CHARACTERIZING DIVERSITY FOR HEAT AND DROUGHT RELATED TRAITS IN HEXAPLOID WHEAT (*Triticum aestivum* L.).

By

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(J-14-M-369)

Thesis submitted to Faculty of Post Graduate Studies
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GENETICS AND PLANT BREEDING

Division of Plant Breeding and Genetics
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Main Campus, Chatha, Jammu 180009
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CERTIFICATE-I

This is to certify that the thesis entitled **"Characterizing diversity for heat and drought related traits in hexaploid wheat (*Triticum aestivum* L.)."** submitted in partial fulfillment of the requirements for the degree of **Master of Science in Genetics and Plant Breeding** to the Faculty of Post-Graduate Studies, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu is a record of bonafide research carried out by **Mr. Sunil Singh Kotwal,** Registration No. **J-14-M-369,** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma. It is further certified that such help and assistance received during the course of investigation have been duly acknowledged.

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CHAPTER I

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) belongs to the family *Poaceae* and is a segmental allohexaploid (2n = 6x = 42, AABBDD). It is the most widely grown crop globally with more than 220 million hectares of cropland producing 715 million tonnes of food grains with a productivity of 3.2 t/ha (FAO, 2015). The yield of wheat has doubled over the last 30 years due to a combination of advanced agronomic practices and improved germplasm through selective breeding (Lopes *et al*., 2014). But the global demand for wheat is expected to rise by 60% by 2050, whereas climate change is anticipated to negatively affect the production by 29% in the same vicinities (Dixon *et al*., 2009). It is estimated that 65 million ha of wheat production area is affected by drought (FAO, 2013). Wheat (*Triticum* spp.), which is one of the first domesticated food crops, represents the first source of calories (after rice) and an important source of proteins in developing countries (Hossain and Teixeira da Silva, 2013a, 2013b). Wheat’s importance is fortified by its global production, occupying 15% of 1500 million ha of arable land (Datta *et al*., 2011) and represents about 30% of the world’s cereal area, with over 220 million ha cultivated worldwide (Cossani and Reynolds, 2012).

In the state of Jammu and Kashmir, wheat is grown over an area of 290.99 thousand hectares with production and productivity of 5819 thousand quintals and 20 quintal per hectares, respectively (Anonymous 2015). Around 70 per cent area under wheat in J&K state is rainfed with no dependable source of irrigation the situation worsens when accompanied by late heat conditions during grain filling. There has been little attempt to breed specifically for drought and heat resistance in wheat due largely to a lack of unique and easily quantifiable plant attributes. A choice of character to study is based upon anticipated effect of each of character on yield under full irrigation and under drought. Any genetic advancement in yield under dry environment is based on some physiological traits. The use of these traits as indirect selection criteria for yield in breeding programme will depend on their relative importance and extent of genetic variation.

The average global temperature is reported to be increasing at a rate of 0.18°C every decade (Hansen *et al.*, 2012). Future climate will also be affected by greater variability in temperature and increased frequency of hot days (Pittock, 2003). To adapt new crop varieties to the future climate, we need to understand how crops respond to elevated temperatures and how tolerance to heat can be improved (Halford, 2009). Water deficit is the main environmental constraint limiting wheat yield, particularly in rainfed areas as grain filling occurs when temperatures are increasing and moisture supply is decreasing. When there is change in ambient temperature, it is accompanied by disturbance in metabolism, which in turn activates heat shock proteins, until new cellular equilibriums are reached. However, temperature above the optimum for growth can be deleterious, causing injury or irreversible damage, which is called heat stress. Wheat heat stress is more harmful during reproductive phase due to direct effect on grain number and dry weight. Terminal heat stress is likely to increase for wheat in near future. Most of the traits related to yield and heat tolerance are controlled by several genes each with minor individual but significant effect when acting together. The potential trait for screening wheat for heat tolerance includes depression of canopy temperature, flag-leaf, stomatal conductance and photosynthetic rate (Farooq *et al*., 2011). All these traits are highly correlated with field performance and grain yield under heat stress. Wheat (*Triticum aestivum* L.) is very sensitive to high temperature and trends in increasing growing season temperatures have already been reported for the major wheat-producing regions (Alexander *et al*., 2006; Hennessy *et al*., 2008). Though, heat stress affects the metabolic pathways at every stage of life of wheat finally leading to yield reduction, the effect of high temperature is particularly severe during grain filling; these losses may be up to 40% under severe stress (Wollenweber *et al*., 2003; Hays *et al*., 2007). Other effects of high temperatures are decreased grain weight, early senescence, shriveled grains, reduced starch accumulation, and altered starch-lipid composition in grains, lower seed germination and loss of vigor (Balla *et al*., 2012).

Drought, also being a very important environmental stress, severely impairs plant growth and development, limits plant production and the performance of crop plants, more than any other environmental factor (Shao *et al*., 2009; Rad *et al*., 2012). As a consequence of severe climatic changes across the globe, threat of the occurrence of more frequent drought spells is predicted. Available water resources for successful crop production have been decreasing in recent years. Furthermore, in view of various climatic change models scientists suggested that in many regions of world, crop losses due to increasing water shortage will further aggravate its impacts. Also available water resources for successful crop production have been decreasing in recent years. As a consequence of severe climatic changes across the globe, threat of the occurrence of more frequent drought spells is predicted. Drought stress can influence plants in terms of membrane integrity, root depth and extension, opening and closing of stomata, cuticle thickness, inhibition of photosynthesis, decrease in chlorophyll content, reduction in transpiration, growth inhibition, hormone composition, protein changes, osmotic adjustment and antioxidant production (Szegletes *et al*., 2000; Lawlor and Cornic 2002; Yordanov *et al*., 2000; Praba *et al*., 2009) to stand with some osmotic changes in their organs. Drought can also cause pollen sterility, grain loss, accumulation of abscisic acid in spikes of drought-susceptible wheat genotypes, and abscisic acid synthesis genes in the anthers (Ji e*t al*., 2010). In relation to current development of cultivars, which are higher yielding even in water-limited environments, one of the major targets is *Triticum* species, being one of the leading human food source, accounting for more than half of total human consumption (Fleury *et al*., 2010; Habash *et al*., 2009). Drought, an environmental stress, is the most significant factor restricting plant growth and crop productivity in agricultural plantations around the world (Tas and Tas, 2007). Wheat is mainly grown on rainfed lands and about 35% of the area of developing countries consists of semiarid environments in which the available moisture constitutes a primary constraint on wheat production (Farshadfar *et al*., 2013). Water is necessary for plant growth and development as it is involved in various physiological functions and is essential for different metabolic activities. Thus, inadequate environmental conditions like drought cause disorders at morphological, physiological, biochemical and molecular levels (Saeedipour, 2012). Drought is a complex and polygenic trait with strong interactions between loci and genotype × environment interactions. Plants use multiple strategies to respond to drought stress and have evolved to adapt to drought via morphological, biochemical and physiological changes through diverse signalling cascades. Hundreds of genes in these pathways controlling the key plant's processes in response to drought stress have been identified by genetic, genomic (at the transcriptomic, proteomic, metabolomic, and epigenetic levels), and transgenic approaches. It is possible to select or create new varieties of crops to obtain a better productivity under water stress if the morpho-anatomical and physio-biochemical characteristics of changes related to drought resistance are understood (Martínez *et al*., 2007). Improving the genetic potential of wheat to drought stress and identification of tolerant genotypes are the main objectives of regional breeding programmes (Hossain *et al*., 2013a, 2013b). Thus, selection and development of new drought-tolerant wheat genotypes that can adapt to climate change is essential to ensure sustainable and productive wheat production (Hagyo *et al*., 2007). Consequently, understanding the physiological mechanisms that enable plants to adapt to water deficit and maintain growth and productivity during a period of stress could help to screen and select heat or drought tolerant genotypes while traits related to this tolerance can be used in wheat breeding programmes (Zaharieva *et al*., 2001).

In the breeding program, it is very important to know the combining ability of inbred lines that are used as parents in hybrids. Combining ability analysis will be helpful in selecting Parents that could produce superior segregates in advance generation. Plant breeders can take advantage from such information on combining ability for developing high yielding lines and hybrids. Therefore knowledge of combining ability is essential for selection of suitable parents for hybridization and identification for promising hybrids in breeding programme. The diallel method of genetic analysis has been widely used to assess the combining ability of parents in hybrids (Miller *et al*., 1980; Kadkol *et al*., 1984; Sherrif *et al*., 1985). The analysis of diallel crossed by the method proposed by Griffing (1956) which partitions the total variation into general combining ability (GCA) of the parent and specific combining ability (SCA) of the crosses have been widely used. Knowledge of GCA and SCA influences yield and its components has become increasingly important for plant breeders in the choice of suitable parents for developing possessing verities in many crop plants (Joshi *et al*., 2004 and Rahim *et al*., 2006). It would be a considerable advantage to be able to estimate the combining ability of parents, genes effects and heterotic effects of crosses before making crosses among varieties. In many studies, GCA effects for parents and SCA effect for crosses were estimated in wheat (Iqbal and Khan, 2006b; Kamaluddin *et al*., 2007). Griffing's approach has been greatly popular among various breeders like Parashar and Janoria (1998), who indicated greater role of additive gene action in the inheritance of grain yield and its components in wheat. Hence, diallel crossing programs have been applied to achieve this goal by providing a systematic approach for the detection of suitable parents and crosses for the investigated characters. From the practical point of view, diallel mating designs provide a very simple and convenient method for the estimation of genetic parameters (Sabaghnia *et al*., 2010). Among various diallel forms, the half diallel method have certain advantages over others, giving maximum information about genetic architecture of a trait, parents and allelic frequency (EL-Maghraby *et al*., 2005 and Iqbal *et al*., 2007). In addition, the diallel cross technique was reported to provide early information on the genetic behaviour of these attributes in the first generation (Topal *et al*., 2004). Griffing used half diallel analysis for combining ability while diallel analysis advocated by Hayman (1954a) and Mather and Jinks (1982) provides reliable method to study the action of genes, genetic components and heritability particularly in autogamous crops, to review the genetic system and gene action involved in the expression of plant attributes, right in the F_1 generation.

Therefore, realizing the importance of heat and drought stress on the production and productivity of wheat, the present study entitled “Characterizing diversity for heat and drought related traits in hexaploid wheat (*Triticum aestivum* L.)” under normal (non-stress) and stress sown (heat and drought stress) condition, is employed to identify the potential candidate heat and drought tolerant genotypes of wheat as well as to identify the best combining parents and their crosses and to know the genetic architecture and mode of inheritance of various morphological and physiological traits related to heat and drought stress with the following objectives:

1. To characterize elite diverse germplasm for morpho-physiological traits related to drought and heat.
2. To study the nature and extent of additive and dominance gene effects involved in the control of drought and heat related attributes.

CHARTER II

REVIEW OF LITERATURE

Keeping in view the climate change, and the present losses as well as losses predicted in future in wheat production due to heat and drought stress around world and India, including parts of Jammu and Kashmir, it is very important to develop the wheat varieties having enhanced heat and drought tolerance in addition to having all desirable agronomic traits. The literature pertaining to various aspects of morphological, physiological traits and genetics of heat and drought tolerance in wheat have been reviewed and have been described as under:

2.1 Heat and drought tolerance

2.2 Evaluation for heat and drought tolerance

- **2.2.1 Genetic variability**
- **2.2.2 Mean performance**
- **2.2.3 Correlation**

2.3 Haymans diallel analysis

- **2.3.1 Combining ability**
- **2.3.2 Gene action**

2.1. Heat and drought tolerance

Declining water resources and global climate change associated with global warming are two global environmental issues. Both factors are anticipated to increase the intensity of drought and heat stress experienced by crops (Reynolds *et al.*, 2007). Drought and heat stress are two most important environmental factors affecting crop growth, development, and yield. Understanding the effect of drought and heat stress will be critical in evaluating the impact of climate change on crop production. Both drought and heat stress affect physiological, growth, development, yield, and quality of crops. Short- and long-term stresses can significantly influence growth and yield processes, particularly when stresses occur at sensitive stages

(Prasad *et al*., 2008). Physiological traits are ideal selection criteria for drought adaptation. Recently, these traits have acquired increasing importance in wheat breeding programs, because of a greater understanding of their relative contribution to grain yield (Araus *et al*., 2002; Reynolds *et al*., 2005; Olivares-Villegas *et al*., 2007). Understanding of physiological traits that determine wheat grain yield in different conditions may be useful for assisting future wheat breeding. Genotypes with physiological traits conferring higher grain yield potential usually perform better under stress conditions. Breeders also need to release cultivars which are adapted to different conditions, so identifying physiological traits that may confer simultaneously high grain yield potential and tolerance to stresses would be essential. These traits must allow the plants to capture more resources or to use them more efficiently (Slafer and Araus, 2007). Reynolds *et al*. (2007) reported that under drought condition, the best expression of canopy temperature and carbon isotope discrimination suggested potential yield gains of approximately 10 and 9% above the best yielding cultivars, respectively; while under heat stress condition, canopy temperature and remobilization of stem carbohydrates suggested potential yield gains of approximately 7 and 9% respectively. They also pointed-out that under drought, canopy temperature associated with water uptake, and carbon isotope discrimination associated with transpiration efficiency and under heat stress, stomatal conductance, leaf chlorophyll content, and canopy temperature were associated with radiation use efficiency. Negative strong correlation between water use and canopy temperature at grain filling stage indicated association between water extraction from soil and canopy cooling at this stage. Olivares-Villegas *et al*. (2007) showed that canopy temperature measured under irrigated and reduced irrigated conditions was not strongly associated with yield, but under drought condition it had significant negative correlation with yield. They noted that genotypes with cooler canopy outperformed in stress condition, but not only for this trait caused higher photosynthetic activity in tolerant group. The relative yield performance of genotypes in stress and favorable environment seems to be a common starting point in identifying the desirable genotypes for stress condition (Mohammadi *et al*., 2010). A number of methods have been proposed to consider yield stability of genotypes in a wide range of environmental conditions, the main objective of those were comparing the performance in the inverse conditions and selecting genotypes adapted to both conditions (Ehdaie *et al*., 1988; Falconer, 1990; Fernandez, 1992). Selection under favorable, stressed, and simultaneously in both conditions were three main strategies, suggested to select tolerant genotypes (Calhoum *et al*., 1994). Several indices have been proposed to describe the behavior of a given genotype under stress and non-stress conditions (Mohammadi *et al*., 2010). An index to determine stress tolerance is stress susceptibility index (SSI) (Fisher and Maurer, 1978). It was based on realized reduction of yield under stressed condition. This index can be used to identify genotypes with yield stability under stressed conditions, and as an indicator index to differentiate between tolerant and sensitive genotypes (Bahar and Yildirim, 2010). Understanding relationship between grain yield and physiological traits, related to abiotic stress tolerance, can be used as efficient tools in breeding programs and identifying ideotypes of the crop for the target environments. On the other hand determination of physiological traits contributing to different abiotic stress tolerance mechanisms is a shortcut to select genotypes for stressed conditions, and then releasing them for the target environments. The objective of this research was to study the relationship between some physiological and phenological traits, grain yield and stress tolerance in wheat genotypes under both terminal drought and heat stresses, as well as to determine the common traits related to tolerance to both stresses.

Farooq *et al*. (2011) Heat stress reduces plant photosynthetic capacity through metabolic limitations and oxidative damage to chloroplasts, with concomitant reductions in dry matter accumulation and grain yield. Genotypes expressing heat shock proteins are better able to withstand heat stress as they protect proteins from heat-induced damage. Heat tolerance can be improved by selecting and developing wheat genotypes with heat resistance. Wheat pre-breeding and breeding may be based on secondary traits like membrane stability, photosynthetic rate and grain weight under heat stress.

Koul and Singh (2011) studied different physiological characters to identify best drought resistant germplasm lines. Drought susceptibility index (DSI) was calculated for different characters over moisture stress and non stress environment. Drought intensity was negative in case of plant height, biomass/plant and 1000 grain weight, number of days to 50% flowering, harvest index. Biomass was important characters and plant height contributed significantly towards biomas under moisture stress condition. DSI value was less than unity for number of day to 50 percent flowering indicating that they flowered earlier under stress condition. For plant height six genotypes were best genotype C-306 and its mutant C-306(M) had DSI of 1.18 for plant height. For 1000 grain weight all genotypes except RSP519 had negative DSI value. Highest negative DSI value was for RSP-526 followed by WH-1009 and WH-773. Parents having better DSI value for most of the characters included HD-2808, RSP-529, WH-773, RSP-524, RSP-554, RSP-555 and SD9-9.

Modarresi *et al*. (2011) studied thermo tolerant wheat genotypes under normal and heat stress (late sowing) conditions. Correlations between indices based on grain filling duration and peduncle length had the same direction with yield showing importance and effectiveness of these two traits and their indices for detection and screening of high yielding and thermo tolerant genotypes under normal and stress condition.

Zarei *et al*. (2013) showed that chlorophyll content, grain filling rate and thousand grain weight were associated with both terminal drought and heat stress tolerance. It can be concluded that under both terminal drought and heat stress conditions, these traits could be more focused in wheat breeding programs. Furthermore, results of slicing of genotype× environmental conditions interaction showed grain yield reduction of durum cultivars were not significant under terminal drought stress as compared to bread wheat genotype. All wheat genotypes showed significant grain yield reduction under terminal heat stress condition, High yielding genotypes under non-stressed condition showed significant grain yield reduction, when subjected to a stressed condition consequently based on stress susceptibility index these genotypes were not classified into tolerant group.

Mason and singh (2014) studied the ability of CT to predict grain yield within the flow of a wheat breeding program and assess its utility as a tool for indirect selection. Overall a negative slope in the heat treatment indicated that a cooler canopy provided a yield benefit under stress, and implementing selection strategies for CT may have potential for breeding tolerant genotypes.

Kaur *et al*. (2016) Drought/heat tolerance is crucial to stabilize and increase food production since domestication has limited the genetic diversity of crops including wild wheat, leading to cultivated species, adapted to artificial environments, and lost tolerance to stress episodes. Breeding for this trait is complicated as it is controlled by polygene’s and their expressions are influenced by various environmental elements Understanding the mechanism of stress tolerance along with a plethora of genes involved in stress signalling network is important for wheat improvement. Integrating physiology and biotechnological tools with conventional breeding techniques will help to develop wheat varieties with better grain yield under stress during reproductive and grain-filling phases.

2.2 Evaluation for heat tolerance

2.2.1 Genetic variability

The quantitatively inherited characters are governed by several gene(s), each gene has small, similar effect which is usually cumulative. These characters are considerably influenced by the environment. The main result of this effect is that the relationship between genotype and phenotype is partially or completely hidden, i.e., the phenotype does not reveal the genotype. As a result, the phenotype is the result of joint action of the genotype and the environment. Obviously, the effect of environment is not heritable and only that part of phenotype that is the result of genotype is heritable. As in crop improvement, the breeder selects plants on the basis of their phenotypes; the effectiveness of selection automatically would depend on the proportion of phenotype due to the genotype. Thus an imperative need of classifying the total variability into its heritable and non-heritable components with the help of genetic parameters, such as genetic coefficient of variation, heritability estimates and genetic advance, is of paramount importance. Statistically, the amount of variation is measured and expressed as the variance. Genotypic variance is a prerequisite for an effective selection. Knowledge of the extent and nature of phenotypic variance is one of the most important points of consideration for the plant breeder. The efficiency of breeding programme mostly depends on the efficiency of selection, which solely depends on the magnitude of variability present in the population and the extent to which the desirable characters are heritable. Genetic coefficient of variation is used to measure the range of genetic variability present in particular quantitative characters.

Ali *et al*. (2008) studied genetic variability in wheat (*Triticum aestivum* L.) germplasm for eight metric traits i.e., plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility %, 1000 grain weight and yield per plant. They reported that genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for yield per plant, number of productive tillers per plant and number of grains per spike. The remaining traits showed moderate to low PCV and GCV estimates.

Riaz-ud-din *et al*. (2010) Significant genotypic differences were observed for all traits studied indicating considerable amount of variation among genotypes for each character under normal and late planting conditions. The maximum reduction was noted for grain yield while tillers m-2 showed less reduction under late planting conditions. Heat stress intensity was high which ultimately lowered the grain yield under late planting conditions. 1000-grain weight was significantly and positively associated with harvest index at genotypic level. Under late planting conditions, grain yield per plot showed significant and positive genotypic correlation coefficients with biomass per plot and harvest index. Characters showing strong association with grain yield indicating selection for these traits are expected to result in yield improvement under normal and late planting conditions.

Shankarrao *et al*. (2010) studied the variability in bread wheat (*Triticum aestivum* L.) grown in Gangetic West Bengal for different yield parameters viz., plant height, days to heading, flowering, maturity, tiller number per plant, length of spike, number of spikes per plant, and per meter square, number of spikelets per spike, number of grains per spike, grain weight per spike, chlorophyll-a, b and total chlorophyll content, thousand grain weight, grain protein content, yield per plant and grain weight per meter square. They observed that genotypes exhibited significant variation for all the characters studied. The estimate of PCV in all the traits studied were greater than those of the GCV, the close proximity between PCV and GCV values for most of the characters indicated less influence of environment on the expression of the characters under study.

Kalimullah *et al*. (2012) studied genetic variability in bread wheat (T*riticum aestivum* L.) germplasm for different traits viz., for number of grains per spike, number of tillers per plant, 1000-grain weight, grain yield per plant and spike density. They reported that estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant and number of tillers per plant. The remaining traits exhibited moderate to low PCV and GCV estimates.

Degewione *et al*. (2013) showed high phenotypic coefficient of variation and genotypic coefficient of variation for grain filling period, number of tillers per plant and grain yield per plot. High genetic coefficient of variation along with high heritability and genetic advance were recorded in grain yield per plot and days to heading.

Priya *et al*. (2013) reported wide range of variability for all characters except days to maturity. They also noticed minimum differences between PCV and GCV in all characters except number of tillers per plant, chlorophyll-b content and grain protein content indicating very little environmental influence on most of these characters, providing enough scope for exploitation of genetic variability through selection on the basis of phenotypic values.

Singh *et al*. (2013a) studied genetic analysis for morphological traits and protein content in bread wheat (*Triticum aestivum* L.) under normal and heat stress environments, and reported that estimates of PCV were generally higher than that of GCV for all the ten traits studied, indicating thereby role of environment in total variability.

