many crops. Moisture stress indicates either the lack or excess of water available for any plant. But the term moisture stress is generally used for deficit moisture conditions. Before attempting breeding programmes on development of stress tolerant cultivars, understanding of the biological mechanisms underlying and the genetic control of such mechanisms is essential. Moisture stress does not affect all aspects of plant growth and development equally. Some processes are highly affected while others are far less affected. The biological yield of the crop is the integrated result of the effects of stress on the various physiological and metabolic processes of the plant like water relations, photosynthesis, respiration, nutrition, growth and development (Rao and Ramamurthy, 1981).

Abiotic stresses are continuously challenging the efforts of scientists working on crop improvement. Large areas in Rajasthan, Madhya Pradesh, Gujarat, Maharashtra, Karnataka and Andhra Pradesh are experiencing severe drought conditions during crop season periodically. To a plant breeder drought tolerance is the ability of one genotype to be more productive with a given amount of soil moisture than other (Quizenberry, 1982).

In other words, drought is shortage of water causing limitation in expression of genetic and economic potential of genotypes. Drought varies in intensity, dimension and time making it a location specific phenomenon. Rainfed wheat is generally grown on stressed soil moisture and often experiences water deficit and high temperature stress during grain development. Voluminous work has been done to develop suitable selection criteria for the development of genotypes tolerant to abiotic stresses. However, selection for moisture stress tolerance in breeding programmes has been impeded by lack of appropriate selection strategies and simple screening techniques. Johnson (1980) suggested that a good screening technique should be rapid, capable of evaluating plant performance at the critical developmental stages, use only small sample and also capable of screening large populations. But the knowledge of seedling screening techniques is meager and also limited by the problems in standardizing the technique of seedling screening under field conditions. One of the important methods of identifying and characterizing drought resistance genotypes is to establish stability in yield, biomass, yield components and other traits through long-term field experiments at the same site or multilocations (Sinha *et al.*, 1986, 1990). Drought resistance could be evaluated as yield stability under the given environment. Drought tolerance could also be defined as the mechanism causing minimum loss in yield in water deficit environment relative to the maximum yield in water constraint free management of the crop.

Several methods have been used and criteria are set to screen the germplasm for drought tolerance such as membrane stability, ion leakage, relative water content (RWC), excised leaf water retention capacity (ELWRC), water potential (WP), chlorophyll index, root shoot ratio, canopy temperature, accumulation of proline and abscisic acid (ABA),

leaf rolling *etc* by various workers. Sinclair and Ludlow (1985) and Scholfield (1988) proposed leaf relative water content as important selection criterion for drought tolerance than other water potential parameters. In 1992, Clarke proposed rate of water loss from excised leaves as a useful criterion for screening wheat genotypes for adoption to dry growing seasons.

Among the various methods of inducing water stress, withholding water and the use of polyethylene glycol (PEG) are found to be efficient. However, Strauss and Agenbag (1998) suggested that the withholding of water is more appropriate due to the possibility of root injury with PEG application. Any screening technique that can be adopted in seedling stage and also on single plant basis will be of great importance to the breeders. Among various traits RWC and ELWRC were reported to be of effective selection criteria for drought tolerance. However, very little work has been done to understand the genetic control of these traits. More systematic studies are warranted to understand the genetics of these traits so that appropriate breeding strategies can be adopted for the crop improvement.

Grain yield in wheat, as in any other crop, is a complex character and is greatly influenced by environmental factors apart from the genetical factors (Grafius, 1959). Arnon (1980) stated that breeding for drought resistance has been a consistent theme of breeding programme but the efforts put in the whole field of breeding have not resulted into significant progress. As against the breeding for biotic stresses, particularly breeding for rust resistance in India, stress breeding has yielded hardly any tangible results. Unlike the identification of specific genes for specific races of rust, it has not been possible to identify any specific gene(s) for drought resistance, except that certain processes such as

osmoregulation or some morphological traits such as tillering, early growth habit (Asana, 1968) *etc.* provide advantage to adaptation to drought. Therefore, adequate knowledge of inter-relationship of factors influencing such complex traits is essential for designing an effective plant breeding programme. Studies on correlation of agronomic and morphophysiological characters are helpful in the investigation of such complex traits. Kheiralla (1994) reported reduction in spike length, 1000-grain weight, and grain yield by 12.47, 8.45 and 40.00 per cent under moisture stress conditions and also showed high significant correlation between grain yield and drought susceptibility index. Similarly, Malik and Wright (1995) studied the inheritance of four physiological traits (net photosynthesis, RWC, WUE and excised leaf water loss) and their correlation with agronomic traits under moisture stress conditions. Generation means and variance analyses of the data suggested simple inheritance of the traits.

For developing superior cultivars that exhibit a great degree of tolerance to abiotic stress particularly moisture stress, it is imperative that the nature of the stress conditions, is defined and diverse range of germplasm needs to be tested for suitable response to stress.

It is also important to analyze and understand the genetic basis of drought tolerance to develop suitable selection criterion for the development of cultivars tolerant to stresses. Keeping these factors in mind, present investigation was carried out with the following objectives:

1. To standardize the technique of screening for seedling survivability under moisture stress.

2. To assess the genetic variability in wheat germplasm to moisture stress with respect to various morpho-physiological and yield characters associated with drought tolerance.
3. To study the correlation between different characters related to drought tolerance.
4. Genetic analysis of morpho-physiological characters, yield and yield components under moisture stress conditions.

## CHAPTER II

# REVIEW OF LITERATURE

Drought tolerance according to Quizenberry (1982), to a plant breeder is the ability of one genotype to be more productive with a given amount of soil moisture than other. For the development of drought tolerant genotypes through crop breeding, suitable screening techniques and the knowledge of the genetic mechanism of tolerance are essential. Johnson (1980) suggested that a good screening technique should be rapid, capable of evaluating plant performance at the critical developmental stages, use only small sample and also capable of screening large populations. The major aspects of the present investigation include

1. Techniques of screening wheat genotypes under moisture stress.
2. To assess the genetic variability in wheat germplasm in relation to drought tolerance.
3. Correlation studies.
4. Genetic analysis of various characters under moisture stress.

The available literature relevant to these aspects was reviewed here under.

### 2.1 SCREENING TECHNIQUES

Sinclair and Ludlow (1985) proposed relative leaf water content (RWC) as more important criteria for selecting drought tolerance than other water potential parameters in wheat.

Winter *et al.*, (1988) conducted several greenhouse and field screening techniques to evaluate the efficiency of various strategies to differentiate drought resistance in five wheat cultivars and concluded that seedling survival after desiccation as the most suitable technique for screening genotypes.

Schonfeld *et al.*, (1988) suggested relative leaf water content as promising selection criterion for drought tolerance in winter wheat compared to water potential, solute potential and turgor pressure and reported high heritability of 64 per cent for the trait relative leaf water content under moisture stress.

An experiment to find out the selection criteria for drought tolerance was conducted by Deshmukh *et al.*, (1991). They reported that ion leakage, drought susceptibility index (DSI) and per cent reduction of RWC in leaves were higher in drought susceptible cultivars as compared to drought tolerant cultivars. Ion leakage was found to be positively correlated with percent reduction in RWC. It was suggested that ion leakage could be used as a selection parameter for screening of drought tolerance in wheat.

The leaf water retention capacity is one of the most important physiological trait in drought tolerant genotypes (Clarke and Mc Caig, 1982) but the trait is characterized by quantitative inheritance, which predominantly controlled by additive genes (Schonfeld *et al.*, 1988). Ritchie *et al.*, (1990) reported that RWC is highly suitable and, therefore, amenable to the selection in moisture stress environments than the traits like 1000 grain weight, number of grains and number of tillers per plant.

Clarke (1992) proposed rate of water loss from excised leaves as a useful criteria for screening wheat genotypes for adaptation to dry growing seasons. Also showed that

RWC screening of phenologically diverse genotypes is possible with low risk of genotypes growth stage interactions, provided that sampling is completed before any genotype reach the heading stage.

Dhanda and Sethi (1998) worked out the effectiveness of excised leaf water loss and RWC as screening tools under moisture stress in combination with growth stage. They found that selection for RWC is more efficient at anthesis time. Golestani Araghi and Assad (1998) evaluated the efficiency of four different criteria consisting of canopy temperature, stomatal resistance, transpiring area and rate of water loss by excised leaves, under optimum and moisture stress conditions. Ultimately canopy temperature, stomatal resistance and rate of water loss were recognized as beneficial drought resistance indicators.

El Hafid *et al.*, (1998) studied the early season drought tolerance and reported that high leaf area index under stress and high tiller survival rate are associated with early season drought resistance. Malik and Aieright (1998) conducted field and pot culture experiments under drought stress to evaluate leaf water potential, osmotic adjustment, relative leaf water content, excised leaf water loss and seedling survival as breeding criteria in spring wheat. The response of the genotypes for the traits at 3<sup>rd</sup> leaf stage and flag leaf stage was similar and hence it is suggested that screening for drought tolerance may be done at seedling stage effectively.

Singh *et al.*, (1999) reported seedling screening for drought tolerance using mortality under stress as criterion and also showed close correspondence between drought tolerance in seedling stage and reproductive stage.

Nagarajan and Rane (2000) studied seedling characters in sand culture under five different moisture regimes. Thirty days after seeding, germination percentage, coleoptile length, longest root length, leaf area, root dry weight, seedling dry weight and total root length were quantified and reported that quantifying early vigour in terms of seedling characters accurately in sand culture can be used for early generation selection of drought tolerant lines.

## **2.2 GENETIC VARIABILITY STUDIES**

A first hand information on the nature and extent of variability in bread wheat genotypes in general and under moisture stress conditions in particular, is essential to understand and develop strategies for the improvement of cultivars. Very few cultivars developed for drought tolerance are performing well under the field conditions. Besides this, much less work has been done to understand the contribution of component characters towards the grain yield under moisture stress. A summary of the literature in this direction is reviewed here.

Chaudhary *et al.*, (1984) evaluated 28 genotypes and found wide variability for weight and volume of seed whereas, less variability existed for kernel density. They suggested selection for longer coleoptile in semi dwarf wheat for moisture stress tolerance.

Tomar *et al.*, (1987) reported existence of wide variability for seed and seedling characters by evaluating ten different characters. Takawale *et al.*, (1989) screened 50 wheat genotypes for the existence of variability. Among 8 different characters studied plant height, spike length and number of productive tillers per plant showed variation.

Plant height, number of grains per panicle and days to 50 per cent flowering were found to have high heritability and high genetic advance.

Yadav *et al.*, (1992) reported high GCV, heritability and genetic advance for traits grain yield per plant, 100- grain weight and number of tillers per plant. Similarly high GCV and PCV for plant height, number of grains/ear and grain yield/plant were reported by Bahadur *et al.*, (1995).

Empilli *et al.*, (1995) evaluated 1344 genotypes of wheat for 17 different characters and showed wide variation for characters heading date, plant height, 1000-grain weight and SDS sedimentation value.

Deswal *et al.*, (1996) reported high heritability and genetic advance for 1000-grain weight, biomass per tiller, number of grains per spike and grain yield per spike in bread wheat. Shimpiger *et al.*, (1996) evaluated 324 wheat genotypes and reported that biological yield per m<sup>2</sup> and harvest index had moderate variability, heritability and genetic advance, whereas number of productive tillers and grain yield has shown high degree of variability and heritability.

Krishnawat and Sharma (1998) reported genetic variability for 11 agronomic and yield characters under both irrigated and drought stress conditions in wheat. GCV and PCV were high for flag leaf area, weight of grains/spike and were moderate for spike length, grain yield/plant and peduncle length.

Farshadfar *et al.*, (2001) reported genetic variation for yield potential, stressed yield, ELWL, RWL, RWC and harvest index under moisture stress conditions and reported high heterosis and heterobeltiosis in the F<sub>1</sub> hybrids for stressed yield, harvest index and spike yield index.

Nagarajan and Rane (2000) reported high genetic variability in different moisture regimes studied for the characters root dry weight, seedling dry weight and total root length. A positive association was observed between these seedling values and known drought tolerance of the genotypes tested.

Bchini *et al.*, (2002) evaluated 16 durum wheat varieties under irrigated and rainfed conditions and showed great genetic variability of root characteristics like length of primary root and thickness of root and above ground parameters.

## **2.3 GENETIC DIVERSITY AND ITS ASSESSMENT**

Identification of promising genotypes with good agronomic base and desired traits of grain yield components besides having resistance to abiotic and biotic stresses is the primary requirement of an effective plant breeding programme. Evaluation of germplasm of a particular crop species collected from different sources helps to increase the availability of a proven broad genetic base. During past ten years, several researchers evaluated wheat genotypes from diverse germplasm of different geographic origins. This lead to a vast repository of genetic diversity for yield and its components traits (Srivastava *et al.*, 1987; Thete *et al.*, 1987; Garg and Gautam, 1988; Singh and Chatrath, 1993). The plant height, days to flowering, flag leaf area, panicle length, number of grains/ear, grain weight/ear, number of productive tillers, 1000- grain weight were some of the important traits contributing to total divergence and served as selection parameters in breeding programmes.

In published literature, there are several methods utilized for the assessment of genetic diversity and grouping of genotypes. The more popularly used ones are:

I. Coefficient of racial likeness (Pearson, 1926)

2. Principal component analysis (Hotelling, 1933)
3. Discriminant Function analysis (Fisher, 1936)
4.  $D^2$  -analysis (Mahalanobis, 1936)
5. Canonical analysis (Rao, 1952)
6. Metroglyph analysis (Anderson, 1957)
7. Sokal's distance (Sokal, 1961)
8. Edward and Cavalli -Sforza's method for cluster analysis (Edward and Cavalli -Sforza, 1965)

Bhatt (1970) suggested the use of multivariate analysis (Mahalanobis  $D^2$  -statistic) on quantitative traits for selecting parents for hybridization in wheat. Forty genotypes of wheat (*Triticum aestivum*) originating from different eco-geographic regions of Australia were grouped into 12 constellations. Bhatt (1973) demonstrated experimentally that the  $D^2$  statistic was more effective in improving yields than selection based on eco-geographic diversity. Bhatt (1976) showed that clustering pattern based on  $D^2$  analysis was stable in four different environments.

Chandra (1977) studied genetic divergence of 57 linseed varieties using Mahalanobis' statistical distance ( $D^2$ ) and metroglyph. They suggested that the metroglyph technique would be suitable for preliminary grouping prior to undertaking  $D^2$  analysis.

Jain *et al.* (1978) assessed genetic divergence in wheat using quantitative traits. However, the distinct complexes were not obtained and the position of strains changed with the change in traits on X and Y axes while plotting glyphs. Mahalanobis  $D^2$  statistic classified the same strains in 13 clusters. The canonical analysis confirmed the clustering pattern determined by  $D^2$  statistic.

Joshi *et al.*, (1979) used Mahalanobis  $D^2$  statistic to study the genetic divergence among nine tetraploid *Triticum* species, each represented by a variety with diagnostic features of that particular species and supported the revised classification of these nine species into two main species

Thete *et al.*, (1987) studied genetic diversity for grain yield and its components in wheat. On the basis of  $D^2$  analysis of data for eight yield components, 50 diverse wheat varieties were grouped into 11 clusters. Clustering patterns were not correlated with geographical distribution.

Kuruvadi (1988) studied genetic divergence among 14 varieties of wheat for 10 yield related characters and grouped them into eight distinct clusters using Mahalanobis  $D^2$  statistic. Analysis of variance revealed considerable variation among the varieties for all 10 characters. The traits contributing most to the divergence were days to flowering, flag leaf area, panicle length and 1000- grain weight.

Satyan *et al.*, (1991) applied metro glyph and canonical analysis to assess the genetic divergence in 121 genotypes of green gram. Metroglyph analysis broadly classified the genotypes into 9 groups. The first canonical root accounted for 99.97 per cent of the total variation and hence, they were able to discriminate the genotypes in a two dimensional graph (Z1-Z2).

Jag-Shoran *et al.*, (1992) derived information on genetic divergence from data on six yield components in 10 winter and 10 spring wheat varieties grown under high fertility/irrigated (E1) and low fertility/rainfed (E2) environments. Based on  $D^2$  analysis, the varieties were grouped into eight and nine clusters for the E1 and E2 environments respectively.

Jagadev (1993) grouped 22 bread wheat genotypes grown under barani condition into seven clusters based on  $D^2$  analysis of nine yield component traits. The characters contributing most to the genetic divergence were 1000-grain weight, days to maturity and grain yield.

Singh (1994) studied 12 yield component traits and five morphological traits in 90 durum wheat genotypes. The genotypes were grouped into seven clusters and had a high level of genetic divergence that was not related to geographical origin. Chaturvedi and Gupta (1995) grouped 44 genotypes of wheat into 13 clusters by analyzing 12 yield component characters. Intra-cluster distances ranged between 0.00 to 36.93 and comparison of cluster means indicated considerable genetic divergence between the groups.

Gupta *et al.*, (1996) assessed the genetic divergence in 51 genotypes of spring wheat by  $D^2$  analysis. Tocher's method grouped the genotypes into 9 and 10 clusters depending on the Tocher's value used (500 and 300, respectively). Protein content, phenol colour reaction and peduncle length contributed towards maximum genetic divergence.

Patil and Bhavsar (1997) evaluated twenty five *Triticum aestivum* and eleven *T. durum* genotypes for five quantitative characters and grouped them into six clusters based on  $D^2$  values. There was no association between clustering pattern and eco-geographical distribution of the genotypes.

Singh and Singh (1998) grouped 23 wheat genotypes into three clusters based on yield components. Number of grains/ear, plant height, days to heading and flag leaf length had high relative contribution to  $D^2$  values.

Deshmukh *et al.*, (1999) analyzed 30 wheat genotypes using  $D^2$  statistic for yield and nine yield component characters. Genotypes were grouped into eight clusters, with the greatest intercluster distance (6.789) being between clusters IV and V. Vishal-Suri *et al.*, (1999) investigated 200 wheat genotypes and grouped them into sixteen clusters using Mahalanobis  $D^2$  statistic, based on eight morphological characters. Grain yield and tiller number were major contributors towards genetic divergence.

Bergale *et al.*, (2001) observed high phenotypic and genotypic coefficients of variation for number of spikes per plant, grain yield per plant, plant height, flag leaf area, and 1000-grain weight. The genotypes were grouped into 11 clusters based on  $D^2$  analysis. Cluster means revealed that plant height had the highest contribution to genetic divergence.

## 2.4 CORRELATION STUDIES

Grain yield in wheat as in other crops is a complex character and is greatly influenced by environmental factors (Grafius,1959). Adequate knowledge of inter-relationship of factors influencing such complex traits, especially under abiotic stress conditions like moisture stress, is essential for designing an effective plant breeding programme. Studies on correlation of agronomic and morpho-physiological characters are helpful in the investigation of the complex characters such as yield. Various studies have been conducted by several workers in relation to the correlation of various attributes to the yield and the literature regarding these studies is cited below:

Jaradat and Konzak (1983) showed that grain yield average over four moisture regimes were significantly correlated with excised leaf water retention capacity and stomatal and cuticular vapour transport resistance.

Sheoran *et al.*, (1986) showed that yield was significantly and positively correlated with spike length, grains/spike, plant height and flag leaf area but negatively correlated with canopy temperature under moisture stress.

Pathak *et al.*, (1986) through correlation studies on wheat under high temperature and moisture stress conditions revealed that grain yield per plant had strong and highly significant positive correlations with grain weight/ear (0.882), plant height (0.740) and ear length (0.614) showing the importance of grain weight/ear and suggesting that an increase in trait may considerably increase the plant yield under stress condition.

Studies on macaroni wheat population by Bangarwa *et al.*, (1987) revealed that five attributes, namely, spikes/plant, plant height, number of spikelets/spike, Spike length and biological yield/plant showed high and positive association with grain yield per plant. Positive correlations were also observed among component traits.

Ehdaie *et al.*, (1989) showed that days to booting, to heading and to anthesis were positively correlated but none of them was significantly associated with days to maturity. The genetic correlation between number of earheads/plant and number of grains/head, 1000-grain weight and harvest index was significantly negative. Harvest index had a negative genetic correlation with days to booting, days to maturity, plant height, number of earheads/plant and straw yield and a positive correlation with number of grains/head, 1000-grain weight and grain yield.

Ehdaie and Waines (1989) showed that plant height was negatively associated with number of grains/head, 1000-grain weight, grain yield and harvest index. Pawar *et al.*, (1990) reported that the phenotypic and genotypic correlations among grain yield and its components in F<sub>4</sub> progenies of wheat crosses, namely, WL 711 X HD 2122 and HD 2122 X Sonalika showed higher genotypic correlation coefficients in magnitude than the phenotypic correlations for almost all the traits in both the crosses. This indicated that the associations between these traits were genotypically inherited. It was also reported that yield was positively and significantly associated with tiller number/plant, number of grains/ear and 1000-grain weight.

Tahara *et al.*, (1990) observed a positive relation between grain yield and RWC measured during anthesis and mid-grain filling, as the high yield selections maintained a significantly higher RWC than the low yield selections.

Chowdhury and Mandal (1991) found positive phenotypic correlation between spikelets/spike, tillers per plant and ear length and yield for three different soil conditions. Deotale *et al.*, (1991) reported a negative correlation ( $r = -0.896$ ) between plant height and yield while a positive correlation between dry matter production ( $r = 0.945$ ), leaf chlorophyll content ( $r = 0.873$ ) and leaf nitrogen content ( $r = 0.982$ ). Dry matter accumulation was positively correlated with chlorophyll content ( $r = 0.934$ ) and leaf N content ( $r = 0.972$ ).

Nachit *et al.*, (1991) evaluated 210 advanced (*Triticum durum*) lines and found that under dry conditions, yield was highly correlated with earliness, leaf rolling mechanism, fertile tillering ability, panicle length and number of spikelets/spike.

Yang *et al.*, (1991) evaluated 3430 world collections of durum wheat for 19 characters under severe moisture stress fields. The rate of excised leaf water loss was used as indicator of drought tolerance, which showed a significant association with plant height, chlorotic leaf spots, days to flowering and days to maturity.

Simple correlation studies by Quayyum *et al.*, (1991) showed that plant height had highly significant and positive association with number of kernels per spike showing that taller plants produced greater number of kernels per spike. The correlations between plant height and weight of kernels per spike and yield per plant were positive and significant which showed that plant height could be used as selection criterion. It was also noted that number of tillers/plant, number of spikelets/spike and spike length had no association with plant height. On the contrary, Bahadur *et al.*, (1993) showed that grain yield was negatively associated with plant height at genotypic level, while the association between these two traits was negligible and positive at phenotypic level which indicated that medium dwarf plant type was desirable in wheat which is well proved by the fact that cultivars with medium height and good tillering are higher yielding than tall types.

Khattak *et al.*, (1992) observed significant variations in chlorophyll and carotenoid contents among five cultivars of wheat. Grain weight and grain yield per unit area were positively correlated to chlorophyll-a, total chlorophyll and carotenoid contents. They also found positive correlations among the pigments and suggested the exploitation of variability in the content of photosynthetic pigments to increase wheat production per unit area.

Bishnoi *et al.*, (1993) studied phenotypic correlation coefficients among nine characters and revealed that tiller number exhibited highly significant positive correlation

with biological yield (0.641) and grain yield (0.436). Spike length also showed high significant positive association with spikelets/spike (0.595) and number of grains/spike (0.384). Highly significant positive association was depicted between biological yield and grain yield (0.774).