Maurya *et al*. (2014) studied genetic variability for seed yield and its component characters in wheat (*Triticum aestivum* L.) and reported highest phenotypic coefficient of variance (PCV) for yield per plant followed 1000 grain weight and number of grains per spike. The highest genotypic coefficient variance (GCV) was observed for yield per plant while the characters 1000 grains weight, grain per spike and spike length showed moderate value of GCV indicating that they could be used as selection indices for yield improvement.

Saeidi *et al*. (2015) Water stress significantly decreased grain yield by decreasing the number of grains per spike. Under water stress from the beginning of stem elongation to flowering stages, Sivandn and DN-11 cultivars had the lowest grain yield. The lowest and the highest reductions in grain yield and biological yield were detected in Marvdasht and DN-11, respectively. Results show that Marvdasht had the highest, while DN-11 had the lowest relative water constant (RWC) and performance index (PI) values. Water stress significantly decreased the chlorophyll content, PI and RWC values, at the same time significantly increased the carotenoid concentration, whereas the maximum quantum yield of photosystem II (Fv/Fm) did not change. According to the results, Pishtaz and Marvdasht cultivars are tolerant against drought stress and can recover very fast after stress is eliminated.

2.2.2 Estimates of heritability and genetic advance

Heritability expresses the proportion of the total variance that is attributable to the average effect of genes. The most important function of the heritability in the genetic study of metric characters is its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. This degree of correspondence between phenotypic values and breeding values is measured by heritability. Plant breeders have calculated heritability estimates in an effort to supply such information.

Ali *et al*. (2008) studied genetic variability in wheat (*Triticum aestivum* L.) germplasm for eight metric traits i.e., plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility %, 1000 grain weight and yield per plant. They reported moderate heritability for number of productive tillers per plant and fertility %. High heritability estimates were recorded for plant height, number of spikelets per spike, number of grains per spike, 1000-grain weight and yield per plant. These traits also indicated high genetic advance (except fertility %).

Majumder *et al*. (2008) reported high heritability coupled with high genetic advance for plant height, grains per spike, 100-grain weight, harvest index and grain yield among 20 spring wheat (*Triticum aestivum* L.) genotypes (varieties or lines).

Shankarrao *et al*. (2010) studied variability for yield parameters in bread wheat (*Triticum aestivum* L.) grown in Gangetic West Bengal, and reported high heritability coupled with high genetic advance (in % of mean) for the grain weight per spike, per plant and per meter square, number of grains per spike, thousand grain weight and the grain protein content indicating the characters to be under additive genetic control and also scope of improvement through direct selection.

Wani *et al*. (2011) studied genetic variability of physiological traits in integration with yield and yield components in wheat (*Triticum aestivum* L.), and observed high heritability and high genetic advance as percent mean for grain yield per plot, harvest index, grains per spike, 1000-grain weight, chlorophyll b and chlorophyll-a, suggesting that selection for these traits may be rewarding.

Kalimullah *et al*. (2012) studied genetic variability in bread wheat (*Triticum aestivum* L.) germplasm for number of grains/spike, number of tillers per plant, 1000-grain weight, flag leaf area, grain yield per plant and spike density. They reported high heritability estimates for all the traits studied. These traits also indicated high expected genetic advance except spike density and number of tillers per plant.

Priya *et al*. (2013) reported high heritability coupled with moderate to low genetic advance for days to heading, days to flowering, plant height and spike length and moderate to high heritability coupled with high genetic advance for number of spikelets per spike, number of grains per spike, weight of grains per spike, chlorophyll-a content, chlorophyll-b content, total chlorophyll content and yield per plant among 49 bread wheat genotypes.

Maurya *et al*. (2014) reported higher heritability, in broad sense, for yield per plant, 1000 grain weight, grain per spike and plant height while moderate heritability observed for days to heading, days to maturity and spike length in bread wheat. High heritability indicates that heritability may be due to higher contribution of genetic component and thus the traits may be improved by progeny selection. Estimates of genetic advance as percent of mean were highest for yield per plant, grains per spike and 1000-grain weight.

Yadav *et al*. (2014) studied genetic variability of yield and its contributing traits among CIMMYT based wheat germplasm, and reported high heritability coupled with high genetic advance for grains per spike and grain yield per plant.

Zeeshan *et al*. (2014) reported high heritability and genetic advance for number of tillers plant, harvest index and grain yield per plant among ten spring wheat genotypes, which confirms their additive gene action.

2.2.3 Mean performance

Mean performance of wheat genotypes for yield, yield contributing and physiological traits associated with heat tolerance under heat stress is the ultimate technique to identify the potential candidate heat tolerant lines of wheat. Mian *et al.* (2007) reported reduction in grain weight due to post anthesis temperature stress.

Khan *et al*. (2007a) studied agronomic evaluation of different bread wheat (*Triticum aestivum* L.) genotypes for terminal heat stress. They reported that all the characters were negatively affected as a result of late sowing yet the genotypes CT-01217, CT-01222 and CT-01085 with grain yield of 4745, 4334 and 4334 kg ha^{-1}, respectively performed well with respect to harvest index (40.5, 31.0 and 36.5%) and medium plant height character (89, 92 and 91 cm) as compared to those of the best check line (Bakhtawar-92) which is an indication that some bread wheat genotypes among existing germplasm may have in built resistance/tolerance against terminal heat stress under late planting condition.

Ubaidullah *et al*. (2007) studied characterization of wheat genotypes for yield and yield associated traits against terminal heat stress. They reported that genotype CT-7 exceeded for spike length and grain weight per spike and CT-10 was better for 1000-grain weight in late sowings than normal sowings whereas CT-7 produced similar number of grain per spike in both sowings indicating that these genotypes have intrinsic potential for higher yields under terminal heat stress. These genotypes exhibited a higher level of productivity under late sowing environments.

Jajarmi (2009) Results indicated significant differences among cultivars, and drought stress levels. In all traits, a significant decrease was observed with increase in stress level. It seems that the length of stem among the other traits has more sensitivity to drought stress. Drought stress reduces the radical length at more than -6 bars The percentage of germination and the velocity of germination lessened when drought stress exceeded more than -12bars. Traits intolerant cultivars did not show a significant decline up to -3 bars.

Rehman *et al*. (2009) studied terminal heat tolerance in wheat and reported that effects of heat stress were lesser in shorter period exposure and more drastic in prolonged exposure of the genotypes to heat, and also reported that the ability of lines to stay green for longer period in heat shock had no direct relationship with seed setting. Hence they revealed that these genotypes can be utilized in breeding programs for development of wheat varieties having heat tolerance at terminal growth stage.

Balouchi *et al.* (2010) screened wheat parents of mapping population for heat and drought tolerance, and detection of wheat genetic variation. They reported that there was a significant genetic variation among the eight varieties that were studied under heat and water stress.

Almeselmani and Deshmukh (2012) studied effect of high temperature stress on physiological and yield parameters of some wheat genotypes recommended for irrigated and rainfed condition and reported significant reductions in all the parameters at all growth stages in all genotypes. Yield and yield components were also adversely affected under late and very late planting. Genotypes recommended for irrigated conditions showed more reductions in leaf area index, relative growth rate, net assimilation rate, chlorophyll content, yield and yield components than the genotypes recommended for rainfed conditions. However, close associations between all growth parameters, yield and yield components were observed and the good performance of the genotypes which is recommended for rainfed condition under high temperature stress which could be because of their ability to maintain high water status in plant tissue and prevent cell from loosing its turgidity.

Sareen *et al*. (2012) evaluated twenty eight synthetic wheat lines for terminal heat tolerance by normal and late planting in field in randomized block design. They reported that synthetic wheat lines S9, S37, S44 and S57 had high thousand grain weight with heat tolerance during both years and genotypes S8, S22, S23, S49 and S77 had poor performance in both environments.

Dhyani *et al*. (2013) evaluated comparative physiological changes in wheat genotypes viz., DBW-140, Raj-3765, PBW-574, K-0-307 and HS-240 under timely and late sown conditions in *Rabi* season. They reported the heat susceptibility index (HIS) for 1000-grain weight, grain weight and grain yield of wheat genotypes viz., HS 240 and K-0-307 was highest as compared with DBW 140, Raj 3765 and PBW 574 genotypes. They also suggested that wheat genotypes are found to differ in their ability to respond to heat, thereby tolerance, which could be useful as genetic stock to develop wheat tolerant varieties in breeding programs.

Sharma *et al*. (2013) studied correlation and heat susceptibility index analysis for terminal heat tolerance in bread wheat and reported that heat susceptibility index values revealed reduction in grain yield in both the years for all the generations of the four crosses. Lowest yield loss was reported in backcross populations of Cross I in both years and among segregating populations of Cross IV observed to be least affected and therefore suggested to be forwarded to further generations and further selection of heat tolerant genotypes.

2.2.4 Correlation

The relationship between the morphological, physiological and biochemical traits related to heat tolerance is very much important in selecting suitable selection criteria for heat tolerance. The association between the traits related to heat tolerance could be better understood through correlation study. On the basis of nature and magnitude of genetic correlation, breeding programs may measure such traits to assist in the selection of heat tolerant genotypes.

Ali *et al*. (2008) carried out association studies in wheat (*Triticum aestivum* L.) germplasm and observed that grain yield per plant showed highly significant positive correlation with number of productive tillers per plant, number of spikelets per spike and number of grains per spike and significant positive correlation with spike length.

Bahar *et al*. (2008) studied the effect of canopy temperature depression on grain yield and yield components in bread and durum wheat and observed that CTD was positively correlated with grain yield, spike yield, and grain numbers per spike. Overall, the results indicated that CTD has played an important role to search physiological basis of grain yield of wheat, and CTD can successfully be used as a selection criterion in breeding programs.

Saint Pierre *et al*. (2010) reported significant negative phenotypic correlation ($r = -0.34$ to -0.75, $P<0.001$) between canopy temperature and grain yield under drought conditions in wheat.

Karimizadeh and Mohammadi (2011) reported canopy temperature depression (CTD) was used to estimate crop yield and to rank genotypes. CTD was measured at three stages, from the emergence of fifty percent of inflorescence (Zadoks Growth Scale54) to watery ripe stage (ZGS71). The results showed that the average values of CTD in durum wheat genotypes changed from 3.3 to 5.7°C at the ZGS69 stage. Genotypes in this stage (ZGS69) had highly significant differences and average of CTD showed that durum wheat canopy was the largest value in all ZGSs under both conditions. The significant and positive correlation of YP, MP, GMP, SSI, STI and

CTD showed that these indices were more effective in identifying high yield genotypes under both conditions.

Guendouz *et al*. (2012) reported that under dryland conditions, grain yield and mean CTD were correlated positively (r = 0.32**). The results of correlation between canopy temperature (CT), canopy temperature depression (CTD) and grain yield suggest that the use of CT and CTD in screening for highly tolerant varieties to drought is similar. The significant correlation of CT and CTD with Mean productivity (MP) and Stress tolerance index (STI) suggests that CTD and/or CT can be favorite selection criteria in plant breeding for drought tolerance.

Grzesiak *et al*. (2012) Seedlings grown under moderate soil drought showed a decrease in dry matter of the top parts and roots and a decrease in the length of seminal, seminal adventitious and nodal roots in comparison to seedlings grown in control conditions. The observed harmful effects of drought stress were more distinct in drought sensitive genotypes. Used in this paper drought susceptibility indexes (DSIGY) were calculated in other experiment by determining the changes in grain yield (GY) under two soil moisture levels (irrigated and drought). The variation of DSIGY for maize ranges from 0.381 to 0.650 and for triticale from 0.354 to 0.578. The correlations between DSIGY and laboratory tests (Seedling Survival) confirmed that they are good indicators of drought tolerance in plants.

Kalimullah *et al.* (2012) reported that grain yield per plant showed highly significant positive correlation with number of tillers per plant and number of grains/spike and significant positive correlation with 1000-grain weight in a set of 41 wheat genotypes.

Paliwal *et al*. (2012) reported negative correlation of CTD with HSITGW, HSIYLD, and HSIGFD which indicates that RILs with high cooling capacity display lower HSI of TGW, YLD, and GFD. They also reported that most of the measured traits under late-sown conditions were significantly correlated to one another. The findings appear to suggest that under late-sown environment, CTD along with TGW and yield may be used as indirect selection criteria for heat tolerance in wheat.

Abdipur *et al*. (2013) studied the correlation of grain yield with canopy temperature depression (CTD) and chlorophyll content (CHL) in wheat under rainfed conditions. The results revealed that CTD had significant correlation with grain yield at anthesis half-way (ZGS 65) and medium milky stage (ZGS 75). The CTD at ZGS 65 appeared to be directly most related to yield for G1, G2, G3 and G4, the genotypes which were well adapted to drought. Chlorophyll content had significant correlation with yield components only at ZGS 75 as only positive significant association of grain yield and chlorophyll content at ZGS 75. So, CTD and CHL at the mentioned stages can be used as potential selection criterions for grain yield and wheat drought tolerance in breeding programs.

Baloch *et al*. (2013) studied correlations of yield and yield attributing traits in wheat (*Triticum aestivum* L.) and reported that tillers per plant, spikelets per spike, number of grains per spike, seed index and harvest index were significantly and positively correlated with grain yield per plant. The higher correlations coefficients of yield components with grain yield suggested that yield components can reliably be used as indirect selection criteria to improve grain yield in wheat.

Sharma *et al*. (2013) reported significant estimates of correlation of grain yield with days to heading, days to anthesis and days to maturity under late sown condition during first year. While under timely sown condition spike length has high estimates of correlation with grain yield in first year itself. Significant estimates were recorded for tillers per plant in both the environments in second year.

Khan *et al*. (2014) studied correlation of some heat tolerant traits of spring wheat (*Triticum aestivum* L.) under late sowing conditions and reported that chlorophyll content of flag leaf both at anthesis and 21 days after anthesis showed significant negative association with canopy temperature (-0.487* and -0.570**, respectively) and grain filling rate (-0.506** and -0.570**, respectively) while it was found positively correlated with grain filling duration (0.538** and 0.508**, respectively). Highly significant negative association (-0.649**) between grains number per spike and 1000-grain weight indicates a competitive demand of both sinks for photosynthates from a common source. Significant negative correlation of heat stress susceptibility indices with days to anthesis, ground coverage, biomass and grain filling rate suggests that these parameters can be useful for discriminating genotypes that have lower susceptibility to heat stress condition. The significant negative association with grain yield also offers solo importance in differentiating heat tolerant genotypes.

Bahari *et al*. (2014) reported that the genotype and the interaction of both factors showed significant differences for germination percent. Germination speed was more sensitive against drought stress compared to germination percent and genotype 2 had highest germination percent. Germination stress indicators (GSI), which was known to select tolerant genotype to drought stress, so genotype 2 was more than others. Also, germination stress indicators (GSI) had a significant positive correlation with the germination speed.

Purushothaman *et al*. (2015) CTD was positively associated with the grain yield and shoot biomass and such association diminished gradually to minimum after 76 DAS. Moreover, CTD at 62 DAS also showed similar positive association with the grain yield recorded in two previous years. The phenotypic variation explained by the markers was the highest at 62 DAS. These results confirm the importance of continued transpiration and the ability of the roots to supply stored soil water under terminal drought. The selection for grain yield through CTD is done best 15 days after the mean flowering time.

2.3 Diallel Analysis

2.3.1 Combining ability

Success of any plant breeding programme depends on the choice of appropriate genotypes as parents in hybridization programme. The combining ability studies of the parents provide information which helps in the selection of better parents for effective breeding. The method for combining ability analysis was developed by Griffing (1956) and is a comprehensive tool for selection of better parents possessing high general and specific combining ability.

Kakar *et al*. (1999) evaluated combining ability analysis of inter-varietal crosses of four bread wheat genotypes for seven characters in diallel fashion. GCA analysis indicated that a large portion of total genetic variation for 4 out of 7 traits was associated with additive genes. SCA was non-significant for all the traits indicating absence of epistasis and dominant gene effects. Parent Jauhar 78 was the best general combiner having positive GCA effect for six traits. Cross Koh-i-noor83 x Mehran89 was the best combination followed by Yecora x Jauhar78, since these crosses exhibited high parent heterosis in at least five traits. GCA effects were more pronounced than SCA effects for all traits except grains per spike.

Khan *et al*. (2000) evaluated five parent diallel involving bread wheat varieties/lines; K-65, LU26S, Tob-66, 6544-6 and KLR-6 to study the inheritance pattern of plant height, number of tiller per plant, 1000-grain weight and grain yield. Highly significant differences were observed among genotypes for all the traits except grain yield per plant for which the differences among genotypes were simply significant. The genotype K-65 appeared to be promising parent for wheat breeding programme.

Singh *et al*. (2002) conducted an experiment to study the combining ability for yield and yield component of bread wheat cultivars in diallel fashion. General combining ability was comparatively higher for days to flowering, plant height, 1000-grain weight and grain yield. Specific combining ability was higher for tillers per plant, spikelets per spike and grains per spike. WH147 was the best general combiner for spikelets per spike and number of grains per spike, while Lok-1 was the best general combiner for days to flowering, tillers per plant, 1000-grain weight and grain yield. CPAN3056, K8504 and DL802-3 were the best general combiners for days to flowering, whereas DL802-3, CPAN3004 and CPAN2099 for plant height and CPAN3056 was the best general combiner for plant height and CPAN3004 and V222 for grain yield per plant.

Mavi *et al*. (2003) performed combining ability analysis in bread wheat using 10 x 10 diallel design in two environments, normal (150kg, E_1) and high nitrogen (300kg, E_2). The parent cultivar PBW343 was the best general combiner for days to heading, number of tillers per plant, grain yield, 1000-grain weight and days to maturity in both environments, followed by C518 and UP2338 for days to heading, grain yield and number of grains per spike in E_2. In general, all combinations of parents, namely those with high x high, high x low and low x low gca effects were involved in the expression of high sca effects.

Joshi *et al*. (2004) analysed the F_1 progenies of a ten parent diallel (excluding reciprocals) of hexaploid wheat (*Triticum aestivum*) for combining ability for quantitative and quality traits. The gca and sca components of variance were significant for all the traits. However, the gca component of variance was predominant indicating the predominance of additive gene effects for the traits studied. Among the parents, Durgapure 65, HD2285, Lok-1, Raj1972 and HD2329 were the best general combiners for tiller per plant, grain yield per plant and 1000-grain weight. The best specific crosses for grain yield were Sonalika x WH157, HD2428 x Durgapure 65, Durgapure 65 x Sonalika, HD2428 x Lok-1 and CPAN3004 x Raj 1972. The parent Raj1972, Lok-1 and HD2285 were the best general combiner for grain yield and protein content.

Siddique *et al*. (2004) calculated combining ability estimates in a 5 x 5 diallel cross of spring wheat cultivars for days to heading, days to maturity, plant height, tillers per plant, grains per spike and grain yield. The analysis of variance revealed highly significant differences for all the traits. The specific combining ability variances were higher than general combining ability variance for all the traits indicating non-additive gene action except for days to heading, days to maturity and plant height, which showed additive gene action. Grains per spike showed both additive and non-additive gene action. Faisalabad 83 and Chakwal 86 were good general combiners while Faisalabad 83 x Chakwal 86 was the best specific combiner.

Saeed *et al*. (2005) conducted combining ability analysis in diallel design in a field experiment to evaluate the performance of bread wheat cultivars. Mean squares of general combining ability (GCA) were non-significant for number of grains per spike, 1000-grain weight and grain yield per plant. Specific combining ability (SCA) mean squares were highly significant for number of grains per spike, 1000-grain weight and grain yield per plant and significant for the number of spikelets per spike.

Kamaluddin *et al*. (2007) studied general and specific combining ability in 11 parent half diallel by evaluation of 55 F_1 progenies of bread wheat involving two traits i.e. 1000-seed weight and seed yield per plant. Analysis of variance for general combining ability (GCA) and specific combining ability (SCA) displayed significant F_1 general and specific combining ability effects for the traits studied. For all the traits GCA effects were more important than SCA effects, indicating that additive genetic effects were predominant. Crosses displaying high SCA effects for seed weight and yield were observed to be derived from parents having various types of GCA effects (high x high, high x low, low x low and medium x low.

Singh *et al.* (2010) studied combining ability analysis for high temperature tolerance in bread wheat (*Triticum aestivum* L. Em. Thell.) involving ten diverse parents and their 45 F_1 and F_2 progenies, and reported significant differences among the parents for *gca* and crosses that of *sca* for all the characters studied. The *gca* and *sca* components of variance were significant for all the traits. Based on general combining ability (*gca*) effects and *per se* performance, parents WH 789 and HD 2881 emerged as good general combiners for grain yield per plant and average to high combiners for most of the yield component characters in case of very late sown condition. These genotype possessed desirable GCA effects for biological yield per plant, number of grains per spike, 1000 - grain weight, tillers per plant, days to heading and harvest index. On the basis of *per se* performance and SCA effects the crosses for grain yield were UP 2614 x HD 2851, WH 789 x PBW 520, HUW 468 x UP 2614 and HUW 468 x PBW 520 which emerged as good specific cross combinations.

Kamaluddin *et al.* (2011) studied combining ability analysis for protein content, days to 50% flowering, days to 50% physiological maturity, number of grains per spike, 1000-grain weight and grain yield per plant in spring wheat in diallel fashion. Additive as well as dominance type of gene action was responsible for expression of these traits. Most of the genotypes were found to be superior general combiner for protein content and other traits studied. Likewise, crosses involving diverse parents showed significant SCA effects for protein content and other traits. To ensure further increase in protein content with optimum maturity duration, combinations of desirable component traits is advocated. Biparental and/or diallel selective mating design would be useful methods for further improvement of protein content with optimum level of maturity time and grain yield in spring wheat.

Singh *et al.* (2012) studied the combining ability of bread wheat and their F_1's in a 7 x 7 diallel fashion excluding reciprocals. The results revealed that the best combinations mostly involved high x low and low x low general combiner for 14 traits under study. There was very rare case in which high x high general combiners were involved for best combinations. On the basis of GCA and SCA effects, 3 parents (i.e. K 7903, K 9465 and HUW 234) and 14 cross combinations (i.e. 5 top crosses, namely HD 2733 x K 7903, HUW 234 X K 9423, HD 2285 x K 2021, HUW 234 x K

2021 and K 9423 x K 2021) were found good general and specific combiners for higher grain yield and also for various yield contributing traits, respectively.

Singh *et al*. (2013b) studied combining ability analysis for high temperature tolerance in bread wheat (*Triticum aestivum* L. Em. Thell.) using 10 x 10 half diallel and reported significant differences among the parents for *gca* and crosses that of *sca* for all the characters studied. The *gca*/*sca* variance ratio below unity in both the generations showed the preponderance of non-additive gene effects for all the characters. Based on general combining ability (*gca*) effects and *per se* performance, parents WH 789 and HD 2881 emerged as good general combiners for grain yield per plant and average to high combiners for most of the yield component characters in case of very late sown condition. On the basis of *per se* performance and SCA effects the crosses for grain yield were UP 2614 x HD 2851, WH 789 x PBW 520, HUW 468 x UP 2614 and HUW 468 x PBW 520 which emerged as good specific cross combinations and were the product of good x good, good x poor or poor x poor general combiners. Hybridization systems, such as multiple crossing and bi-parental mating could be useful in the genetic improvement for further amelioration of grain yield per plant in bread wheat.

Ram *et al*. (2014) studied genetic analysis for terminal heat stress in bread wheat (*Triticum aestivum* L. Em. Thell.) using 10 x 10 half diallel and reported that parents HUW-234 followed by PBW-175, HD-2888 and DBW-14 in both normal and heat stress environment having good GCA along with high per se performance for canopy temperature depression and cell membrane thermo-stability could be used as donor for terminal heat tolerance in breeding programme. For CTD and CMS h^2(ns) estimates were high. Since the identified genotypes can cope up the effect of heat stress, they can be utilized for developing heat tolerant genotypes.

2.3.2 Gene action

Combining ability analysis of cultivars is important to exploit the relevant type of gene action for a breeding programme. If specific combining ability is predominant, it can be used in hybrid breeding programme. In other breeding programme only that segment of total genetic variance, which results from additive genes can be used since subsequent inbreeding retains them.

Joshi *et al*. (2003) conducted genetic analysis in 10 x 10 half diallel bread wheat progenies planted under early (25 October), normal (20 November) and late (20 December) sowing dates. Both additive and non-additive gene effects were present in the material under study. However, the ratio of additive/non-additive genetic variance revealed that there was preponderance of additive gene effects in the expression of yield per plant, protein content and other yield contributing traits studied. Both the gene effects were highly influenced by the environment.

Rahman *et al*. (2003) studied genetic analysis of yield and quality chatacters in spring wheat in seven cultivars and their F_1's obtained from a diallel cross without reciprocals. Diallel analysis revealed the presence of epistasis for the characters plant height, spikes per plant, grains per spike, 1000-grain weight, grain yield per plant and protein content. Partial dominance was showed by the characters days to maturity, plant height, grains per spike, 1000-grain weight and protein content. Among these gene actions partial dominance could easily be exploited through conventional breeding.

Singh *et al*. (2003) studied the genetics of yield and related traits in bread wheat by means of 10 x 10 half diallel progenies under three diverse environments. The component analysis indicated that both additive (D) and dominance components (H_1 and H_2) were significant. However, the relative magnitude of the dominance component was higher than the additive component, indicating the preponderance of dominance in controlling the inheritance of the characters studied. The value of F exhibited an excess of dominant alleles in the parents and the environment component E was non-significant for this trait. The average degree of dominance $(H_1/D)^{1/2}$ was within the range of over dominance. The ratio of $H_2/4H_1$ indicated symmetrical distribution of the genes for days to heading. The value of h^2/H_2 was less than one in all traits.

Tomar and kumar (2004) have reported that seedling survivability as efficient selection criteria for drought tolerance in wheat. They observed that when genotypes start wilting when no irrigation was applied after sowing and studying there recovery response after irrigation based on the days taken for recovery (Seedling survivability) genotypes can be grouped as susceptible (withered early) and drought tolerant (resume growth). They also studied the inheritance of this trait and concluded that it is under single dominant gene control.

Farshadfar *et al*. (2008) studied gene action and epistatic effect for drought indicators and found that both additive and non-additive gene action were significant for grain yield in water stress condition. Only additive gene action was predominant for heading date in the rainfed condition.

Farooq *et al*. (2011a) studied genetic analysis of relative cell injury percentage and some yield contributing traits in wheat under normal and heat stress conditions. They reported that additive component of genotypic variation (D) was significant for all studied traits and more significant than the H_1 and H_2 dominance components. Values of the gene proportion with positive and negative effects in the parents ($H_1/4H_1$) demonstrated an unequal distribution of dominant genes in the parents for almost all the traits except for flag leaf area, grain yield per plant, and harvest index which showed an equal distribution of dominant genes under stress conditions. High heritability estimates were found for days to heading, days to maturity, flag leaf area and grain yield under both regimes. Moderately high estimates were found for biomass per plant and harvest index.

Farooq *et al*. (2011b) studied inheritance pattern of yield attributes in spring wheat at grain filling stage under different temperature regimes. They reported that additive component of variance (D) was significant and more than dominance variance H_1 and H_2 for spike density and grain yield per plant under both temperature regimes showing preponderance of additive effects. Grains per spike showed prevalence of dominant gene action under both conditions. Spikelets per spike and spike weight showed dominance effects under normal conditions and additive ones under heat stress. Estimates of narrow sense heritability were moderate to high in almost all the traits except for spikelets per spike under normal conditions in which it was low.

Tammam and Abd El-rady (2011) conducted genetical studies on some morpho-physiological traits in some bread wheat crosses under heat stress conditions and they reported that both additive and non-additive gene effects controlled the genetic system of plant height (cm), spike length (cm), days to heading and days to maturity. The additive gene effects were the most prevalent type under both the sowing dates. The positive and negative alleles were unequally distributed among the parents for all traits under the two planting dates. The parents had more positive alleles for all traits in both generations under both the sowing dates except in the F_1 hybrids under late sowing for heading date and in F_1 and F_2 generations under late sowing for maturity date which exhibited more negative alleles. Heritability values were high in both broad and narrow-sense for these characters. The previous results revealed that selection could be effective for developing these traits in segregating generations.

Irshad *et al*. (2014) studied genetics of some polygenic traits in hexaploid bread wheat in high temperature stress and showed that additive component of variation (D) was significant ($P<0.01$) and prominent over H_1 and H_2 components for days to anthesis, grains per spike, 1000-grain weight, grain yield per plant and dry biomass per plant at maturity while dominant genes were mainly controlling factors for spike length and was confidently sustained by the value of $H_1/D^{1/2}$. Values of h^2 and $H_2/4H_1$ demonstrated asymmetrical and unequal distribution of dominant genes in parents for most of the characters. Spike length, dry biomass per plant at maturity, grains per spike, 1000-grain weight and grain yield per plant exhibited high narrow sense heritability due to the existence of additive gene action with partial dominance suggesting that these traits might be useful for the development of high temperature stress tolerant varieties by modified pedigree selection method.

Kumar *et al*. (2015) studied estimates of genetic parameters for grain yield, agro-morphological traits and quality attributes in bread wheat (*Triticum aestivum*) using 10 x 10 half diallel mating design and reported significant additive and dominant components for all the traits. They showed positive and significant value of ‘F’ for yield and quality components in F_1 crosses which indicated the preponderance of dominant and positive genes in the parents. The estimates of h^2 were found highly significant for number of productive tillers/ plant, flag leaf area, spike length, spikelets/ spike, biological yield/ plant, grain yield/ plant and gluten content, whereas, non-significant values were reported for rest of the traits. The value of ($H_2/4H_1$) for all the traits indicated the asymmetrical distribution of positive and negative alleles among the parents. The proportion of dominant and recessive genes indicated presence of dominant alleles in the parents for these traits. The ratio of h^2/H_2

revealed that more than one major gene group was responsible for controlling these traits.

Nazir *et al*. (2015) studied pattern of inheritance in some yield related parameters in spring wheat (*Triticum aestivum* L.) using diallel design and reported that additive and non-additive component were significant for all the traits showing the importance of both these components in inheritance of the studied traits. The graphical representation showed that tiller number for each plant, height of plant, grain number per spike and weight of 1000 grains were controlled by partial dominance with additive type of gene action. Over-dominance was observed in weight of grains per spike. Complete dominance was observed for spikelet number per spike and grain yield per plant. Non-allelic interaction was absent for all the traits studied. The distribution of dominant and recessive genes for yield traits was also studied and noted that line 9437 being closer to the origin had maximum contribution of dominant genes for grain yield per plant. The estimates of narrow sense heritability (h^2_{ns}) were higher for plant height and grain number per spike indicating better chance for improvement following selection procedure in these traits. The traits governed by additive genes and partial dominance should be selected in early segregating generation. In traits showing over dominance, delayed selection would be better to practice.

CHAPTER III

MATERIAL AND METHODS

The present study entitled **“**Characterizing diversity for heat and drought related traits in hexaploid Wheat (*Triticum aestivum* L.**)”** was carried out at the Research Farm of Division of Plant Breeding and Genetics, Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Main Campus, Chatha, Jammu during *Rabi* 2014-15 and 2015-16 under two different environments designated as N (normal irrigation) and S (stress) conditions.

Sher-e-Kashmir University of Agricultural Science and Technology of Jammu, Chatha is situated at an altitude of 332 m above sea level with 32^0 39’ degree N latitude and 74^0 degree 58’ E longitude with an annual rainfall of 1000 mm and, represents sub-tropical conditions.

3.1 Experimental Material

The experimental material of the present study comprises twenty true breeding lines of hexaploid wheat received from ICARDA, Syria in the form of DBSYT-2011nursery IC, collections from IIWR, Karnal and maintained in the Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Science and Technology, Jammu (Table 3.1). The present study was carried under two different experiments.

3.1.1 Experiment No.1

Twenty different germplasm lines were evaluated for various morphological and physiological drought and heat related traits during *Rabi* 2014-15 to characterize these lines for heat and drought. Based on their diversity performance seven elite lines were selected for further study in experiment number two.

Table 3.1: Wheat varieties, there source and pedigree used for the evaluation of heat and drought stress:

GENOTYPE	SOURCE	PEDIGREE
PBW 175	PAU, Ludhiana (Punjab)	HD2160/WG1205
RGP 1	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 2	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 3	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 7	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 11	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 12	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 15	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 16	ICARDA, Syria	DBSYT-2011-ICARDA
RGP 18	ICARDA, Syria	DBSYT-2011-ICARDA
DWR 1	DWR, Karnal (Haryana)	IC-296681
DWR 13	DWR, Karnal (Haryana)	IC-296768
DWR 16	DWR, Karnal (Haryana)	IC-309871
DWR 17	DWR, Karnal (Haryana)	IC-309872
DWR 18	DWR, Karnal (Haryana)	IC-309873
PBW 644	PAU, Ludhiana (Punjab)	PBW 175/ HD 2643
PBW 550	PAU, Ludhiana (Punjab)	WH594/RAJ3858/W485
DBW 14	DWR, Karnal (Haryana)	Raj 3765/PBW343
HD 3040	IARI, Delhi	WR1027/HD2851
RAJ 3765	SKRUS, ARS, Durgapur, Raipur (raj.)	HD2402/VL639

3.1.2 Experiment No.2

The seven lines evaluated for heat and drought stress namely PBW-175, RGP1, RGP12, RGP18, DWR13, DWR16 and DWR17 were crossed in a half diallel fashion during Rabi 2014-2015 to obtain 21 F_1' s . All the 21 F_1 along with their parents were raised in a randomized block design with three replications under normal (date of sowing 24th November) and stress condition (drought and terminal heat stress in polyhouse, date of sowing 11th December). Each entry was sown in three rows of 1 m each, with plant-to-plant and row-to-row distance of 10 and 25 cm, respectively.

3.2 Recording of observations

Data on the following parameters were recorded on randomly selected five plants from each wheat genotype used for evaluation as well as crosses/ parent of half diallel in three replications at an appropriate time from each experiment on the following morphological and physiological traits:

3.2.1 Morphological traits

3.2.1.1 Days to 50 per cent flowering:

The number of days from date of sowing to date when 50 percent of plants flowered of in the rows was recorded.

3.2.1.2 Days to maturity: The number of days taken from date of sowing to the full maturity of crop was recorded

3.2.1.3 Plant height (cm):

Height of the plant in centimetres was recorded from the ground level to the top of the ear (excluding awns) of the main shoot of each plant at the time of maturity.

3.2.1.4 Number of tillers per plant:

At maturity the number of fertile tillers per plant were counted and averaged.

3.2.1.5 Number of grains per ear:

Five ears from each of the five selected plants in each progeny from each replication were taken at maturity stage prior to harvesting. Number of grains of each ear was counted separately after thrashing them manually and the mean data obtained was represented as number of grains per ear for each progeny.

3.2.1.6 Grain yield per plant (g):

The grain yield of five randomly selected plants from each progeny was weighed in grams. Average of five plants was worked out.

3.2.1.7 Harvest index:

Harvest index was calculated as ratio of grain yield to biological yield (excluding roots) and expressed in percentage .i.e.

Harvest index (%) = Economic yield per plant/ Biological yield per plant× 100

3.2.1.8 1000 grain weight (g):

One thousand grains from each genotype were counted and weighed in grams on electrical balance.

3.2.2 Physiological traits

3.2.2.1 Relative leaf water content (RWC):

To measure RWC at grain filling stage, three fresh flag leaves were detached from each plot and weighed immediately to record fresh weight. Fresh leaves were floated in distilled water for 24 hours. Excess water of leaves was wiped-off and weight to record saturated weight, and then oven-dried at 70 ^{0}C for 48 hours for dried weight measurement. The RWC was computed using the following equation:

RWC (%) = [(W-DW) / (TW-DW)] x 100,

Where,

W – Sample fresh weight

TW – Sample turgid weight

DW – Sample dry weight.

3.2.2.2 Canopy temperature (CT):

Canopy temperature was measured with an infrared thermometer at the grain filling stage as described by Reynolds et al. (1998) and Olivares-Villegas et al. (2007). Five measurements per plot were taken. Canopy temperature was recorded by a handheld infrared thermometer (IMPAC Electronic GmbH, Germany) on bright sunny days between 1 and 3 pm at grain filling stage. For each plot five measurements were made at approximately 0.5-1 m distance from the edge of the plot and approximately 50 cm above the canopy with an approximate angle of 30^0- 60^0 from horizontal giving a canopy view of 10cm × 25 cm (Ayenesh et al., 2002).

3.2.2.3 Canopy temperature depression (CTD):

Canopy temperature depression was calculated using formula as, CTD = Ambient temperature – canopy temperature. Ambient temperature was measured after recording observation in each plot, using a handheld thermometer.

3.2.2.4 Germination stress index (GSI):

In the laboratory experiment twenty five seeds from each line were germinated in Petri dishes under two different stress and non-stress water regimes in the seed germinator. In the stress and non-stress condition 10ml of polyethylene glycol 6000 with – 0.8 MPa osmotic potential and 10ml of distilled water were used in the Petri dishes, respectively. During ten days the number of germinated seeds were recorded and promptness index (PI) and germination stress index (GSI) were calculated using the formula of Bouslama and Schapaugh (1984);

(Promptness index) PI = nd_2 (1.0) +nd_4 (0.8) + nd_6 (0.6) + nd_8 (0.4) +nd_{10} (0.2)

Where, $nd_{2,}$ $nd_{4,}$ $nd_{6,}$ $nd_{8,}$ and nd_{10} are the percentage of germinated seeds in the 2^{nd}, 4^{th}, 6^{th}, 8^{th}, and 10^{th} day respectively.

GSI = (PI under stress condition)/ (PI under non stress condition) × 100

3.2.2.5 Seedling survivability:

In the experiment twenty five genotypes of wheat were screened at the seedling stage in plastic boxes in greenhouse conditions for moisture stress. The plastic boxes were filled with a mixture of soil, sand and F.Y.M. in 50:45:50 ratios.

The boxes were given equal quantity of water twelve hours before sowing to ensure good germination. Twenty five seeds were sown in rows at uniform depth of 3cms. No irrigation was provided after sowing. When most of the genotypes stated withering after 35 days, the boxes were irrigated on 43rd day to study the recovery response (seedling survivability) of the genotypes. Based on the days taken for recovery wheat genotype withered early were grouped as susceptible while the genotypes resume growth showed a better response and were classified as drought tolerant.

3.2.2.6 Drought susceptibility index (DSI):

Drought susceptibility index for grain yield was calculated by the formula given by Fisher and Maurer (1978) and Clark *et at.* (1984). It was assessed by measurement of trait under water stress and non-moisture stress.

Stress intensity D=1-[Mean γ_D all genotypes/mean γ_P of all genotypes]

Where, γ_D = grain yield under drought stress.

γ_P = grain yield under non stress condition.

D = stress intensity

Then, DSI= [1-YD/YP] / D Where,YD = Mean of the genotype in stress

YP = Mean of the genotype in non- stress

3.3 Statistical Analysis

The observations recorded for the various morphological and physiological traits were subjected to the following statistical analysis:

3.3.1 Mean performance

The mean or average of the each of above recorded traits was used to test the performance of the 20 wheat genotypes used in present study under non-stress and stress conditions.

3.3.2 Analysis of variance

To test the significance of differences among different genotypes used in the study, the data on mean values for different characters was analysed as per standard statistical procedure for randomized block design (Panse and Sukhatme, 1984). Different biometrical measures that were used to explain dispersion of variability includes:

1. **Range**: It was expressed as the difference between the lowest value and the highest value present in the observation for each trait.

2. **Standard deviation (σ):** Expressed in terms of square root of variance.

$$\text{SD} = \sqrt{Var} = \sqrt{\sigma^2} = \sigma$$

3. **Variance**: Expressed as the average of squared deviation of all the individual observation from the mean. Mathematically

$$\text{Variance (var.) or } \sigma^2 = \frac{\sum (x - \bar{x})^2}{N - 1}$$

4. **Standard error (SE)**: Expressed as the mean difference between sample estimates of mean and the population parameter µ i.e. it is the measure of uncontrolled variation present in a sample. Mathematically

$$\text{Standard error} = \frac{\text{Standard deviation}}{\sqrt{\text{N}}}$$

Where,

X_i = i^{ih} observation of a given character.

N = Total number of observations

Var/σ^2 = Variance of sample

In fact, S.E is the SD of means and is expressed as SE_m

5. Coefficient of variation (CV):

CV (%) = Standard deviation /Mean x100

The analysis of variance was carried for different genotypes of bread wheat

(a) Analysis of variance for different wheat genotypes

Source of variation	d.f	MSS	Expectation of MSS
Replications	(r-1)	M_r	
Genotypes	(g-1)	M_g	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (g-1)	M_e	σ^2_e
Total	rg-1		

Where,

r = number of replications

g = number of genotypes

M_r = Mean sum of square due to replications

M_g = Mean sum of square due to genotypes

M_e = Mean sum of square due to error

The genotypic, phenotypic and environmental variances were estimated as suggested by Lush (1940).

1. **Genotypic variance**

$$V_g \text{ or } V = \frac{M_g - M_e}{r}$$

2. **Phenotypic variance**:

$$V_P \text{ or } \sigma^2_p = M_g + M_e$$

The phenotypic and genotypic variance was further used to compute coefficient of variation as suggested by Burton (1952).

1. **Phenotypic coefficient of variation (PCV)**

$$\text{PCV (\%)} \quad \frac{\sqrt{\text{Phenotypic Variance}}}{\text{Mean}} \times 100$$

$$= \quad \frac{\sqrt{V_p}}{\overline{X}} \quad or \quad \frac{\sigma p}{\overline{X}} \times 100$$

2. **Genotypic coefficient of variation (GCV):**

$$\text{GCV (\%)} \quad = \quad \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean}} \times 100$$

$$= \quad \frac{\sqrt{V_g}}{\overline{X}} \quad \text{or} \quad \frac{\sigma_g}{\overline{X}} \times 100$$

Where,

$\sigma_{p,}$ and σ_g are phenotypic and genotypic standard deviation respectively.

The PCV and GCV were classified as follows as suggested by Sivasubramaniam and Madhavamanon (1973).

Low : less than 10%

Moderate : 10-20%

High : More than 20%

3.4.3 Genetic parameters

1. **Heritability (broad sense) h^2_{bs}:** It was calculated by the method adopted by Lush (1940) and expressed as percentage**.**

$$\textbf{Heritability (broad sense) (\%)} \quad = \quad \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

$$= \quad \frac{\sigma^2_g}{\sigma^2_p}$$

As suggested by Johnson *et al.* (1955) heritability values were categorized as fallows.

Low : less than 30%

Moderate : 30-60%

High : More than 60%

2. Genetic advance (GA):

The expected genetic gain or advance under selection was estimated by following method as suggested by Johnson *et al.* (1955)

$$\text{Genetic advance (GA)} = \sigma_p \text{ x } h^2 \text{ x } k$$

Where,

σ_p = Phenotypic standard deviation of the original population for the character

h^2 = Heritability coefficient

k = Selection differential at particular level of selection intensity, which is 2.06 for 5 per cent selection intensity

$$\text{Genetic advance as percent of means} = \frac{\text{Genetic advance}}{\text{Mean}}$$

Genetic advance as percent of mean was calculated as suggested by Johnson *et al.* (1955)

Low : Less than 10%

Moderate : 10-20%

High : More than 20%

3.4.4 Correlation

3.4.4.1.Correlation coefficient:

The estimates of genotypic correlation coefficient among various characters were worked out by using the formulae suggested by Miller *et al*. (1958). The genotypic correlation coefficient (r_g) is expressed as follows:

$$r_g(X_1\ X_2) = \frac{\sigma_g X_1 X_2}{\sqrt{(\sigma_g^2 X_1)(\sigma_g^2 X_2)}}$$

r_g = genotypic correlation between x_1 and x_2

$\sigma_g\ x_1\ x_2$ = genotypic covariance between the two traits

$\sigma_g^2\ x_1$ = genotypic variance of the first trait

$\sigma_g^2\ x_2$ = genotypic variance of the second trait

Estimation of genotypic covariance components between two traits ($\sigma_g\ x_1\ x_2$) were derived as follows:

$$\sigma_g\ x_1\ x_2 = \frac{\text{MSPT} - \text{MSPE}}{r}$$

$\sigma_e\ x_1\ x_2$ = MSPE

$\sigma_p\ x_1\ x_2$ = $\sigma_g\ x_1\ x_2 + \sigma_g\ x_1\ x_2$

Where,

$\sigma_g\ x_1\ x_2$ = genotypic covariance between the two traits

$\sigma_e\ x_1\ x_2$ = error covariance between the two traits

$\sigma_p\ x_1\ x_2$ = phenotypic covariance between the two traits

MSPT = mean sum of products due to treatment

MSPE = mean sum of product due to error

For calculating correlation coefficient, the sum of products and the sum of squares at error levels were deducted from their respective values at varietal levels to obtain genotypic variances and covariances. These genotypic variances and covariances components were used to compute genotypic correlation coefficients between various traits.