Mohan *et al.*, (1993) reported through correlation studies that grain yield was positively correlated with biological yield, effective tillers per metre, length of ear, number of grains per ear, grain weight per ear and nutrient uptake ability.

Cedola *et al.*, (1994) analyzed the correlation between leaf water status, morphological parameters and susceptibility index, and reported that high moisture stress tolerance was associated with reduced water potential, RWC, osmotic potential at full turgidity and leaf tensile strength.

Reynolds *et al.*, (1994) measured morpho-physiological traits on 16 spring wheat genotypes under hot, irrigated conditions on two sowing dates (December and February) and reported significant correlations of biomass at maturity, grains/m<sup>2</sup>, days to anthesis and days to maturity with yields. They also reported significant correlation of flag leaf photosynthesis measured at booting, anthesis and during grain filling with yield. Singh and Sharma (1994) observed that grain yield was significantly and positively associated with tiller number, biological yield and grains per ear but harvest index was negatively correlated with biological yield in wheat.

Al Hakim *et al.*, (1995) attempted to transfer drought tolerance from *T. polonicum* to *T. durum* using indirect selection. The accumulation of soluble sugars was positively correlated with RWC or stress tolerance of genotypes. A negative correlation was found

between RWC and proline content under moisture stress and a positive correlation was reported between grain yield and RWC in the F<sub>2</sub> population,

Johnson *et al.*, (1996) observed negative correlation between grain yield and grain weight in wheat. Heerden (1996) reported a positive correlation between the ability to maintain RWC levels and drought tolerance.

Kheiralla *et al.*, (1997) reported a significant negative correlation between grain yield under moisture stress and drought susceptibility index. Rana and Sharma (1997) evaluated 25 diverse wheat genotypes for 7 yield components and showed that grain yield has strong positive correlation with biological yield, grains per spike, tillers per m<sup>2</sup> and harvest index under both moisture stress and irrigated conditions.

Islam *et al.*, (1998) showed significant negative correlation between grain yield under moisture stress and percentage reduction in RWC and significant positive correlation of grain yield with germination percentage in Poly ethylene glycol. Mentewab and Sarrafi (1998) studied 60 doubled haploids developed from two parents under drought conditions. Genetic correlation showed an association of low RWL and low Water Potential (WP) with high yield and most of its related traits, while high leaf water potential was associated with high 1000- grain weight and HI. Multivariate analysis identified genotypes associating high RWC, low leaf WP and good yield.

Bhutta and chowdhry (1999) observed positive significant correlation coefficients between stomatal frequency, osmotic pressure, flag leaf area and tillers per plant with grain yield per plant. Ismail *et al.*, (1999) studied the relationships of yield and drought susceptibility index with morphophysiological traits under drought and irrigated

conditions. Correlation study revealed a significant positive association of number and weight of grains per spike with grain yield.

Nagarajan and Rane (2000) showed that the longest root length, root dry weight, seedling dry weight and total root length had high correlation with per cent reduction in biomass and grain yield.

Merah (2001) evaluated 144 durum wheat genotypes from different geographical origin, under rainfed mediterranean conditions, for RWC, osmotic potential, grain yield, above ground biomass and harvest index (HI). The correlation analysis has revealed significant positive associations between water status traits and both grain yield and HI.

## **2.5 PATH COEFFICIENT STUDIES**

Information on the correlation of agronomic and morphological characters with yield is helpful in the identification of the components of this complex character, yet these do not provide precise information on the relative importance. With increasing number of variables, it becomes necessary to measure the contribution of these variables to the observed correlation and hence partition the correlation coefficients into unidirectional and alternate pathways. The path coefficient analysis permits a critical examination of specific factors that produce a given correlation and could be successfully employed in formulating an effective selection strategy. Wright (1921) suggested path coefficient analysis to understand the influence of one variable upon another and permit the partitioning of correlation coefficients into components of direct and indirect effect.

Dewey and Lu (1959) discussed the utility of path coefficient analysis and employed this technique to establish the relative importance of seed size, spikelets/ spike,

fertility and plant size as determiners of seed yield in crested wheat grass. Fertility and plant size had a strong direct and indirect influence upon seed yield, respectively.

Paroda and Joshi (1970) reported high direct and positive effect of all yield components except for the grains per ear that showed the negative direct effect on the yield. The high positive correlation of grain weight and grains per ear with grain yield was due to high positive indirect effect of weight of grains per ear.

Bhatt (1973) concluded that tiller number per plant is an important yield component in wheat. Jaimini *et al.*, (1974) observed high positive effect of spikes/plant, which in turn influence the grain yield. Quick (1978) indicated the high direct effect of tiller number on grain yield. The negative indirect effect of tiller number through kernel weight and kernel per spike reduced the correlation of kernel weight and kernel per spike with yield.

Pathak *et al.*, (1986) reported that grain weight per ear, plant height and ear length showed high correlations with grain yield. Grain weight per ear had the highest direct effect on yield and was considered as an important trait in selecting for tolerance to heat. It was followed by number of effective tillers per plant.

Bangarwa *et al.*, (1987) revealed through path analysis that biological yield and spike length made the maximum contributions to grain yield and these traits were recommended as selection criteria for improving grain yield. Jadhav and Jadon (1987) reported that tillers per plant and grain weight per spike had the greatest direct effect on yield. Shamsuddin (1987) through correlation and path coefficient studies from 30 wheat cultivars revealed that spikes per plant, grains per spike, 1000-grain weight, glume weight per plant, biological yield and harvest index were directly related to yield per

plant, flag leaf area was indirectly correlated with yield through biological yield and glume yield.

Ehdaie and Waines (1989) showed positive direct effects of days to maturity, plant height and number of heads per plant but they were partially or completely counterbalanced by their negative indirect effects through number of grains per head, 1000-grain weight and harvest index. They showed that late and tall genotypes tended to produce more heads per plant, but with fewer numbers of grains per head, smaller grain size and lower harvest index and flag-leaf area and showed that biological yield, harvest index, grain filling period and days to anthesis had high direct effect on yield.

Studies of Pawar *et al.*, (1990) revealed that the direct effect of component characters on grain yield indicated that tillers per plant had largest contribution followed by grain number and 1000-grain weight in cross between WL 711 x HD 2122, whereas, on the contrary, the character 1000-grain weight had largest contribution followed by number of grains per ear and number of tillers per plant.

Chowdhury and Mandal (1991) worked on eight yield characters and reported that days to maturity showed the highest direct effect on yield and suggested that for improved yield, selection could be followed for larger number of tillers/plant, spikelets/spike, plant height and number of grains/ear.

Multiple correlation and regression studies by Quayyum *et al.*, (1991) on bread wheat revealed that number of tillers per plant and kernel weight per spike is the effective yield components as they showed significant contributions towards yield per plant.

Wang *et al.*, (1991) through the correlation and path analysis on 14 wheat cultivars revealed grain number and weight of the main spike, 1000-grain weight and fertile spikelets, but not plant height, spikes/plant and spike length, were significantly

correlated with grain yield/plant. It was also shown that the direct contribution of grain weight on the main spike to grain yield/plant was highest, followed by spikes/plant. On the contrary, Kumar and Singh (1993) reported spike length had the greatest positive direct effect on grain yield.

Analysis carried out on four yield components by Shelembi *et al.*, (1992) showed that grains per spike exerted the greatest direct influence on grain yield, but also had a negative indirect influence which reduced the coefficients between grain weight and spikes per meter row with yield, even though there were strong direct contributions by both the traits. Since the three variables recorded negative correlations and opposite effects to yield, they suggested that the breeders need to compromise between the three in order to maximize grain yield.

The estimates of path coefficients by Bahadur *et al.*, (1993) revealed that direct contributions towards grain yield was maximum through 1000-grain weight followed by tiller number, number of seeds per ear, number of spikelets and ear length. Plant height had negative direct contribution. It was also reported that indirect effects of tiller number, spikelet number and number of seeds per ear were higher when compared with indirect effects via other variables and these variables also had high direct effects and correlations on grain yield as compared to other variables. Therefore, they suggested that tiller number, spikelet number, number of seeds per ear and 1000-grain weight appeared to be major components of grain yield and should be given utmost consideration in selection for breeding for high grain yield in wheat.

Farshadfar *et al.*, (1993) used path coefficient analysis to partition the phenotypic correlations and reported that root density and root length showed the highest correlations

with total biomass ( $r = 0.84$  and  $0.83$  respectively) as well as the highest direct effects on biomass ( $r = 0.58$  and  $0.36$  respectively).

Singh and Sharma (1994) through path analysis indicated that biological yield and harvest index were the most important yield components and suggested that they may be used as selection criteria for grain yield in wheat populations, since the two traits showed positive high direct effects on grain yield.

Simane (1998) reported that the direct effect of number of spikes per  $m^2$  on grain yield was positive and significant. However, the indirect effect via kernels per spike and kernel weight was negative. Kernel filling period had a strong influence on grain yield via kernel weight. Kernel per spike had the highest direct effect on grain yield.

## 2.6 GENE ACTION

Nass and Jui (1985) and Li *et al.*, (1991) reported that grain yield was controlled by additive effects, whereas Nanda *et al.*, (1983) reported the importance of both additive as well as epistasis effects. Sawant and Jain (1985) found significant additive effects for yield per plant along with dominance effects. Importance of dominance effect in determining the grain yield has been reported by Gill *et al.*, (1986) and Prodanovic (1993), of over-dominance by Chaudhary *et al.*, (1985) and, of non-additive effects in general by Sharma *et al.*, (1986), Sharma and Singh (1983), Yadav and Singh (1987) and Maloo (1988). The importance of both additive and non-additive effects for yield has been reported by Kumar *et al.*, (1983), Ekse and Demir (1984), Redhu *et al.*, (1986), Qari *et al.*, (1986), Thombre *et al.*, (1985), Singh *et al.*, (1986 b), Ahmed *et al.*, (1986), Singh *et al.*, (1986), Malik *et al.*, (1988), Ibrahim (1993) and Menon and Sharma (1995) and of dominance and epistasis by Walia *et al.*, (1995).

There are several reports on the combining ability analysis for 1000-grain weight indicating importance of both additive and non-additive effects (Chaudhary *et al.*, 1985; Singh and Paroda, 1985; Singh *et al.*, 1985; Qari *et al.*, 1986; Singh *et al.*, 1986; Narula, 1987; Malik *et al.*, 1988 and Menon and Sharma, 1995). A large number of workers have observed importance of additive effects for this character (Ekse and Demir, 1984; Nekheva and Kalashnik, 1985; Shamanin *et al.*, 1985; Singh *et al.*, 1986; Redhut *et al.*, 1986; Li *et al.*, 1991; and Walia *et al.*, 1995). However, along with additive effects, importance of epistasis has been reported by Nanda *et al.*, (1983) and Mahdy (1988) and that of dominance by Sawant and Jain (1985), Khan *et al.*, (1986), and Prodanovic (1993). Senpati *et al.*, (1994) reported the predominant role of non-additive gene action in the inheritance of 1000-grain weight.

The number of effective tillers/plant is also one of the most investigated character, with most of reports indicating importance of both additive and non-additive effects. There are, however, few reports that claim otherwise. Radhu *et al.*, (1986) studied grain yield per plant and six other characters and reported additive gene action to be the main factor controlling number of tillers per plant. Chaudhary *et al.*, (1985) and Lonc and Zahewski (1991) indicated the importance of overdominance, whereas Nanda *et al.*, (1983) observed epistasis to be important in the expression of this character. The predominance of both additive and non-additive types of gene action has been reported by Singh and Paroda (1985), Sawant and Jain (1985), Thombre *et al.*, (1985) Kraljevic-Balalic (1986), Qari *et al.*, (1986), Singh *et al.*, (1986), Malik *et al.*, (1988), and Mahdy (1988). The importance of non-additive effects has been reported by Li *et al.*, (1991), Senpati *et al.*, (1994) and of dominance effects by Prodanovic, (1993).

There are several reports on the combining ability analysis for number of grains per ear indicating the importance of additive effects (Rasal *et al.*, 1991; Li *et al.*, 1991),

non-additive effects (Senapati *et al.*, 1994), overdominance (Lonc and Zahewski, 1991), dominance (Prodanovic 1993) and additive and non-additive (Menon and Sharma, 1995).

Several workers have subjected the character plant height to combining ability analysis. Chaudhary *et al.*, (1985); Shamanin *et al.*, (1985); Redhu *et al.*, (1986); Rasal *et al.*, (1991) and Li *et al.*, (1991) have reported the importance of additive gene effects for controlling this trait. However, role of dominance effects (Sawant and Jain, 1985) and partial dominance (Singh *et al.*, 1985; Lonc Zahewski, 1991) have also been reported. Khan *et al.*, 1986) studied a 4 X 4 complete diallele and observed overdominance for plant height. Importance of both additive and non-additive effects have been reported by Ekse and Demir (1984); Sharma *et al.*, (1984); Singh and Paroda, (1985); Singhal *et al.*, (1985); Thombre *et al.*, (1985); Ahmed *et al.*, (1986); Singh *et al.*, (1986) and Malik *et al.*, (1988).

For trait peduncle length Iqbal *et al.*, (1991) reported the importance of partial dominance for controlling this trait. Rasal *et al.*, (1991) studied the combining ability of seven quantitative characters in 6 genetically diverse wheat varieties and reported that additive gene effects were predominant for spikelets/spike. Similar results also have been reported by Prodanovic, (1993) and Walia *et al.*, (1995). Li *et al.*, (1991) reported non-additive effects, on the other hand Yadav and Mishra (1992) reported both additive and non-additive effects. Lonc and Zahewski (1991) reported the importance of over dominance for controlling this trait.

Reports on the combining ability analysis for ear length revealed that this character was governed by additive effects (Li *et al.*, 1991; Walia *et al.*, 1995). Partial dominance has been reported by Lonc and Zahewski (1991).

Chaudhary *et al.*, (1989) evaluated parents, F<sub>1</sub>'s, F<sub>2</sub>'s, and backcrosses of 5 crosses under moisture stress and reported digenic interaction for leaf water potential, RWC, osmotic potential and leaf diffusive conductance. Kheiralla (1994) reported overdominance in favourable environment and partial dominance under drought stress for the characters grain yield and earliness.

Malik and Wright (1995) studied the genetics and correlation of four physiological traits (net photosynthesis, water use efficiency, RWC and ELWL) with agronomic traits under drought conditions. Generation mean and variance analysis of the data suggested simple inheritance for these traits.

Toth- Lokos *et al.*, (1997) studied the inheritance of RWC and mass of flag leaf. In both the cases additive gene effects were predominant. Overdominance was also observed in the case of RWC. Sutka *et al.*, (1997) studied the drought tolerance in wheat using varietal chromosome substitution and alien addition lines and reported that RWC, RWL, drought susceptibility index and phenotypic stability were controlled by genes located on chromosomes 1A, 5A, 7A, 4B, 5B, 1D, 3D, and 5D.

Islam *et al.*, (1998) reported that the additive component of variation is more important than the non-additive component for RWC and ion leakage under moisture stress conditions. Subhani and chowdhry (2000) evaluated a 6 X 6 diallele cross to determine the nature of genetic mechanism controlling some morphophysiological traits like tiller/plant, plant height, spike length, grains/spike, 1000- grain weight, grain yield/plant under irrigated and drought stress conditions. Additive genetic effects were found to be more important than non-additive effects with the exception of yield/plant, which appeared to be more closely linked to non-additive genetic effects.

Mai-Kodomi *et al.*, (1999) elucidated the inheritance of seedling drought tolerance in cowpea. Segregation analysis revealed that the drought tolerance is a dominant trait and both Type 1 and Type 2 reactions are controlled by a single dominant gene but the genes are different in two types. Test of allelism revealed that Type 1 is dominant over Type 2 reaction.

Farshadfar *et al.*, (2000) found high broad sense heritability estimates for HI, grain yield and earliness under moisture stress. Additive gene action was found to be predominant for grain yield, HI, RWC and chlorophyll fluorescence. Farshadfar *et al.*, (2001) evaluated the genetic background of quantitative criteria of drought tolerance. Genetic analysis exhibited overdominance in the inheritance of stressed yield, RWL, ELWRC, HI and Biomass, while RWC and yield potential were controlled by the additive type of gene action.

## CHAPTER III

# MATERIALS AND METHODS

The present investigations were carried out at the Division of Genetics, IARI, New Delhi and Regional Research Station, Wellington, during 1999 to 2002. The experimental field in Delhi is located at an altitude of 228.6 m above mean sea level with 28°40' N latitude and 77°12' E longitudes. The region has a sub-tropical and semi-arid climate with hot dry summer and cold winters. The soil type is loam to sandy loam. The mean annual rainfall is around 710 mm (average of past 30 years), most of which is received during July to September.

The details of the materials and methodology followed are described below

### 3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of 185 germplasm lines including land races, indigenous, exotic and newly developed genotypes. These genotypes were screened for moisture stress tolerance using different criteria in the field as well as in glass house separately. In the glass house 185 wheat genotypes were screened for moisture stress tolerance using the seedling survivability as criterion. Under field conditions only 70 genotypes were screened for moisture stress tolerance using morpho-physiological characters as criterion.

Based on the screening results, genotypes were identified as diverse lines for stress tolerance and stress susceptibility to generate respective  $F_1$  hybrid. In the off-season (*Kharif* 2000), at Wellington, segregating generations ( $BC_1$ ,  $BC_2$  and  $F_2$ ) were

produced. During *rabi* 2000-2001, the parents along with  $F_1$ 's and segregating generations were grown under moisture stress to find out the mode of inheritance of different traits.

## **3.2 EXPERIMENTAL METHODOLOGY AND RECORDING OF OBSERVATIONS**

### **3.2.1 GLASS HOUSE EXPERIMENT:**

Experiments were conducted in the glass house to standardize a technique of seedling screening for moisture stress tolerance using seedling survivability as criterion. The experiment was conducted in wooden boxes of 90 X 60 X 15 Cm<sup>3</sup> dimensions. The wooden boxes were filled with a mixture of soil: sand: FYM in 50:45:5 ratio. All the boxes were given equal quantity of water 12 hours before sowing to ensure good germination. Seeds were sown in rows spaced 10 cm apart and the spacing between plants within a row was 2 cm. Seeds were placed at a uniform depth of 3 cm by making holes in the soil. Single seed was placed in each hole and then filled with same soil mixture. No irrigation was given after sowing and the seedlings were left undisturbed. After 15 days the topsoil in the boxes was loosened manually. Data was recorded on duration of survival of the genotypes. When most of the genotypes started wilting, the boxes were irrigated to study the recovery response of the genotypes. Earliest dying and latest dying genotypes were selected as diverse lines. Crosses between these diverse lines were taken up in the field.

The parents and  $F_1$ s were raised in the *rabi* season of 2000-2001 to generate  $F_2$  seed and also to produce sufficient quantity of  $F_1$  seed. During *rabi* 2001-2002 all the

parents, F<sub>1</sub>s and F<sub>2</sub>s were raised in the wooden boxes in the similar fashion as that of genotypic screening. The F<sub>2</sub> segregation pattern for the character seedling survivability was studied.

The F<sub>2</sub> and back cross generation data is subjected to Chi-square test of goodness of fit. Chi-square was calculated using the formula

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

Where, O = Observed Frequency of a class

E = Expected Frequency of a class

### 3.2.2 FIELD EXPERIMENT

During *rabi* 2000-2001 two sets of germplasm lines were sown, one in the field and the other in net house. The field crop was grown under irrigated condition to ensure the successful crossing programme. The land was thoroughly worked to fine tilth in the net house. The land was irrigated to saturation and levelled properly. The entire area to be sown was protected from all sides from rain by erecting a temporary polyhouse. The polyhouse was provided with window like structures on the sides to facilitate the free air movement. Seeds were sown manually in rows of 1 m length with a spacing of 25 cm between rows and 7.5 cm between plants within a row. Each row represented a single genotype. No irrigation was provided till the maturity of the crop. The material was raised in a randomized block design with two replications.

In the field the seeds were sown by hand in rows of 1.5 m long. Each row represents a single genotype. Thirty cm spacing between rows and 10 cm between plant to plant was adopted. The field was irrigated at regular intervals to ensure good crop. The material in the field was utilized as a crossing block to produce  $F_1$  seed. A random sample of 10 plants from each genotype was taken for recording single plant data on various morphological, physiological and agronomical traits. The procedure adopted in recording the data is discussed as under.

#### **3.2.2.1. Plant Height:**

Height of the plant from the ground level to the tip of the main ear excluding awns was recorded in centimeters (cm) at the time of maturity.

#### **3.2.2.2. Number of productive tillers/plant:**

The number of spike bearing tillers was counted for each randomly selected plant.

#### **3.2.2.3. Peduncle length:**

The length of peduncle was measured in centimeters (cm) from the flag leaf node to the base of the spike of the main tiller.

#### **3.2.2.4. Spike length:**

The length of the main spike was also measured in centimeters (cm) from base to the tip of the ear excluding awn.

#### **3.2.2.5. Number of spikelets/spike:**

The total number of spikelets present on the main spike was counted and recorded.

#### **3.2.2.6. Number of grains/main spike:**

The main ear head of each selected plant was threshed separately and the number of grains was counted.

#### **3.2.2.7. Grain yield/main spike:**

The main spike was threshed separately from each plant and the weight of the grains was recorded in grams (g) on an electronic balance.

#### **3.2.2.8. Thousand-grain weight:**

From the individual plant produce 250 grains were counted at random and their weights were recorded on an electronic balance. The weights were multiplied by four so as to convert it into 1000- grain weight.

#### **3.2.2.9. Relative Leaf Water Content (RWC):**

The relative leaf water content was estimated at the anthesis stage. Flag leaf of single plant was excised from all the genotypes to estimate the RWC in percent. The leaves were collected early in the morning and immediately transported to the lab by keeping the leaves in polythene bags. Fresh weight (FW) of each leaf was measured immediately and the leaf was cut into 4 cm long pieces. These leaf pieces were placed in petriplates containing distilled water at room temperature. After four hours, the samples were quickly and carefully blotted dry with tissue paper and turgid weight (TW) was determined. Then the samples were kept for drying in seed envelopes in an oven at 80°C for 24 hours. Then the dry weight (DW) of each sample was recorded separately. Relative leaf Water Content was calculated following the formula given by Barrs and Wetherley (1962).

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

### 3.2.2.10. Excised Leaf Water Retention Capacity (ELWRC):

The excised leaf water retention capacity (ELWRC) was estimated at anthesis stage. Penultimate leaf of individual plants was excised from ten randomly selected plants in each genotype. The leaves were collected in the morning and transported to the laboratory by placing them in polythene bags. The fresh weight (FW) of each sample was recorded immediately by an electronic balance, and the leaf was placed on the table at room temperature for six hours. After six hours the individual leaf samples were again weighed to record the flaccid weight (FW). Then the samples were kept in seed envelopes and oven dried at 80°C for 24 hours. The dry weight (DW) was recorded. The excised leaf water retention capacity was estimated using the formula given by Clarke (1987)

$$\text{ELWRC} = \frac{\text{Fresh weight} - \text{weight after 6 hours}}{\text{Fresh weight} - \text{Dry weight}} \times 100$$

Based on the estimates of physiological traits, RWC and ELWRC, contrasting genotypes were selected to attempt crosses. The material present in the field was utilized for generating F<sub>1</sub> seed. At the time of panicle emergence from the boot leaf, the spikelets were emasculated and covered with a crossing bag. On the following day the emasculated ear heads were pollinated with the respective pollen parent by go-go method, and the bags were closed again to prevent contamination from other pollen sources. The crossed

plants were labelled properly. At the time of harvesting the crossed spikes were harvested separately and individual spikes were threshed.