3.5 Combining ability analysis

7 inbred parental lines, 21 F_1 hybrids (half diallel crosses) were used for half diallel analysis .These 28 wheat progenies were evaluated in stress and non-stress conditions to record physiological and morphological traits.

3.5.1 Analysis of variance

Before proceeding to the biometrical genetic analysis of the data, it is essential to test the genotypic differences among the entries. The data for different traits were statistically analysed on the basis of model described as under:

$X_{ij} = \mu + gi + b_j + e_{ij}$

Where,

X_{ij} = observation of the i^{th} genotype in the j^{th} block

μ = general mean

g_i = effect of the i^{th} genotype

b_j = effect of the j^{th} block

e_{ij} = random error associated with i^{th} genotype and j^{th} block.

The assumptions of the model are:

1. The observations are independent
2. The different effects in the model are additive, and
3. Errors in the model are normally and independently distributed with mean zero and variance

Analysis of variance based on this mathematical model led to the following breakup of the variance components for all the traits under study.

Source of variation	**d.f.**	**S.S.**	**M.S.**	**Expectation of mean squares**	**F-calculated**
Replication	r-1	S1	S1/(r-1)= Mr	$\sigma^2 e + t\, \sigma^2 b$	Mr/Me
Genotypes	t-1	S2	S2/(t-1)= Mt	$\sigma^2 e + r\, \sigma^2 g$	Mt/Me
Error	(r-1) (t-1)	S3	S3/(r-1) (t-1)= Me	$\sigma^2 e$	

Where,

r = number of replications

t = number of genotypes

Mr = mean squares due to replications

Mt = mean squares due to genotypes

Me = mean squares due to error

σ^2_g = variance due to genotypes

σ^2_b = variance due to blocks

σ^2_e = error variance

3.5.1 Analysis of variance for combining ability

The combining ability analysis was carried out in F_1 and parents following Method 2, Model I of Griffing (1956) for the estimation of variances and combining ability effects, as the reciprocals were not included in the study and consisted of only parents and one set of F_1s. The mathematical model used is as follows:

X_{ij} = $\mu + g_i + g_j + S_{ij} + \Sigma_k \Sigma_l e_{ijkl}$

i, j = 1,2, …………….p (parents)

k = 1.2, ……………..b (replications) and

l = 1, 2, …………….c (sample of plants)

Where,

μ = mean common to all parents

gi = general combining ability (gca) effect of ith parent

g_j = General combining ability (gca) effect of jth parent

s_{ij} = Specific combining ability (sca) effect for the cross between the ith and jth parent such that $s_{ij} = s_{ji}$,

e_{ijkl} = Environmental effect associated with ijklth individual observation

For combining ability estimates the degrees of freedom for genotypes was further divided into gca and sca as indicated below.

ANOVA table for combining ability

Source of variation	d.f.	SS	MS	Expectation of mean squares
GCA	p-1	S_g	M_g	$\sigma^2 + (p+2)\ (1/p-1)\ \Sigma_{gl}^2$
SCA	p(p-1)/2	S_s	M_s	$\sigma^2 + [2/p\ (p-1)]\ \Sigma_j\ \Sigma_j\ S_{ij}^2$
Error	m	S_e	M_e	σ^2

Where

Sg (SS due to gca)

$$= \frac{1}{n+2}\left[E\ (xi + xii)^2 - \frac{4}{n}x^2 .....\right]$$

Ss (SS due to sca)

$$= E_i = \sum{}_j x_{ij}^2 - \frac{1}{n+2}(x_i + x_{ii})^2 + \frac{2x^2 ....}{(n+1)(n+2)}$$

Where,

r is the number of blocks

m is the error d.f.

n is the number of parents

The error mean square Me' was obtained after dividing the error mean square (me) from R.B.D. ANOVA by the number of replications (r).

The significance of mean square due to gca (Mg) and sca (Ms) were tested against the error mean square (Me') by 'F' test at $p = 0.05$ and $p = 0.01$.

The ratio of unbiased estimates of the variance due to sea (σ^2 s) and variance due to gca (σ^2 g) was also calculated for each character

Where,

$$\sigma^2 s \quad = \quad Ms - Me' \text{ and } \sigma^2 g = (Mg - Me') / n+2$$

Estimates of Combining Ability Effects and their Standard Errors:

The estimates of the gca and sea effects were worked out only for those characters where variances due to sca and gca were significant.

gca effect of parent i was calculated as under:

$$g_i \quad = \quad \frac{1}{(n+2)}(x_i + x_{ii}) - \frac{2x_{\dots}}{n}$$

sca effect of cross ixj was calculated as under:

$$s_{ij} \quad = \quad x_{ij} - \frac{1}{(n+2)}(x_i + x_{ii} + x_{ij} + x_{jj}) + \frac{2}{(n+1)(n+2)} x_{\dots}$$

Where,

x_i = total, of array involving ith parent

x_{ij} = total of array involving jth parent

x_{ii} = parental value of ith parent

x_{ij} = parental value of jth parent

x_{ii} = total of all $\frac{n(n+1)}{2}$ items of diallel table

The standard errors to test the significance of sca and gca effects were worked out as follows:

$$SE_{(gi)} = \left[\frac{n-1}{n(n+2)} Me' \right]^{1/2}$$

$$SE_{(sij)} = \left[\frac{n^2+n+2}{(n+1)(n+2)} Me' \right]^{1/2}$$

3.5.2 Diallel Analysis

3.5.2.1 Component analysis (Hayman, 1954b)

The component analysis of the diallel cross was carried out by the method of Hayman (1954a). The analysis is based on following assumptions:

1) Dipliod segregation
2) No reciprocal effects
3) Homozygous parents
4) No epistasis
5) No multiple allelism, and
6) Independent genes distribution among parents.

In order to satisfy the assumptions for diallel analysis, the following general assumptions were used:

a) t^2- test (Hayman, 1954b)

The uniformity of Wr, Vr indicates the validity of assumptions made by Hayman (1954).

The testing is done by using following formula:

t^2 = [(n-2)/4] [Var Vr-Var $Wr)^2$]/ [Var Vr x Var Wr) – cov^2 (Vr, Wr)]

Where,

Var = variance

Cov = covariance

N = number of parents

Vr = variance of r^{th} array

Wr = the covariance between the parents and their offsprings in n^{th} array

This is tested against the table value of F with 4 and (n-2) degrees of freedom. Significant values indicate failure of hypothesis.

b) Analysis of (Wr, Vr) regression

Another way of testing the hypothesis is through the regression coefficient

b = Cov (Wr, Vr)/Var (Vr)

These texts have been described in detail by Mather and Jinks (1971)

Genetic components of variation were calculated from the diallel table following the method given by Hayman (1954b). These components of variance were derived by constructing a group of equations based on various parameters derived from the diallel table, as given below:

Expectations of F1 diallel:

V_p = D + E

V_r = 1/4D + 1/4H_1- 1/4F + n +1/2n E

W_r = 1/2D – 1/4F + 1/n E

V_m = 1/4D – 1/4H_1 – 1/4H_2- 1/4F + 1/2n E

Where,

D = Component of variation due to the additive effects of genes

H_1 = Component of variation due to the dominance effects of genes

H_2 = Proportion of dominance variation due to positive and negative effects of genes

h_2 = Net dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses)

F = The mean of F_1 over the arrays. It indicates the relative frequency of dominant and recessive alleles in the parents. It may take the negative or positive sign if there is an excess of recessive or dominant alleles, respectively. If both kinds of alleles are equally distributed the F will be zero, $H_1 = H_2 = h^2$.

Estimates of genetic components in F_1 diallel

D = $V_p – E$

H_1 = $V_p + 4Vr-4Wr-(3n-2)\ E/n$

H_2 = $4Vr-4Vm-2E$

h^2 = $4\ (Ml_1 – Ml_0)2-4(n-1)\ E/n^2$

F = $2\ V_p\ -4Wr\ -2\ (n-2)\ E/n$

Where,

V_p = Variance of parents

V_r = variance of the rth array

V_r = mean variance of arrays

W_r = the covariance between the parents and their offspring in the rth array

W_r = mean covariance between the parents and their offspring in all the arrays

V_m = variance of array means

Ml_1-Ml_0 = difference between the means of parents and their progenies

E = expected environmental component of variation

Using the above equations, the calculations of genetic components were done and tested following the details given by Singh and Chaudhary (1979). The standard errors were calculated by using the equations ½ Var (Wr –Vr) = S^2, and the terms of the main diagonal of covariance matrix given by Hayman (1954b) as corresponding multipliers.

3.5.2.2 Proportion of genetic components

The following ratios of the genetic components were worked out:

a) Degree of dominance

The mean degree of dominance was calculated using the formula as proposed by Hayman (1954b)

Mean degree of dominance = $(H_1/D)^{1/2}$

If the value of this ratio is zero, there is no dominance

If value equal to 1, then there is complete dominance

If it is greater than zero but less than unity (1), there is partial dominance; and

If it is greater than 1, it denotes over-dominance.

b) Proportion of genes with positive and negative effects in the parents is given by:

$H_2/4H_1$

Denotes the “proportion of genes with positive and negative effects in the parents”, and if the ratio is equal to 0.25, indicates symmetrical distribution of positive and negative genes.

c) Proportion of dominant and recessive genes in the parents

$$Kd/kr = [(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$$

If the ratio equal to 1, indicative of equality of dominant and recessive genes

If it is greater than 1, indicative of excess of dominant genes

If it is less than 1, indicative of recessive genes.

d) Number of group of genes which exhibit dominance

h^2/H_2

It is an approximate measure of the sets of genes exhibiting dominance and detectable biometrical genetic analysis.

e) The correlation coefficient (r) between the parental measurement (Y_r) and the parental order of dominance (Wr-Vr)

It was calculated as:

$$r\ (Y_r, Wr + Vr) = \text{Cov.}\ (Y_r, Wr + Vr) / [\text{Var.}\ Y_r\ \text{Var.}\ (Wr + Vr)]^{1/2}$$

When r is near to unity, the recessive genes are positive

When r is approximately unity, the dominant genes are positive

When r is small, presence of equal proportion of dominant genes having positive and negative effects.

f) Heritability:

Heritability in narrow sense was estimated from the mean variance of arrays by the following formula (Crumpacker and Allard, 1962) for each trait separately.

$$1/4D / [1/4\ D + ¼\ H_1 - 1/4\ F + E]$$

CHAPTER IV

EXPERIMENTAL RESULTS

The present study entitled, **"Characterizing diversity for heat and drought related traits in hexaploid wheat (*Triticum aestivum* L.)"** was undertaken by evaluating twenty genotypes of hexaploid wheat to generate information on the genetic variability and character association to screen heat and drought parents during *Rabi* 2014-15. To determine the nature and extent of gene effects 21 F_1s generated in a half diallel fashion, evaluated under normal and stress (drought and heat) conditions during *Rabi* 2015-16. Stress (heat and drought) were, however, of mild levels so as to ensure comparable plant populations under study. The observed variance for various morphological and physiological characters were analysed following suitable procedures. Combining ability and component analysis were done. The results obtained have been presented under the following sub-heads:

4.1 EVALUATION OF WHEAT GENOTYPES

- **4.1.1 Analysis of variance and components of variation**
- **4.1.2 Genetic variability**
- **4.1.3 Correlation**

4.2 COMBINING ABALITY ANALYSIS

- **4.2.1 Analysis of variance for experimental design**
- **4.2.2 Analysis of variance for combining ability**
- **4.2.3 General combining ability (GCA) effects**
- **4.2.4 Specific combining ability (SCA) effects**
- **4.2.5 Hayman's diallel analysis**

4.1 EVALUATION OF WHEAT GENOTYPES

The study was undertaken to evaluate twenty wheat genotypes for different morphological and physiological traits related to heat and drought tolerance, to identify best heat and drought tolerant lines. The results of this experiment are presented:

4.1.1 Analysis of variance and components of variation

Twenty wheat genotypes were analyzed in randomized block design with three replications under normal and stress environment conditions during *Rabi* 2014-15. Analysis of variance is presented in Table 4.1. The analysis of variance revealed that all the mean squares for genotypic differences were highly significant for all the morphological and physiological traits under both normal and stress environment conditions. The result indicates that there were sufficient genotypic differences for all the traits in both the environments.

4.1.2. Genetic variability for morphological and physiological traits

The estimate of general mean, range, genotypic and phenotypic variance, coefficient of variation, heritability and genetic advance is presented in table 4.2. The individual mean performance of twenty wheat genotypes for all the characters studied is presented in Appendix 1.

Among the morphological characters studied the genotypic differences were significant for days to 50% flowering. The range of variation varied from 105-114 and 78-99 days with overall mean of 110.10 and 91.89 days, under normal and stress conditions, respectively. Results presented in Table 4.2 exhibited that averages of days to 50% flowering were significantly affected by heat and drought stress treatment, and were reduced by 16.53 % of normal (110.1days). Under normal environment condition, RGP7 and RGP18 with mean days to heading of 105 days each was the earliest to flower, followed by RGP1 (106 days) and PBW175 (108 days). Whereas genotype DWR17 was late in flowering (114 days). Under stress environment condition, DWR13 was the earliest to flower with mean days to heading of 78 days, followed by RGP18 and PBW175 with 80 and 88 days respectively. Late sown wheat variety DWR16 was the late in flowering (99 days). The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 35.35 and 52.54, 4.24 and 6.97 per cent respectively. The phenotypic and genotypic coefficients of variations were low under normal and stress environment conditions i.e. 6.58 and 2.87, 5.40 and 2.24 per cent, respectively.

Table 4.1: Analysis of variance for morphological and physiological traits in hexaploid wheat under normal (N) and stress (S) environments.

Source of variation	d.f.	E	Mean squares						
			Days to 50% flowering (days)	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000-grain weight (g)**
Replications	2	N	43.71	2.01	124.80	3.84	31.50	0.59	3.60
		S	7.75	1.59	7.02	0.76	12.05	0.19	7.26
Genotype	19	N	95.23**	125.37**	384.53**	15.07**	182.94**	28.18**	60.86**
		S	15.45**	33.84**	122.80**	13.59**	53.85**	26.08**	25.50**
Error	38	N	3.71	4.76	5.59	1.53	2.73	3.91	3.55
		S	2.72	4.29	5.57	0.72	2.98	2.66	5.97

*, ** **significant at 5% and 1% level, respectively**

Source of variation	d.f.	E	Mean squares						
			Harvest index (%)	**Relative leaf water content (%)**	**Canopy temperature ^{0}C (grain filing)**	**Canopy temperature depression ^{0}C (grain filing)**	**Drought susceptibility index**	**Germination stress index (%)**	**Seedling survivability**
Replications	2	N	19.92	4.72	0.44	0.82	-	-	-
		S	10.96	18.10	0.02	1.32	0.22	2.09	2.58
Genotype	19	N	367.94**	216.67**	1.71**	44.02**	-	-	-
		S	159.48**	59.32**	3.71**	12.47**	3.01**	119.22**	45.24**
Error	38	N	70.82	76.41	0.38	1.48	-	-	-
		S	58.3	17.55	0.68	3.65	0.42	3.48	0.88

*, ** **significant at 5% and 1% level, respectively.**

Table 4.2: Estimates of mean, range, PCV, GCV, ECV, heritability $(h^2)_{bs}$ and genetic advance (GA) for different morphological and physiological traits of hexaploid wheat genotypes under normal (N) and stress (S) environments.

Estimates	**Days to 50% flowering (days)**		**Days to maturity (days)**		**Plant height (cm)**		**No. of tillers per plant**		**No. of grains/ ear**		**Grain yield per plant (g)**		**1000-grain weight (g)**	
Environment	N	S	N	S	N	S	N	S	N	S	N	S	N	S
CD(0.05)	0.23	1.02	1.05	3.42	2.32	1.15	0.04	0.40	0.08	0.59	3.27	1.34	0.13	3.94
Mean(X±SEm)	**110.1±0.95**	**91.9±0.59**	**146.7±0.05**	**127.8±1.20**	**87.8±0.32**	**81.8±0.91**	**9.7±0.19**	**5.19±0.49**	**39.6±0.04**	**35.1±0.99**	**11.0±0.56**	**6.4±0.47**	**39.5±0.11**	**29.0±0.99**
Range	105-114	78-99	144-150	112-135	74-97	66-92	8-13.6	3.1-9.3	30-55	26-42	8.7-14.7	4.2-10.4	33.1-47.2	21.5-37.5
Var. genotypic	35.35	4.24	61.87	9.85	109.61	45.74	4.51	4.29	60.07	22.64	8.09	8.47	30.10	6.57
Var. phenotypic	52.54	6.97	71.63	14.15	165.21	71.32	6.05	5.02	102.81	28.57	12.00	9.14	40.66	12.37
PCV (%)	6.58	2.87	5.77	2.94	5.72	9.32	25.36	43.17	19.55	15.23	31.49	47.24	16.14	12.13
GCV (%)	5.40	2.24	5.36	2.42	5.04	8.27	21.89	39.91	17.57	13.56	25.86	45.47	13.89	10.84
ECV (%)	0.45	1..05	0.27	2.03	1.45	2.67	16.00	15.91	15.68	8.64	0.19	1.51	2.83	1.10
Heritability $(h^2)_{bs}$	67.28	60.83	86.37	69.61	77.79	64.13	74.55	85.46	82.50	79.24	67.42	92.67	74.03	53.11
GA (% mean)	7.01	4.11	5.15	5.28	17.55	8.06	48.79	73.79	16.11	10.55	36.94	95.65	66.99	21.34

*, ** **significant at 5% and 1% level, respectively**

Contd.......

Estimates	Harvest index (%)		Relative leaf water content (%)		Canopy temperature ^{0}C (grain filing)		Canopy temperature depression ^{0}C (grain filing)		Drought susceptibility index		Germination stress index (%)		Seedling survivability (%)	
Environment	N	S	N	S	N	S	N	S	N	S	N	S	N	S
CD(0.05)	21.60	12.62	15.21	6.92	0.03	0.02	0.70	1.15	-	0.28	-	1.05	-	0.04
Mean(X±SEm)	**31.4±1.06**	**25.8±0.55**	**62.3±1.21**	**49.2±0.56**	**24.2±0.38**	**27.7±0.54**	**3.41±0.69**	**1.25±0.03**	-	**0.19±0.38**	-	**53.8±0.86**	-	**65.9±0.89**
Range	24-39	16-33	53-73	43-64	22.8-26	25.7-29.1	1.8-6.5	-0.5-3.6	-	-1.89-2.85	-	36-72	-	46-78
Var. genotypic	165.70	53.72	71.19	23.92	0.45	0.95	14.18	4.94	-	0.86	-	352.14	-	114.53
Var. phenotypic	236.53	92.03	105.98	31.48	0.84	1.81	15.66	6.59	-	1.28	-	455.29	-	186.18
PCV (%)	27.86	37.18	16.52	11.40	3.79	4.86	19.77	18.37	-	91.16	-	13.82	-	6.10
GCV (%)	25.81	28.41	13.54	10.94	2.77	3.52	18.96	17.56	-	52.63	-	12.75	-	5.78
ECV (%)	2.32	2.99	4.76	8.51	2.57	3.18	4.73	3.34	-	3.26	-	1.99	-	2.25
Heritability $(h^2)_{bs}$	85.85	58.37	67.17	75.98	53.57	52.49	73.85	64.26		33.33		40.04		89.80
GA (% mean)	17.72	21.81	6.80	9.38	4.19	4.98	49.70	37.46	-	31.46	-	56.88	-	25.51

*, ** **significant at 5% and 1% level, respectively**

Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 67.28 and 60.83 per cent, respectively. Genetic advance as per cent of mean were low under both normal (7.01) and stress (4.11) environment conditions.

Days to maturity exhibited significant genotypic differences its range varied from 144-150 days and 112-135 days, under normal and stress condition respectively, with an overall mean of 146.72 under normal and 127.81 days under stress conditions. The averages of maturity duration were significantly affected by heat and drought stress treatment, which reduced by 12.88% of normal (146.72 days). Under normal environment condition, genotypes RGP12 and RGP18, were the earliest to mature with mean maturity duration of 144 days each, followed by HD3040 (145 days), whereas DWR17 and DWR16 were the late in maturity (150 days each). Under stress environment conditions, genotypes DWR13 was the earliest to mature with mean maturity duration of 112 days followed by RGP18 (114) and PBW175 (124), whereas, genotype DWR17 were the late in maturity with mean maturity duration of 135 days. The phenotypic variance was higher in magnitude 71.63 and 61.87 as compared to the corresponding estimate of genotypic variance 14.15 and 9.85 per cent. The PCV and GCV were low under both normal and stress conditions i.e. 5.77and 2.94, 5.36 and 2.42 per cent, respectively for this trait. Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 86.37and 69.61 per cent, respectively. Genetic advance as per cent of mean were low under both normal and stress conditions i.e. 5.15 and 5.28 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for plant height under both normal and stress conditions which ranged from 74-97 and 66-92 cm, respectively, with an overall mean of 87.71 and 81.80 cm under normal and stress environment conditions, respectively. The averages of plant height were significantly affected by heat and drought stress treatment, and were reduced by 6.73% of normal (87.71 cm). Under normal environment condition, RGP1 and RGP12 were the shortest with mean plant height of 74 cm each, followed by DWR16 (76 cm). DWR13 and PBW175 was the tallest with plant height of 97cm each. Under stress environment conditions, maximum plant height was recorded in DWR13 and DWR17 (92 cm each) followed by PBW175 (89) cm. whereas, RGP12 was shortest with 66cm plant height. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 165.21 and 109.61; 71.32 and 45.74 per cent, respectively. The PCV and GCV were low under both normal and stress conditions i.e. 5.72 and 9.32, 5.04 and 8.27 per cent, respectively. Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 77.79 and 64.13 per cent, respectively. Genetic advance as per cent of mean were moderate under normal and low under stress conditions i.e. 17.55 and 8.06 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for tillers per plant under both normal and stress conditions which ranged from 8-13.6 and 3.1-9.3 tillers per plant, respectively, with an overall mean of 9.70 and 5.19 tillers per plant under normal and stress environment conditions, respectively. The averages of tillers per plant were significantly affected by heat and drought stress treatment, and were reduced by 46.49% of normal (9.70). Under normal environment condition, genotypes DWR16 had the highest number of tillers (13.6), followed by PBW175 (12.6), RGP18 (11.8) and PBW550 (10.9). Genotypes RGP1 and RAJ3765 had the lowest number of effective tillers (8.0 each). Under stress environment condition, DWR16 and RGP12 had the highest number of effective tillers (9.3 and 8.7 respectively) followed by DWR17 (7.5). Genotypes PBW175, RGP18 and PBW644 had the lowest number of effective tillers (3.0 each). The phenotypic variance was higher in magnitude 6.05 and 4.51 as compared to the corresponding estimate of genotypic variance 5.02 and 4.29 per cent. The phenotypic and genotypic coefficients of variation were higher both under normal and stress conditions. Estimate of heritability (h^2_{bs}) were 74.55% and 52.35%, under stress and normal condition respectively. Genetic advance as per cent of mean were high under both normal and stress sown conditions i.e. 48.79 and 73.79 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for grains per ear under both normal and stress environment conditions which ranged from 30-55 and 26-42 grains per ear, respectively. The overall mean was 39.59 and 35.11 grains per ear under normal and stress environment conditions, respectively. The averages of grains per ear were significantly affected by heat and drought stress treatment, and were reduced by 11.32% of normal (39.59 grains per ear). Under normal environment condition, genotypes PBW644 had the highest number of grains per ear (55) followed by RAJ3765 (53) and DWR17 (52) whereas RGP15 had lowest number of grains per ear. Under stress condition, genotypes RGP12 and DWR16 had the highest number of grains per ear (42), followed by RGP11 (41) whereas RGP1 had the lowest number of grains per spike. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 102.81 and 60.07, 28.57 and 22.64 per cent, respectively. The PCV and GCV were moderate under both conditions i.e. 19.57 and 13.56, 7.57 and 13.56 per cent, respectively. Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 82.50 and 79.24 per cent, respectively. Genetic advance as per cent of mean was moderate under both normal and stress conditions i.e. 16.11 and 10.55 per cent, respectively.

Significant differences were exhibited by genotypes for grain yield per plant under both normal and stress environment conditions which ranged from 8.7-14.7 and 4.2-10.4 grams, respectively. The overall mean was 11.01 and 6.41 grams under normal and stress conditions, respectively. The averages of yield per plant were significantly affected by heat and drought stress treatment, and were reduced by 41.78% of normal (11.01). Under normal environment condition, DWR16 had the highest grain yield per plant (14.70), followed by RGP18 (13.80), PBW175 (13.60) and DWR13 (13.30) whereas, RGP1 and RGP12 had the lowest grain yield per plant of 8.70 and 8.80 grams respectively. Under stress sown condition, DWR13 had the highest grain yield per plant (10.40), followed by RGP18 (9.80), DWR16 (9.70), PBW175 (8.2) and RGP12 (8.0) whereas, RGP1, and DWR17 had the lowest grain yield per plant of 4.20 grams each. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 12.00 and 8.09, 9.14 and 8.47 per cent respectively. The PCV and GCV were high under both normal and stress conditions i.e. 31.49 and 47.27, 25.86 and 45.47 per cent respectively. Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 67.42 and 92.67 per cent, respectively. Genetic advance as per cent of mean were high under both normal and stress conditions i.e. 36.94 and 95.65 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for 1000-grain weight under both normal and stress environment conditions which ranged from 33.1-47.2 and 21.5-37.5 grams, respectively. The overall mean was 39.49 and 29.10 grams under normal and stress conditions, respectively. The averages of 1000-

grain weight were significantly affected by heat and drought stress treatment, and were reduced by 26.31% of normal (39.49). Under normal environment condition, genotypes PBW175 had the highest 1000-grain weight (47.20), followed by DWR14 (46.70), DWR13 (46.40) and RGP18 (45.60). Genotypes RGP1 and DWR16 had the lowest 1000-grain weight of 33.10 gram. Under stress environment condition, PBW175 had the highest 1000-grain weight (37.50), followed by DWR16 (35.10) and HD3040 (32.2). Genotypes RGP1 and RGP2 had the lowest 1000-grain weight of 21.50 grams each. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 40.66 and 30.10, 12.37 and 6.57 per cent respectively. The PCV and GCV were moderate for this trait under both normal and stress conditions. Estimate of heritability (h^2_{bs}) were high under normal and moderate under stress conditions i.e. 74.03 and 53.11 per cent, respectively. Genetic advance as per cent of mean were high under both normal and stress sown conditions i.e.66.99 and 21.34 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for harvest index under both normal and stress conditions which ranged from 24-39 and 16-33 per cent, respectively. The overall mean was 31.41 and 25.79 per cent under normal and stress conditions, respectively. The averages of harvest index were significantly affected by heat and drought stress treatment, and were reduced by 17.89% of normal (31.41). Under normal environment condition, PBW550 had the highest value of harvest index (39) followed by DWR13 (37) and HD3040 (36). RGP1 and PBW175 had the lowest value of harvest index 24 and 26 per cent respectively. Under stress condition, RGP 18 and DWR 13 had the highest per cent of harvest index 33 per cent each, followed by RAJ3765, 31 per cent. PBW157 and RGP1 had the lowest value of harvest index i.e.16 per cent. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance under both conditions i.e. 236.53 and 165.70, 92.03 and 53.72 per cent, respectively. The PCV and GCV were high for this trait under both normal and stress conditions. Estimate of heritability (h^2_{bs}) were high under normal and moderate under stress conditions i.e. 85.85 and 58.37 per cent, respectively. Genetic advance as per cent of mean were moderate under normal and high under stress conditions i.e.17.72 and 21.81 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for relative leaf water content under both normal and stress conditions which ranged from 57-73 and 43-64 per cent respectively. The overall mean was 62.31 and 49.19 per cent under normal and stress conditions, respectively. The averages of relative water content were significantly affected by heat and drought stress treatment, and were reduced by 21.05% of normal (62.31). Under normal sown condition, DWR13, RGP18 and RGP12 had the highest per cent of relative leaf water content of 73 per cent, followed by PBW175 (72). Lowest per cent of relative water content was recorded for RGP1, DWR17 and HD3040 (53 per cent). Under stress condition, RGP18 had the highest per cent of relative water content of 64 per cent, followed by DWR16 (53), RGP1 (52), PBW175 and RGP12 (51 per cent each). DWR13 and DWR17 had lowest per cent of relative water content 43 per cent respectively. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 105.98 and 71.19, 31.48 and 23.92 per cent respectively. The PCV and GCV were moderate under both normal and stress conditions i.e. 16.52 and 11.40, 13.54 and 10.42 per cent, respectively. Estimate of heritability (h^2_{bs}) were high under both normal and stress environment conditions i.e. 67.17and 75.98 per cent, respectively. Genetic advance as per cent of mean were low under both normal and stress conditions i.e. 6.80 and 9.38 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for Canopy temperature (grain filling stage) under both normal and stress environment conditions which ranged from 22.8-26 and 25.7-29.1^{o}C, respectively, with an overall mean of 24.23^{o}C under normal and 27.67^{o}C under stress conditions, respectively. The averages of canopy temperature (CT) were significantly affected by heat and drought stress treatment, and were increased by 14.19% of control (24.23). Under normal environment condition, RGP18 had the lowest value of CT of 22.8^{o}C, followed by DWR16 (23.2), DWR13 (23.3) and PBW175 (23.4). Genotype DWR17 had the highest value of CT followed by PBW550. Under stress environment condition, RGP18 had lowest value of CT of 25.7^{o}C, followed by DWR13, PBW175 and RGP1. Genotype DWR17 had the highest value of CT of 29.1^{o}C followed by DWR16 and RGP12. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 0.84 and 0.45, 1.81 and 0.94 per cent respectively. The PCV and GCV were low for this trait under both conditions i.e.

3.79 and 4.86, 2.77 and 3.52, per cent, respectively. Estimate of heritability (h^2_{bs}) were moderate under both normal and stress sown conditions i.e. 53.57 and 52.49 per cent, respectively. Genetic advance as per cent of mean were low under both normal and stress conditions i.e. 4.19 and 4.89 per cent, respectively.

Genotypes exhibited significant differences in their mean performance for Canopy temperature depression (CTD) under both normal and stress environment conditions which ranged from 1.8-6.5 and -0.5-3.6^{o}C, respectively, with an overall mean of 3.41^{o}C under normal and 1.25^{o}C under stress conditions. The averages of CTD (grain filling stage) were significantly affected by heat and drought stress treatment, and were reduced by 63.34% of control (3.41). Under normal sown condition, DWR13 had the highest value of CTD of 6.5^{o}C, followed by RGP18 (5.1), RGP12 (4.5) and PBW175 (4.1). DWR17 had the lowest value of CTD of 1.8^{o}C. Under stress sown condition, RGP12 and RGP18 had the highest value of CTD of 3.6^{o}C, followed by PBW175 (3.5) and DWR16 (3.1), Whereas, DWR17, RGP11 and RGP1 had the lowest value of CTD. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 15.66 and 14.18, 6.59 and 4.94 per cent, respectively. The phenotypic and genotypic coefficients of variation were moderate for this trait under both normal and stress conditions i.e. 19.77 and 18.37, 18.96 and 17.56 per cent, respectively. Estimate of heritability (h^2_{bs}) were high under both normal and stress sown conditions i.e. 73.85 and 64.26 per cent, respectively. Genetic advance as per cent of mean were high under both normal and stress sown conditions i.e. 49.70 and 37.46 per cent, respectively.

Drought susceptibility index (DSI) was calculated for grain yield over moisture stress and non-stress using formula as suggested by Fischer and Maurer (1978).Genotypes exhibited significant differences in their mean performance for drought susceptibility index under stress environment conditions which ranged from -1.89 to 2.85 per cent, with an overall mean of 0.19 per cent under stress condition. Parents having low drought susceptibility index value (drought resistant) for grain yield are DRW13, DWR16, RGP18, PBW175 whereas; RGP1 and DWR17 have high DSI value (drought sensitive) for grain yield. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 1.28 and 0.86 per cent, respectively. The phenotypic and genotypic coefficients of variation were high for this trait i.e. 91.16 and 52.63 per cent, respectively. Estimate of heritability (h^2_{bs}) were low i.e. 33.33 per cent. Genetic advance as per cent of mean were high i.e. 31.46 per cent.

Genotypes exhibited significant differences in their mean performance for germination stress index (GSI), which ranged from 26-72 per cent, with an overall mean of 53.80 per cent. Highest value of germination stress index was recorded for DWR13 (72), DWR16 (71), RGP18 (70), RGP12 (69) and RGP7 (67) per cent. Genotypes with lowest GSI value were RGP1 and DWR17 (36 per cent each). The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 455.29 and 352.14 per cent, respectively. The phenotypic and genotypic coefficients of variation were moderate for this trait i.e. 13.82 and 12.75 per cent, respectively. Estimate of heritability (h^2_{bs}) were low i.e. 40.04 per cent. Genetic advance as per cent of mean were high i.e. 56.88 per cent.

Genotypes exhibited significant differences in their mean performance for seedling survivability (SS), ranged from 46-78 per cent with an overall mean of 65.90. Seedling survivability involves screening germplasm lines which discriminate between drought tolerance and susceptibility under artificial moisture stress conditions. High seedling survivability per cent was recorded in DWR13 followed by RGP18, PBW175 and DWR16. Low per cent of seedling survivability was recorded in RGP1. The phenotypic variance was higher in magnitude as compared to the corresponding estimate of genotypic variance i.e. 186.18 and 114.53 per cent, respectively. The phenotypic and genotypic coefficients of variation were low for this trait i.e. 6.10 and 5.78 per cent, respectively. Estimate of heritability (h^2_{bs}) were high i.e. 89.80per cent. Genetic advance as per cent of mean were high i.e. 25.51 per cent.

4.1.3 Correlation

The genotypic correlation coefficients among various morphological and physiological traits related to heat and drought tolerance under normal and stress conditions are presented in Table 4.3 and, 4.4 respectively.

Under normal environment condition, days to 50% flowering showed positive and highly significant correlation with days to maturity (0.490**) and relative water content (0.448**), but negative and significant correlation with plant height

(-0.373**). Days to maturity showed positive and significant correlation with days to 50% flowering (0.490**), canopy temperature (0.476**) and canopy temperature depression (0.396**). Plant height showed positive and significant correlation with number of tillers per plant (0.387**), grain yield per plant (0.331*), canopy temperature (0.485**) and canopy temperature depression (0.380*), but negative and significant association with days to 50% flowering (-0.373**). Number of tillers per plant showed positive and significant association with plant height (0.387**), number of grains per ear (0.539**), yield per plant (0.569**), relative water content (0.617**) and canopy temperature depression (0.478**), but showed negative and significant association with canopy temperature (-0.487**). Number of grains per ear showed positive and highly significant association with number of tillers per plant (0.539**), grain yield per plant (0.641**), harvest index (0.474**) and relative water content (0.562**), but showed negative and highly significant correlation with canopy temperature (-0.576**). Also showed positive and significant association with canopy temperature depression (0.321*). Grain yield per plant showed positive and highly significant correlation with number of tillers per plant (0.569**), number of grains per ear (0.641**), 1000-grain weight (0.534**), harvest index (0.616**) and canopy temperature (0.652**). Also, it is positively and significantly associated with plant height (0.331*) and relative water content (0.335*). Yield per plant showed negative and significant association with canopy temperature depression (-0.462**). 1000-grain weight showed positive and highly significant association with grain yield per plant (0.534**), canopy temperature (0.679**) and harvest index (0.651**). Also, it is positively and significantly associated with relative water content (0.363*). Harvest index showed positive and highly significant association with number of grains per ear (0.474**), 1000-grain weight (0.651**), yield per plant (0.616**), relative water content (0.681**), and canopy temperature (0.488**), but showed negative and significant association with canopy temperature depression (-0.315*). Relative water content showed positive and highly significant association with days to 50% flowering (0.448**), number of tillers per plant (0.617**), number of grains per ear (0.562**), harvest index (0.681**) and canopy temperature (0.716**), but showed negative and high significant association with canopy temperature depression (-0.593**). Also it showed positive and significant association with grain yield per plant (0.335*) and 1000-grain weight (0.363*). Canopy temperature showed positive and highly significant association with days to maturity (0.476**), plant height

Table 4.3: Genotypic correlation coefficients among various morphological and physiological traits under normal (N) environment of hexaploid wheat genotypes.

Genotypic correlation coefficients among various morphological and physiological traits under normal (N) environment of hexaploid wheat genotypes.

	DF	DM	PH	NTP	NGE	GYP	TGW	HI	RWC	CT	CTD
DF	…	0.490 **	-0.373 **	0.105	-0.220	-0.193	-0.094	0.213	0.448**	-0.210	-0.254
DM			-0.097	0.041	-0.113	-0.438	-0.308	-0.183	-0.283	0.476 **	0.396**
PH				0.387 **	0.234	0.331 *	0.012	-0.128	0.239	0.485**	0.380**
NTP					0.539 **	0.569**	0.278	0.247	0.617**	-0.487 **	0.478**
NGE						0.641 **	0.267	0.474 **	0.562**	-0.576**	0.321*
GYP							0.534**	0.616 **	0.335 *	0.652**	-0.462**
TGW								0.651**	0.363*	0.679**	0.284
HI									0.681**	0.488 **	-0.315 *
RWC										0.716**	-0.593 **
CT											-0.556**
CTD											

*, ** **significant at 5% and 1% level, respectively; DF (days to 50% flowering), DM (days to maturity), PH (plant height), NTP (number of tillers per plant), NGE (number of grains per ear), GYP (grain yield per plant), TGW (1000-grain weight), HI (harvest index), RWC (relative leaf water content), CT (canopy temperature at grain filling stage), and CTD (canopy temperature depression taken at grain filling stage).**

(0.485**), grain yield per plant (0.652**), 1000- grain weight (0.679**), harvest index (0.488**) and relative water content (0.716**) but showed negative and highly significant correlation with canopy temperature depression (-0.556**). Canopy temperature depression showed positive and highly significant association with number of tillers per plant (0.478**), days to maturity (0.396**) and plant height (0.380**). Also, it showed negative and highly significant association with yield per plant (-0.462**), relative water content (-0.593**) and canopy temperature (-0.556**). Also it showed positive and significant association with number of grains per ear (0.321*).

Under stress environment condition, days to 50% flowering showed positive and highly significant association with days to maturity (0.545**) and relative water content (0.637**) but negative and significant association with canopy temperature (-0.413**). Days to maturity showed positive and highly significant correlation with plant height (0.550**), relative water content (0.513**), canopy temperature (0.539**) and canopy temperature depression (0.450**). Also it is positively and significantly associated with 1000-grain weight (0.365*) and grain yield per plant (0.363*). Plant height showed positive and highly significant association with days to maturity (0.550**), number of tillers per plant (0.519**), canopy temperature (0.440**) and canopy temperature depression (0.409**). Tillers per plant showed positive and highly significant association with plant height (0.519**), number of grains per ear (0.571**), grain yield per plant (0.624**), canopy temperature (0.434**) and canopy temperature depression (0.550**). Also it showed positive and significant association with harvest index (0.336*) and relative water content (0.336*). Number of Grains per ear showed positive and highly significant association with Grain yield per plant (0.572**), relative water content (0.539**) and number of tillers per plant (0.519**). It also recorded positive and significantly associated with harvest index (0.363*) and canopy temperature (0.307*). Grain yield per plant showed positive and highly significant correlation with number of tillers per plant (0.624**), number of grain per ear (0.572**), 1000-grain weight (0.468**), harvest index (0.467**) relative water content (0.621**) and canopy temperature depression (0.588**), but negatively and significantly associated with canopy temperature (-0.449**) and drought susceptibility index (-0.364*). 1000-grain weight showed positive and highly significant association with grain yield per plant (0.468**),

Table 4.4: Genotypic correlation coefficients among various morphological and physiological traits under stress (S) environment of hexaploid wheat genotypes.

	DF	DM	PH	NTP	NGE	GYP	TGW	HI	RWC	CT	CTD	DSI	GSI	SS
DF		0.545**	-0.231	0.070	0.166	-0.085	-0.082	0.227	0.637**	-0.413**	-0.042	-0.116	-0.059	-0.243
DM			0.550**	0.227	0.069	0.363*	0.365*	0.276	0.513**	0.539**	0.450**	-0.261	-0.052	-0.205
PH				0.519**	0.135	0.139	0.118	0.071	0.031	0.440 **	0.409**	0.190	0.190	-0.011
NTP					0.571**	0.624**	0.303	0.355*	0.336*	0.434**	0.550**	0.254	0.126	-0.179
NGE						0.572**	0.032	0.363*	0.539**	0.307*	0.161	0.112	0.062	-0.255
GYP							0.468**	0.467**	0.621**	-0.449**	0.588**	-0.364*	0.170	0.027
TGW								0.624**	0.456**	0.489**	0.636**	0.354*	0.361*	0.389*
HI									0.395*	0.437**	0.372*	-0.085	-0.169	-0.199
RWC										0.612**	0.508**	-0.468**	-0.578**	-0.657**
CT											0.395*	0.452**	-0.439**	- 0.560**
CTD												0.384**	-0.088	-0.504**
DSI													0.535**	0.671**
GSI														0.689**
SS														

*, ** **significant at 5% and 1% level, respectively; DF (days to 50% flowering), DM (days to maturity), PH (plant height), NTP (number of tillers per plant), NGE (number of grains per ear), GYP (grain yield per plant), TGW (1000-grain weight), HI (harvest index), RWC (relative leaf water content), CT (canopy temperature at grain filling stage), CTD (canopy temperature depression taken at grain filling stage), DSI (drought susceptibility index), GSI (germination stress index) and SS (seedling survivability**

harvest index (0.624**), relative water content (0.456**), canopy temperature (0.489**) and canopy temperature depression (0.636**). Also, it is positively and significantly associated with drought susceptibility index (0.354*), germination stress index (0.361*), seedling survivability (0.389*) and days to maturity (0.365*). Harvest index showed positive and highly significant association with grain yield per plant (0.467**), 1000-grain weight (0.624**) and canopy temperature (0.437**). Also, it is positively and significantly associated with number of tillers per plant (0.355*), number of grains per ear (0.363*), relative water content (0.395*) and canopy temperature depression (0.372*). Relative water content showed positive and highly significant correlation with days to 50% flowering (0.637**), days to maturity (0.513**), number of grains per ear (0.539**), grain yield per plant (0.621**), canopy temperature (0.612**) and canopy temperature depression (0.508**), but it recorded negative and highly significant association with drought susceptibility index (-0.468**), germination stress index (-0.578**) and seedling survivability (-0.657**). Canopy temperature showed positive and highly significant association with days to maturity (0.539**), plant height (0.440**), number of tillers per plant (0.434**), 1000-grain weight (0.489**), harvest index (0.437**), relative water content (0.612**) and drought susceptibility index (0.452**), but showed negative and highly significant association with days to 50% flowering (-0.413**), grain yield per plant (-0.449**) and seedling survivability (-0.560**). Canopy temperature depression showed positive and highly significant association with days to maturity (0.450**), plant height (0.409**), number of tillers per plant (0.550**), grain yield per plant (0.588**), 1000-grain weight (0.636**) and relative water content (0.508**), but showed negative and highly significant association with seedling survivability (-0.504**). It is also positively and significantly associated with harvest index (0.372*) and canopy temperature (0.395*). Drought susceptibility index showed positive and significant association with canopy temperature (0.452**), canopy temperature depression (0.384**), germination stress index (0.535**), seedling survivability (0.671**) and 1000- grain weight (0.354*). Also showed negative and significant association with relative water content (-0.468**) and grain yield per plant (-0.364*). Germination stress index showed positive and significant correlation with drought susceptibility index (0.535**), seedling survivability (0.689**) and1000-grain weight (0.361*). It showed negative and significant association with relative water content (-0.578**) and canopy temperature (-0.439**). Seedling survivability recorded positive and significant correlation with drought susceptibility index (0.671**), germination stress index (0.689**) and1000-grain weight (0.389*). Also recorded negative and highly significant association with relative water content (-0.657**), canopy temperature (-0.560**) and canopy temperature depression (-0.504**).