During summer 2001, all the parents along with  $F_1$  s were sown in a crossing block at Wellington, in two staggered sowings at 15 days interval. Seeds were sown in rows of 1.5 m length with a spacing of 30 Cm between rows and 15 Cm between plants within a row. Crosses were made between  $F_1$  (as female parent) and both the corresponding parents to generate  $BC_1$  and  $BC_2$  generations. The  $F_1$ s were selfed as well to generate  $F_2$  seed. The crossed and selfed seeds were harvested and threshed separately.

During *rabi* 2001, the parents,  $F_1$ s and the segregating generations ( $BC_1$ ,  $BC_2$  and  $F_2$ ) were raised in the net house. The net house area was protected from rains by erecting the polyhouse. Before taking up the sowing the plot was irrigated to saturation and levelled properly. Sowings were taken up manually in well prepared soil. The seed material of four different crosses was sown in rows spaced at 30 cm apart. Plant to plant spacing of 7.5 Cm was adopted. The material was raised in Randomized complete block design with three replications. No irrigation was provided after sowing till maturity. Data on morphological parameters was recorded on ten randomly selected plants from each parent and the  $F_1$ 's, 15 plants each from  $BC_1$  and  $BC_2$ , and 40 plants each from  $F_2$  in every replication in all the crosses. The data was subjected to appropriate statistical methods.

### 3.3 STATISTICAL ANALYSIS

Replication wise, mean values of each genotype and each character were calculated and used for statistical analysis. The data were analyzed at the Bio-informatics

Centre (BIC), Indian Agricultural Research Institute, New Delhi. Statistical procedures followed are described hereunder.

### 3.3.1 Analysis of Variance

Difference between genotypes for different characters were tested for significance by using Analysis of variance technique (Panse and Sukhatme, 1954). Analysis of variance was done on the basis of the following model.

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where;

$Y_{ij}$  = Phenotypic observation of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  replication.

$\mu$  = general mean

$g_i$  = effect of the  $i^{\text{th}}$  genotype

$r_j$  = effect of the  $j^{\text{th}}$  replication

$e_{ij}$  = random error associated with  $i^{\text{th}}$  genotype and  $j^{\text{th}}$  replication.

The structure of Analysis of variance (ANOVA) was as follows:

#### ANOVA

| SOURCE       | df            | MSS | EXPECTED MSS               | F-VALUE |
|--------------|---------------|-----|----------------------------|---------|
| Replication  | (r-1)         | Mr  | $\sigma_e^2 + g\sigma_r^2$ | Mg/Me   |
| Treatment    | (g-1)         | Mg  | $\sigma_e^2 + r\sigma_g^2$ |         |
| Error        | (r-1)(g-1)    | Me  | $\sigma_e^2$               |         |
| <b>Total</b> | <b>(rg-1)</b> |     |                            |         |

where, r = number of replications

g = number of genotypes

Mr, Mg and Me = Mean sum of squares due to replication, genotype and error, respectively.

$$\sigma_e^2 = \text{Error variance} = Me$$

$$\sigma_g^2 = \text{Genotypic variance} = [(Mg-Me)/r] \text{ and}$$

$$\sigma_p^2 = \text{Phenotypic variance} = \sigma_g^2 + \sigma_e^2$$

MSS due to genotypes were tested against the error variance using F test at  $P = 0.05$  or  $P = 0.01$  with  $V_1$  and  $V_2$  degrees of freedom, where  $V_1$  is the degree of freedom for highest value of variance and  $V_2$  is the degree of freedom for lower value of variance.

### 3.3.2 PHENOTYPIC AND GENOTYPIC CORRELATION COEFFICIENTS

Phenotypic and genotypic correlation coefficients were calculated by the formula suggested by AI-Jibouri *et al.*, (1958) using the variance and covariance estimates from Analysis of Variance and Analysis of Covariance tables.

Phenotypic correlation coefficient ( $r_{pl.2}$ )

$$\frac{\sigma_{pl.2}^2}{\sigma_{pl.1} \cdot \sigma_{pl.2}}$$

Genotypic correlation coefficient ( $r_{gl.2}$ )

$$= \frac{\sigma_{gl.2}^2}{\sigma_{gl.1} \cdot \sigma_{gl.2}}$$

where,

$r_{pl.2}$  and  $r_{gl.2}$  are the phenotypic and genotypic correlation coefficient, respectively.

$\sigma_{pl.2}^2$  and  $\sigma_{gl.2}^2$  are the phenotypic and genotypic covariances between character 1 and 2.

$\sigma_{pl.1}$  and  $\sigma_{pl.2}$  are the phenotypic standard deviation for character 1 and 2, respectively, and

$\sigma_{gl.1}$  and  $\sigma_{gl.2}$  are the genotypic standard deviations for character 1 and 2, respectively.

### 3.3.3 PATH COEFFICIENT ANALYSIS

The genotypic and phenotypic correlation coefficients were further partitioned into direct and indirect effects as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

In the present study, grain yield/spike was taken as an effect and assumed to be influenced by all other 9 characters directly or indirectly (via a third variable). The variation in grain yield unexplained by these characters (causes) was presumed to have been contributed by a residual effect which was correlated with other factors.

Path coefficients were obtained by solving the simultaneous equations, which express the basic relationship between path coefficients and correlation coefficients. The general formula may be written as

$$r_{iy} = \sum_{j=1}^n r_{ij} \cdot P_{jy}$$

where,

$r_{iy}$  = Coefficient of correlation between causal factors  $x_i$  and dependent variable  $y$ ,

$r_{ij}$  = Coefficient of correlation between factors  $i$  and  $j$ .

$P_{jy}$  = Direct effect of variable  $j$  upon the variable  $y$ .

Residual factor was obtained as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

where,

$$R^2 = \sum_{j=1}^n P_{iy}^2 + 2 \sum_{i=1}^n P_{iy} r_{ij} P_{jy}$$

Which is the square of the multiple correlation coefficient (R) and is known as coefficient of determination.

### 3.3.4 MAHALANOBIS' D<sup>2</sup>- STATISTIC

To measure the genetic divergence between two populations, Mahalanobis (1936) gave a statistic known as Mahalanobis' statistic. This statistic is useful in multivariate analysis of quantitative characters to assess the genetic divergence between populations.

#### 3.3.4.1 BASIC CONCEPT:

If  $x_1, x_2, \dots, x_p$  be the multiple measurements available on each individual and  $d_1, d_2, \dots, d_p$  as  $X_1^1 - X_1^2, X_2^1 - X_2^2, \dots, X_p^1 - X_p^2$ , respectively, be the difference in the means on  $i^{\text{th}}$  character, for 1<sup>st</sup> and 2<sup>nd</sup> population, then Mahalanobis D<sup>2</sup> statistic is defined as follows :

$$pD^2 = b_1 d_1 + b_2 d_2 + \dots + b_p d_p$$

Here,  $b_i$  values are to be estimated such that the ratio of variance between the population to variance within the population is maximum. In terms of variance and covariance, the D<sup>2</sup> values is obtained as follows

$$pD^2 = W_{ij} (X_i^1 - X_i^2) (X_j^1 - X_j^2)$$

where,

$W_{ij}$  is the (i and j)<sup>th</sup> element in the inverse of estimated variance -covariance matrix.

#### 3.3.4.2 COMPUTATION OF D<sup>2</sup> VALUES

For each of the pairs of combinations, the mean deviation *i.e.*,  $Y_i^1 - Y_i^2$  with  $i = 1, 2, 3, \dots, p$  was computed and  $D^2$  was calculated as the sum of the squares of these deviations *i.e.*,

$$D^2 = \sum_{i=1}^n (Y_i^1 - Y_i^2)^2$$

e.g. in the present study, the 02 value between two genotypes based on the measurement of  $p$  characters were measured as follows :

$$D^2 = (Y_1^1 - Y_1^2)^2 + (Y_2^1 - Y_2^2)^2 + \dots + (Y_n^1 - Y_n^2)^2$$

#### 3.3.4.3 TESTING THE SIGNIFICANCE OF D<sup>2</sup> VALUES

The  $D^2$  values were obtained for a pair of genotypes and were taken as the calculated value for  $\chi^2$  and were tested against the tabulated value of  $\chi^2$  for  $n$  degree of freedom,

Where,

$n$  = number of characters studied.

#### 3.3.4.4 GROUPING OF GENOTYPES INTO VARIOUS CLUSTERS (TOCHER'S METHOD)

The first step in the grouping of the genotypes into distinct clusters is to arrange these genotypes in the order of their relative distances from each other. A simple device following Rao (1952, pp. 363) were to start with two closely associated groups having low  $D^2$  from the first two and so on. If at any stage the average  $D^2$  of the group from those already listed appeared to be high, this group was taken out from the former cluster. If the change in average  $D^2$  within a cluster due to inclusion of another group was found

appreciable then the newly added group has to be taken outside the cluster. No formal rules can however, be laid down in the formulation of these clusters, but the only criterion is that, on an average the  $D^2$  values between any two genotypes within a group is much smaller than those belonging to the two different groups. If a group consists of only one genotype, this rule cannot be applied, as it is a separate group by itself.

### 3.3.5 GENERATION MEAN ANALYSIS

The mean values were computed for each generation of  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  for each cross over three replications. The variances and the corresponding standard errors of the means were computed from the deviations of the individual values from the pooled mean for six generations in each cross.

#### 3.3.5.1 STUDY OF MEANS

The adequacy of the data for a simple additive dominance model was tested utilizing the A, B and C scaling tests of Mather (1949).

$$\text{Scale A} = 2\overline{BC}_1 - \overline{P}_1 - \overline{F}_1 = 0$$

$$\text{Scale B} = 2\overline{BC}_2 - \overline{P}_2 - \overline{F}_1 = 0$$

$$\text{Scale C} = 4\overline{F}_2 - 2\overline{F}_1 - \overline{P}_1 - \overline{P}_2 = 0$$

Where,

$\overline{P}_1$ ,  $\overline{P}_2$ ,  $\overline{F}_1$ ,  $\overline{F}_2$ ,  $\overline{BC}_1$  and  $\overline{BC}_2$  are the means of different generations over three replications.

The variance of the quantities A, B and C were calculated from the respective variances of the different generations as follows.

$$V_A = 4V\overline{BC}_1 + V\overline{P}_1 + V\overline{F}_1$$

$$V_B = 4V\overline{BC}_2 + V\overline{P}_2 + V\overline{F}_1$$

$$V_C = 16\overline{VF_2} + 4\overline{VF_1} + \overline{VP_1} + \overline{VP_2}$$

Where,

$V_A$ ,  $V_B$  and  $V_C$  are the variances of A, B and C

$\overline{VP_1}$ ,  $\overline{VP_2}$ ,  $\overline{VF_1}$ ,  $\overline{VF_2}$ ,  $\overline{VBC_1}$  and  $\overline{VBC_2}$  are the mean variances of  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  generations respectively.

The standard error of A, B and C were obtained as  $V_A$ ,  $V_B$  and  $V_C$  respectively and were utilized for testing the significance of deviation of the scales from zero. The additive dominance model was considered inadequate when atleast any one of the three scales was found to deviate significantly from zero.

### 3.3.5.2 JOINT SCALING TEST

The model proposed by Cavalli (1952) was adopted to estimate the goodness of fit (chi-square) of additive, dominance model. The three parameters m, d and h derived from the additive dominance model were estimated by the weighted least square method (Mather, 1949). From these parameters, the expected generation means were calculated as follows:

$$\overline{P_1} = m - (d)$$

$$\overline{P_2} = m + (d)$$

$$\overline{F_1} = m + (h)$$

$$\overline{F_2} = m + 1/2(h)$$

$$\overline{BC_1} = m - 1/2(d) + 1/2(h)$$

$$\overline{BC_2} = m + 1/2(d) + 1/2(h)$$

Where,

- m = population mean  
(d) = additive component  
(h) = dominance component

The adequacy of the simple additive, dominance model was tested statically by goodness of fit between the expected generation means and the observed generation means. when the scaling tests and chi-square test indicated inadequacy of simple additive dominance model, a six parameter model (Hayman, 1958) was adopted assuming digenic interaction. Perfect fit estimates of six parameters m, (d), (h), (i), (j) and (l) were estimated as follows.

$$\begin{aligned} m &= \overline{F_2} \\ (d) &= \overline{BC_1} - \overline{BC_2} \\ (h) &= 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2} + \overline{F_1} - 1/2(\overline{P_1}) - 1/2(\overline{P_2}) \\ (i) &= 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2} \\ (j) &= \overline{BC_1} - 1/2(\overline{P_1}) - \overline{BC_2} + 1/2(\overline{P_2}) \\ (l) &= \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2} \end{aligned}$$

The data were refitted following Cavalli's (1952) least square method by eliminating the parameters one by one to increase the precision and test the adequacy of the best fit model.

The standard errors of the above parameters were calculated and 't' test was applied to test the significance of deviation of the parameters.

## **CHAPTER IV**

### **RESULTS**

The experimental results obtained in the present investigation are presented according to the different experiments. The results are described in the following sub headings.

1. Screening for drought tolerance using seedling survivability as a selection criterion.
2. To assess the genetic variability among the different wheat genotypes for tolerance to moisture stress.
3. Genetic analysis of various attributes.

#### **4.1 SEEDLING SURVIVABILITY STUDIES:**

Success of any breeding programme depends on suitable screening technique adopted for a particular trait or combination of traits. Available literature suggests various methods of screening techniques for drought tolerance. Plant breeders and plant physiologists have devised various strategies and evolved standardized techniques for screening wheat germplasm tolerant to drought conditions. The available methods of screening are not very easy to adopt in case of  $F_2$  segregating populations. Genetic improvement of crop involves selection of genotypes in segregating population of a cross, however, the selection for drought tolerance is not feasible with the available means of screening. Hence a simple method of screening germplasm lines using

**Table 1: Reaction of different genotypes to the seedling screening for drought tolerance**

| S. No. | Duration of seedling survivability under screening conditions |                            |                                |
|--------|---------------------------------------------------------------|----------------------------|--------------------------------|
|        | Less than 30 days after sowing                                | 30 to 35 days after sowing | More than 35 days after sowing |
| 1.     | Lal Bahadur / <i>A. squarrosa</i> derivative                  | NING 8319                  | NI 5439                        |
| 2.     | Choti lerma                                                   | MARIS/ALDS                 | Kundan                         |
| 3.     | 47A/ ALBORZ                                                   | HD 2012                    | UP 2338                        |
| 4.     | Sardari                                                       | WR 368                     | NIAW 588                       |
| 5.     | Zardak                                                        | WH 748                     | HW 2044                        |
| 6.     | Kalyansona                                                    | WR 1092                    | HW 3081                        |
| 7.     | RS 820                                                        | HD 2780                    | HD 2687                        |
| 8.     | JWS 92                                                        | IND 06                     | K 8027                         |
| 9.     | HD 2643                                                       | RL-84-1                    | HI 1494                        |
| 10.    | HS 240                                                        | Akbar                      | WBM 1304                       |
| 11.    | CNT 8                                                         | HW 3035                    | NP 718                         |
| 12.    | HD 2329                                                       | BH 146                     | PBW 514                        |
| 13.    | Halna                                                         | Deckson 98A                | HW 2099                        |
| 14.    | Lok Barati                                                    | PBW 343                    | HUW 538                        |
| 15.    | NIAW 590                                                      | CPAN 1492                  | RS 634                         |
| 16.    | MP 1136                                                       | HD 2784                    |                                |
| 17.    | HD 2839                                                       | Lok Bold                   |                                |
| 18.    | Raj 4005                                                      | HW 971                     |                                |
| 19.    | Chinese Spring                                                | NIAW 877                   |                                |
| 20.    | Sunstar*6/ C80-1                                              | PBW 175                    |                                |
| 21.    | NIAW 880                                                      | WLT 6                      |                                |
| 22.    | Charter                                                       | K 8823                     |                                |
| 23.    | Amigo/Agent                                                   | WR 95                      |                                |
| 24.    | Chaunmai #18                                                  | K 2620                     |                                |
| 25.    | HW 2022                                                       | HD 2009                    |                                |
| 26.    | Punjab 85                                                     | Kharchia                   |                                |
| 27.    | HW 1042                                                       | HD 2014                    |                                |
| 28.    | Annapurna                                                     | WR 368                     |                                |
| 29.    | Agent                                                         | IND 11                     |                                |
| 30.    | Bakhtawar                                                     | IND 07                     |                                |
| 31.    | Oleson Dwarf                                                  | WR 251                     |                                |
| 32.    | HD 2380                                                       | RL-4-81                    |                                |
| 33.    | Fenman                                                        | KRL-1-4                    |                                |
| 34.    | BH 1166                                                       | HUW 540                    |                                |
| 35.    | HP 1633                                                       | GW 1172                    |                                |
| 36.    | K 65                                                          | RL-22-1092                 |                                |
| 37.    | JWS 68                                                        | CBW 509                    |                                |
| 38.    | Sonalika                                                      | HUW 533                    |                                |

|     |             |           |   |
|-----|-------------|-----------|---|
| 39. | HI 1077     | NIAW 34   |   |
| 40. | RS 420      | MACS 2496 |   |
| 41. | T 555       | C 306     |   |
| 42. | UP 2538     | HPW 184   |   |
| 43. | SKW 178     | UP 2537   |   |
| 44. | HI 1489     | HW 2045   |   |
| 45. | Pissi Local | HPW 190   |   |
| 46. | MP 1124     | HD 2747   |   |
| 47. | RW 3542     | HW 2004   |   |
| 48. | Lok 45      | HD 2687   |   |
| 49. | MP 1128     | HW 3026   |   |
| 50. | HW 2040     | GW 173    |   |
| 51. | HD 2798     | HD 2793   |   |
| 52. | Lok 1       | HI 8591   | , |
| 53. | MP 3066     | HW 3063   |   |
| 54. | DBW 14      | HW 2002   |   |
| 55. | RS 634      | HI 1501   |   |
| 56. | Narmada 4   | TL 2915   |   |
| 57. | T 2707      |           |   |
| 58. | VL 819      |           |   |
| 59. | WLT 2       |           |   |
| 60. | VL 831      |           |   |
| 61. | HS 424      |           |   |
| 62. | DL 788-2    |           |   |
| 63. | HPW 190     |           |   |
| 64. | Veery's     |           |   |
| 65. | DWR-95-91   |           |   |
| 66. | Kite        |           |   |
| 67. | DI 105      |           |   |
| 68. | HUW 234     |           |   |
| 69. | DI 9        |           |   |
| 70. | Sel 111     |           |   |
| 71. | EC 368168   |           |   |
| 72. | KRL 20      |           |   |
| 73. | Raj 3765    |           |   |
| 74. | MACS 6098   |           |   |
| 75. | VL 825      |           |   |
| 76. | NW 1076     |           |   |
| 77. | NIAW 301    |           |   |
| 78. | UP 262      |           |   |
| 79. | KRL 25      |           |   |
| 80. | Raj 4016    |           |   |
| 81. | Kanchan     |           |   |
| 82. | PH 171      |           |   |
| 83. | RW 3542     |           |   |

|      |          |  |  |
|------|----------|--|--|
| 84.  | RW 3553  |  |  |
| 85.  | HUW 542  |  |  |
| 86.  | UP 3526  |  |  |
| 87.  | Raj 4017 |  |  |
| 88.  | HUW 206  |  |  |
| 89.  | HUW 545  |  |  |
| 90.  | HD 2767  |  |  |
| 91.  | HW 2040  |  |  |
| 92.  | HD 2755  |  |  |
| 93.  | SHUN-4   |  |  |
| 94.  | HW 4011  |  |  |
| 95.  | HD 2818  |  |  |
| 96.  | HD 2795  |  |  |
| 97.  | HI 1503  |  |  |
| 98.  | HW 2820  |  |  |
| 99.  | Raj 415  |  |  |
| 100. | HW 4028  |  |  |
| 101. | Raj 4021 |  |  |
| 102. | Raj 418  |  |  |
| 103. | HD 2821  |  |  |
| 104. | HW 3094  |  |  |
| 105. | Raj 4022 |  |  |
| 106. | Transec  |  |  |
| 107. | HD 2791  |  |  |
| 108. | HW 737   |  |  |
| 109. | RS 519   |  |  |
| 110. | HW 3060  |  |  |
| 111. | HD 2808  |  |  |
| 112. | Raj 420  |  |  |
| 113. | HW 1085  |  |  |
| 114. | Inquilab |  |  |



Plate I : Seed sowing in wooden boxes under glass house conditions



Plate II : Seedlings showing typical symptoms of drying



**Plate III : Seedling recovery after the resumption of irrigation**

survivability of seedlings under extreme conditions of moisture stress as a selection criterion was adopted in the present study. One hundred and eighty five wheat genotypes of diverse origin were screened in wooden boxes under moisture stress in glass house conditions (Plate I). Based on the response of the genotypes, in terms of days of survival, the genotypes were grouped into three categories. The results obtained are presented in the Table 1.

Many genotypes started withering from 20<sup>th</sup> day of germination but at the same time a few genotypes were still healthy. The withering started from the basal leaf (tip to bottom of the leaf) turning into brown colour and consequently complete drying. Thus withering progressed from bottom to top leaves (Plate II). Complete seedling death started from the 26<sup>th</sup> day onwards and by 30<sup>th</sup> day most of the genotypes exhibited seedling death. Those germplasm lines that survived beyond 30 days are not very healthy (showed wilting of lower leaves) but could survive for some more time. Many of the lines completely died between 30<sup>th</sup> and 35<sup>th</sup> day after sowing. Remaining genotypes also started withering after 35 days and, therefore, to study the recovery of these seedlings, irrigation was resumed on 43<sup>rd</sup> day after sowing. Few of the genotypes like NIAW 588, UP 2338, Kundan, Deckson 98A started recovering and also regained growth, though not vigorous. Among the recovered genotypes, NIAW 588 produced spike with one or two seeds (Plate III), Kundan and Deckson 98A produced an empty spike. Those genotypes, which died before 35 days, did not recover after resuming irrigation. Most prominent genotypes which died earliest include Sonalika, JWS 98, HD 2329, Halna, MC 3, Sardari, Kalyansona Chinese Spring, Punjab 85, Olesson Dwarf, Annapurna, MC 8, Raj 4017, Pissi local, MP 1124, HW 3035, Kite, Lok 45 etc. The genotypes which survived upto 35



Plate IV : Differential response of parents, HW 2044 and MP 1136 under seedling screening in glasshouse conditions



Plate V :  $F_2$  segregation pattern for seedling survivability in the cross MP 1136 x HW 2044

days after sowing include Ning 8319, WR 1019, Deckson 98A, WR 251, RL-4-1, GW 1172, Kharchia 65, C306, Ind 06, WLT 6, HW 971, K 8823, WH 748 etc. The genotypes, which survived beyond 40 days after sowing and recovered after resuming irrigation include NI 5439, Kundan, UP 2338, NIAW 588, HW 3081, RS 634, K 8027, HI 1494, PBW 514, and HUW 538. The genotype C306, which is a well-known drought tolerant genotype in the Indian subcontinent did performed moderately. All the seedlings of C306 could survive only for 33 to 35 days after sowing.

Keeping in view the seedling survivability as a selection criterion for drought tolerance, the parents,  $F_1$  and  $F_2$  segregating generations of two crosses (MP1136 x HW2044 and HW3081 x C306) were screened following the procedure mentioned earlier. The data on the segregation pattern of seedling survivability is presented in Table 2. All the parents and the different populations studied showed clear differences in their response to the artificial drought situation created under controlled conditions. The seedling survivability permitted easy grouping of individual seedlings into drought tolerant and susceptible genotypes.