4.2 Combining Ability Analysis

Combining ability diallel analysis was carried out for morphological and physiological traits under normal (N) and stress (S) conditions. Study was undertaken to determine the analysis of variance, the general combining ability (GCA) and specific combining ability (SCA) variances, general combining ability and specific combining ability effects as per the method described by Griffing, (1956). Results obtained for all the traits under both normal and stress sown conditions are interpreted as under:

4.2.1 Analysis of variance

Analyses of variance were carried for morphological and physiological traits under normal and stress environment conditions and results are presented in the Table 4.5. The analysis of variance revealed significant differences among parents and hybrids for all the characters over both the environments indicating the presence of genotypic variability, different responses of genotypes to water deficit and possible selection of drought and heat tolerant genotypes. This indicated the presence of considerable variation among the genotypes for each trait under study. Most of the characters had higher mean squares under non-stress environment except number of grains per ear, canopy temperature and canopy temperature depression, indicating better expression of different characters in non-stress environment as compared to drought and heat stress environment.

4.2.2 Analysis of variance for combining ability

The results of combining ability analysis in half diallel analysis was performed by Method 2, Model-I of Griffing, (1956) for normal (N) and stress (S) environment conditions both for morphological and physiological traits (Table 4.6). The result showed that mean squares due to general combining ability (gca) and specific

Table 4.5: Analysis of variance for morphological and physiological traits in 7 x 7 half diallel sets in hexaploid wheat under normal (N) and stress (S) environments.

			Mean squares						
Source of variation	**d.f.**	**E**	**Days to 50% flowering (days)**	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000-grain weight (g)**
Replications	2	N	0.14	0.56	0.24	0.56	0.45	0.11	0.67
		S	0.11	0.32	0.43	0.49	0.22	0.37	0.38
Treatments	27	N	19.48 **	42.96 **	322.40 **	6.26 **	35.17 **	11.88**	71.92 **
		S	2.01 **	3.24 **	64.01 **	3.28 **	39.12 **	1.14**	18.29 **
Parents	6	N	10.10**	36.89 **	833.73 **	4.76**	38.81 **	5.52**	62.51 **
		S	3.41**	4.11**	105.55**	3.71* *	49.21 **	2.25**	24.34 **
Hybrids	20	N	23.25 **	46.93 **	288.36**	3.61 **	28.98 **	13.88 **	62.62 **
		S	1.64 **	3.14 **	53.73 **	2.42 **	37.86 **	1.46 **	17.35**
Parents Vs hybrids	1	N	0.25	122.10 **	935.06 **	0.14	137.21 **	10.08**	314.43 **
		S	0.67	91.19**	12.39**	0.75	3.89	0.16	0.83
Error	54	N	1.24	0.70	5.10	0.57	0.89	0.93	0.76
		S	0.16	0.68	1.59	0.37	0.90	0.30	0.44
Total	83	N	2.16	2.53	42.66	51.21	21.53	6.44	23.90
		S	3.43	2.16	32.43	12.65	24.86	4.58	6.25

*, ** **significant at 5% and 1% level, respectively**

Contd……

			Mean squares						
Source of variation	**d.f.**	**E**	**Harvest index (%)**	**Relative leaf water content (%)**	**Canopy temperature ^{0}C (grain filing)**	**Canopy temperature depression ^{0}C (grain filing)**	**Drought susceptibility index**	**Germination stress index (%)**	**Seedling survivability**
Replications	2	N	0.25	0.97	0.14	0.46	-	-	-
		S	0.37	0.38	0.43	0.20	0.02	0.51	0.07
Treatments	27	N	319.07 **	20.36**	0.78 **	1.98 **	-	-	-
		S	58.71 **	14.71 **	1.87 **	9.80 **	0.46 **	1438.38 **	201.65 **
Parents	6	N	429.05 **	11.42**	2.49 **	2.90 **	-	-	-
		S	69.82 **	11.28**	2.91**	6.48**	0.65**	789.70 **	205.71 **
Hybrids	20	N	285.62 **	25.25 **	2.24**	1.80 **	-	-	-
		S	139.12**	13.52 **	2.82**	8.55**	0.19 **	1704.86 **	206.40 **
Parents Vs hybrids	1	N	328.09**	136.16**	11.27 **	0.04	-	-	-
		S	383.91 **	98.01 **	12.57 **	54.84 **	0.02	0.96	82.29 **
Error	54	N	1.09	0.32	0.18	0.61	-	-	-
		S	2.33	1.17	0.74	0.37	0.03	0.87	1.47
Total	83	N	59.66	12.80	0.37	1.04	-	-	-
		S	38.22	9.80	1.10	7.03	0.43	468.49	66.55

*, ** **significant at 5% and 1% level, respectively**

Table 4.6: Analysis of variance for combining ability for morphological and physiological traits in 7 x 7 diallel sets under normal (N) and stress (S) environments.

			Mean squares						
Source of variation	**d.f.**	**E**	**Days to 50% flowering (days)**	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000-grain weight (g)**
GCA	6	N	7.90 **	14.02**	96.60 **	1.45 **	10.72 **	4.37 **	21.08 **
		S	2.98 **	11.06**	44.05**	1.20 **	8.01**	1.17**	7.01 **
SCA	21	N	6.08 **	17.26 **	110.56 **	11.83 **	12.01 **	3.84 **	24.80 **
		S	1.57**	8.35 **	1.08 **	14.84 **	14.49 **	14.47 **	0.44 **
Error	54	N	2.41	0.90	1.03	0.19	1.63	1.31	0.25
		S	0.38	0.56	0.86	0.12	0.96	0.10	0.14

*, ** **significant at 5% and 1% level, respectivel**

			Mean squares						
Source of variation	**d.f.**	**E**	**Harvest index (%)**	**Relative leaf water content (%)**	**Canopy temperature ^{0}C (grain filing)**	**Canopy temperature depression ^{0}C (grain filing)**	**Drought susceptibility index**	**Germination stress index (%)**	**Seedling survivability**
GCA	6	N	47.80 **	7.50 **	0.31 **	0.73 **	-	-	-
		S	25.52 **	2.08**	0.66 *	1.96	0.42 **	402.46 **	112.25 **
SCA	21	N	123.08 **	6.58 **	0.24 **	0.64 **	-	-	-
		S	17.83 **	5.70 **	0.61 **	3.64 **	0.60 **	501.45 **	54.35 **
Error	54	N	0.36	0.10	0.06	0.02	-	-	-
		S	0.79	0.39	0.23	1.79	0.01	0.29	0.49

*, ** **significant at 5% and 1% level, respectively**

combining ability (sca) under normal and stress (heat and drought) were significant for all the traits for both normal and stress environments indicating the involvement of additive and non- additive gene action in their inheritance, except for gca of canopy temperature depression in stress environment.

4.2.3 General combining ability (GCA) effects

The general combining ability (GCA) effects of seven parents both in normal and stress environment conditions were statistically analyzed by Griffing's Method 2 Model I which are presented in the Table 4.7.

The result for days to 50% flowering showed that three of seven parental genotypes, RGP18 (-1.10 & -0.98), DWR13 (-1.06 & -0.79) and DWR17 (-0.66 & -0.42) displayed negative significant GCA effects under both normal and stress environment conditions. Parental lines PBW175 (1.16 & 0.96), RGP12 (0.75 & 0.85) and DWR16 (0.75 & 0.65) exhibited highly significant positive GCA effects under both normal and stress environment conditions. Days to maturity showed that three out of seven genotypes viz., DWR16 (-4.35 and -3.04), RGP18 (-3.24 and -2.04) and DWR17 (-1.84 and -1.70) exhibited negative significant GCA effects under both normal and stress environment conditions. RGP1 (3.05 and 1.37) and RGP12 (1.13 and 2.26) recorded positive significant GCA effects under both normal and stress environment conditions.

The results for plant height showed that three out of seven genotypes viz., DWR13 (-2.89 and -3.31), RGP12 (-2.05 and -3.35) and DWR17 (-1.41 and -2.34) exhibited negative significant GCA effects under both normal and stress environment conditions. RGP18 (2.43 and 2.17) recorded positive significant GCA effects under both normal and stress environment conditions.

Number of tillers per plant exhibited positive significant GCA effects for DWR16 (1.18 and 0.91) under both normal and stress conditions whereas, genotype RGP18 (-1.16 and -1.07) displayed negative significant GCA effect under both normal and stress environment conditions.

Three of seven genotypes showed positive significant GCA effects viz., PBW175 (0.52 and 1.86), DWR16 (1.55 and 2.69) and DWR17 (1.61 and 1.32) for Number of grains per ear under both normal and stress environment conditions.

Table 4.7: Estimates of general combining ability effects for morphological and physiological traits in 7 x 7 diallel set based on Griffing's Method 2 Model 1 under normal (N) and stress (S) environments.

Genotype	**E**	**Days to 50% flowering (days)**	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000 grain weight**
PBW175	N	1.16 **	1.24**	4.93 **	-0.45**	0.52 **	0.98 **	2.10 **
	S	0.96**	0.07	-2.56 **	0.55**	1.86 **	0.90**	-0.72 **
RGP12	N	0.75**	1.13**	-2.05 **	0.42 **	-1.69**	0.02	0.40 *
	S	0.85**	2.26**	-3.35 **	-0.73**	-0.48 **	-0.55**	-0.43 **
RGP1	N	0.76**	3.05**	0.08	-0.47**	-0.77**	-0.66 **	1.34 **
	S	0.02	1.37**	0.15	0.23 **	-0.71 **	-1.20 **	0.16
DWR16	N	0.75**	-4.35**	1.70**	1.18**	1.55 **	0.85 **	1.55 **
	S	0.65 **	-3.04**	0.64	0.91**	2.69**	-0.72**	1.03 **
RGP18	N	-1.10 **	-3.24**	2.43**	-1.16**	1.23**	1.02**	-2.25 **
	S	-0.98**	-2.04 **	2.17 **	-1.07**	-0.08	1.10**	-0.52**
DWR13	N	-1.06 **	-0.89**	-2.89**	0.04	0.89 **	0.56**	0.32 *
	S	-0.79 **	0.01	-3.31**	-0.52 **	-0.66 **	0.82 **	1.51 **
DWR17	N	-0.66**	-1.84**	-1.41**	-0.98**	1.61 **	-0.07	-0.35 *
	S	-0.42**	-1.70 **	-2.34 **	0.04	1.32**	0.13	0.72 **
S.E. (gi)	N	0.11	0.23	0.15	0.11	0.17	0.11	0.38
	S	0.17	0.18	1.83	0.15	0.12	0.21	0.29
S.E. (gi-gi)	N	0.19	0.35	0.23	0.17	0.25	0.16	0.58
	S	0.28	0.27	2.79	0.23	0.18	0.32	0.44

*, ** **significant at 5% and 1% level, respectively**

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Genotype	**E**	**Harvest index (%)**	**Relative leaf water content (%)**	**Canopy temperature ^{0}C (grain filing)**	**Canopy temperature depression ^{0}C (grain filing)**	**Drought susceptibility index**	**Germination stress index (%)**	**Seedling survivability**
PBW175	N	0.02	0.49 **	-0.37 **	0.12 **	-	-	-
	S	0.05	0.10	-0.15 **	0.10**	-0.02	3.07 **	1.27 **
RGP12	N	-2.24**	1.77**	-0.22 **	0.34 **	-	-	-
	S	-0.36 **	0.57**	0.20 **	-0.43 **	0.20**	-9.60 **	1.40 **
RGP1	N	1.25 **	-0.11**	0.23 **	-0.83 **	-	-	-
	S	0.70 **	0.61**	-0.48 **	-0.13 **	0.03	2.20 **	-3.50 **
DWR16	N	1.23 **	-0.71 **	0.05 **	0.32 **	-	-	-
	S	-1.11**	-0.57 **	0.21 **	-0.35 **	0.18 **	-9.37**	1.84 **
RGP18	N	-0.01	0.95**	-0.06 **	0.19**	-	-	-
	S	-2.64 **	0.60**	-0.13**	0.16**	-0.43**	2.88 **	2.73**
DWR13	N	1.56 **	0.74**	-0.08 **	0.15 **	-	_	-
	S	-0.83**	0.99**	-0.47 **	0.28 **	-0.35**	7.31 **	2.61 **
DWR17	N	0.47 **	0.45**	0.12**	-0.36 **	-	_	-
	S	1.58 **	-0.07	-0.30 **	0.90 **	0.85**	3.52 **	0.51 **
S.E. (gi)	N	0.02	0.05	0.01	0.04	-	_	-
	S	0.03	0.10	0.01	0.01	0.08	0.41	0.53
S.E. (gi-gi)	N	0.11	0.08	0.02	0.05	-	_	-
	S	0.04	0.16	0.02	0.02	0.12	0.62	0.81

*, ** **significant at 5% and 1% level, respectively**

Parents RGP12 (-1.69 and -0.48) and RGP1 (-0.77 and -0.71) exhibited negative significant GCA effects under both normal and stress sown conditions.

Grain yield per plant showed that RGP18 (1.02 and 1.10), PBW175 (0.98 and 0.90) and DWR13 (0.56 and 0.82) had positive significant GCA effects under normal and stress conditions for yield per plant. Negative significant GCA effects were found in RGP1 (-0.66 and -1.20) under both normal and stress conditions.

Two of seven parental genotypes, DWR16 (1.55and 1.03) and DWR13 (0.32 and 1.51) displayed positive significant GCA effects for 1000-grain weight under both normal and stress environment conditions. Genotype RGP18 (-2.25 & -0.52) exhibited significant negative GCA effects in both normal and stress environment conditions.

The results for harvest index showed that RGP1 (1.25 and 0.70) and DWR17 (0.47 and 1.58) had positive significant GCA effects under normal and stress conditions for harvest index. Negative significant GCA effects was found in RGP12 (-2.24 and -0.36) under both normal and stress conditions.

Parents RGP12 (1.77 and 0.57), RGP18 (0.95 and 0.60) and DWR13 (0.74 and 0.99) displayed positive significant GCA effects for relative leaf water content under normal and stress conditions. Whereas, genotypes DWR16 (-0.71 & -0.57) exhibited negative significant GCA effects under both normal and stress conditions.

Canopy temperature (grain filling stage) recorded negative significant GCA effects were observed in PBW175 (-0.37 &-0.15), DWR13 (-0.08 and -0.47) and RGP18 (-0.06 & -0.13) under normal and stress conditions. DWR16 exhibited positive significant GCA effects under normal and stress conditions.

Canopy temperature depression (grain filling stage) had positive significant GCA effects for genotype RGP18 (0.19 & 0.16), DWR13 (0.15 & 0.28) and PBW175 (0.12 & 0.10) under normal and stress conditions. Whereas, genotype RGP1 exhibited negative significant GCA effects under normal and stress conditions.

Drought susceptibility index had negative significant GCA effects for RGP18 (-0.43) and DWR13 (-0.35). Whereas, genotypes RGP12, DWR16 and DWR17 exhibited positive significant GCA effects under stress conditions.

Germination stress index had positive significant GCA effects for DWR13 (7.31), DWR17 (3.52), PBW175 (3.07), RGP18 (2.88) and DWR16 (2.20), whereas RGP12 (-9.60) and DWR16 (-9.37) exhibited negative significant GCA effects under stress conditions.

Positive significant GCA effects were observed in RGP18 (2.73), DWR13 (2.61), RGP12 (1.40), DWR16 (1.84), PBW175 (1.27) and DWR17 (0.51). Whereas, RGP1 (-3.50) exhibited negative significant GCA effects under stress conditions for Seedling survivability.

4.2.4 Specific combining ability (SCA) effects for morphological and physiological traits

Estimates of specific combining ability (SCA) effects for morphological and physiological traits under normal (N) and stress environment (S) conditions statistically analyzed by Griffing's Method 2 Model I are presented in Table 4.8.

For days to 50% flowering crosses, PBW175 x RGP18, PBW175 x DWR13, RGP12 x RGP1, RGP12 x DWR16, RGP12 x DWR13, RGP12 x RGP1, RGP12 x DWR17, DWR16 x DWR17 and DWR13 x DWR17 showed negative significant SCA effects under normal and stress conditions. Crosses viz., PBW175 x RGP12, PBW175 x RGP1, PBW175 x DWR16, DWR16 x RGP18 and RGP18 x DWR17 exhibited positive significant SCA effects under both conditions.

For days to maturity, crosses PBW175 x RGP12, PBW175 x RGP18, RGP12 x DWR17, RGP1 x RGP18, RGP1 x DWR13, DWR16 x DWR17 and RGP18 x DWR13 showed negative significant SCA effects under both normal and stress conditions. Crosses viz., PBW175 x DWR16, RGP12 x RGP18, RGP1 x DWR17 and DWR13 X DWR17 exhibited positive significant SCA effects under both conditions.

Crosses RGP12 x RGP18, RGP12 x DWR13, RGP1 x DWR16, RGP1 x DWR13, DWR16 x RGP18 and DWR16 x DWR17 showed negative significant SCA effects under both normal and stress conditions for plant height. Crosses viz., PBW175 x RGP1, PBW175 x RGP18, PBW175 x DWR17, RGP12 x DWR17 and DWR13 x DWR17 exhibited positive significant SCA effects under both normal and stress conditions.

Table 4.8: Estimates of specific combining ability effects for morphological traits in a 7 x 7 diallel set based on Griffing's Method 2 Model 1 under normal (N) and stress (S) environments.

Crosses	E	**Days to 50% flowering (days)**	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000-grain weight (g)**
PBW175 X RGP12	N	0.52**	-1.69**	11.33 **	-0.27	4.81 **	1.69**	-1.49 **
	S	0.32**	-0.21**	0.38	-0.64	3.17**	1.10 **	5.51**
PBW175 X RGP1	N	2.78**	1.77**	14.94 **	1.52 **	-7.15 **	2.03 **	3.74 **
	S	0.66**	-0.55**	1.51**	0.71 **	-5.35 **	0.60 **	1.24 **
PBW175 X DWR16	N	0.85**	1.47**	9.51 **	-1.06**	-4.66 **	-2.44**	-5.04 **
	S	0.40 **	0.19 **	-0.35	-1.03 **	-5.95 **	-0.33 **	-3.55 **
PBW175 X RGP18	N	-0.73**	-1.94 **	8.89 **	-0.16	0.62 **	0.72**	4.66 **
	S	-1.05**	-1.16 **	0.92 **	-0.49	0.34 **	-0.80**	4.11 **
PBW175 X DWR13	N	-2.67**	6.18 **	11.64 **	-0.49	0.02	-0.43**	-3.08 **
	S	-0.97**	-0.47**	0.44	-0.44	-0.03	1.32 **	-0.77 *
PBW175 X DWR17	N	-4.74 **	0.35**	9.39 **	0.32	1.18**	-0.11	8.26 **
	S	0.06	-1.92 **	2.38**	-0.01	0.49**	-0.04	-0.81 *
RGP12 X RGP1	N	-0.48 **	-8.45 **	7.17**	1.68**	-1.44**	1.10**	-4.90
	S	-1.36 **	0.01	-0.50	1.11 **	0.03	0.36**	-4.55 **
RGP12 X DWR16	N	-0.93**	4.25**	-1.39*	1.75**	2.22**	3.80 **	6.66 **
	S	-0.83**	-0.58**	-0.07	1.49 **	3.62 **	0.98 **	-0.01
RGP12 X RGP18	N	2.78**	5.51 **	-3.07**	-1.54**	-1.72**	1.46**	-0.63
	S	-0.68 **	1.38 **	-1.86**	-1.03 **	-3.20 **	0.71 **	0.49
RGP12 X DWR13	N	-1.26**	-2.38**	-7.21**	-1.28**	-3.33 **	-1.16**	9.12 **
	S	-0.40**	0.08	-5.37 **	- 0.48	-3.88 **	-0.99 **	0.90 *
RGP12 X DWR17	N	-1.67**	-0.37**	9.96 **	-0.97 *	-3.54**	-1.70**	-1.87 **
	S	-0.56**	-0.69**	6.90 **	0.40	-4.05 **	0.76 **	-1.61 **
RGP1 X DWR16	N	0.99**	-3.34 **	-2.12**	-0.10	0.37 **	3.55 **	-1.95 **
	S	-0.57**	0.68**	-2.68 **	-0.06	0.45**	0.59**	-0.60
RGP1 X RGP18	N	2.37**	-4.08**	-0.26	-0.02	0.02	-1.84**	1.09 *
	S	-1.34 **	-0.95**	4.31**	0.18	0.03	-0.71 **	0.39
RGP1 X DWR13	N	-2.33**	-1.31**	-6.67**	-0.65	2.61**	1.04**	3.52 **
	S	-0.17	-0.42 **	-4.29 **	-0.24	4.26**	-0.03	-0.33
RGP1 X DWR17	N	-0.41**	4.84**	2.25**	-0.40	1.09 **	-1.94**	0.51
	S	0.77**	1.64 **	-1.66**	0.19	-0.02	-0.58**	-0.86 *

***, ** significant at 5% and 1% level, respective**

Contd…

Crosses	**E**	**Days to 50% flowering (days)**	**Days to maturity (days)**	**Plant height (cm)**	**No. of tillers per plant**	**No. of grains/ ear**	**Grain yield per plant (g)**	**1000-grain weight (g)**
DWR16 X RGP18	N	1.11 **	3.95**	-6.19 **	-0.27	2.03**	-0.98**	4.98 **
	S	0.40**	-0.88**	-3.86**	-0.70 *	3.80**	-0.04	-0.73 *
DWR16 X DWR13	N	1.74**	-2.60 **	-0.49	-0.92 *	-0.58 **	0.41**	1.41 **
	S	0.14	0.16	3.23**	0.01	2.79**	0.94 **	3.20 **
DWR16 X DWR17	N	-0.67**	-0.45**	-4.12 **	1.69**	-3.25 **	-1.97**	-3.27 **
	S	-1.16**	-0.71**	-6.45 **	1.55**	0.02	0.73**	0.84 *
RGP18 X DWR13	N	-4.74 **	-2.34 **	0.62	1.24 **	-0.84**	-0.99 **	3.44 **
	S	0.03	-0.55**	0.08	1.22**	0.82**	-0.05	-1.13 **
RGP18 XDWR17	N	0.85**	0.04	6.59**	0.08	3.26 **	1.63**	1.44 **
	S	0.73**	-1.66 **	-2.79**	0.44	4.56**	0.03	1.34 **
DWR13 XDWR17	N	-1.48**	0.92**	2.99**	1.78 **	1.43**	1.20**	-4.14 **
	S	-0.47**	2.05 **	7.32 **	1.15**	3.55**	0.70**	-0.05
S.E. (Sij)	N	0.15	0.19	0.78	0.81	0.03	0.12	0.35
	S	0.18	0.07	0.61	0.65	0.04	0.06	0.72
S.E. (Sij-Sik)	N	0.22	0.28	1.05	1.21	0.05	0.18	0.52
	S	0.27	0.11	0.91	0.97	0.05	0.10	1.07
S.E. (Sij-Skl)	N	0.21	0.27	1.11	1.13	0.05	0.17	0.49
	S	0.26	0.10	0.86	0.91	0.05	0.09	1.00