The parents, their  $F_1$  progeny and  $F_2$  population of the cross MP 1136 X HW 2044 were screened and analyzed genetically. All the 18  $F_1$  seedlings, that germinated, survived up to 42 days after sowing as that of the tolerant parent HW 2044 indicating that the survivability of seedlings is a dominant character. All seedlings of MP 1136 (susceptible parent) died completely by 30<sup>th</sup> day after sowing. Out of 113  $F_2$  seedlings germinated, 87 seedlings survived beyond 36<sup>th</sup> day and majority of the seedlings recovered with the resumption of irrigation on 42<sup>nd</sup> day after sowing and 26 seedlings die before 30<sup>th</sup> day (Plates IV and V). The dead seedlings could not recover with the

**Table 2: Segregation of seedling survivability in F<sub>2</sub> and BC<sub>1</sub> derived from two cross combinations**

|                   | Number of seeds sown | Number of seeds germinated | Reaction (No. of seedlings) |                           | Ratios tested | $\chi^2$ value at 1 d.f | P         |
|-------------------|----------------------|----------------------------|-----------------------------|---------------------------|---------------|-------------------------|-----------|
|                   |                      |                            | Death before 30 DAS         | Recovery after irrigation |               |                         |           |
| HW 3081 X C306    |                      |                            |                             |                           |               |                         |           |
| P <sub>1</sub>    | 26                   | 20                         | 1                           | 19                        |               |                         |           |
| P <sub>2</sub>    | 26                   | 18                         | 14                          | 4                         |               |                         |           |
| F <sub>1</sub>    | 21                   | 20                         | 0                           | 20                        |               |                         |           |
| F <sub>2</sub>    | 140                  | 125                        | 29                          | 96                        | 3:1           | 0.216                   | 0.70-0.50 |
| BC <sub>1</sub>   | 64                   | 57                         | 30                          | 27                        | 1:1           | 0.157                   | 0.70-.050 |
| HW 2044 X MP 1136 |                      |                            |                             |                           |               |                         |           |
| P <sub>1</sub>    | 26                   | 21                         | 2                           | 19                        |               |                         |           |
| P <sub>2</sub>    | 26                   | 20                         | 20                          | 0                         |               |                         |           |
| F <sub>1</sub>    | 20                   | 18                         | 0                           | 18                        |               |                         |           |
| F <sub>2</sub>    | 130                  | 113                        | 26                          | 87                        | 3:1           | 0.238                   | 0.70-0.50 |

of irrigation. The observed values when subjected to chi-square test for significance, fitted well in to expected ratio of 3:1 (survived : dead).

The parental genotypes, HW 3081 and C306, their  $F_1$ ,  $F_2$  and back cross generations were also subjected to similar conditions of screening as mentioned earlier. All the  $F_1$  plants like one of the parents survived up to 40<sup>th</sup> day of sowing indicating that seedling survivability is a dominant trait. In the  $F_2$  population, 96 seedlings out of 125 survived till 40<sup>th</sup> day after sowing and recovered with the resumption of water. Twenty nine seedlings withered by 30<sup>th</sup> day after sowing and did not recover after the resumption of irrigation. In case of back cross population, out of 57 plants 27 recovered after 42<sup>nd</sup> day with the resumption of irrigation, while 30 seedlings died completely and did not recover. The observed value in both survived and dead classes fitted well in the expected ratio of 3:1 with a chi square value of 0.216. The data observed in backcross generation fitted well in expected ratio of 1(survived): 1(dead) with chi square value (0.157) being non-significant. The backcross data validated the proposed segregating ratio in  $F_2$  generation.

## **4.2 GENETIC VARIABILITY**

### **4.2.1 ANALYSIS OF VARIANCE**

Analysis of variance for 10 characters (Table 3) indicated that the differences among the treatments (Genotypes) were highly significant for all the characters studied.

### **4.2.2 MEAN PERFORMANCE**

The mean performances of the genotypes for all the 10 characters studied are shown in the Table 4.

**Table 3: Analysis of variance for 10 characters in 70 diverse germplasm lines of wheat**

| S. No. | Character                             | Replications | Treatments | Error      |
|--------|---------------------------------------|--------------|------------|------------|
|        | <b>Degrees of freedom</b>             | <b>2</b>     | <b>69</b>  | <b>138</b> |
| 1      | Plant height                          | 65.62**      | 454.61**   | 6.04       |
| 2      | Number of tillers/plant               | 0.00219      | 0.848**    | 0.0035     |
| 3      | Peduncle length                       | 11.96**      | 110.74**   | 1.036      |
| 4      | Spike length                          | 1.074**      | 8.002**    | 0.0956     |
| 5      | No. of spike lets/spike               | 2.73**       | 25.79**    | 1.00       |
| 6      | No. of grains/spike                   | 4.453**      | 350.73**   | 1.548      |
| 7      | Grain yeield/spike                    | 0.0219**     | 0.388**    | 0.002      |
| 8      | 1000-grain weight                     | 10.09**      | 64.395**   | 1.368      |
| 9      | Excised leaf water retention capacity | 16.171**     | 235.158**  | 1.864      |
| 10     | Relative leaf water content           | 36.31**      | 177.295**  | 6.501      |

\*\* , \* :- significant at 1 and 5 per cent

**Table 4: Mean performance of different genotypes under moisture stress**

| S.No | Genotypes   | PH    | TN   | PL    | SL   | SL/SP | GN    | GY/SP | TW    | ELWRC | RWC   |
|------|-------------|-------|------|-------|------|-------|-------|-------|-------|-------|-------|
| 1    | Baktawar    | 59.12 | 1.10 | 22.76 | 8.81 | 16.81 | 30.30 | 1.00  | 33.07 | 40.78 | 63.81 |
| 2    | MP 1128     | 57.64 | 1.00 | 23.99 | 4.47 | 7.06  | 29.30 | 0.94  | 32.11 | 36.51 | 68.87 |
| 3    | SKW 178     | 72.46 | 2.05 | 29.49 | 9.27 | 13.98 | 58.50 | 2.03  | 34.69 | 45.49 | 66.54 |
| 4    | BH 146      | 81.76 | 1.57 | 31.05 | 7.84 | 11.91 | 35.10 | 1.38  | 39.26 | 28.73 | 75.88 |
| 5    | HW 2022     | 51.26 | 1.20 | 19.13 | 5.53 | 9.61  | 36.20 | 1.12  | 30.88 | 37.46 | 68.19 |
| 6    | HD 2329     | 67.74 | 2.10 | 30.58 | 9.05 | 14.45 | 31.70 | 1.50  | 40.65 | 40.75 | 77.53 |
| 7    | UP 2532     | 60.61 | 1.16 | 20.88 | 8.12 | 11.16 | 20.50 | 0.76  | 37.46 | 40.15 | 72.21 |
| 8    | MP 1124     | 70.75 | 1.20 | 20.99 | 7.82 | 12.9  | 27.60 | 0.73  | 26.22 | 41.20 | 63.94 |
| 9    | WR 251      | 59.99 | 1.00 | 26.37 | 6.77 | 8.52  | 15.10 | 0.62  | 41.21 | 45.60 | 66.78 |
| 10   | HUW 234     | 55.63 | 1.10 | 21.87 | 7.44 | 12.50 | 32.00 | 1.16  | 36.32 | 44.20 | 65.38 |
| 11   | NING 8319   | 55.13 | 1.20 | 18.91 | 6.22 | 10.22 | 21.30 | 0.80  | 37.83 | 26.23 | 73.82 |
| 12   | HW 3026     | 81.93 | 1.10 | 30.14 | 9.46 | 13.86 | 34.40 | 1.42  | 41.34 | 55.49 | 66.26 |
| 13   | Lok bold    | 68.79 | 1.00 | 30.62 | 6.31 | 9.35  | 15.18 | 0.86  | 36.89 | 33.07 | 71.28 |
| 14   | HPW 190     | 45.50 | 1.00 | 16.98 | 5.93 | 9.32  | 15.40 | 0.39  | 24.92 | 36.28 | 65.71 |
| 15   | HW 2040     | 42.73 | 1.10 | 16.85 | 6.68 | 7.68  | 13.30 | 0.44  | 33.24 | 27.31 | 70.60 |
| 16   | K 9107      | 75.09 | 1.20 | 25.80 | 9.55 | 14.10 | 26.40 | 1.01  | 38.46 | 34.43 | 68.55 |
| 17   | HW 2044     | 68.44 | 1.50 | 33.42 | 7.86 | 11.17 | 29.00 | 1.53  | 39.68 | 50.22 | 86.20 |
| 18   | WH 744      | 73.94 | 1.40 | 30.91 | 9.76 | 13.66 | 31.9  | 1.59  | 41.24 | 47.97 | 78.80 |
| 19   | HUW 206     | 68.17 | 1.40 | 24.74 | 8.19 | 15.12 | 34.2  | 1.17  | 34.39 | 31.94 | 68.16 |
| 20   | Lok 45      | 59.66 | 1.10 | 25.67 | 6.84 | 12.12 | 28.5  | 1.18  | 41.64 | 32.90 | 68.63 |
| 21   | RW 3542     | 65.25 | 1.10 | 23.85 | 6.57 | 10.43 | 36.2  | 1.25  | 34.61 | 30.51 | 69.97 |
| 22   | NIAW 34     | 43.17 | 1.10 | 14.34 | 5.15 | 9.28  | 15.9  | 0.62  | 38.74 | 52.26 | 71.40 |
| 23   | HW 2099     | 73.06 | 1.20 | 27.88 | 7.96 | 13.86 | 29.5  | 1.25  | 40.31 | 38.19 | 64.44 |
| 24   | HI 1489     | 63.12 | 1.00 | 24.72 | 5.79 | 11.25 | 29.7  | 1.06  | 35.72 | 36.92 | 65.15 |
| 25   | Lok 44      | 63.03 | 1.10 | 25.33 | 7.61 | 13.85 | 33.1  | 1.15  | 34.65 | 35.56 | 72.17 |
| 26   | Pissi local | 78.10 | 1.20 | 26.57 | 8.35 | 13.65 | 25.4  | 1.06  | 41.83 | 53.92 | 64.86 |
| 27   | HPW 184     | 61.22 | 1.00 | 23.45 | 7.65 | 13.65 | 28.8  | 1.00  | 34.56 | 40.75 | 61.90 |
| 28   | HW 2047     | 50.90 | 1.00 | 18.85 | 5.90 | 13.17 | 21.2  | 0.56  | 26.05 | 46.54 | 69.34 |
| 29   | HW 3035     | 57.61 | 1.20 | 23.31 | 5.55 | 9.10  | 17.4  | 0.58  | 33.44 | 23.76 | 79.38 |
| 30   | HD 2747     | 53.91 | 1.00 | 25.10 | 7.81 | 12.00 | 28.2  | 1.11  | 39.33 | 36.90 | 72.93 |
| 31   | NI 5439     | 77.20 | 1.90 | 31.02 | 7.29 | 15.27 | 38.7  | 1.41  | 36.60 | 54.46 | 74.51 |
| 32   | HP 1851     | 61.25 | 1.10 | 23.35 | 7.47 | 14.11 | 34.7  | 1.16  | 33.41 | 34.31 | 74.47 |
| 33   | HW 2034     | 67.82 | 1.30 | 24.80 | 9.15 | 16.61 | 43.10 | 1.48  | 34.32 | 29.26 | 78.51 |
| 34   | JWS 68      | 83.60 | 1.90 | 34.75 | 7.49 | 14.96 | 40.10 | 1.70  | 40.44 | 27.12 | 80.74 |
| 35   | HI 1502     | 77.88 | 2.10 | 30.02 | 7.02 | 13.66 | 41.20 | 1.56  | 37.84 | 28.75 | 76.92 |
| 36   | HW 2004     | 93.00 | 2.10 | 38.02 | 8.20 | 15.12 | 42.80 | 2.01  | 40.61 | 42.35 | 65.43 |

|                   |             |       |      |       |       |       |       |       |       |       |       |
|-------------------|-------------|-------|------|-------|-------|-------|-------|-------|-------|-------|-------|
| 37                | UP 2338     | 73.22 | 1.90 | 29.74 | 9.65  | 16.53 | 49.50 | 1.84  | 37.17 | 21.74 | 91.81 |
| 38                | HW 2045     | 76.31 | 2.00 | 25.26 | 9.82  | 19.75 | 47.40 | 1.82  | 38.31 | 50.22 | 86.20 |
| 39                | HUW540      | 82.50 | 1.30 | 32.35 | 10.80 | 16.02 | 51.00 | 1.78  | 34.87 | 37.94 | 62.10 |
| 40                | Akbar       | 74.57 | 1.50 | 31.17 | 9.07  | 15.70 | 36.70 | 1.71  | 41.23 | 41.88 | 77.40 |
| 41                | HW 2033     | 72.46 | 2.00 | 28.44 | 8.77  | 16.72 | 46.40 | 1.64  | 35.36 | 33.25 | 78.89 |
| 42                | HD 2687     | 76.80 | 2.00 | 36.57 | 8.53  | 13.07 | 39.60 | 1.57  | 39.46 | 33.35 | 78.90 |
| 43                | HW 3035     | 73.77 | 1.70 | 29.47 | 8.56  | 13.41 | 29.50 | 1.24  | 40.22 | 35.25 | 66.60 |
| 44                | UP 2537     | 74.81 | 1.90 | 31.51 | 9.59  | 13.51 | 31.70 | 1.43  | 40.38 | 40.11 | 72.21 |
| 45                | RL-84-1     | 75.48 | 1.30 | 28.29 | 8.86  | 16.02 | 40.00 | 1.08  | 26.87 | 31.62 | 71.14 |
| 46                | CPAN 1492   | 69.24 | 2.00 | 26.11 | 8.29  | 12.23 | 30.60 | 1.00  | 32.78 | 34.32 | 66.46 |
| 47                | K 8027      | 85.21 | 1.90 | 31.17 | 8.74  | 14.39 | 34.70 | 1.20  | 34.57 | 30.17 | 72.86 |
| 48                | PBW 343     | 68.40 | 1.50 | 24.64 | 8.18  | 13.71 | 29.10 | 0.99  | 34.08 | 51.56 | 77.96 |
| 49                | Deckson     | 66.00 | 2.00 | 23.06 | 11.72 | 19.83 | 42.50 | 1.17  | 27.58 | 32.22 | 71.33 |
| 50                | NIAW 588    | 79.70 | 1.30 | 33.51 | 11.92 | 19.28 | 54.60 | 2.10  | 38.67 | 23.92 | 82.85 |
| 51                | MACS 2496   | 71.53 | 2.00 | 25.97 | 9.49  | 17.27 | 48.60 | 1.68  | 34.78 | 27.53 | 78.54 |
| 52                | K 9903      | 89.67 | 1.90 | 44.54 | 10.53 | 13.39 | 41.30 | 1.64  | 39.71 | 57.14 | 69.18 |
| 53                | NIAW 590    | 71.48 | 1.40 | 30.76 | 9.09  | 11.72 | 28.20 | 0.80  | 28.29 | 39.42 | 69.38 |
| 54                | HW 1042     | 61.00 | 1.50 | 26.00 | 6.23  | 11.71 | 27.40 | 1.02  | 37.21 | 35.9  | 73.43 |
| 55                | DBW 14      | 78.43 | 2.60 | 28.76 | 10.03 | 16.83 | 44.70 | 1.71  | 38.25 | 27.24 | 75.20 |
| 56                | RW 857      | 85.29 | 2.50 | 34.96 | 10.11 | 13.09 | 39.60 | 1.65  | 39.83 | 29.35 | 79.06 |
| 57                | WR 544      | 72.72 | 1.90 | 34.55 | 9.04  | 13.76 | 32.60 | 1.33  | 40.42 | 45.60 | 66.79 |
| 58                | RS 634      | 99.49 | 2.10 | 35.40 | 11.21 | 19.23 | 49.70 | 2.20  | 39.04 | 44.67 | 65.46 |
| 59                | Lok Barathi | 83.10 | 1.90 | 35.83 | 8.46  | 12.55 | 20.10 | 1.12  | 39.85 | 37.69 | 76.01 |
| 60                | Lok 1       | 71.78 | 2.10 | 33.62 | 8.10  | 11.08 | 22.60 | 1.04  | 41.30 | 52.03 | 62.75 |
| 61                | HW 3036     | 68.28 | 1.70 | 26.24 | 7.88  | 14.50 | 37.00 | 1.38  | 37.26 | 55.49 | 61.22 |
| 62                | RL 22-1092  | 74.39 | 3.20 | 34.23 | 11.26 | 20.80 | 47.80 | 0.97  | 20.28 | 34.96 | 70.68 |
| 63                | K 9909      | 76.81 | 2.30 | 37.10 | 8.32  | 11.97 | 28.30 | 1.08  | 38.08 | 48.00 | 75.23 |
| 64                | HD 2839     | 66.52 | 1.20 | 24.98 | 8.35  | 13.88 | 36.50 | 1.16  | 31.90 | 36.81 | 66.90 |
| 65                | HD 2784     | 62.50 | 1.10 | 23.65 | 9.70  | 12.23 | 8.00  | 0.30  | 37.62 | 53.08 | 75.81 |
| 66                | MP 3066     | 97.95 | 1.50 | 40.14 | 11.21 | 18.85 | 52.40 | 1.88  | 35.96 | 29.86 | 79.56 |
| 67                | Kundan      | 71.75 | 2.00 | 33.11 | 8.99  | 15.05 | 32.72 | 1.90  | 43.77 | 38.49 | 92.89 |
| 68                | MP 1136     | 94.54 | 2.50 | 40.47 | 9.12  | 16.81 | 48.55 | 1.95  | 37.81 | 39.90 | 89.54 |
| 69                | HW 3081     | 80.04 | 1.90 | 28.81 | 11.20 | 14.53 | 45.83 | 2.03  | 38.11 | 29.98 | 88.32 |
| 70                | C306        | 95.85 | 3.35 | 38.44 | 8.59  | 16.10 | 41.00 | 1.69  | 37.56 | 47.57 | 73.58 |
| <b>Grand mean</b> |             | 70.97 | 1.59 | 28.36 | 8.376 | 13.72 | 33.83 | 1.281 | 36.32 | 38.52 | 72.79 |
| <b>SD</b>         |             | 1.86  | 0.18 | 1.19  | 0.48  | 0.54  | 2.86  | 0.09  | 1.59  | 3.08  | 2.47  |
| <b>CV</b>         |             | 2.62  | 11.7 | 4.22  | 5.78  | 3.99  | 8.48  | 7.04  | 4.39  | 8.00  | 3.39  |

PH : Plant height  
SL : Spike length  
TW : 1000-grain weight  
ELWRC : Excised leaf water retention capacity

TN : Number of tillers/plant  
SL/SP : Number of spikelets/ spike  
GY/SP : Grain yield/ main spike

PL : Peduncle length  
GN : Number of grains/spike  
RWC : Relative leaf water content

#### **4.2.2.1 Plant height:**

The genotypes showed a grand mean of 70.972 cm for plant height. The plant height ranged from 52.73 cm (HW 2040) to 99.49 cm (RS 634). Genotypes MP 3066 (97.95 cm), MP1136 (94.54 cm), C306 (95.85 cm) and HW 2004 (93 cm) have shown higher plant height.

#### **4.2.2.2 Number of productive tillers/ plant:**

The highest mean number of productive tillers/plant was exhibited by the genotype C306 (3.35). Many genotypes recorded only one tiller. Genotypes that recorded only one tiller include MP 1128, WR 251, Lok Bold, HPW 190, HI 1489, HPW 184, HW 2047, and HD 2747. The grand mean for tiller number is 1.596.

#### **4.2.2.3 Peduncle length:**

Peduncle length ranged between 14.34 cm (NIAW 34) and 44.54 cm (K 9903) with a grand mean of 28.36 cm.

#### **4.2.2.4 Spike length:**

The genotype NIAW 588 recorded the maximum spike length among the genotypes (11.92 cm) whereas MP 1128 showed the least spike length (4.47 cm). The grand mean is 8.376 cm.

#### **4.2.2.5 Number of spikelets/spike:**

The grand mean of 13.728 was observed for the number of spikelets/spike. The number of spikelets per spike ranged from 7.06 (MP 1128) to 20.8 (RL-22-1092).

#### **4.2.2.6 Number of grains/ spike:**

SKW 178 (58.5) produced the highest mean number of grains/spike and the genotype HW 2784 (8 grains) recorded the least number of grains/spike. The grand mean for the character is 33.829.

#### **4.2.2.7 Grain yield/main spike:**

Maximum grain yield/main spike was recorded in RS 634 (2.2 gm) and the genotype H W 2 784 recorded the lowest grain yield/main spike ( 0.3 gm) with a grand mean of 1.281 gm.

#### **4.2.2.8 1000-grain weight:**

The highest and lowest values for 1000-grain weight were recorded for Kundan (43.77 gm) and RL-22-1092 (20.28 gm), respectively.

#### **4.2.2.9 Relative Leaf Water Content:**

Relative Leaf Water Content (RWC) showed a grand mean of 72.729 per cent. Highest relative leaf water content was noted for the genotype Kundan (92.89 %) whereas it was lowest in the genotype HW 3036 (61.22%).

#### **4.2.2.10 Excised leaf water retention capacity:**

Mean Excised leaf water retention capacity of genotypes ranged from 21.74 per cent (UP 2338) to 57.14 per cent (K 9903) with the grand mean of 38.52 per cent.

## **4.3 CORRELATION STUDIES**

The phenotypic and genotypic correlations among ten different morphophysiological characters were worked out using 70 different genotypes. The results of the genotypic and phenotypic correlations are presented in the Table 5.

### **4.3.1 GENOTYPIC CORRELATIONS**

Usually the genotypic correlations are higher than the phenotypic correlations with similar sign and are reflected in the results obtained in the present study. All the characters under study have shown positive significant correlation with the grain yield/spike except excised leaf water retention capacity, which showed a negative correlation.

Plant height showed positive significant correlation with various characters like number of tillers/plant (0.637), peduncle length (0.880), spike length (0.658), number of spikelets/spike (0.601), number of grains/spike (0.632) and grain yield/spike (0.620). Plant height had positive non-significant correlation with 1000-grain weight, Relative Leaf Water Content and Excised Leaf Water Retention Capacity.

Positive significant associations were recorded for the number of tillers/plant with plant height (0.637), peduncle length (0.651), number of grains/spike (0.563) and grain yield/main spike (0.585). However it had positive non-significant correlation with all the other characters studied.

The character peduncle length exhibited positive significant correlation with plant height (0.880), number of tillers/plant (0.651), spike length (0.588) and grain yield/main

**Table 5: Genotypic and phenotypic correlation coefficients for 10 different characters**

| Character | PH   | TN     | PL      | SL     | SL/SP   | GN      | TW     | ELWRC  | RWC    | GY/SP   |
|-----------|------|--------|---------|--------|---------|---------|--------|--------|--------|---------|
| PH G      | 1.00 | 0.637* | 0.880** | 0.658* | 0.601*  | 0.632*  | 0.326  | 0.046  | 0.430  | 0.620*  |
| PH P      | 1.00 | 0.613* | 0.849** | 0.638* | 0.576*  | 0.615*  | 0.316  | 0.045  | 0.381  | 0.603*  |
| TN G      |      | 1.00   | 0.651*  | 0.491  | 0.520   | 0.563*  | 0.084  | 0.006  | 0.321  | 0.585*  |
| TN P      |      | 1.00   | 0.629*  | 0.482  | 0.509   | 0.525   | 0.083  | 0.004  | 0.305  | 0.566*  |
| PL G      |      |        | 1.00    | 0.588* | 0.412   | 0.504   | 0.402  | 0.104  | 0.431  | 0.576*  |
| PL P      |      |        | 1.00    | 0.574* | 0.411   | 0.490   | 0.380  | 0.107  | 0.402  | 0.564*  |
| SL G      |      |        |         | 1.00   | 0.802** | 0.629*  | 0.085  | -0.016 | 0.379  | 0.587*  |
| SL P      |      |        |         | 1.00   | 0.764** | 0.619*  | 0.080  | -0.015 | 0.351  | 0.572*  |
| SL/SP G   |      |        |         |        | 1.00    | 0.776** | -0.085 | -0.076 | 0.349  | 0.577*  |
| SL/SP P   |      |        |         |        | 1.00    | 0.750** | -0.081 | -0.071 | 0.322  | 0.569*  |
| GN G      |      |        |         |        |         | 1.00    | -0.045 | -0.207 | 0.568* | 0.702** |
| GN P      |      |        |         |        |         | 1.00    | -0.039 | -0.206 | 0.561* | 0.685** |
| TW G      |      |        |         |        |         |         | 1.00   | 0.252  | 0.389  | 0.568*  |
| TW P      |      |        |         |        |         |         | 1.00   | 0.224  | 0.366  | 0.561*  |
| ELWRC G   |      |        |         |        |         |         |        | 1.00   | -0.219 | -0.167  |
| ELWRC P   |      |        |         |        |         |         |        | 1.00   | -0.217 | -0.161  |
| RWC G     |      |        |         |        |         |         |        |        | 1.00   | 0.866** |
| RWC P     |      |        |         |        |         |         |        |        | 1.00   | 0.815** |
| GY/SP G   |      |        |         |        |         |         |        |        |        | 1.00    |
| GY/SP P   |      |        |         |        |         |         |        |        |        | 1.00    |

\*\* and \*: significant at 1 and 5 per cent

Plant height

Number of tillers/plant

Peduncle length

Spike length

SL/SP: Number of spikelets/spike

GN: Number of grains/spike

TW: 1000-grain weight

ELWRC: Excised leaf water retention capacity

RWC: Relative leaf water content

GY/SP: Grain yield/ main spike.

spike (0.576). However, with all the other characters it has positive non-significant association.

Spike length exhibited significant positive association with plant height (0.658), peduncle length (0.588), number of spikelets/spike (0.802), number of grains/spike (0.629) and grain yield/main spike (0.587). Spike length has negative non-significant association with Excised Leaf Water Retention Capacity.

Number of spikelets/spike behaved similar to that of spike length. It had a significant positive association with plant height (0.601), spike length (0.802), number of grains/spike (0.776) and grain yield/main spike (0.577). Number of spikelets/spike showed a negative non-significant association with 1000-grain weight and Excised Leaf Water Retention Capacity.

Significant positive correlations were observed between number of grains/spike and plant height (0.632), number of tillers/plant (0.563), spike length (0.629), number of spikelets/spike (0.776), Relative Leaf Water Content (0.568) and grain yield/main spike (0.702). Number of grains/spike exhibited negative non-significant correlation with 1000-grain weight and Excised Leaf Water Retention Capacity.

Positive significant correlation was noticed between 1000-grain weight and grain yield/main spike (0.568), however, it showed non-significant association with all the remaining traits studied.

Excised Leaf Water Retention Capacity does not show significant association with any of the characters studied in the present investigation.

Positive significant correlations were recorded between Relative Leaf Water Content and number of grains/spike (0.568) and grain yield/main spike (0.866). However,

Relative Leaf Water Content showed positive correlation with all the other characters under study except excised leaf water retention capacity.

#### **4.3.2 PHENOTYPIC CORRELATIONS:**

It is evident from the Table 4 that plant height has positive significant correlation with various characters like number of tillers/plant (0.613), peduncle length (0.849), spike length (0.638), number of spikelets/spike (0.576), number of grains/spike (0.615), and grain yield/main spike (0.603). Plant height showed positive non-significant correlation with 1000-grain weight, Relative Leaf Water Content and excised leaf water retention capacity.

Significant positive associations were recorded between number of tillers per plant and plant height (0.613), peduncle length (0.629), and grain yield/main spike (0.566). However it had positive non-significant correlation with all the other characters studied.

Peduncle length exhibited positive significant correlation with plant height (0.849), number of tillers/plant (0.629), spike length (0.574) and grain yield/main spike (0.564). It showed positive non-significant association with all the other characters studied.

Spike length exhibited significant positive association with plant height (0.638), peduncle length (0.574), number of spikelets/spike (0.764), number of grains/spike (0.619) and grain yield/main spike (0.572). However, spike length showed negative non-significant association with excised leaf water retention capacity.

No of spikelets/spike had a significant positive association with plant height (0.576), spike length (0.764), number of grains/spike (0.750) and grain yield/main spike

(0.569). Whereas it showed a negative non-significant association with 1000-grain weight and excised leaf water retention capacity.

Significant positive correlations were observed between number of grains/spike and plant height (0.615), spike length (0.619), number of spikelets/spike (0.750), Relative Leaf Water Content (0.561) and grain yield/main spike (0.685). However, the same trait exhibited negative non-significant correlation with 1000-grain weight and excised leaf water retention capacity.

Thousand-grain weight had a positive significant correlation with only grain yield/main spike (0.561) and showed non-significant association with all the other traits studied.

Excised leaf water retention capacity does not show any significant association with any of the characters studied in the present investigation.

Significant positive correlations were shown by relative leaf water content with number of grains/spike (0.561) and grain yield/main spike (0.815). However, relative leaf water content had positive correlation with all the other characters under study except excised leaf water retention capacity.

#### **4.4 PATH COEFFICIENT ANALYSIS**

The differences due to genotypes under study were significant indicating sufficient genetic variability was available in the material selected for the experiment. Path coefficient analysis reveals, in quantitative terms, the contribution of different variables towards the expression of any dependent variable. The direct and indirect effects were worked out separately. Each character influences other character directly or through the influence via third character i.e., indirect effect. In the present investigation

grain yield/spike is taken as dependent variable and remaining nine characters viz., plant height, number of tillers/plant, peduncle length, spike length, number of spikelets/spike, number of grains/main spike, 1000-grain weight, Excised leaf water retention capacity and Relative Leaf Water Content as independent variables. The phenotypic and genotypic path analysis representing the direct and indirect effects of various characters have been presented in Table 6 and 7.

#### **4.4.1 PHENOTYPIC PATH COEFFICIENT ANALYSIS**

In a broad sense majority of the characters have positive direct effects, although few have shown negative direct effect on grain yield/main spike. The sum of negative direct effects when compared to the sum of positive direct effects is negligible. Results indicated that the maximum positive direct effect on grain yield/main spike was due to Relative Leaf Water Content (0.539) followed by number of grains/spike (0.290), number of spikelets/spike (0.192), 1000-grain weight (0.175), peduncle length (0.055), and plant height (0.055). Negative direct effects were recorded for number of tillers/plant (-0.005), spike length (-0.069) and excised leaf water retention capacity (-0.019).

The indirect effects revealed that most of the characters had very low contributions towards grain yield/main spike via other characters. However, few characters have shown higher magnitude of indirect effects through other characters than directly influencing the grain yield/main spike. For convenience only indirect effects of comparatively higher magnitude have been depicted here. Interestingly all the characters studied have indirect effect on grain yield/main spike via Relative Leaf Water Content. Plant height had positive indirect effect of 0.111, 0.178, and 0.205 via number of spikelets/spike, number of grains/spike and Relative Leaf Water Content respectively. Number

**Table 6: Phenotypic path coefficients showing direct and indirect effects**

| Character | PH    | TN            | PL           | SL            | SL/SP        | GN           | TW           | ELWRC         | RWC          |
|-----------|-------|---------------|--------------|---------------|--------------|--------------|--------------|---------------|--------------|
| PH        | 0.055 | -0.003        | 0.046        | -0.044        | 0.111        | 0.178        | 0.055        | -0.001        | 0.205        |
| TN        | 0.034 | <b>-0.005</b> | 0.034        | -0.033        | 0.098        | 0.152        | 0.015        | 0.000         | 0.164        |
| PL        | 0.046 | -0.003        | <b>0.055</b> | -0.036        | 0.079        | 0.142        | 0.066        | -0.002        | 0.217        |
| SL        | 0.035 | -0.002        | 0.029        | <b>-0.069</b> | 0.147        | 0.179        | 0.014        | 0.000         | 0.189        |
| SL/SP     | 0.031 | -0.003        | 0.023        | -0.053        | <b>0.192</b> | 0.217        | -0.014       | 0.001         | 0.173        |
| GN        | 0.34  | -0.003        | 0.027        | -0.043        | 0.144        | <b>0.290</b> | -0.007       | 0.004         | 0.239        |
| TW        | 0.017 | 0.000         | 0.021        | -0.005        | -0.016       | -0.011       | <b>0.175</b> | -0.004        | 0.197        |
| ELWRC     | 0.003 | 0.000         | 0.006        | 0.001         | -0.014       | -0.060       | 0.039        | <b>-0.019</b> | 0.117        |
| RWC       | 0.021 | -0.002        | 0.022        | -0.024        | 0.062        | 0.129        | 0.064        | 0.004         | <b>0.539</b> |

**Note:** Direct effects on main diagonal.

PH: Plant height

TN: Number of tillers/plant

PL: Peduncle length

SL: Spike length

SL/SP: Number of spikelets/spike

GN: Number of grains/spike

TW: 1000-grain weight

ELWRC: Excised leaf water retention capacity

RWC: Relative leaf water content

of tillers/plant showed indirect effects through number of grains/spike (0.152) and Relative Leaf Water Content (0.164). Peduncle length had shown indirect influence through number of grains/spike (0.142) and Relative Leaf Water Content (0.217). Spike length exhibited positive indirect effects via number of spikelets/spike (0.147), number of grains/spike (0.179) and Relative Leaf Water Content (0.189). The character number of spikelets/spike showed indirect effects via number of grains/spike (0.217) and Relative Leaf Water Content (0.173). Number of grains/spike and 1000-grain weight has shown higher magnitudes of indirect effects on grain yield/main spike via Relative Leaf Water Content, the magnitude of indirect effects is 0.239 and 0.197 respectively. Excised leaf water retention capacity had a negative indirect effect of  $-0.060$  (via number of grains/spike) and  $-0.177$  (via Relative Leaf Water Content) on grain yield/main spike. Relative Leaf Water Content exhibited positive indirect effect via number of grains/spike (0.129) and 1000-grain weight (0.064).

#### **4.4.2 GENOTYPIC PATH COEFFICIENT ANALYSIS**

Genotypic path coefficients have similar direct and indirect effects on grain yield/main spike as that of the phenotypic path coefficient. Magnitude of genotypic path coefficient is relatively higher compared to the phenotypic path coefficients. It is evident from the results (Table 7) that Relative Leaf Water Content had the highest positive direct effect on grain yield/main spike (0.587) among various characters studied. Other characters showing positive direct effects include number of grains/spike (0.307), 1000-grain weight (0.196), number of spikelets/spike (0.191), peduncle length (0.067) and number of tillers/plant (0.002) whereas other characters namely plant height, spike length and excised leaf water retention capacity showed negative direct effects. Spike length

**Table 7: Genotypic path coefficients showing direct and indirect effects**

| Character    | PH            | TN           | PL           | SL            | SL/SP        | GN           | TW           | ELW<br>RC     | RWC          |
|--------------|---------------|--------------|--------------|---------------|--------------|--------------|--------------|---------------|--------------|
| <b>PH</b>    | <b>-0.009</b> | 0.001        | 0.059        | -0.051        | 0.115        | 0.194        | 0.064        | -0.001        | 0.249        |
| <b>TN</b>    | -0.006        | <b>0.002</b> | 0.044        | -0.038        | 0.099        | 0.163        | 0.016        | 0.000         | 0.186        |
| <b>PL</b>    | -0.008        | 0.001        | <b>0.067</b> | -0.043        | 0.078        | 0.155        | 0.079        | -0.003        | 0.249        |
| <b>SL</b>    | -0.006        | 0.001        | 0.037        | <b>-0.078</b> | 0.153        | 0.193        | 0.017        | 0.000         | 0.219        |
| <b>SL/SP</b> | -0.006        | 0.001        | 0.028        | -0.062        | <b>0.191</b> | 0.238        | -0.017       | 0.002         | 0.201        |
| <b>GN</b>    | -0.006        | 0.001        | 0.034        | -0.049        | 0.148        | <b>0.307</b> | -0.009       | 0.005         | 0.271        |
| <b>TW</b>    | -0.003        | 0.000        | 0.027        | -0.007        | -0.016       | -0.014       | <b>0.196</b> | -0.006        | 0.225        |
| <b>ELWRC</b> | 0.000         | 0.000        | 0.007        | 0.001         | -0.014       | -0.064       | 0.049        | <b>-0.025</b> | -0.121       |
| <b>RWC</b>   | -0.004        | 0.001        | 0.029        | -0.029        | 0.066        | 0.144        | 0.076        | 0.005         | <b>0.578</b> |

**Note:** Direct effects on main diagonal.

PH: Plant height

TN: Number of tillers/plant

PL: Peduncle length

SL: Spike length

SL/SP: Number of spikelets/spike

GN: Number of grains/spike

TW: 1000-grain weight

ELWRC: Excised leaf water retention capacity

RWC: Relative leaf water content

exhibited highest negative direct effect of  $-0.078$  followed by excised leaf water retention capacity ( $-0.025$ ) and plant height ( $-0.009$ ). Different characters have positive and negative direct path coefficients on the grain yield/main spike, however, the magnitude of total positive direct effects are far higher than sum of negative direct effects.

The results of indirect effects of genotypic path coefficients (Table 5) revealed that all the characters studied have considerable amount of influence on the grain yield/main spike through other characters. All the characters studied showed high positive indirect effect on grain yield/main spike via Relative Leaf Water Content. However, excised leaf water retention capacity has a negative indirect effect through Relative Leaf Water Content on grain yield/main spike.

Plant height, which exhibited negative direct effect on grain yield/main spike, had positive indirect effect via number of spikelets/spike ( $0.115$ ), number of grains/spike ( $0.194$ ) and Relative Leaf Water Content ( $0.249$ ) and negative indirect effect via spike length ( $-0.051$ ). Number of tillers/plant exhibited positive indirect effect through number of spikelets/spike ( $0.099$ ), number of grains/spike ( $0.163$ ) and Relative Leaf Water Content ( $0.186$ ). Positive indirect effects were recorded by peduncle length via number of grains/spike ( $0.155$ ), 1000-grain weight ( $0.079$ ) and Relative Leaf Water Content ( $0.249$ ). Spike length also showed positive indirect effects through number of spikelets/spike ( $0.153$ ), number of grains/spike ( $0.193$ ) and Relative Leaf Water Content ( $0.219$ ). Negative indirect effect of  $-0.062$  was recorded by number of spike lets/spike via spike length, however, it also exhibited positive indirect effect via number of grains/spike ( $0.238$ ) and Relative Leaf Water Content ( $0.201$ ). 1000-grain weight and number of

grains/spike have positive indirect effect via Relative Leaf Water Content (0.225 and 0.271 respectively). The physiological parameter excised leaf water retention capacity showed positive influence through 1000-grain weight (0.049) and negative indirect effect via number of grains/spike (-0.064) and Relative Leaf Water Content (-0.121).

All the characters studied have significant contribution towards the expression of grain yield/main spike. However, they are not sufficient for the entire expression. Thus there is a residual effect of 0.1594 (phenotypic) and 0.098 (genotypic) left over.

## **4.5 GENETIC DIVERGENCE ANALYSIS**

Knowledge of the extent of genetic divergence in the existing germplasm is very essential before attempting any crop improvement programme. Divergence analysis of 70 different genotypes grown under different agro-climatic zones of India was carried out. The data was subjected to Mahalanobis'  $D^2$  statistic. The results obtained are presented hereunder.

### **4.5.1 MAHALANOBIS' $D^2$ STATISTIC**

The  $D^2$  values that determine the statistical distance among the various genotypes reflecting their genetic diversity was estimated pair-wise for all the genotypes under study using 10 different morphophysiological characters. Based on the  $D^2$  -values, the genotypes were grouped into different constellations adopting Tocher's method. Seventy genotypes under study were grouped into 8 clusters. The details of the group constellations are presented in the Table 8.

The cluster I contained highest number of genotypes (13), namely, MP 1128, HW2022, UP 2532, WR 251, HUW 234, Ning 8319, Lok Bold, Lok 45, RW 3542, HI 1489, HW 3035, HD 2747 and HW 1042. Twelve genotypes were included in cluster IV

**Table 8: Group constellation of the genotypes based on Mahalanobis'  $D^2$**

| Cluster | Number of genotypes | Genotypes included                                                                                                     |
|---------|---------------------|------------------------------------------------------------------------------------------------------------------------|
| I       | 13                  | MP 1128, HW2022, UP 2532, WR 251, HUW 234, Ning 8319, Lok Bold, Lok 45, RW 3542, HI 1489, HW 3035, HD 2747 and HW 1042 |
| II      | 11                  | Baktawar, MP 1124, K 9107, HUW 206, Lok 44, HPW 184, HP1851, RL-84-1, CPAN 1492, NIAW 590 and HD 2839                  |
| III     | 7                   | Pissi local, HW 3045, Lok Bharati, Lok-1, HW 3036, K 9909, and HD 2784                                                 |
| IV      | 12                  | SKW178, NW 2034, UP 2338, HW 2045, HUW 540, NW 2033, Deckson 98A, NIAW 588, MACS/2496, DBW 14, RL-22-1092, and HW 3081 |
| V       | 4                   | HPW 190, HW 2040, NIAW 34, and HW 2047                                                                                 |
| VI      | 6                   | HW 2004, K 9903, RS 634, MP 3066, MP 1136, and C-306                                                                   |
| VII     | 11                  | HD 2329, HW 3026, HW 2044, WH 744, HW 2099, NI 5439, Akber, UP 2537, PBW 343, WR 544, AND Kundan                       |
| VIII    | 6                   | BH 146, JWS 68, HI 1502, HD 2687, K 8027, and RW 857                                                                   |

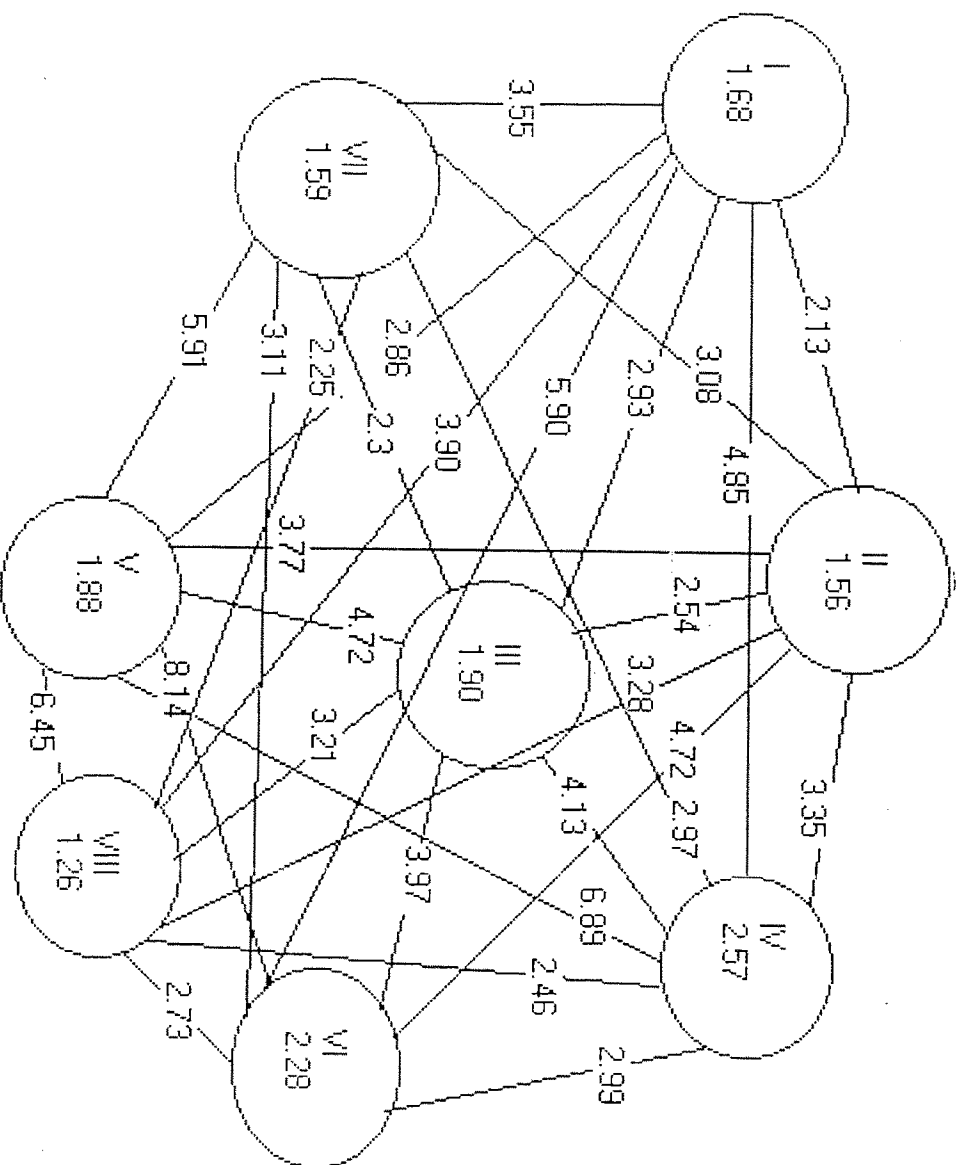


**Fig :CLUSTER DIAGRAM SHOWING INTER AND INTRA CLUSTER DISTANCES**

viz., SKW178, NW 2034, UP 2338, HW 2045, HUW 540, NW 2033, Deckson 98A, NIAW 588, MACS/2496, DBW 14, RL-22-1092, and HW 3081. Cluster II and VII consisted of eleven genotypes each. Genotypes included in cluster II are Bakhtawar, MP 1124, K 9107, HUW 206, Lok-44, HPW 184, HP1851, RL-84-1, CPAN 1492, NIAW 590 and HD 2839 and that of cluster VII are HD 2329, HW 3026, HW 2044, WH 744, HW 2099, NI 5439, Akber, UP 2537, PBW 343, WR 544, AND Kundan. Seven genotypes were placed in cluster III, namely, Pissi local, HW 3045, Lok Bharati, Lok-1, HW 3036, K 9909, and HD 2784. Clusters VI and VIII were formed by six genotypes each. The genotypes included in cluster VI are HW 2004, K 9903, RS 634, MP 3066, MP 1136, and C306 and cluster VIII comprised of BH 146, JWS 68, HI 1502, HD 2687, K 8027, and RW 857 genotypes. Lowest number of genotypes (4) is placed into cluster V, namely, HPW 190, HW 2040, NIAW 34, and HW 2047. The distribution of 70 genotypes among eight clusters was relatively uniform and reasonable.

#### **4.5.2 INTRA AND INTER CLUSTER DISTANCES**

The intra and inter cluster distances are presented in Table 9 and Fig. 1. Highest inter cluster distance was observed between the clusters V and VI (8.143) followed by clusters V and IV (6.898), clusters V and VIII (6.458), clusters V and VII (5.917) and clusters VI and I (5.909). Moderate inter cluster distances were observed between clusters VI and II (4.720), clusters V and III (4.727), clusters I and II (4.859), III and IV (4.139), VI and III (3.976) and clusters I and VIII (3.901). The distance between clusters II and I was minimum (2.173) followed by between the clusters VII and VIII (2.255).