*, ** **significant at 5% and 1% level, respectively**

Contd…

Crosses	E	Harvest index (%)	Relative leaf water content (%)	Canopy temperature ^{0}C (grain filing)	Canopy temperature depression ^{0}C (grain filing)	Drought susceptibility index	Germination stress index (%)	Seedling survivability
PBW175 X RGP12	N	4.13 **	-3.43 **	-0.46 **	1.32 **	-	-	-
	S	2.21 **	-0.12	-0.54**	0.35**	0.28 **	13.87 **	-11.56 **
PBW175 X RGP1	N	9.50**	1.77**	-0.34 **	0.42**	-	-	-
	S	-0.78*	1.78**	0.51**	1.51**	0.04	10.43 **	-3.11 **
PBW175 X DWR16	N	-6.01**	-0.30	-0.06 **	-0.20	-	-	-
	S	0.49	-0.25	0.01	0.14	-0.12	-23.87 **	-4.00 **
PBW175 X RGP18	N	-5.47**	1.06**	-0.82 **	0..47 **	-	-	-
	S	-0.89*	2.28**	-0.71**	0.68**	0.88**	33.89 **	-0.89
PBW175 X DWR13	N	2.18**	-0.40*	0.44**	1.02 **	-	-	-
	S	-1.96**	-1.97**	-0.62**	-0.34**	0.03	-20.54 **	12.00 **
PBW175 X DWR17	N	-5.45**	1.26**	-0.76 **	-0.01	-	-	-
	S	-8.27 **	-1.12**	-0.87**	0.11	0.01	9.68 **	9.33 **
RGP12 X RGP1	N	3.72**	1.23 **	-0.42 **	-0.80 **	-	-	-
	S	2.67**	-0.41	-0.48**	0.92**	0.65**	33.01 **	14.22 **
RGP12 X DWR16	N	-0.68	1.42 **	0.03	-0.02	-	-	-
	S	0.60	1.41**	0.02	0.12	0.10	13.80 **	-2.67 **
RGP12 X RGP18	N	-4.97**	-0.05	-0.50 **	0.35**	-	-	-
	S	1.86**	0.48	-0.80**	1.99**	-0.57 **	16.13 **	0.44
RGP12 X DWR13	N	-4.34**	0.07	0.17 **	0.06	-	-	-
	S	-8.38 **	-1.34**	0.74**	2.38**	0.11	-10.12 **	-6.67 **
RGP12 X DWR17	N	8.13**	-0.03	0.01	-0.97 **	-	-	-
	S	1.34**	-1.34**	0.02	1.29**	0.28 **	-25.27 **	2.67 **
RGP1 X DWR16	N	-0.68	3.48 **	-0.37**	-0.60 **	-	-	-
	S	-0.58	-3.55 **	0.61**	0.53**	0.09	35.88 **	5.78 **
RGP1 X RGP18	N	9.25**	-2.43**	0.61**	0.74 **	-	-	-
	S	-3.15**	-1.41**	0.85**	2.36**	0.01	-20.24 **	0.89
RGP1 X DWR13	N	-16.22 **	1.17**	1.20**	-0.27 **	-	-	-
	S	-4.04**	3.43 **	1.04 **	-0.94**	0.08	-3.80 **	-2.22 **
RGP1 X DWR17	N	22.00 **	-0.79 **	0.03	-0.22**	-	-	-
	S	0.18	4.88 **	0.02	0.11	-0.33**	23.12 **	-12.89 **

***, ** significant at 5% and 1% level, respectively**

Contd…

Crosses	E	Harvest index (%)	Relative leaf water content (%)	Canopy temperature ^{0}C (grain filing)	Canopy temperature depression ^{0}C (grain filing)	Drought susceptibility index	Germination stress index (%)	Seedling survivability
DWR16 X RGP18	N	3.01**	-0.80**	-0.62**	-1.19**	-	-	-
	S	2.89**	-0.25	0.48**	-1.44**	0.73**	40.22 **	8.89 **
DWR16 X DWR13	N	-9.30**	2.70**	-0.57**	0.74 **	-	-	-
	S	1.62**	0.89**	-0.46**	1.71**	-0.30**	24.05 **	8.01 **
DWR16 X DWR17	N	9.10**	-3.70 **	0.90 **	-1.08 **	-	-	-
	S	1.63**	0.89**	0.81**	0.59**	-0.46**	-21.32 **	-1.78 *
RGP18 XDWR13	N	-0.01	-0.75**	-0.27**	0.46**	-	-	-
	S	-0.05	-0.91**	-0.18**	-0.79**	-0.40**	-15.35**	0.01
RGP18 XDWR17	N	-3.50**	-0.20	-0.21**	0.08	-	-	-
	S	-5.19**	-3.10 **	-0.22**	0.13	0.70**	16.12 **	3.33 *
DWR13 XDWR17	N	-9.90**	3.55 **	0.37 **	0.35**	-	-	-
	S	2.11**	1.53**	1.27 **	0.81**	-0.65**	18.62 **	-5.78 *
S.E. (Sij)	N	0.78	0.38	0.04	0.09	-	-	-
	S	0.61	0.51	0.03	0.24	0.20	1.01	1.31
S.E. (Sij-Sik)	N	1.15	0.56	0.05	0.14	-	-	-
	S	0.90	0.75	0,05	0.36	0.29	1.50	1.94
S.E. (Sij-Skl)	N	1.11	0.53	0.05	0.13	-	-	-
	S	0.86	0.71	0.05	0.24	0.28	1.40	1.82

*, ** **significant at 5% and 1% level, respectively**

Crosses PBW175 x RGP1, RGP12 x RGP1, RGP12 x DWR16, DWR16 x DWR17, RGP18 x DWR13 and DWR13 x DWR17 revealed positive significant SCA effects under both normal and stress conditions for number of tillers per plant whereas, crosses PBW175 x DWR16 and RGP12 x RGP18 showed negative significant SCA effects under normal and stress conditions.

For number of grains per ear crosses, PBW175 x RGP12, PBW175 x RGP18, PBW175 x DWR17, RGP12 x DWR16, DWR16 x RGP18, RGP18 x DWR17, RGP1 x DWR16, DWR16 x DWR17 and DWR13 x DWR17 showed positive significant SCA effects under both conditions. Other crosses, PBW175 x RGP1, PBW175 x DWR16, RGP12 x RGP18, RGP12 x DWR13 and RGP12 x DWR17 exhibited negative significant SCA effects under normal as well as stress conditions.

Grain yield per plant showed positive significant SCA effects in crosses, PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP1, RGP12 x RGP18, RGP1 x DWR16, DWR16 x DWR13, RGP18 x DWR13 and DWR13 x DWR17 under normal and stress conditions. Negative significant SCA effects were recorded in RGP12 x DWR13, RGP1 x RGP18, RGP1 x DWR17 and DWR16 x DWR13 under both conditions.

Crosses viz., PBW175 x RGP1, PBW175 x RGP18, RGP12 x DWR13, DWR16 x DWR13 and RGP18 x DWR17 revealed positive significant SCA effects under normal as well as stress conditions for 1000-grain weight. Crosses, PBW175 x DWR16 and PBW175 x DWR13 showed negative significant SCA effects under normal and stress conditions.

Positive significant SCA effects for harvest index was found in PBW175 x RGP12, RGP12 x RGP1, RGP12 x DWR17, DWR16 x DWR13 and DWR16 x DWR17 under normal and stress environment conditions. Other crosses PBW175 x RGP18, PBW175 x DWR17, RGP12 x DWR13, RGP1 x DWR13 and RGP18 x DWR17 exhibited negative significant SCA effects under both conditions.

Positive significant SCA effects are found in PBW175 x RGP1, PBW175 x RGP18, RGP12 x DWR16, RGP1 x DWR13 and DWR13 x DWR17 under both normal and stress conditions. Crosses, PBW175 x DWR13, RGP1 x RGP18 and

RGP18 x DWR13 showed negative significant SCA effects under both conditions for Relative leaf water content.

For canopy temperature (grain filling stage) negative significant SCA effects were found in crosses PBW175 x RGP12, PBW175 x RGP18, PBW175 x DWR17, RGP12 x RGP1, RGP12 x RGP18, RGP18 x DWR13 and RGP18 x DWR17 under both normal and stress environment conditions. Whereas crosses RGP12 x DWR13, RGP1 x RGP18, DWR18 x RGP18, DWR16 x DWR17and DWR13 x DWR17 showed positive significant SCA effects under both conditions.

Canopy temperature depression for crosses viz., PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP1, RGP12 x RGP18, DWR16 x DWR13 and DWR13 x DWR17 exhibited positive significant SCA effects for this trait under both normal and stress environment conditions. Crosses, RGP12 x RGP18, RGP1 x DWR13, DWR16 x DWR13 and DWR13 x DWR17 showed negative significant SCA effects under both conditions.

In crosses PBW175 x RGP12, RGP12 x RGP18, RGP1 x DWR17, DWR16 x DWR13, DWR16 x DWR17, RGP18 x DWR13 and DWR13 x DWR17 drought susceptibility index (grain yield) exhibited negative significant SCA effects under stress conditions. Crosses, PBW175 x RGP18, RGP12 x RGP1, RGP12 x DWR17, DWR16 x RGP18, and RGP18 x DWR17 showed positive significant SCA effects under stress conditions.

In crosses PBW175 x RGP12, PBW175 x RGP18, PBW175 x RGP1, PBW175 x DWR17, RGP12 x RGP1, RGP1 x DWR16, RGP12 x DWR16, RGP1 x DWR17, DWR16 x RGP18, DWR16 x DWR13, RGP18 x DWR17 and DWR13 x DWR17 Germination stress index exhibited positive significant SCA effects under stress environment conditions. Other crosses PBW175 x RGP1, PBW175 x DWR16, PBW175 x DWR17, RGP12 x RGP1, RGP12 x DWR16, RGP1 x DWR17, DWR16 x RGP18, DWR16 x DWR13, RGP18 x DWR17 and DWR13 x DWR17 showed negative SCA effects under stress environment conditions.

For seedling survivability positive significant SCA effects are found in PBW175 x DWR13, PBW175 x DWR17 PBW175 x RGP1, RGP12 x RGP1, RGP12 x DWR17, RGP1 x DWR16, DWR16 x RGP18, DWR16 x DWR13 and RGP18 x

DWR17 for this trait under stress environment conditions. Whereas, crosses PBW175 x RGP12, PBW175 x RGP1, PBW175 x DWR16, PBW175 x RGP18, RGP12 xDWR16, RGP12 xDWR13, RGP1 x DWR13, RGP1 x DWR17, DWR16 x DWR17 and DWR13 x DWR17 showed negative SCA effects under stress conditions.

4.2.5 Hayman's diallel analysis

Results of genetic components of variation, their ratio along with standard error and correlation coefficient among morphological and physiological traits under normal (N) and stress environment (S) conditions was computed according to Hayman, (1954a) and used by Hayman, (1958) and are presented in Table 4.9.

4.2.5.1 Days to 50% flowering

The estimates of additive (D) and dominance components (H_1 and H_2) were found to be significant under both normal and stress environment conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of days to 50% flowering. The measure of net dominance h^2 was positive and significant under both conditions indicating that the dominant genes are in the positive direction. The estimates of F were also positive and significant under normal condition while positive and non-significant under stress condition. The estimates of mean degree of dominance $(H_1/D)^{1/2}$indicated partial dominance under both condition. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.86 under normal environment condition and 1.66 under stress environment condition suggesting again an excess of dominant alleles in the parents. The ratio of h^2/H_2 less than unity under both environment conditions. The heritability in narrow sense was found to be moderate (0.67) under normal condition but low (0.22) under stress condition.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

Table 4.9: Estimates of components of genetic variation and degree of dominance in a 7 x 7 half diallel sets for morphological and physiological traits under normal (N) and stress (S) environments.

Component	**E**	Days to 50% flowering (days)	Days to maturity (days)	Plant height (cm)	No. of tillers per plant	No. of grains/ ear	Grain yield per plant (g)	1000-grain weight (g)
D	N	1.94*±0.98	26.58*±2.76	259.24*±16.37	21.06*±0.25	7.94*±0.53	3.96*±0.40	20.58*±6.99
	S	0.75*±0.24	6.47*±0.74	30.42*±8.13	0.11±0.27	10.40*±2.14	0.01±0.15	7.96±3.69
H_1	N	19.89*±4.69	54.27*±1.48	458.61*±39.41	1.65*±0.62	39.85*±10.62	13.39*±5.86	96.12*±16.84
	S	10.44*±0.59	31.09*±5.80	51.17*±19.59	1.78*±0.66	31.63*±1.15	4.52*±0.38	12.88*±8.89
H_2	N	17.96*±4.13	49.05*±8.59	256.54*±34.72	2.69*±0.54	37.05*±2.35	11.12*±5.16	85.19*±14.84
	S	11.48*±1.68	28.05*±4.93	10.57*±1.63	2.89*±1.74	32.43*±5.75	5.20*±1.35	11.62*±2.19
h^2	N	1.79*±0.38	50.91*±3.53	351.91*±34.72	0.30±0.36	23.15 *±6.28	1.25±3.47	58.54*±9.97
	S	1.46*±0.52	23.03*±2.30	48.83*±11.26	0.50±0.58	13.72*±1.54	1.51±3.33	20.65*±3.83
F	N	4.67*±0.77	-1.36 ±6.72	442.97 *±39.27	0.61±0.30	16.10±10.58	0.51±5.84	3.02±4.31
	S	3.54±2.15	18.29*±3.28	47.26*±23.59	0.58±0.30	29.09*±5.13	0.06±0.38	-0.08±5.62
E	N	2.38*±0.68	5.70±3.09	0.25±1.10	0.19±0.76	1.41±2.27	1.27±0.86	0.25±2.47
	S	0.04±0.28	0.12±0.82	0.10±0.27	0.03±0.29	0.59±0.96	0.33±0.22	0.14±1.30
$(H1/D)^{1/2}$	N	0.80	3.12	0.83	6.96	2.24	4.87	2.16
	S	0.38	1.97	0.69	3.94	2.33	3.08	1.80
$(H_2/4H_1)$	N	0.22	0.19	0.14	0.22	0.17	0.20	0.22
	S	0.23	0.23	0.20	0.21	0.21	0.23	0.19
(kd/kr)	N	1.86	1.69	1.85	1.51	2.65	1.20	1.69
	S	1.66	1.13	1.77	1.04	1.88	1.39	0.78
h^2 / H_2	N	0.53	1.20	1.37	0.11	0.85	0.13	0.68
	S	0.44	1.07	1.05	0.17	0.09	0.02	0.06
H (n)	N	0.67	0.56	0.56	0.32	0.85	0.50	0.49
	S	0.22	0.46	0.43	0.19	0.39	0.16	0.39
t^2	N	2.47	0.12	0.17	2.01	0.02	1.32	1.52
	S	0.47	0.26	0.02	0.92	0.89	1.39	0.04
r	N	0.37	0.80	0.86	0.49	0.37	0.59	0.08
	S	0.24	0.69	0.49	0.47	0.39	0.09	0.03
b ± S.E. (b)	N	0.38±0.20	0.88±0.26	0.97±0.07	0.62±0.24	0.39±0.23	0.74±0.17	0.42±0.58
	S	0.29±0.37	0.74±0.56	0.55±0.44	0.89±0.12	0.52±0.44	0.88±0.26	0.07±0.41

***, indicate that value is significant as it exceeds 1.96 after dividing with its standard error**

Contd……

Component	E	Harvest index (%)	Relative leaf water content (%)	Canopy temperature ^{0}C (grain filing)	Canopy temperature depression ^{0}C (grain filing)	Drought susceptibility index	Germination stress index (%)	Seedling survivability
D	N	3.98*±0.48	2.58*±0.21	0.76*±0.08	0.76*±0.16	-	-	-
	S	0.14±0.32	0.03*±0.01	0.72*±0.21	0.46*±0.11	0.53*±0.105	5.24*±1.31	68.09*±15.03
H_1	N	523.71*±72.29	19. 65*±6.24	1.06*±0.19	2.82*±0.40	-	-	-
	S	42.47*±13.02	16.97*±7.90	1.89*±0.50	9.03*±1.40	0.05*±0.02	37.73*±7.04	11.48*±2.78
H_2	N	336.04*±51.81	17.15*±5.50	0.59*±0.17	1.49*±0.35	-	-	-
	S	3.30*±0.95	14.34*±6.96	1.25*±0.44	8.59*±2.99	0.63*±0.04	33.05*±5.99	9.72*±2.37
h^2	N	0.47±0.58	6.22±5.25	0.19±0.20	0.40±1.02	-	-	-
	S	36.47*±11.42	9.60*±4.67	2.22*±0.30	2.30*±2.01	0.01*±0.003	4.03±4.01	0.57±1.58
F	N	0.80±1.11	5.50±4.39	0.20 ±0.29	1.68±0.40	-	-	-
	S	0.13±1.21	0.03±0.02	0.14±0.50	0.02±1.55	0.91±1.62	1.19±7.64	2.67±3.02
E	N	0.09±0.14	0.09±0.23	0.03±0.14	0.24±0.50	-	-	-
	S	9.44*±1.91	0.12±0.48	0.02±0.03	0.24±0.29	0.02±0.21	0.07±0.99	0.47±1.39
$(H1/D)^{1/2}$	N	0.73	2.76	1.18	1.92	-	-	-
	S	0.75	1.75	1.52	1.61	1.93	2.96	1.87
$(H_2/4H_1)$	N	0.21	0.21	0.20	0.22	-	-	-
	S	0.20	0.22	0.21	0.16	0.21	0.23	0.22
(kd/kr)	N	0.64	0.57	1.64	0.92	-	-	-
	S	0.42	0.48	1.46	0.98	1.47	1.23	1.39
h^2 / H_2	N	0.14	0.30	0.35	0.06	-	-	-
	S	0.02	0.45	0.50	0.01	0.22	0.33	0.19
H (n)	N	0.38	0.22	0.48	0.26	-	-	-
	S	0.17	0.27	0.30	0.15	0.39	0.62	0.37
t^2	N	0.22	2.30	0.19	0.60	-	-	-
	S	0.66	1.97	0.39	0.41	0.47	2.14	0.35
r	N	0.43	0.25	0.03	0.11	-	-	-
	S	0.14	0.23	0.16	0.42	0.03	0.10	0.17
b ± S.E. (b)	N	-0.32±0.48	-0.22±0.48	0.61±0.09	-0.11±0.16	-	-	-
	S	0.20±0.21	0.40±0.51	0.19±0.21	0.41±0.48	-0.19±0.28	0.12±0.34	0.47±0.59

***, indicate that value is significant as it exceeds 1.96 after dividing with its standard error**

4.2.5.2 Days to maturity

The estimates of genetic components D, H_1 and H_2 were found to be significant under both normal and stress environment conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of the trait. The measure of net dominance h^2 was positive and significant under both conditions indicating that the dominant genes are in positive direction. The estimates of F were negative and non-significant under normal environment condition while positive and significant under stress environment condition. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait which emphasized the importance of non-additive component under both normal and stress conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.69 under normal environment condition and 1.13 under stress environment condition suggesting an excess of recessive alleles under normal environment condition and dominant alleles under stress condition in the parents. The ratio of h^2/H_2 was more than unity under both normal and stress environment conditions indicating that at least one gene or gene group was responsible for expression of this trait under both conditions. The heritability in narrow sense was found to be moderate under both normal (0.56) and stress environment (0.46) conditions.

Correlation between *per se* performance of the parents (Yr) and parental order of dominance (Wr+Vr) was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.3 Plant height

The estimates of genetic components D, H_1 and H_2 were found to be significant under normal and stress environment conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of plant height. The value of h^2 was positive and significant under both conditions indicating that the dominant genes are in the positive direction. The estimate of F was positive and significant under both conditions indicating that dominant genes were in excess than recessive ones in the parents under both conditions. The mean degree of dominance $(H_1/D)^{1/2}$ indicated partial dominance under both normal and stress conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.85 under normal and 1.77 under stress environment condition suggesting an excess of dominant alleles in the parents. The ratio of h^2/H_2 was high and positive under both normal and stress environment conditions indicating that at least one gene or gene group was responsible for expression of this trait under both conditions. The heritability in narrow sense was found to be moderate under both normal (0.56) and stress (0.43) conditions.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.4 Number of tillers per plant

The estimates of additive (D) and dominance components (H_1 and H_2) were found to be significant under both normal and stress environment conditions while D was non-significant under stress environment condition indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of the trait. The measure of net dominance h^2 was positive and non-significant for both conditions. The estimates of F were also positive and non-significant under both conditions. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance under both condition. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.51 under normal environment condition and 1.04 under stress environment condition suggesting again an excess of dominant alleles in the parents under both conditions. The ratio of h^2/H_2 was less than unity under both normal and late sown conditions. The heritability in narrow sense was found to be moderate under both conditions.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.5 Number of grains per ear

The results regarding the genetic components of variation for number of grains per ear revealed that additive component (D) and the dominance components (H_1 and H_2) were found to be significant under both conditions, thereby, indicating that both additive and non-additive type of gene effects controlled this trait. The measure of net dominance h^2 was positive and non-significant under normal environment condition while positive and significant under stress environment condition. The estimates of F were also positive and non-significant under both conditions. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over-dominance under both normal and stress sown conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 2.65 under normal environment condition and 1.88 under stress environment condition suggesting again an excess of dominant alleles in the parents under both conditions. The ratio of h^2/H_2 was less than unity under both normal and stress environment conditions. The heritability in narrow sense was found to be high under normal (0.85) and moderate under stress (0.39) condition.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.6 Grain yield per plant

The estimates of additive (D) and dominance components (H_1 and H_2) were found to be significant under both normal and stress conditions while D was non-significant under stress environment conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of the trait. The measure of net dominance h^2 was positive and non-significant under both conditions indicating positive directions of dominant genes. The estimates of F were positive but non-significant under both conditions indicating that dominant genes were in excess under both conditions. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over-dominance under both normal and stress environment conditions thus emphasizing the importance of non-additive component of genetic variance in the inheritance of grain yield per plant. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.20 under normal and 1.39 under stress environment condition suggesting dominant alleles in the parents. The ratio of h^2/H_2 was low and positive under both normal and stress conditions indicating that this value has been under estimated. The heritability in narrow sense was found to be moderate under normal and low under stress condition.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.7 1000-grain weight

The results regarding the genetic components of variation for 1000-grain weight revealed that D, H_1 and H_2 were found to be significant under both conditions while D was non-significant under stress condition indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of the trait. The measure of net dominance h^2 was positive and significant under normal environment condition but positive and non-significant under stress environment condition indicating that the dominant genes are in positive direction. The estimates of F were positive and significant under normal environment condition while negative and non-significant under stress environment condition. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance under both conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.69 under normal and 0.78 under stress sown condition. The ratio of h^2/H_2 was less than 1 under both conditions. The heritability in narrow sense was found to be moderate under both normal (0.49) and stress (0.39) conditions.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant under both conditions indicating that recessive genes had positive effect and dominant genes were mostly negative.