It is evident from the results that the intra cluster distance is highest in the cluster IV (2.571) followed by within the cluster VI (2.289) having 12 and 6 genotypes

**Table 9: Inter and intra cluster distances ( $D^2$  values) for 10 characters**

| Cluster number | I     | II    | III   | IV    | V     | VI    | VII   | VIII  | Intra cluster distance |
|----------------|-------|-------|-------|-------|-------|-------|-------|-------|------------------------|
| <b>I</b>       | 0.000 |       |       |       |       |       |       |       | 1.680                  |
| <b>II</b>      | 2.173 | 0.000 |       |       |       |       |       |       | 1.560                  |
| <b>III</b>     | 2.938 | 2.546 | 0.000 |       |       |       |       |       | 1.906                  |
| <b>IV</b>      | 4.859 | 3.356 | 4.139 | 0.000 |       |       |       |       | 2.571                  |
| <b>V</b>       | 2.862 | 3.770 | 4.727 | 6.898 | 0.000 |       |       |       | 1.884                  |
| <b>VI</b>      | 5.909 | 4.720 | 3.976 | 2.992 | 8.143 | 0.000 |       |       | 2.289                  |
| <b>VII</b>     | 3.552 | 3.081 | 2.300 | 2.974 | 5.917 | 3.113 | 0.000 |       | 1.592                  |
| <b>VIII</b>    | 3.901 | 3.285 | 3.218 | 2.467 | 6.458 | 2.736 | 2.255 | 0.000 | 1.266                  |

**Table 10: Cluster means of 70 genotypes for ten characters**

| Cluster number | PH    | TN   | PL    | SL    | SL/SP | GN    | GY/SP | TW    | ELWRC | RWC   |
|----------------|-------|------|-------|-------|-------|-------|-------|-------|-------|-------|
| <b>I</b>       | 59.20 | 1.12 | 23.88 | 6.43  | 10.38 | 25.92 | 0.958 | 36.51 | 35.39 | 70.46 |
| <b>II</b>      | 67.39 | 1.28 | 25.14 | 8.33  | 14.03 | 31.85 | 1.04  | 32.23 | 36.46 | 67.92 |
| <b>III</b>     | 73.47 | 1.71 | 30.36 | 8.48  | 12.77 | 24.41 | 1.03  | 39.45 | 47.92 | 68.92 |
| <b>IV</b>      | 74.57 | 1.96 | 28.70 | 10.26 | 17.34 | 48.32 | 1.68  | 34.36 | 32.81 | 77.58 |
| <b>V</b>       | 45.57 | 1.05 | 16.75 | 5.91  | 9.86  | 16.47 | 0.50  | 30.73 | 40.59 | 69.26 |
| <b>VI</b>      | 95.08 | 2.24 | 39.42 | 9.81  | 16.58 | 45.95 | 1.89  | 38.44 | 43.58 | 73.79 |
| <b>VII</b>     | 73.14 | 1.63 | 30.81 | 8.75  | 14.00 | 32.54 | 1.46  | 39.83 | 45.88 | 75.90 |
| <b>VIII</b>    | 81.77 | 1.99 | 33.09 | 8.28  | 13.51 | 38.38 | 1.51  | 38.56 | 29.57 | 77.39 |

PH: Plant height

TN: Number of tillers/plant

PL: Peduncle length

SL: Spike length

SL/SP: Number of spikelets/spike

GN: Number of grains/spike

TW: 1000-grain weight

ELWRC: Excised leaf water retention capacity

RWC: Relative leaf water content

respectively. This is closely followed by cluster III (1.906) and cluster V (1.884). The cluster VIII showed minimum intra cluster distance (1.266). Thus the genotypes included in clusters III, IV, V and VI revealed maximum diversity among them and also contributed to higher inter cluster distances.

#### **4.5.3 CLUSTER MEANS**

The cluster means for each character was calculated by averaging the total of the mean values of each genotype belonging to that particular cluster. The calculated cluster means for various characters were presented in Table 10. The cluster V consisting of HPW 190, HW 2040, NIAW 34, and HW 2047 genotypes exhibited lowest cluster mean values for all the morphological or yield attributes studied in the present investigation. Whereas, for the physiological characters the cluster mean is neither highest nor lowest compared to other cluster means. Character wise cluster means for cluster V are plant height (45.575), number of tillers/ plant (1.05), peduncle length (16.755), spike length (5.915), number of spikelets/spike (9.862), number of grains/spike (16.475), grain yield/main spike (0.502), and 1000-grain weight (30.737). The description of the highest cluster means for each character is described in the following paragraph.

##### **4.5.3.1 Plant height:**

Cluster VI consisting of six genotypes had the highest mean plant height of 95.08 cm followed by cluster VIII (81.773 cm); the cluster VIII also consists of six genotypes only.

##### **4.5.3.2 Number of tillers/plant:**

Highest average number of tillers per plant was recorded by cluster VI (2.241) closely followed by cluster VIII (1.995) and cluster IV (1.962).

#### **4.5.3.3 Peduncle length:**

Cluster VI recorded the highest mean peduncle length (39.428 cm) followed by cluster VIII (33.09 cm) and cluster VII (30.811 cm).

#### **4.5.3.4 Spike length:**

The cluster IV that included 12 genotypes recorded highest mean spike length of 10.263 cm. It is closely followed by cluster VI with a mean spike length of 9.81 cm.

#### **4.5.3.5 Number of spikelets/spike:**

The clusters IV and VI recorded highest mean number of spike lets per spike (17.345 and 46.583 respectively).

#### **4.5.3.6 Number of grains/spike:**

Cluster IV showed highest mean number of grains per spike (48.327) followed by cluster VI (45.958). The cluster VIII has a mean of 38.382.

#### **4.5.3.7 Grain yield /main spike:**

Reasonable variation is found in the mean grain yield per spike among the clusters. The cluster mean ranged between 0.502 g (cluster V) and 1.895 g (cluster VI). Towards the higher value the cluster VI is followed by cluster IV (1.687 g), cluster VIII (1.51 g) and cluster VII (1.46 g).

#### **4.5.3.8 1000- grain weight:**

The cluster means for 1000- grain weight are very close. Highest cluster mean was recorded by cluster VII (39.831 g) followed very closely by cluster III (39.451g), cluster VIII (38.566g) and cluster VI (38.448g). Lowest cluster means were recorded by cluster V (30.737 g) and cluster II (32.236g).

#### **4.5.3.9 Relative Leaf Water Content:**

The cluster IV exhibited the highest mean Relative Leaf Water Content (77.580%) followed very closely by cluster VIII (77.393%). However, the clusters II and III recorded the lowest mean Relative Leaf Water Content values (67.898 % and 68.925 % respectively).

#### **4.5.3.10 Excised Leaf Water Retention Capacity:**

Lowest value of excised leaf water retention capacity indicated the higher tolerance of genotypes to moisture stress conditions. The cluster VIII showed the lowest mean excised leaf water retention capacity (29.578%) followed by cluster IV (32.812%) and cluster I (35.393%). Highest mean excised leaf water retention capacity was recorded by the genotypes classified in cluster III (47.922%) and cluster VII (45.883%).

### **4.6 GENERATION MEAN ANALYSIS**

The mean data obtained from the six generations of all the four crosses (Kundan x HD2329, MP1136 x HW2044, HW3081 x HD2839 and HW3081 x C306) for ten different characters were subjected to A, B and C scaling tests to know the presence of epistasis. Then the data were analyzed using six parameter model (Hayman, 1958) and three parameter model of Cavalli's (1952) joint scaling test and tested for goodness of fit. When the additive dominance model was found inadequate, sequential model fit scheme was employed. Either the best fit model (non-significant  $\chi^2$  value) or the one having the lowest  $\chi^2$  value was considered appropriate to know the gene action. The mean data for all the four crosses for ten characters is presented in Table 11. The data on genetic components are presented cross-wise and have been described accordingly hereunder.

Table 11. Mean data for six generation ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of four crosses

| Generation               | 1     | 2     | 3     | 4    | 5     | 6     | 7     | 8    | 9     | 10   |
|--------------------------|-------|-------|-------|------|-------|-------|-------|------|-------|------|
| <b>Kundan x HD 2329</b>  |       |       |       |      |       |       |       |      |       |      |
| $P_1$                    | 93.57 | 42.41 | 71.43 | 2.33 | 33.11 | 8.88  | 14.53 | 2.27 | 30.35 | 1.78 |
| $P_2$                    | 73.08 | 42.12 | 66.60 | 2.40 | 28.71 | 8.90  | 15.23 | 1.92 | 31.03 | 1.50 |
| $F_1$                    | 90.14 | 40.00 | 76.18 | 3.03 | 34.49 | 10.20 | 16.50 | 2.65 | 38.57 | 2.07 |
| $F_2$                    | 87.97 | 39.77 | 72.34 | 3.11 | 31.78 | 9.60  | 16.21 | 2.26 | 36.68 | 1.74 |
| $BC_1$                   | 88.49 | 33.02 | 73.54 | 2.67 | 32.48 | 9.71  | 15.94 | 2.32 | 35.36 | 1.78 |
| $BC_2$                   | 86.93 | 41.92 | 74.81 | 3.58 | 33.44 | 9.99  | 16.93 | 2.28 | 40.56 | 1.80 |
| <b>MP 1136 x HW 2044</b> |       |       |       |      |       |       |       |      |       |      |
| $P_1$                    | 89.90 | 50.82 | 87.99 | 2.25 | 37.97 | 8.49  | 14.94 | 2.13 | 41.57 | 1.69 |
| $P_2$                    | 71.00 | 49.08 | 73.94 | 2.43 | 34.19 | 8.86  | 13.87 | 1.84 | 33.97 | 1.52 |
| $F_1$                    | 90.89 | 50.62 | 88.32 | 2.65 | 38.65 | 10.06 | 15.53 | 2.38 | 43.41 | 1.88 |
| $F_2$                    | 88.70 | 45.04 | 87.33 | 3.20 | 39.43 | 9.69  | 16.00 | 2.27 | 43.17 | 1.82 |
| $BC_1$                   | 90.51 | 42.87 | 86.85 | 2.76 | 37.80 | 9.95  | 17.14 | 2.64 | 48.53 | 2.08 |
| $BC_2$                   | 88.99 | 43.81 | 86.82 | 2.55 | 37.65 | 9.87  | 16.26 | 2.24 | 42.00 | 1.74 |
| <b>HW 3081 x HD 2839</b> |       |       |       |      |       |       |       |      |       |      |
| $P_1$                    | 87.63 | 28.93 | 75.63 | 1.66 | 58.50 | 10.72 | 15.35 | 2.31 | 37.98 | 1.55 |
| $P_2$                    | 68.90 | 44.94 | 75.90 | 1.93 | 30.53 | 8.82  | 15.27 | 2.17 | 43.83 | 1.70 |
| $F_1$                    | 89.10 | 27.78 | 78.03 | 1.74 | 31.80 | 9.91  | 16.72 | 3.24 | 54.84 | 2.39 |
| $F_2$                    | 87.70 | 37.57 | 84.70 | 4.28 | 33.16 | 10.58 | 17.24 | 2.40 | 40.76 | 1.79 |
| $BC_1$                   | 91.72 | 37.90 | 86.64 | 2.71 | 32.01 | 11.50 | 18.31 | 2.84 | 47.58 | 2.06 |
| $BC_2$                   | 90.21 | 38.46 | 75.78 | 2.55 | 30.72 | 10.08 | 17.53 | 2.54 | 44.30 | 1.71 |
| <b>HW 3081 x C 306</b>   |       |       |       |      |       |       |       |      |       |      |
| $P_1$                    | 88.43 | 26.56 | 78.91 | 2.07 | 30.58 | 11.50 | 16.81 | 2.63 | 38.91 | 2.05 |
| $P_2$                    | 72.13 | 49.82 | 96.70 | 4.17 | 38.73 | 9.06  | 16.07 | 2.48 | 44.50 | 1.76 |
| $F_1$                    | 88.99 | 39.26 | 99.48 | 4.27 | 41.29 | 11.74 | 19.47 | 3.11 | 46.83 | 2.24 |
| $F_2$                    | 86.88 | 41.25 | 85.90 | 2.99 | 34.79 | 9.74  | 16.53 | 2.38 | 37.83 | 1.74 |
| $BC_1$                   | 89.56 | 38.46 | 87.96 | 3.57 | 33.90 | 11.09 | 18.70 | 2.25 | 0.84  | 1.69 |
| $BC_2$                   | 88.72 | 41.54 | 91.77 | 4.13 | 36.91 | 10.05 | 18.38 | 2.57 | 42.94 | 1.90 |

1. Relative leaf water content, 2. Excised leaf water retention capacity, 3. Plant height, 4. Number of tillers per plant, 5. Peduncle length, 6. Spike length, 7. Number of spikelets per spike, 8. Spike weight, 9. Number of grains per spike, 10. Grain yield per main spike

Table 12. A, B and C scaling tests and the genetic components of the cross Kundan x HD 2329

| Generation                                    | 1            | 2             | 3            | 4            | 5            | 6           | 7            | 8           | 9             | 10           |
|-----------------------------------------------|--------------|---------------|--------------|--------------|--------------|-------------|--------------|-------------|---------------|--------------|
| <b>A,B,C, Scaling test</b>                    |              |               |              |              |              |             |              |             |               |              |
| A                                             | -6.71*±2.95  | -16.37*±7.17  | 1.55*±0.67   | -6.62**±1.27 | -2.63±2.14   | -2.63*±1.33 | 0.85±2.79    | -1.27*±0.53 | 1.79*±0.41    | -1.32*±0.61  |
| B                                             | 0.64±3.71    | 1.72±1.49     | 6.84*±2.67   | 1.72*±0.74   | 3.68±2.26    | 0.87*±0.34  | 2.13**±0.24  | -0.90±1.20  | 11.51**±5.51  | 0.92*±0.47   |
| C                                             | -5.03±7.39   | -5.42*±2.46   | -1.64±2.84   | -1.64*±0.78  | -3.78±3.48   | 1.22±2.02   | 2.06**±0.39  | -1.46*±0.65 | 8.19**±3.19   | 1.47*±0.69   |
| <b>Haynains 6 parameters model</b>            |              |               |              |              |              |             |              |             |               |              |
| m                                             | 87.97**±1.70 | 39.77**±6.81  | 72.34**±2.02 | 3.11**±0.33  | 31.78**±0.71 | 9.59*±0.22  | 16.26**±0.81 | 2.25**±0.10 | 36.67**±1.18  | 1.73**±0.16  |
| d                                             | 1.56*±0.78   | -8.90*±4.04   | -1.27*±0.52  | -0.90±0.41   | -0.95*±0.42  | -1.27*±0.59 | -0.98**±0.32 | 1.63**±0.22 | -5.21**±1.24  | -3.63**±0.19 |
| h                                             | 0.76*±0.36   | -11.49*±4.59  | 14.48**±2.76 | 0.71*±0.31   | 8.31**±2.65  | 2.32**±0.12 | 2.54**±0.76  | 1.73**±0.62 | 12.99**±2.91  | 0.68*±0.27   |
| i                                             | -1.04*±0.45  | -9.22*±4.63   | 7.34±9.35    | 4.54**±0.23  | 4.73±3.51    | 1.00*±0.49  | 0.92*±0.41   | 1.18±0.61   | 5.12**±1.42   | 0.96*±0.51   |
| j                                             | -3.67*±1.53  | -9.22*±4.49   | -3.70*±1.60  | -0.87*±0.35  | -3.15**±1.07 | -0.76±0.71  | -0.83*±0.39  | -0.98±0.74  | -4.85**±1.14  | -2.32*±1.16  |
| l                                             | 7.12±10.84   | -23.87**±8.50 | -13.62±12.47 | -1.73*±0.71  | -5.77±5.38   | -2.22±3.37  | -3.91**±0.65 | -0.92*±0.43 | -18.43**±3.39 | 1.37*±0.59   |
| <b>Joint scaling test (3 parameter model)</b> |              |               |              |              |              |             |              |             |               |              |
| m                                             | 87.81**±0.64 | 41.24**±0.64  | 69.37**±0.64 | 2.51**±0.63  | 30.86**±     | 8.96**±0.64 | 15.11**±0.64 | 2.06**±0.64 | 31.71**±0.64  | 1.60**±0.64  |
| d                                             | 4.50**±0.63  | -1.66*±0.63   | 1.69*±0.63   | -0.90*±0.36  | 1.56*±       | -1.06*±0.51 | -1.47*±0.62  | 1.14*±0.56  | -1.31±0.63    | 1.02*±0.42   |
| h                                             | 1.30*±0.61   | -3.28*±1.18   | 7.47**±1.18  | 0.81*±0.35   | 3.53**±      | 1.39**±0.61 | 1.85*±0.81   | 1.51*±0.65  | 8.89**±1.18   | 4.02**±1.18  |
| ( $\chi^2$ ) (3)                              | 8.352*       | 48.092**      | 29.038**     | 18.554**     | 4.94         | 14.21**     | 32.56**      | 19.59**     | 174.32**      | 92.43**      |
| <b>Best fit model</b>                         |              |               |              |              |              |             |              |             |               |              |
| m                                             | 85.01**±2.08 | 36.89**±2.08  | 70.01**±2.08 | 3.38*±1.38   | -            | 9.24**±2.08 | 16.34**±2.08 | 2.09**±0.71 | 36.83**±2.08  | 13.87**±2.08 |
| d                                             | 5.24*±0.70   | 6.14**±1.21   | 2.43**±0.70  | -0.77*±0.32  | -            | -1.06*±0.41 | -1.35*±0.62  | 2.14**±0.65 | -3.41**±1.12  | 1.37*±0.62   |
| h                                             | 4.84*±2.03   | 2.21**±0.48   | 6.66**±2.77  | -1.28*±0.66  | -            | 1.04**±0.31 | 1.56**±0.71  | 3.21*±1.60  | 4.41**±1.25   | 6.79**±2.77  |
| i                                             | 3.17*±1.42   | -             | -            | -0.98*±0.42  | -            | 1.31*±0.58  | -            | -           | -5.80*±3.01   | 2.47**±0.92  |
| j                                             | -            | -             | -7.41**±3.16 | -            | -            | -           | -1.39**±0.24 | -           | -9.71**±2.42  | -1.34*±0.58  |
| l                                             | -7.35*±3.16  | -18.09**±1.92 | -            | -0.79*±0.30  | -            | -           | -1.27**±0.11 | -1.33*±0.61 | -             | -            |
| $\chi^2$                                      | (1)=0.939    | (2)=10.551**  | (1)=9.43*    | (1)=10.361*  | -            | (2)=2.73    | (1)=12.37**  | (2)=8.19*   | (1)=80.73**   | (1)=35.02**  |

1. Relative leaf water content, 2. Excised leaf water retention capacity, 3. Plant height, 4. Number of tillers per plant, 5. Peduncle length, 6. Spike length, 7. Number of spikelets per spike, 8. Spike weight, 9. Number of grains per spike, 10. Grain yield per main spike

Table 13. A, B and C scaling tests and the genetic components of the cross MP 1136 x HW 2044

| Generation                                    | 1             | 2            | 3             | 4            | 5            | 6            | 7            | 8           | 9             | 10           |
|-----------------------------------------------|---------------|--------------|---------------|--------------|--------------|--------------|--------------|-------------|---------------|--------------|
| <b>A,B,C, Scaling test</b>                    |               |              |               |              |              |              |              |             |               |              |
| A                                             | 0.22±0.08     | -15.70±11.02 | -2.59±0.22    | 0.61±0.59    | -1.02±3.23   | 1.36*±0.69   | 3.79**±1.12  | 0.77*±0.24  | 12.05±9.09    | 0.99±0.84    |
| B                                             | 16.10*±3.69   | -12.07±7.12  | 11.39**±1.49  | 2.64**±0.74  | 2.46**±0.56  | 0.80**±0.22  | 3.13**±0.93  | 0.25±0.58   | 6.62±6.53     | 1.08**±0.47  |
| C                                             | 12.11±7.49    | -20.98±14.06 | 10.74±7.42    | 2.80*±0.98   | 8.26*±3.93   | 1.29*±0.51   | 4.14**±1.51  | 0.33±0.41   | 10.34±12.29   | 3.13*±0.70   |
| <b>Haynains 6 parameters model</b>            |               |              |               |              |              |              |              |             |               |              |
| m                                             | 88.69**±1.82  | 45.03**±2.61 | 87.32**±5.80  | 3.19**±0.14  | 39.43**±1.39 | 9.69**±0.50  | 16.03**±1.12 | 2.26**±0.17 | 43.17**±2.21  | 1.82**±0.13  |
| d                                             | 1.51*±0.68    | -0.94*±0.41  | 2.99*±0.98    | 0.91**±0.34  | 1.40*±0.61   | 0.89**±0.34  | 0.87**±0.32  | 4.01*±1.19  | 6.52*±2.74    | 3.31**±0.25  |
| h                                             | 14.65**±6.18  | -6.11**±1.24 | 5.40**±1.97   | -1.86*±0.89  | -4.25**±1.97 | 2.26**±0.23  | 3.91**±1.49  | 1.07**±0.26 | 14.03**±1.23  | 0.63**±0.27  |
| i                                             | 1.21*±3.09    | -6.78±14.48  | -1.95*±0.84   | -2.17**±0.74 | -6.83±7.85   | 0.88**±0.21  | 2.78±1.83    | 6.89±9.38   | 8.36±11.59    | 0.35*±0.17   |
| j                                             | -7.93**±1.86  | -1.81±6.24   | -6.99**±1.24  | -1.03*±0.51  | -1.74±3.09   | 2.76**±0.74  | 0.93**±0.30  | 2.57*±1.17  | 2.72±5.44     | 2.45**±0.28  |
| l                                             | -20.53*±10.03 | 34.55*±13.65 | -6.83±4.17    | 1.55**±0.48  | 5.39**±0.13  | -3.05**±0.31 | -9.71*±3.74  | -1.71±1.45  | -27.07**±1.93 | -1.02**±0.12 |
| <b>Joint scaling test (3 parameter model)</b> |               |              |               |              |              |              |              |             |               |              |
| m                                             | 81.76**±0.64  | 47.69**±0.64 | 81.79**±0.64  | 2.46**±0.64  | 36.40**±0.64 | 8.83**±0.64  | 14.93**±0.64 | 2.05**±0.64 | 39.17**±0.64  | 1.65**±0.46  |
| d                                             | 7.86**±0.63   | 5.05**±0.63  | 5.62**±0.63   | 3.01**±0.63  | 1.54±0.86    | 1.31**±0.16  | 1.60**±0.61  | 1.93**±0.63 | 4.34*±1.84    | 1.35**±0.36  |
| h                                             | 11.75**±1.18  | -1.58±0.70   | 8.19**±1.18   | 0.43*±0.38   | 2.89**±0.98  | 1.55**±0.29  | 1.65**±0.051 | 0.89**±0.11 | 7.04**±1.17   | 1.27**±0.12  |
| ( $\chi^2$ ) (3)                              | 45.58**       | 7.01         | 27.60**       | 20.39**      | 114.37**     | 37.3**       | 113.53**     | 11.79**     | 2.82          | 114.21**     |
| <b>Best fit model</b>                         |               |              |               |              |              |              |              |             |               |              |
| m                                             | 88.78**±2.08  | -            | 87.09**±2.08  | 4.51**±0.49  | 36.07**±0.70 | 7.79**±1.19  | 14.40**±0.71 | 2.65**±0.64 | -             | 1.60**±0.47  |
| d                                             | 70.83**±0.63  | -            | 7.24**±0.70   | -3.01**±0.63 | 1.54±1.25    | 1.31*±0.54   | 5.37*±2.69   | 1.42±0.86   | -             | 8.65**±1.71  |
| h                                             | 20.86**±1.24  | -            | 1.47*±0.56    | -3.42*±1.42  | 6.28**±2.32  | 5.31**±1.25  | 7.12**±2.39  | 4.59**±1.18 | -             | 1.82*±0.69   |
| i                                             | -             | -            | -6.00**±2.24  | -2.17*±0.96  | -            | 0.88**±0.31  | -            | -           | -             | -            |
| j                                             | -             | -            | -13.99**±3.16 | -            | -            | 1.66*±0.38   | 5.15**±2.13  | -           | -             | 1.49**±0.31  |
| l                                             | -7.95**±2.24  | -            | -             | 1.55**±0.62  | -3.71*±175   | -3.05**±0.73 | -6.02**±2.32 | -           | -             | -1.54**±0.33 |
| $\chi^2$                                      | (2)=6.93*     | -            | (1)=0.866     | (1)=3.92*    | (2)=43.21**  | (1)=12.58**  | (1)=20.46**  | (2)=7.39    | -             | (1)=40.61**  |

1. Relative leaf water content, 2. Excised leaf water retention capacity, 3. Plant height, 4. Number of tillers per plant, 5. Peduncle length, 6. Spike length, 7. Number of spikelets per spike, 8. Spike weight, 9. Number of grains per spike, 10. Grain yield per main spike

In the cross Kundan x HD 2329, the additive dominance model was found to be adequate only for character peduncle length. The scaling tests and genetic parameters were presented in Table 12. All the three genetic parameters viz., m, d and h were found to be significant with non-significant  $\chi^2$  value. This is further confirmed by the non-significance of all the three scaling tests, A, B and C. For rest of the characters, three parameter model was found to be inadequate. For these characters either all or any of the three scaling tests was found to be significant. Under the best fit model, the four parameters m, d, h and i were significant with non-significant  $\chi^2$  value for spike length. For characters excised leaf water retention capacity and spike weight, genetic components m, d, h, and l were found to be important. Further the dominance (h) and dominance x dominance (l) components possessed opposite sign. However, for the character plant height four parameters viz., m, d, h and j were found to be significant.

The five genetic parameters m, d, h, i and l were found to be significant for three traits viz., relative leaf water content, number of tillers/ plant, and number of spikelets/ spike. Further, (h) and (l) components showed opposite sign for RWC and number of spikelets/ spike. For characters number of grains/ spike and grain yield/ main spike, the five parameters model, m, d, h, i and j was found to be best fit but with highly significant  $\chi^2$  values among the different combinations.

The additive dominance model was found to be adequate for characters excised leaf water retention capacity and number of grains/ spike in the cross MP 1136 x HW 2044 (Table 13). While for the rest of the characters the three parameter model was found to be inadequate. Significance of one or more among A, B, and C scaling tests further supports the inadequacy of the additive dominance model. Under best fit model, four

Table 14. A, B and C scaling tests and the genetic components of the cross HW 3081 x HD 2839

| Generation                                    | 1              | 2             | 3             | 4            | 5            | 6            | 7             | 8            | 9             | 10           |
|-----------------------------------------------|----------------|---------------|---------------|--------------|--------------|--------------|---------------|--------------|---------------|--------------|
| <b>A,B,C, Scaling test</b>                    |                |               |               |              |              |              |               |              |               |              |
| A                                             | 6.71±4.84      | 19.08±9.74    | 19.63**±1.26  | 2.01±1.41    | 3.72*±1.31   | 2.97**±0.14  | 4.55**±1.24   | 2.13**±0.39  | 2.33±1.93     | -1.31±0.79   |
| B                                             | 22.42**±5.19   | 4.20**±1.70   | -2.37*±1.14   | 1.41±0.93    | -0.88±1.35   | 1.42*±0.57   | 3.06±2.93     | -0.32±0.46   | -10.07**±1.09 | -6.76*±2.91  |
| C                                             | 16.0±89.91     | 20.84*±9.89   | 31.19*±12.71  | 10.05*±3.89  | 10.01**±1.67 | 2.96**±0.29  | 4.88*±2.18    | -1.37**±0.25 | -28.47**±5.33 | -7.19**±2.55 |
| <b>Haynains 6 parameters model</b>            |                |               |               |              |              |              |               |              |               |              |
| m                                             | 87.70**±2.15   | 37.57**±5.88  | 84.69**±2.54  | 4.28**±0.97  | 33.16**±0.30 | 10.58**±0.13 | 17.23**±0.16  | 2.39**±0.41  | 40.75**±0.53  | 1.78**±0.12  |
| d                                             | 1.50±2.63      | -0.57±11.83   | 10.85**±3.80  | 0.76±0.83    | 1.28*±0.58   | 1.46*±0.62   | 0.78*±0.31    | 2.97**±0.27  | 3.28±3.90     | 0.84**±0.16  |
| h                                             | 23.90**±10.40  | -6.71*±3.01   | -11.68**±1.94 | -6.67**±2.39 | -4.98**±1.44 | 1.06**±0.14  | 4.14**±1.36   | 2.17**±0.61  | 34.66**±4.18  | 1.03*±0.35   |
| i                                             | 13.06±10.11    | 2.43*±1.10    | -13.95*±6.75  | -6.62**±2.43 | -7.17*±3.47  | 0.91*±0.37   | 2.73*±1.34    | 1.18*±0.60   | 20.73**±1.39  | 0.98**±0.33  |
| j                                             | -7.85*±3.52    | 7.43±9.24     | 10.99**±1.82  | 2.98±1.84    | 2.30±2.17    | 0.95**±0.11  | 0.74±1.81     | 0.25±0.33    | 6.20±4.72     | 0.72**±0.019 |
| k                                             | -42.22**±14.46 | -25.72**±8.33 | -3.29±3.46    | 3.18*±1.48   | 4.33±3.85    | -4.80**±1.25 | -10.35**±2.76 | -0.99±1.19   | -12.99**±2.81 | 1.42*±0.71   |
| <b>Joint scaling test (3 parameter model)</b> |                |               |               |              |              |              |               |              |               |              |
| m                                             | 80.45**±1.67   | 38.92**±6.14  | 77.69**±6.68  | 2.29**±0.26  | 29.97**±1.97 | 10.08**±1.17 | 15.90**±1.15  | 2.19**±0.46  | 39.61**±2.61  | 1.69**±0.26  |
| d                                             | 7.79*±3.48     | -6.51*±3.21   | 2.06*±0.83    | -0.74±0.49   | -0.55*±0.23  | 1.05*±0.46   | 0.99*±0.39    | 1.15*±0.56   | -1.68*±0.48   | 1.29**±0.34  |
| h                                             | 13.02**±2.26   | -7.17**±1.84  | 4.20**±1.12   | 0.44**±0.11  | 2.74**±1.02  | 0.45*±0.19   | 2.01*±0.78    | 0.94**±0.18  | 12.64**±2.14  | 0.53*±0.23   |
| ( $\chi^2$ ) (3)                              | 86.00**        | 66.92**       | 98.73**       | 14.67**      | 16.68**      | 71.27**      | 74.50**       | 6.10         | 52.26**       | 20.11**±     |
| <b>Best fit model</b>                         |                |               |               |              |              |              |               |              |               |              |
| m                                             | 65.20**±4.94   | 36.93**±7.07  | 91.72**±2.08  | 8.41**±1.49  | 34.04**±2.08 | 9.77**±1.70  | 18.90**±2.08  | 1.05*±0.51   | 28.11**±2.08  | 1.13**±0.28  |
| d                                             | 7.79**±0.63    | -6.51**±0.64  | -1.34*±0.62   | -0.93±0.64   | -0.95*±0.46  | 0.94*±0.41   | 4.41**±0.77   | 0.75**±0.27  | -2.92**±0.71  | 7.51**±0.75  |
| h                                             | 66.10**±11.89  | 13.31**±3.29  | -13.57**±2.77 | -9.86**±1.18 | -2.40**±0.27 | 3.71**±0.32  | 2.01*±0.97    | 3.17**±1.18  | 27.21**±2.77  | 1.24**±0.27  |
| i                                             | 13.05**±4.89   | -             | -15.90**±2.24 | -6.61**±2.48 | -4.60*±2.24  | -            | 3.40±0.97     | 1.18*±0.39   | 13.03**±2.24  | 0.63*±0.24   |
| j                                             | -              | -             | 21.93**±3.16  | -            | -            | 1.03*±0.48   | 1.48*±1.42    | -            | 12.41**±3.16  | 1.54*±0.41   |
| l                                             | -42.19**±7.34  | -22.46**±3.36 | -             | 3.18*±1.27   | -            | -3.57**±1.33 | -             | -0.99*±0.37  | -             | -            |
| $\chi^2$                                      | 2.29           | (2)=15.73**   | (1)=2.04      | (2)=12.96**  | (2)=2.47     | (1)=21.03**  | (2)=1.98      | (1)=1.41     | (1)=31.54**   | (1)=7.79*    |

Relative leaf water content, 2. Excised leaf water retention capacity, 3. Plant height, 4. Number of tillers per plant, 5. Peduncle length, 6. Spike length, 7. Number of spikelets per spike, 8. Spike weight, 9. Number of grains per spike, 10. Grain yield per main spike

parameters were significant with significant  $\chi^2$  values for traits RWC, peduncle length and spike weight. The genetic parameters m, d, h and l were found to be significant for RWC and peduncle length. Further, the dominance (h) and dominance x dominance (l) components possessed opposite sign. For the trait spike weight, four parameters: m, d, h and j were found to be significant with significant  $\chi^2$  value.

Five genetic parameters were found to be significant for the rest of the characters studied. The genetic components m, d, h, i and j were found to be important for plant height. In case of number of tillers/ plant and spike length, the five genetic parameters which showed significance include m, d, h, i and l. for the traits number of spikelets/ spike and grain yield/ main spike, m, d, h, j and l were found to be important. The dominance (h) and dominance x dominance (l) components have opposite sign for the traits number of tillers/ plant, spike length, number of spikelets/ spike and grain yield/ main spike. But the  $\chi^2$  values were found to be significant in all these cases.

In cross HW 3081 x HD 2839, one or more parameters among A, B and C scaling tests were found to be significant for all the traits studied (Table 14). Thus the simple additive dominance model was found to be inadequate to explain the genetic basis of various traits studied in this cross. When proceeded further for the best fit model either four or five parameter model was found to be satisfying with non-significant  $\chi^2$  or lowest possible  $\chi^2$  value among different combinations.

Four genetic components were found to be significant for the traits excised leaf water retention capacity and peduncle length. In the case of ELWRC, the genetic components m, d, h and l were significant while for peduncle length, m, d, h and i showed significance with non-significant  $\chi^2$  values. Five parameter model was found to

Table 15. A, B and C scaling tests and the genetic components of the cross HW 3081 x C 3061

| Generation                                    | 1              | 2            | 3             | 4            | 5             | 6            | 7            | 8             | 9              | 10           |
|-----------------------------------------------|----------------|--------------|---------------|--------------|---------------|--------------|--------------|---------------|----------------|--------------|
| <b>A,B,C, Scaling test</b>                    |                |              |               |              |               |              |              |               |                |              |
| A                                             | 1.70±3.86      | 11.10**±2.63 | -5.46±3.86    | 0.60±0.94    | -4.46**±1.33  | -1.13±0.87   | -0.16±1.04   | -1.24**±0.30  | -13.35**±6.65  | -0.90**±0.29 |
| B                                             | 16.32**±4.22   | -5.99±6.19   | -12.63**±2.75 | -0.16±1.13   | -6.20**±1.34  | -0.69±1.51   | 1.21±0.98    | -0.45±0.29    | -5.44±5.87     | -0.19±0.17   |
| C                                             | 8.99**±3.96    | 10.09**±2.09 | -33.98**±4.40 | -3.01±1.98   | -13.11**±3.42 | -5.16**±2.06 | -6.96**±1.87 | -1.82**±0.77  | -35.03**±13.18 | -1.34**±0.62 |
| <b>Haynains 6 parameters model</b>            |                |              |               |              |               |              |              |               |                |              |
| m                                             | 86.88**±1.91   | 41.24**±4.83 | 85.89**±1.03  | 2.98**±0.67  | 34.79**±0.68  | 9.73**±0.32  | 16.53**±0.31 | 2.37**±0.16   | 37.83**±2.10   | 1.73**±0.12  |
| d                                             | 0.83**±0.28    | -3.08±3.20   | -3.81**±1.78  | -0.56**±0.21 | -3.01**±0.48  | 1.03**±0.52  | 0.32±0.44    | -0.31**±0.13  | -2.10**±0.65   | -0.21±0.36   |
| h                                             | 17.74**±8.92   | -3.91**±1.49 | 26.05**±6.20  | 4.49**±1.30  | 8.88**±3.09   | 4.74**±1.98  | 10.40**±1.70 | 0.68±0.74     | 16.72**±1.93   | 0.57±0.23    |
| i                                             | 9.03±8.90      | -4.98**±2.03 | 15.88**±6.15  | 3.44**±1.21  | 2.44±2.91     | 3.33**±1.41  | 8.02**±1.55  | 0.12±0.72     | 16.23**±3.16   | 0.24±0.48    |
| j                                             | -7.30**±2.38   | 8.54**±3.51  | 3.58±2.34     | 0.38±0.71    | 0.86±0.83     | -0.22±0.71   | -0.68±0.60   | -0.39**±0.19  | -3.95±3.22     | -0.35**±0.13 |
| j                                             | -27.06**±11.92 | -0.11±2.45   | 2.21±1.01     | -3.88±2.50   | 8.22**±3.93   | -1.50±3.24   | -9.08±2.59   | 1.57±0.93     | 2.55**±1.20    | 0.85±0.64    |
| <b>Joint scaling test (3 parameter model)</b> |                |              |               |              |               |              |              |               |                |              |
| m                                             | 81.60**±6.14   | 38.78**±3.64 | 87.23**±8.89  | 3.15**±0.54  | 33.83**±3.47  | 10.06**±1.46 | 16.94**±1.16 | 2.39**±0.51   | 44.21**±4.61   | 1.80**±0.61  |
| d                                             | 6.68**±0.83    | 9.91**±1.36  | -6.67**±1.63  | -0.87**±0.31 | -3.70**±0.54  | 1.21**±0.65  | 0.87±0.63    | -63.33**±1.75 | 1.05**±0.50    | 0.71**±0.32  |
| h                                             | 10.03**±2.19   | 1.66**±0.53  | 8.11**±1.38   | 0.98**±0.42  | 5.42±1.41     | 1.15**±0.11  | 2.24**±1.02  | 0.40±1.08     | -1.65**±0.63   | 0.22**±0.10  |
| ( $\chi^2$ ) (3)                              | 44.66**        | 34.30**      | 63.93**       | 0.598        | 12.19**       | 1.24         | 31.02**      | 0.32          | 68.95**        | 1.75         |
| <b>Best fit model</b>                         |                |              |               |              |               |              |              |               |                |              |
| m                                             | 87.78**±2.18   | 43.17**±4.94 | 73.42**±4.94  | -            | 34.87**±0.70  | 79.08**±2.08 | 14.60**±2.08 | 2.49**±0.61   | 30.11**±4.94   | 1.80**±0.57  |
| d                                             | 8.14**±0.79    | -9.91**±0.63 | -6.67**±1.63  | -            | -3.87**±0.63  | 1.21**±0.56  | 1.01**±0.47  | 7.19**±0.71   | 1.05**±0.43    | 1.42**±0.70  |
| h                                             | 2.20**±0.27    | 3.79**±1.12  | 23.83**±11.89 | -            | 5.60**±2.29   | 3.88**±1.72  | 5.19**±2.17  | 4.58**±1.18   | 14.16**±1.18   | 0.23**±0.11  |
| i                                             | -9.03**±3.81   | 4.98**±0.48  | 15.88**±4.89  | -            | -             | 2.44**±0.22  | 2.64**±1.26  | -             | 16.23**±4.89   | -            |
| j                                             | -              | 1.17**±0.53  | -             | -            | -             | -            | -            | -7.83**±3.16  | -              | 7.09**±1.31  |
| j                                             | -27.05**±7.31  | -            | 2.22**±0.97   | -            | 11.48**±3.36  | -            | -1.37**±0.31 | -             | 2.55**±0.73    | -            |
| $\chi^2$                                      | (1)=1.35       | (1)=29.64**  | (2)=8.91*     | -            | (1)=40.25**   | (2)=6.18     | 1.52         | 1.95          | 18.87**        | 14.60**      |

. Relative leaf water content, 2. Excised leaf water retention capacity, 3. Plant height, 4. Number of tillers per plant, 5. Peduncle length, 6. Spike length, 7. Number of spikelets per spike, 8. Spike weight, 9. Number of grains per spike, 10. Grain yield per main spike

be adequate to explain the genetic basis of remaining traits under study in this cross. The parameters m, d, h, i and j were found significant in case of plant height, number of spikelets/ spike and grain yield/ main spike. For the characters RWC, number of tillers/ plant, spike weight and number of grains/ spike, m, d, h, i and l were significant. Here the  $\chi^2$  values were non-significant only for RWC and spike weight. The dominance (h) and dominance x dominance (l) components possessed opposite sign in case of RWC, number of tillers/ plant and spike weight. However, they possessed similar sign in case of number of grains/ spike but the  $\chi^2$  value is highly significant in this case. For the trait spike length, m, d, h, j and l were found to be significant with significant  $\chi^2$  value.

The genetic components for various characters for the cross HW 3081 x C 306 was presented in Table 15. In the cross HW 3081 x C 306, all the three scaling tests (A, B and C) were found to be non-significant only for the trait number of tillers/ plant. The genetic parameters m, d and h were significant and the  $\chi^2$  value is non-significant. Thus the additive dominance model was found to be adequate for this trait. For the rest of the traits the three parameter model was not adequate.

Under the best fit model four parameters were found to be significant for the traits, peduncle length (m, d, h and l with non-significant  $\chi^2$  value), spike length (m, d, h and i with non-significant  $\chi^2$  value), spike weight and grain yield/ main spike (m, d, h and j uniformly for both the traits). For the rest of the traits five parameter model suited well to explain the genetic basis. The five genetic components m, d, h, i and l were found to be significant for four characters viz., RWC, plant height, number of spikelets/ spike and number of grains/ spike. But the non-significant  $\chi^2$  values were recorded only for RWC and number of spikelets/ spike. The genetic components h and l possessed opposite sign

in case of RWC and number of spikelets/ spike and similar sign for plant height and number of grains/ spike (but with highly significant  $\chi^2$  values). Genetic parameters m, d, h, i and j were found to be important for the character excised leaf water retention capacity.

## CHAPTER V.

### DISCUSSION

The moisture stress environments are highly variable, therefore; selection in breeding populations for drought tolerant genotypes to give high yield is difficult. The traits that influence yield performance under moisture stress have variable expression in different years. Therefore, the improvement in yield observed under irrigated and environments with optimum rainfall cannot be compared with water limited environments. Several workers have identified various morpho-physiological traits associated with drought tolerance, which may complement conventional breeding methods and in yield improvement under dryland conditions (Turner, 1986; Ludlow and Muchow, 1990; and Blum, 1989). However, it has been observed that no single criterion for selecting drought tolerant genotypes has been successful in any breeding programme. There are a few reports, where seedling survivability has been used for selecting genotypes of cowpea (Singh et al., 1999) for moisture stress environments. The present investigation was, therefore, undertaken to screen genotypes on the basis of seedling survivability and to work out the genetics of seedling survivability to ensure formulation of an effective breeding methodology for moisture stress tolerance.

#### **5.1 SEEDLING SURVIVABILITY STUDIES:**

In the present investigation a different method of screening for moisture stress tolerance was tried for its suitability and standardization. When the seedlings were screened under artificially created drought, different genotypes have shown diverse responses for seedling survivability duration. Majority of the genotypes (Table 1) started

withering after 25 days of sowing. The varietal differences were most pronounced between 25 to 35 days, when the most drought susceptible varieties like HD 2329, Halna, Kalyansona, Chinese Spring, Annapurna, Kite and MP 1124 showed early seedling mortality and stopped growing. The leaves started drying from leaf tip to base. The shoot also started drying gradually and shown the symptoms of declining turgidity. The characteristic features of moisture stress were visible as compared to the genotypes, which showed the symptoms of survival, as their leaves and shoot were green. Few genotypes survived for longer duration of time (about 40 days from the date of sowing) and majority survived for moderate to less duration (35 and 30 days, respectively). It was interesting to note that many of those genotypes released for dryland conditions performed better in seedling screening. Genotypes reported to be tolerant to drought conditions on field and survived longer during screening under artificial moisture stress conditions include NI 5439, Kundan, HW 3081, WBM 1304, NP 718, HW 2099, UP-2338, NIAW 588, K 8027, HI 1494 and HUW 538. The genotype C306, a well-known drought tolerant variety across the wheat zones in the country survived for moderate duration only. The mechanism that makes C306 highly tolerant to drought is not very well defined. However, C306 has been characterized a drought tolerant genotype as it has established itself a stable genotype in yield, biomass and other traits under field experimentation at multilocations (Sinha et al., 1986, 1990). It has spreading habit at early stage, non-synchronous, high tillering and deeper root system and also has ability to translocate pre-anthesis assimilates to developing grains during stress (Aggarwal and Sinha, 1984; Sarvanan, 1996). While studying the physiological parameters like relative leaf water content, water potential, excised leaf water retention capacity, the genotype

C306 did not record a favourable pattern for the above mentioned traits as compared to other genotypes. It is likely that the drought tolerance mechanism in C306 must be activated at a later stage than seedling. In spite of poor drought and wilt scores it performs better than any other variety under drought conditions in the farmers fields. However, the genotypes NI 5439, K 8027 and Kundan, which are in cultivation under drought conditions fall well within the score of >40 days of seedling survivability. The pattern of wilting and seedling survivability of different varieties substantiates the visual observations made under field conditions. Very few workers have (Winte *et al.*, 1988; Malik and Aeright, 1998; Singh *et al.*, 1999 and Nagarajan and Rane, 2000) emphasized the seedling survivability and seedling characters as useful screening criteria for moisture stress tolerance. The present study grouped the genotypes into three distinct classes based on their response to seedling screening technique adopted.

### **5.1.1 INHERITANCE OF SEEDLING SURVIVABILITY**

Genetic control of the character seedling survivability under moisture stress has not been studied so far in wheat. There is a report of monogenic control of seedling mortality under moisture stress in cowpea (Singh *et al.*, 1999).

Inheritance of seedling survivability under moisture stress was studied in two crosses. The drought tolerant and drought susceptible parents for these crosses were selected from the results obtained from the seedling screening experiment described earlier. The F<sub>1</sub> plants of the cross C-306 X HW 3081 survived after 40 days and also recovered growth after the resumption of irrigation indicating that seedling survivability is dominant over seedling mortality. The F<sub>2</sub> population of the above cross segregated in a expected ratio of 3 (survived): 1 (dead) with Chi square value of 0.216, indicating that

the trait is under the control of single dominant gene. The BC<sub>1</sub> progenies (F<sub>1</sub> X C306) segregated into 1 (survived) : 1 (dead) ratio with a Chi square value of 0.1578, which validated the hypothesis proposed for F<sub>2</sub> segregation that the trait seedling survivability in moisture stress condition is governed by a single dominant gene.

In another cross, MP 1136 x HW 2044, all the plants of F<sub>1</sub> survived for about 40 days as that of dominant parent (HW 2044) and also recovered after resuming irrigation. The observation in F<sub>1</sub> indicated dominant gene control of seedling survivability. In the F<sub>2</sub> generation a ratio of 3 (survived): 1 (dead) was observed. The observed ratio fitted well in the expected ratio with a Chi square value of 0.252. This clearly implies that the seedling survivability under moisture stress condition is under single dominant gene control. The results obtained were in consonance with the earlier reports of Singh *et al.*, (1999) in cowpea, who also reported a single dominant gene controlling the seedling survivability under moisture stress.

## **5.2 CORRELATION STUDIES**

The aim in most crop improvement programmes is to increase the productivity. Grain yield is a complex character and is the manifestation of cumulative effect of various component characters. Direct selection for such complex traits is not desirable and hence the information on the interdependence of individual characters is essential. These component characters are not independent in their action but are interlinked and they may also bring simultaneous change in other characters too. Thus, it is necessary to find out the direction and degree of association between two characters at phenotypic and genotypic levels as suggested by Worleg *et al.*, (1976).

One of the major objectives in the present investigation was to study the association of grain yield with other morpho-physiological traits under moisture stress conditions. In the present study it was found that the grain yield/main spike has positive significant correlation with all the characters except the excised leaf water retention capacity. The association of plant height and grain yield/spike was significant and positive at both genotypic and phenotypic levels. It also exhibited positive significant association with other characters like number of tillers/plant, peduncle length, spike length, number of spikelets/spike and number of grains/spike. The results were in conformity with the earlier reports of Sheoran *et al.*, (1986), Pathak *et al.*, (1986), Bangarwa (1987) and Quayyum *et al.*, (1991). Number of tiller/plant showed positive significant association with peduncle length, number of grains/spike and grain yield/spike. These results were in accordance with the previous reports made by Pawar *et al.*, (1990), Chowdhury and Mandal (1991), Bishnoi *et al.*, (1993), Singh and Sharma (1994), Rana and Sharma (1997). Positive significant correlation was observed between peduncle length, spike length, and grain yield/spike. All the characters related to spike viz., spike length, number of spikelets/spike and number of grains/spike showed positive significant associations among themselves and also independently with the grain yield/spike. These results were in consonance with the observations made by Bangarwa *et al.*, (1987), Ehdaie *et al.*, (1989), Pawar *et al.*, (1990), Chowdhury and Mandal (1991), Bishnoi *et al.*, (1993), Mohan *et al.*, (1993), Singh and Sharma (1994), Rana and Sharma (1997). The trait 1000-grain weight exhibited positive significant correlation with grain yield/spike. These observations are in concordance with the earlier reports of Ehdaie *et al.*, (1989), Pawar *et al.*, (1990), Quayyum *et al.*, (1991), and Mentewab and Sarrafi

(1998). The grain yield/spike is also had positive association with RWC. Positive association of water status related characters with the grain yield were reported earlier by many workers like Tahara *et al.*, (1990), Cedola (1994), Al Hakim *et al.*, (1995), Johnson *et al.*, (1996), Islam *et al.*, (1998), Mentewab and Sarrafi (1998), and Merah (2001).

From the results obtained on the character association, it is interesting to note that the grain yield/spike is independent of ELWRC and it had a negative non-significant association. Hence it can be interpreted that selection for ELWRC under moisture stress conditions may not form an effective selection criterion. A few workers reported ELWRC as an effective screening tool for screening wheat genotypes for drought tolerance like Järdat and Konzak (1983), and Yang *et al.*, (1991).

From the foregoing discussion it can be concluded that the RWC and other yield attributes that showed positive significant correlations with grain yield/spike should be given prime importance during any wheat improvement programme for the development of moisture stress tolerance. Among the various physiological traits reported by different workers (Sinclair and Ludlow, 1985; Scholfield *et al.*, 1988; Clarke, 1992; and Dhanda and Sethi, 1998), RWC appear to be very effective selection criterion for drought tolerance screening. In the present investigation also RWC exhibited high positive significant correlation with grain yield/spike. Hence this trait can be very effectively utilized indirect selection of drought tolerant genotypes. As RWC can be measured on single plant basis, screening the segregating populations is also feasible and also helps in enhancing the pace of any crop improvement programme. It can also be interpreted from the above discussion that RWC can become a very good screening tool to distinguish drought tolerant genotypes with high precision and ease.

### 5.3 PATH COEFFICIENT ANALYSIS

Path coefficient is a standardized partial regression coefficient, which permits the separation of correlation coefficients into direct and indirect effects (Wright, 1921). To understand the direct contribution of any independent variable on dependent variable, it is essential to resort to path coefficient analysis. Correlation coefficient does not always gives precise information regarding the direct relation between any two variables. To know the real direct contribution of any character towards grain yield/spike (dependent variable) the path analysis is obvious.

In the present study many characters exhibited sufficiently high correlation coefficients with grain yield/spike, to establish their importance in the selection programmes for crop improvement in wheat. But when resorted to path coefficient analysis, it revealed that they were not very important as merely revealed by the correlation studies. It is evident from the data presented in Table 5 (phenotypic and genotypic path coefficients) that the characters such as RWC, number of grains/spike, spikelets/spike and 1000-grain weight have considerably high positive direct effect on grain yield/spike. The traits plant height, and peduncle length have negligible direct positive effects, whereas number of tillers/plant, number of spikelets/spike and ELWRC showed negative direct effects. These results are in consonance with the reports of Paroda and Joshi (1970), Pathak *et al.*, (1986), Bangarwa *et al.*, (1987), Shamsuddin (1987), Pawar *et al.*, (1990), Chowdhury and Mandal (1991), Wang *et al.*, (1991), Shelembi *et al.*, (1992), Bahadur (1993).

The characters number of tillers/plant and spike length showed negative direct effects, but the correlation analysis revealed positive significant association with grain

yield/spike. These traits exhibited higher magnitudes of indirect effect through other characters thus showing positive significant correlation. ELWRC also showed negative direct and indirect effects on grain yield/spike.

It is interesting to note that the residual effect (phenotypic) was only 0.1594, which indicated that more than 80 per cent of the total genotypic variability of grain yield has been explained by the traits included in the present study. The remaining amount of genetic variability may be contributed by other characters, which were not included in the present study and the environmental factors.

Based on the present investigations on correlation analysis and path coefficient analysis, the characters like RWC, number of grains/spike, number of spike lets/spike and 1000-grain weight may be considered highly dependable and reliable for adoption in any selection programme aiming at development of moisture stress tolerant genotypes.

## **5.4 GENETIC DIVERSITY STUDIES**

Analysis of genetic diversity analysis has been considered as an important prerequisite for any hybridization programme intended to develop high yielding progenies. This is very essential specially when the breeding programme aims at abiotic stress tolerance. Testing of existing genetic diversity for abiotic stress tolerance helps in identifying suitable genotypes for hybridization programme. In this regard, several researchers evaluated germplasm from diverse from diverse geographic origin and that lead to a huge repository of genetic diversity for various morphophysiological characters, yield and its component traits (Srivastava *et al.*, 1987; Garg and Gautam, 1988; Singh and Chatrath, 1993). In this context, 70 genotypes of bread wheat were analyzed for the

extent of genetic diversity present under moisture stress conditions, which could be used for future hybridization programmes.

#### 5.4.1 MAHALANOBIS' $D^2$ STATISTIC

Using Mahalanobis'  $D^2$  analysis all the 70 genotypes could be grouped into 8 clusters using ten different morpho-physiological traits. A perusal of the cluster means indicated that the cluster V containing minimum number of genotypes (four) also had lowest means for majority of the characters studied viz., plant height, number of tillers/plant, peduncle length, spike length, number of spikelets/spike, number of grains/spike and 1000-grain weight. The clusters II and VIII showed lowest values for RWC and ELWRC respectively. Cluster IV consisting of 12 genotypes exhibited highest values for spike length, number of spikelets/spike, number of grains/spike and RWC whereas the cluster VI including 6 genotypes recorded highest values for plant height, number of tillers/plant, peduncle length and grain yield/main spike. Clusters III and VII recorded highest values for traits ELWRC and 1000-grain weight respectively. It is interesting to note that the genotypes belonging to different eco-geographic areas were included in the same cluster. This indicates that there is less or no association between clustering pattern and eco-geographical distribution of the genotypes. Bhatt, 1970; Thete *et al.*, 1987; and Garg and Gautam, 1988 have shown that the diversity is not necessarily related to the genetic diversity alone. Also the clustering of genotypes from different ecogeographic locations into one cluster could be attributable to possible free exchange of breeding materials or even varieties from one place to another (Sharma and Hore, 1997). This may also be due to the fact that the unidirectional selection practiced for a particular trait in several places produced similar phenotypes, which were aggregated in

one cluster irrespective of their distant geographic origin (Somayajulu *et al.*, 1970). On the other hand many genotypes originating from one place were scattered over different clusters. Such genetic diversity among the genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the base populations, past history of selection, and degree of general combining ability (Murthy and Arunachalam, 1966). This fact is also supported by wide inter cluster distances observed among them, especially the clusters I, V, VI, VII and VIII have shown higher amount of inter cluster distances with other clusters. The clusters IV and VI also exhibited higher intra cluster distances. The cluster means of these two clusters are also of higher order for majority of the traits studied. Since the hybridization among the genotypes of same cluster may not produce good specific combiners, the putative parents for hybridization programme should thus belong to different and diverse clusters with high cluster means for the desired characters. At the same time, *per se* performance of constituents of diverse clusters should also be considered for selection of parental lines.

## 5.5 GENERATION MEAN ANALYSIS

### 5.5.1 Kundan x HD2329:

In the cross Kundan x HD 2329, the three parameter model (m, d and h) exhibited good fit ( $\chi^2$  value at 3 degrees of freedom being non-significant and m, d and h being significant) for peduncle length. The dominance component showed preponderance over the additive genetic component. Hence, for the improvement of this trait heterosis breeding or population improvement programme could be resorted. For the rest of the characters this model does not appear to be appropriate. The inadequacy of additive dominance model provides the evidence of presence of epistasis for various traits studied.

This is further strengthened by the fact that any one or more of the A, B and C scaling tests were found to be significant in all these traits. When the data was subjected to sequential model fitting through the elimination of the non-significant parameters, a significant reduction was observed in  $\chi^2$  values. Among the various combinations available the best fit model was selected based on non-significant  $\chi^2$  value or the model with lowest possible  $\chi^2$  value. The four parameter model was found to be fit for characters excised leaf water retention capacity, spike weight (m, d, h and l); plant height (m, d, h and j) and spike length (m, d, h and i). Preponderance of additive genetic component over dominance was found in case of ELWRC and spike length. The dominance component is predominant over additive component in case of traits plant height and spike weight. Five parameter model fit well for RWC, number of tillers/ plant and number of spikelets/ spike. For all the three characters significant role of m, d, h, i and l components of gene action were commonly observed. For characters RWC, ELWRC, number of spikelets/ spike and spike weight, dominance (h) and dominance x dominance (l) components were significant and possess opposite sign indicating duplicate type of epistasis. The genetic parameters m, d, h, i and j were significant commonly for traits number of grains/ spike and grain yield/ main spike. But the  $\chi^2$  values were found to be highly significant indicating the role of higher order gene interactions or presence of linkage. Overall in this cross the dominance component showed preponderance over the additive genetic component. The dominance component can be exploited by adopting heterosis breeding or population improvement strategies for the crop improvement.

### 5.5.2 MP 1136 x HW 2044:

Simple additive dominance model was adequate to explain the genetic basis of characters excised leaf water retention capacity and number of grains/ spike in the cross MP 1136 x HW 2044. Adequacy of additive dominance model indicates the absence of epistasis and thus the traits are under the control of simple inheritance. Additive genetic component is predominant over dominance component for the trait ELWRC. The dominance component showed preponderance over additive component for number of grains/ spike. For rest of the traits three parameter model was found inadequate indicating the presence of epistasis. Significance of one or more of the three scaling tests viz., A, B and C, further confirmed the presence of epistatic or higher order of gene interactions in the determination of these traits. Significant reduction in  $\chi^2$  value was recorded when the data was subjected to sequential model fitting by eliminating non-significant parameters. Four parameter model was found to be best suited for the traits RWC, peduncle length and spike weight. Genetic components m, d, h and l were significant commonly for RWC and peduncle length. While, the parameters m, d, h and j were significant for spike weight. The h and l components have opposite signs indicating duplicate type of epistasis governing the traits RWC and peduncle length. However, in case of peduncle length the  $\chi^2$  value is highly significant indicating the presence of higher order gene interactions or linkage.

Five parameter model was found to fit well for the traits plant height (m, d, h, i and j); number of tillers/ plant, spike length (m, d, h, i and l for both traits); number of spikelets/ spike and grain yield/ main spike (m, d, h, j and l for both the traits). The additive component is predominant over dominance component in case of traits plant

height, number of tillers/ plant and grain yield/ main spike. These traits can be improved by fixing the additive genetic component using pedigree method of breeding and/or single seed descent method. The dominance component showed preponderance over additive genetic component in determining the traits spike length and number of spikelets/ spike. These traits can be improved by adopting heterosis breeding or population improvement schemes.

### **5.5.3 HW 3081 x HD 2839:**

The three parameter model is inadequate to explain the genetic behaviour of all the traits studied in the cross HW 3081 x HD 2839 indicating the existence of epistasis. Further confirmation to this fact is provided by the significance of any of the three scaling tests (A, B and C scaling tests). The data was subjected to near best fit model through elimination of non-significant parameters. Finally the best fit model was selected based on the non-significant or lowest possible  $\chi^2$  value.

Four parameter model was found fit for excised leaf water retention capacity (m, d, h and l were significant) and peduncle length (m, d, h and i were significant). The h and l components were showing opposite signs in case of trait ELWRC indicating the role of duplicate type of epistasis. The additive genetic component is predominant over the dominance component in case of peduncle length. The dominance component can be exploited in crop improvement programme by adopting heterosis breeding.

Five parameters m, d, h, i and j were found significant commonly for the traits plant height, number of spikelets/ spike and grain yield/ main spike. The dominance component is predominant in case of plant height whereas, the additive genetic component is predominant in the traits number of spikelets/ spike and grain yield/ main

spike. The genetic parameters  $m$ ,  $d$ ,  $h$ ,  $i$  and  $l$  were significant for characters RWC, number of tillers/ plant, spike weight and number of grains/ spike. The dominance component showed preponderance over the additive component in all these four characters. The dominance ( $h$ ) and dominance x dominance ( $l$ ) components have opposite sign with non-significant  $\chi^2$  values for RWC and spike weight indicating the presence of duplicate gene control. The predominance of dominance component in these traits can be exploited for crop improvement by heterosis breeding or recurrent selection.

#### **5.5.4 HW 3081 x C 306:**

In the cross HW 3081 x C 306, the additive dominance model was found adequate for number of tillers/ plant indicating the absence of epistatic gene interactions. This is further confirmed by the non-significance of all the three scaling tests (A, B and C). The dominance component is slightly higher than the additive component. For the rest of the traits three parameter model is found inadequate indicating the presence of epistasis or higher order gene interactions. Sequential model fitting was resorted to know the genetic control of these traits and best fit model was selected for each trait.

Four parameter model explains the genetic control of characters viz., peduncle length, spike length, spike weight and grain yield/ main spike. The genetic parameters  $m$ ,  $d$ ,  $h$  and  $l$  (peduncle length),  $m$ ,  $d$ ,  $h$  and  $i$  (spike length) and  $m$ ,  $d$ ,  $h$  and  $j$  (for both spike weight and grain yield/ main spike) were found to be important. Preponderance of dominance was observed for characters peduncle length and spike length whereas; additive genetic component is predominant in case of spike weight and grain yield/ main spike. The genetic components  $h$  and  $l$  possessed similar sign for the trait peduncle length

but with very high  $\chi^2$  value indicating the presence of higher order gene interactions or the presence of linkage.

Five genetic parameters, m, d, h, i and l are significant for the traits RWC, plant height, number of spikelets/ spike and number of grains/ spike. The parameters h and l have opposite sign for RWC and number of spikelets/ spike with non-significant  $\chi^2$  values. This indicates the duplicate type of epistasis governing these traits. Similar sign for genetic parameters h and l was observed in case of characters plant height with lower  $\chi^2$  value indicating the presence of complementary gene action. For the trait excised leaf water retention capacity, the genetic parameters m, d, h, i and j were found to be significant. The additive genetic component is predominant over dominance component in this trait. Overall in the cross HW 3082 x C 306, the dominance component is predominant over additive component. In case of both the physiological traits the additive genetic component is predominant over dominance. When these traits need to be improved the fixable genetic variance can be exploited through pedigree or single seed descent method of plant breeding. Heterosis breeding and population improvement methods are more suitable to exploit the dominance component.

Overall perusal of the results among the four crosses studied, duplicate type of epistasis was found to be important in the control of the trait RWC. Similar result of duplicate gene control for RWC was earlier reported by Chaudhary *et al.*, (1989). The additive genetic component is found to be predominant over the dominance component in case of both the physiological traits, RWC and ELWRC studied. These findings are in accordance with the earlier findings of Toth-Lokos *et al.*, (1997), Islam *et al.*, (1998) and Farshadfar *et al.*, (2001). Both additive and dominance were found to be important for the

characters plant height, number of tillers/ plant and peduncle length. Similar observations were reported by many workers like Singh and Paroda (1985), Kraljevic-Balalic (1986), Malik *et al.*, (1988), Yadav and Mishra (1992) and Walia *et al.*, (1995). For the trait spike length the dominance component was found to be predominant over additive component in all the four cross combinations studied. Additive genetic component is predominant for the traits number of spikelets/ spike, spike weight and grain yield/ main spike. For these traits even the higher order gene interactions or linkages were evident in different cross combinations. Similar results were observed by earlier workers like Sawant and Jain (1985), Li *et al.*, (1991), Menon and Sharma (1995), Subhani and Chaudhary (2000). The dominance component is most predominant over the additive component in the inheritance of number of grains/ spike. For this character complementary type of epistasis was found in the cross HW 3081 x C 306 while, higher order interactions were prevalent in the crosses Kundan x HD 2329 and HW 3081 x HD 2839. Importance of non-additive effects for number of grains/ spike has been reported by Senapati *et al.*, (1994).

The prevalence of duplicate type of epistasis in the inheritance of certain traits indicating that these traits may be improved through recurrent selection or biparental mating designs. This would help in exploiting the duplicate type of non-allelic interaction and allow recombination and concentration of genes having cumulative effects in the population.

The overall perusal of the results indicates that epistasis is the integral part of genetic architecture of the parent material used in the present investigation. Hence breeders cannot ignore the epistatic component. Therefore, both fixable and non-fixable

gene effects should be exploited following suitable breeding programme keeping the specific objectives in mind.

## CHAPTER VI

### SUMMARY

The present investigation entitled “ **Genetics of drought tolerance in bread wheat (*Triticum aestivum* L.)**” was taken up with one hundred and eighty five wheat genotypes of diverse origin. All these genotypes were screened in wooden boxes under artificial moisture stress in the glass house conditions. The seeds were sown in wooden boxes of 90x60x15 cu. cm. filled with soil, sand and FYM mixture. Before sowing, each box was given equal quantity of water to ensure uniformity and proper germination of the seeds. Thereafter, no irrigation was provided till most of the genotypes exhibited mortality. The selection criterion adopted was the seedling survivability under moisture stress conditions. The wheat genotypes exhibited differential response to the screening conditions. Majority of the genotypes (114 lines) started wilting from 20 days after sowing. Basal leaves are the first to show the drying symptoms; within a leaf, the drying started from tip to bottom. One hundred and fourteen genotypes showed complete death between 26 to 30 days after sowing. Fifty six genotypes survived till 35 days after sowing and only fifteen genotypes survived beyond this period. Irrigation was resumed on 43<sup>rd</sup> day after sowing to study the recovery response. Only fifteen genotypes resumed growth and a few among them could complete their life cycle by producing either one or two seeds.

Efforts have been made to study the inheritance of seedling survivability under moisture stress conditions. The parents, F<sub>1</sub> progeny and F<sub>2</sub> populations of the crosses

MP 1136 x HW 2044 and HW 3081 x C306 were screened under similar conditions as mentioned earlier. The survivability reaction of  $F_1$  progeny was similar to that of the dominant parent, in both the crosses. This indicated that the seedling survivability is a dominant trait. The  $F_2$  segregation pattern in both the crosses was studied. The observed values in both the crosses fitted well into the expected ratio of 3:1 (survived: dead). This confirms that the seedling survivability is controlled by a single dominant gene.

Genetic variability studies were taken up using ten different morpho-physiological characters in seventy wheat genotypes under moisture stress conditions in nethouse. The  $D^2$  values that determine the statistical distance among various genotypes reflecting their genetic diversity indicated the presence of considerable divergence among the genotypes studied. The seventy genotypes studied were grouped into eight clusters. Highest numbers of genotypes (13) were accommodated in the cluster I and lowest (4) in cluster V. Maximum inter cluster distance was observed between the clusters V and VI (8.143) and the minimum was between clusters I and II (2.173). Maximum and minimum intra cluster distances were recorded by the clusters IV (2.571) and VIII (1.266), respectively. The genotypes included in clusters III, IV, V and VI revealed maximum diversity among them and also contributed to higher inter cluster distances.

Grain yield is a complex character and hence the direct selection for yield is not desirable. Therefore, the information on the inter dependence of individual characters is essential. These component characters are not independent in their action and may also exhibit indirect action via other traits. To understand the inter dependence of various characters, correlation and path coefficient analyses were conducted in the present investigation. It was found that the grain yield/ main spike had positive significant

correlations with all the characters studied except for the excised leaf water retention capacity (ELWRC). Path coefficient analysis revealed that the characters such as relative leaf water content (RWC), number of grains/ spike, number of spikelets/ spike and 1000-grain weight had considerably high positive direct effects on grain yield/ main spike. These characters may be considered highly dependable and reliable for adoption in any selection programme aiming at development of moisture stress tolerant genotypes in wheat.

To understand the inheritance pattern of various morpho-physiological characters, four crosses (Kundan x HD 2329, MP 1136 x HW 2044, HW 3081 x HD 2839 and HW 3081 x C306), were subjected to generation mean analysis. The mean data obtained from the six generations of the four crosses for ten different characters were subjected to A, B and C scaling tests to know the presence of epistasis. Then the data was subjected to six parameter and three parameter models. When these models were found inadequate, sequential model fit scheme was adopted to understand the genetic control of the traits. Duplicate type of epistasis was found to be important in the control of RWC among all the four crosses studied. Traits under the control of duplicate type of epistasis can be improved through recurrent selection or biparental mating designs. The additive genetic component is predominant over the dominance component in case of both the physiological traits studied (RWC and ELWRC). Both additive and dominance components were found to be essential in determining the plant height, number of tillers/ plant and peduncle length. The dominance component was found predominant over additive component in the determination of spike length and number of grains/ spike. The dominance component could be very efficiently exploited by heterosis breeding or

population improvement programmes. The additive component is more important for the characters number of spikelets/ spike, spike weight and grain yield/ main spike. Additive genetic variance is the fixable genetic component and could be improved by following pedigree method or single seed descent method of breeding.

The overall trend of results indicated that epistasis is the integral part of genetic architecture of the parent material used in the present study. Suitable breeding strategies need to be adopted to exploit both fixable and non-fixable gene effects judiciously to achieve the specific objectives.

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