4.2.5.8 Harvest index

The results regarding the genetic components of variation for harvest index revealed that additive component (D) and dominance components (H_1 and H_2) were found to be significant under both conditions, while D was non-significant under stress environment conditions thereby, indicating that both additive and non-additive type of gene effects controlled this trait. The value of h^2 was positive and non-significant under normal environment condition while positive and significant under stress environment condition. The estimates of F were positive and non-significant under both conditions. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated partial dominance under both normal and stress environment conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was less than 1 under both normal and stress conditions suggesting again on recessive alleles in the parents. The ratio of h^2/H_2 was less than unity under both normal and stress conditions indicating that this value has been under estimated. The heritability in narrow sense was found to be moderate under normal (0.38) and low under stress (0.17) conditions.

Correlation between *per se* performance of the parents and dominance order was negative but non-significant under normal condition and positive and non-significant under stress condition.

4.2.5.9 Relative leaf water content

The results regarding the genetic components of variation for relative leaf water content revealed that additive component (D) and dominance components (H_1 and H_2) were found to be significant under both conditions, thereby, indicating that both additive and non-additive type of gene effects controlled this trait. The value of h^2 was positive and non-significant under normal environment condition while negative and non-significant under stress environment condition. The estimates of F were positive and non-significant under both conditions. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance under both conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was less than 1 under both normal and stress conditions suggesting again on recessive alleles in the parents. The ratio of h^2/H_2 was less than unity under both normal and stress environment conditions indicating that this value has been under estimated. The heritability in narrow sense was found to be low under both normal (0.22) and stress (0.17) conditions.

Correlation between *per se* performance of the parents and dominance order was negative but non-significant under normal environment condition and positive and non-significant under stress condition.

4.2.5.10 Canopy temperature

The estimates of additive (D) and dominance components (H_1 and H_2) were found to be significant under normal and stress conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of this trait. The measure of net dominance h^2 was positive and non-significant under normal sown condition but positive and significant under stress environment condition indicating that the dominant genes are in positive direction. The estimates of F were positive but non-significant under both conditions indicating that dominant genes were in excess under both conditions. The mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait which emphasized the importance of non-additive component under both normal and stress sown conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.64 under normal and 1.46 under stress sown condition suggesting again on dominant alleles in the parents. The ratio of h^2/H_2 was low and positive under both conditions indicating that this value has been under estimated. The heritability in narrow sense was found to be moderate under both normal (0.48) and stress (0.30) conditions.

Correlation between *per se* performance of the parents and dominance order was negative but non-significant under both conditions.

4.2.5.11 Canopy temperature depression

The estimates of additive (D) and dominance components (H_1 and H_2) were found to be significant under normal and stress sown conditions indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of this trait. The measure of net dominance h^2 was positive and non-significant under normal sown condition but positive and significant under stress sown condition indicating that the dominant genes are in positive direction. The estimates of F were positive but non-significant under both conditions indicating that dominant genes were in excess under both conditions. The mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait which emphasized the importance of non-additive component under both normal and stress conditions. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 0.92 under normal and 0.98 under stress sown condition suggesting on recessive alleles in the parents. The ratio of h^2/H_2 was low and positive under both normal and stress sown conditions indicating that this value has been under estimated. The heritability in narrow sense was found to be low under both normal (0.26) and stress sown (0.15) conditions.

Correlation between *per se* performance of the parents and dominance order was negative but non-significant under normal sown condition and positive and non-significant under stress sown condition.

4.2.5.12 Drought susceptibility index (grain yield)

The estimates of genetic components D, H_1 and H_2 were found to be significant indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of Drought susceptibility index. The value of h^2 was positive and significant. The estimates of F were positive and non-significant. The mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait which emphasized the importance of non-additive component. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.47. The ratio of h^2/H_2 was positive. The heritability in narrow sense was found to be moderate Correlation between *per se* performance of the parents and dominance order was negative but non-significant.

4.2.5.12 Germination stress index

The estimates of genetic components D, H_1 and H_2 were found to be significant indicating that both additive and non-additive components of genetic variance were important in determining the genetic control of the trait. The value of h^2 was positive and non-significant, indicating the positive direction of dominant genes. The estimates of F were positive and non-significant indicating that dominant genes were in excess. The mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.23 suggesting dominant alleles in the parents. The ratio of h^2/H_2 was low and positive. The heritability in narrow sense was found to be high (0.62).

Correlation between *per se* performance of the parents and dominance order was positive but non-significant.

4.2.5.14 Seedling survivability

The results regarding the genetic components of variation for seedling survivability revealed that additive (D) and dominance components (H_1 and H_2) were found to be significant under both conditions, thereby, indicating that both additive and non-additive type of gene effects controlled this trait. The value of $h^2$and F was positive and non-significant. The mean degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for this trait. The ratio of $H_2/4H_1$ which was less than expected theoretical value of 0.25 under both conditions revealed asymmetric distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes (kd/kr) in the parents was 1.39 suggesting dominant alleles in the parents. The ratio of h^2/H_2 was less than unity. The heritability in narrow sense was found to be moderate.

Correlation between *per se* performance of the parents and dominance order was positive but non-significant.

CHAPTER V

DISCUSSION

Wheat (*Triticum aestivum* L.) one of the largest cereal crop of the world, is a most important staple food of about two billion people (36% of the world population), and also it is the second most important source of food and income after rice in India. Drought (water stress) and heat stress (increases in above-optimum air temperatures) often occur simultaneously, but they can have very different effects on various physiological, growth, developmental, and yield processes. Although drought and heat stresses have been extensively studied independently, relatively little is known about how their combination affects crop productivity. Heat and drought stress are currently the leading threat on world's food supply, limiting wheat yield. The extent and severity of stress affected agricultural land is predicted to worsen as a result of inadequate irrigation resources, declining water tables and global warming. Drought/heat tolerance is crucial to stabilize and increase food production. Domestication has limited the genetic diversity of crops including wild wheat, leading to cultivated species, adapted to artificial environments, and lost tolerance to stress conditions.

There are several mating designs by which we can develop crop material for its genetic analysis. Some of the common designs used today are North Carolina designs (Comstock and Robinson, 1952), the combining ability technique (Griffing, 1956), triple test cross method and diallel mating design (Hayman, 1954a, b; Jinks, 1954, Kang, 2003). The diallel cross is among the most commonly used biometrical technique in early segregating generation which provides reliable information on the pattern of inheritance of variation in the plant material. Thus it is used to study the genetic basis of variation in various morphological, physiological and biochemical traits of wheat.

In order to choose the best hybrid combinations, a large number of subjectively chosen varieties are crossed. It would be a considerable advantage to be able to estimate the combining ability of parents and gene effects of crosses before making crosses among varieties. Diallel crossing programs have been applied to achieve this goal by providing a systematic approach for the detection of suitable parents and crosses for the characters under study. In addition, diallel analysis gives plant breeders the opportunity to choose the most efficient selection method by allowing them to estimate various genetic parameters, Singh and Chaudhary (1979). The general combining ability and specific combining ability effects and their variance are very effective genetic parameters of direct utility to decide the next phase of the breeding programme, it also enables the plant breeder to decide about hybrid or pureline breeding, the selection of F_1's for a multiple crossing or a composite breeding programme and the possibility of employing appropriate selection techniques like modified mass selection, recurrent selection and reciprocal recurrent selection.

Results of the present study **"Characterizing diversity for heat and drought related traits in hexaploid wheat (*Triticum aestivum* L.)"** are discussed in the light of available literature and explanation wherever possible is provided for the trends revealed by these observations under following heads.

5.1 EVALUATION FOR HEAT AND DROUGHT STRESS

5.1.1 Mean performance

5.1.2 Variability analysis

5.1.3 Correlation

5.2 COMBINING ABALITY ANALYSIS

5.2.1 Analysis of variance

5.2.2 Analysis of variance for combining ability

5.2.3 General combining ability

5.2.4 Specific combining ability

5.2.5 Components of genetic variation

5.1 Evaluation for heat and drought stress

5.1.1 Mean performance

Screening for heat and drought tolerance is a useful tool to select the most tolerant genotypes. This can be done under laboratory, green house in pots and under field condition; however, of the all of these methods, field condition bioassay is the most successful and effective method for screening since the evaluation can cover all stages of plant growth and development and thus the data is more realistic than using the other methods (Vaezi *et al.*, 2010).

The present results revealed that the mean of traits such as days to 50% flowering, days to maturity, plant height, number of grains per ear, number of tillers per plant, 1000-grain weight, grain yield per plant, harvest index, canopy temperature depression, relative water content, drought susceptibility index, germination stress index and seedling survivability were decreased under heat and drought stressed environments. Several studies under field conditions through stress environment, also reported decrease in mean of such characters. (Mian *et al*., 2007; Khan *et al*., 2007a; Almeselmani and Deshmuch, 2012). The trait viz., canopy temperature was increased under terminal heat and drought stress by 14.19% of control.

Analyses of the data of the present study indicated that the reduction of grain yield under heat and drought stress was apparently due to the reduction in all the yield components, particularly number of tillers per plant which showed greater reduction 46.49%, followed by 1000-grain weight 26.31%, harvest index 17.89 % and number of grains per ear 11.31% (Garcia del Moral *et al*., 1991; Guendouz *et al*., 2012). Heat and drought stress was reported to reduce the ability of plant to maintain normal anthesis and pollination and to produce tillers thereby reduceing the opportunity of producing ears (Wardlaw and Wrigley, 1994). The severity of the stress increased when the heat stress applied at anthesis and grain filling stages than on at one stage alone (McDonald *et al*., 1983; Macas *et al*., 1999; Mullarkey and Jones, 2000; Tewolde *et al*., 2006). The decrease in 1000-grains weight under heat stress is due to reduction of the duration between anthesis and physiological maturity (Warrington *et al*., 1977), which is associated with a reduction in grain weight (Warrington *et al*., 1977; Shpiler and Blum, 1991). Reduction in number of grains per ear result due to high temperature during floret development that may cause complete sterility (Saini and Aspinall, 1982). The grain filling duration were reduced by heat and drought stress in genotypes differing in grain weight stability and is likely to occur due to the heat and drought stress which forces plant to complete its grain formation in relatively lesser time (Dias and Lidon, 2009).

The adverse effect of heat and drought stress on relative leaf water content, canopy temperature and canopy temperature depression coincided with general trend of the effect of heat stress on physiological processes in plants. Canopy temperature depression has been used in various practical applications including evaluation of plant response to environmental stress (Ehrler *et al.*,1978; Idso, 1982; Howell *et al.*,1986), irrigation scheduling (Hatfield, 1982), and to evaluate cultivars for water use (Pinter *et al.*, 1990), tolerance to heat (Amani *et al.*, 1996) and drought (Blum *et al.*, 1989; Rashid *et al.*, 1999). Relative water content through its relation to cell volume closely reflects the balance between water supply to the leaf and transpiration rate. Drought tolerant genotypes possess more relative water content as compared to susceptible type. Genotypes RGP18, RGP12, DWR16 and PBW175 had high relative water content under both conditions. Canopy temperature depression (CTD) has been used to assess plant water status because it represents an overall, integrated physiological response to drought and high temperature (Amani *et al.*, 1996). The difference between canopy temperature (CT) under normal and stressed conditions equals 14.19%, this result is in agreement with the finding of Talebi (2011) and Guendouz (2012), and water stress affects positively to canopy temperature. Blum *et al.*, (1989) used canopy temperatures of drought stressed wheat genotypes to characterize yield stability under various moisture conditions. Drought stressed plants displayed higher canopy temperature than well watered plants (Siddique *et al.*, 2000). High CTD has been used as selection criteria to improve tolerance to drought and heat (Amani *et al.*, 1996; Ayeneh *et al.*, 2002). The genotypes with negative values of CTD suggests that these genotypes are very sensitive to water stress.CTD is used as a tool for predicting performance under water stress conditions (Reynolds *et al.*, 1997). Increase in CTD might have been occurred due to increased respiration and decreased transpiration resulting from stomatal closure (Siddique *et al.*, 2000). The reduction in canopy temperature depression resulting this from terminal heat stress in wheat was also reported by Mohammadi *et al.* (2012), and is possibly due to adverse effect of heat stress that causes reduction in tillering and plant canopy development. Drought susceptibility index (DSI) is considered as potential indicator for drought resistance of a genotype. Improved drought resistance is inversely related to DSI indicating that one ranking would have lowest DSI value for population. In other words low drought susceptibility index is synonymous with high drought resistance (Hamdi and Erskine 1996). D- Value (drought intensity) was negative in case of genotypes DWR13, DWR16, RGP11, DWR1, RGP18, RGP12 and PBW175. These negative values indicate that these genotypes were less affected under heat and drought stress condition as compared to other genotypes for grain yield. Germination stress index is one of the most suitable criteria for screening drought tolerance genotypes (Ehdaei *et al*., 1991). Genotypes with higher germination stress index were more drought tolerant (Sapara *et al*., 1991). Maximum value of germination stress index was observed in DWR13 followed by DWR16, RGP18 and RGP12. All these genotypes were performing better under stress conditions. The present results are conformity with earlier reports of (Ashraf and Abu-Shakara, 1978). Therefore, polyethylene glycol induced water stress can be used effectively for low cost evaluation of drought resistance in large number of cultivars as most of the cultivars having drought resistance capabilities had higher germination stress index. Seedling survivability is a basic requirement for improvement of drought resistance is the available of a rapid and reliable method for screening large number of breeding material for drought resistance. Singh *et al*. (1999) suggested a simple method to screen germplasm lines using seedling survivability, which accurately discriminates between drought tolerance and susceptibility under artificial moisture stress condition. Maximum number of seedling died without irrigation up to 30 days in genotypes RGP1. Genotypes DWR13 followed by RGP18, PBW175 and DWR16 recovered most after withering. Tomar and Kumar (2004) also reported similar results for genotype C306.

Heat stress causes disruptions in the structure and function of chloroplasts, and reductions in chlorophyll content and photosynthesis was also reported by Xu *et al.* (1995).

Results of the present work exhibited differential response of the test cultivars of wheat to terminal heat and drought stress. This suggests that these differences were due to genetic variations among the test cultivars to heat and drought stress since all treatments were carried out under similar conditions. The differential response of genotypes of wheat crop to terminal heat and stress has been reported and well documented by several investigators (Ubaidullah *et al*., 2007; Mohammadi and Karimizadeh, 2012; Sareen *et al*., 2012; Dhyani *et al*., 2013; Zarei *et al*., 2013).

The present study demonstrated that DWR13, RGP18, DWR16, PBW175 and RGP12 are the most tolerant cultivars to drought and heat since they had highest values of grain yield under heat stress, while DWR17 and RGP1 were the most heat and drought sensitive cultivars as low grain yield was obtained when grown at terminal heat and drought stress condition. Subsequent data analyses revealed that the heat and drought tolerant cultivars appeared superior in most of the yield and yield related traits, relative leaf water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index, and seedling survivability compared to the heat sensitive cultivars.

5.1.2 Variability analysis

Analysis of variance for different morpho-physiological traits as depicted in Table 4.2 revealed that all the 20 genotypes differed significantly for most of these traits with respect to all the traits under study for both normal and stress conditions.

5.1.2.1 Morphological traits

Different genetic parameters that were used to explain the variability revealed that, the component of analysis of total variability into genotypic and phenotypic variance, coefficient of genotypic and phenotypic variability, heritability and genetic advance are helpful in improving efficiency of selection in segregation populations. Overall phenotypic variance was higher in magnitude than corresponding genotypic variation for most of the characters in both environments. Germination stress index, seedling survivability, relative leaf water content and harvest index had high estimates of phenotypic varianceas compared to other traits. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were moderate to high for number of tillers per plant, number of grains per ear, grain yield per plant, 1000-grain weight and harvest index under both conditions. However, in case of days 50% flowering, days to maturity and plant height, a low level of PCV and GCV was recorded under both conditions. Similar findings have been reported by Ali *et al*. (2008), Abinasa *et al*. (2011), Kalimullah *et al*. (2012), Degewione *et al*. (2013), Kumar *et al*. (2013a), Maurya *et al*. 2014.

Estimates of heritability and genetic advance expressed as per cent of mean were high to moderate for most of the morphological characters in these genotypes, however, estimate of genetic advance for days to 50% flowering and days to maturity were recorded to be low under both conditions. Panse (1957) stressed the importance of heritability in addition to mean performance and variability. The present study revealed high heritability for most of the morphological characters and these findings are in accordance with early reports of different workers in wheat breeding (Ali *et al*., 2008; Majumder *et al*., 2008; Degewione *et al*., 2013; Maurya *et al*., 2014; Yadav *et al*., 2014; Zeeshan *et al*., 2014).

5.1.2.2 Physiological traits

Analysis of variance for different physiological traits as depicted in Table 4.2 revealed that all the 20 genotypes differed significantly for most of these traits with respect to all the traits under study for both normal and stress conditions. The present study revealed high heritability for most of the physiological characters and these findings are in accordance to early reports with different workers in wheat breeding (Pinter *et al*., 1990; Amani *et al*., 1996; Blum *et al*., 1989; Rashid *et al*., 1999; Guendouz *et al*., 2012; Grzesiak *et al*., 2012).

Different genetic parameters that were used to explain the variability revealed that PCV and GCV were moderate for most of the physiological traits under both conditions, except canopy temperature (under both condition) and seedling survivability where, low PCV and GCV was recorded. These results are supported with the findings of Shankarrao *et al*. (2010), Tsegaye *et al*. (2012) and Priya *et al*. (2013).

Estimates of heritability and genetic advance expressed as per cent of mean were high for most of the physiological traits in the wheat genotypes under both conditions, however, estimate of genetic advance for number of grains per ear and seedling survivability were recorded to be moderate which is desirable for exercising selection. Panse (1957) also stressed the importance of heritability in addition to mean performance and variability. High level of heritability and high genetic advance was observed for most of the physiological traits. These findings are in accordance with early reports of various workers (Shankarrao *et al*., 2010; Wani *et al*., 2011; Priya *et al*., 2013).

Johnson *et al.* (1955) suggested that high heritability combined with high genetic advance will be more useful than heritability alone in predicting the performance of the progenies of selected lines. Accordingly in the present investigation high heritability with high genetic advance as per cent of mean was observed with respect to number of tillers per plant, 1000-grain weight, grain yield per plant, canopy temperature depression and seedling survivability, under both conditions indicating the presence of additive gene effects in controlling these characters. Similar findings were also reported by Ali *et al*. (2008), Majumder *et al*. (2008), Shankarrao *et al*. (2010), Wani *et al*. (2011), Kalimullah *et al*. (2012), Priya *et al*. (2013),Yadav *et al*. (2014) and Maurya *et al*. (2014).

5.1.3 Correlation

The correlation coefficients among grain yield, yield contributing and physiological traits related to heat and drought tolerance under normal and stress environment conditions are presented in Table 4.4 and Table 4.5, respectively. The results revealed that the positive correlation between number of tillers per plant and canopy temperature depression suggested that dense canopies keep the crop canopy cooler and hence increases the CTD.

Under stress conditions, grain yield and mean CTD were correlated positively (r = 0.58**), this correlation is similar to other studies (Blum *et al*., 1989; Royo *et al*., 2002); but under normal condition CTD correlated negative with grain yield (r = -0.46**) (Table 4.4). In this study, positive correlation between CTD and grain yield suggests that CTD has been used for selection in breeding programs. High CTD has been used as selection criterion to improve tolerance to heat and drought (Amani *et al*., 1996; Ayeneh *et al*., 2002). Under stress condition canopy temperature (CT) correlated negative with grain yield (r = -0.44**). Similar results were reported by Talebi (2011) in wheat. Similar results of correlation between canopy temperature (CT), canopy temperature depression (CTD) and grain yield suggests that the use of CT and CTD in screening for high tolerant cultivars to heat and drought is similar. Drought susceptibility index and canopy temperature were correlated positively (0.45**) as stability in grain yield was estimated for each genotype by the drought susceptibility index derived from the yield difference stress and non-stress environments. It was compared with midday canopy temperature under drought stress, which expressed the relative plant water status for each genotype, positive correlation between canopy temperature, indicated that drought-susceptible genotypes which suffered relatively greater loss under stress also tended to be under great water-stress and had warmer canopies at midday (Blum *et al*., 1989).

Positive and significant correlation of grain yield per plant with number of grains per ear, number of tillers per plant, 1000-grain weight, harvest index and relative leaf water content indicates that each yield contributing trait contributes equally to grain yield per plant under heat and drought stress, similar findings have been reported by Paliwal *et al*. (2012) and Baloch *et al*. (2013).

5.2 Combining ability analysis

Griffing (1956) proposed a more general procedure for half diallel analysis in which mean measurement of a cross is partitioned into two major components apart from a general mean (u) and an environmental component (i) the contribution of the parents, the general combining ability (gca) effect and (ii) the excess over and above the sum of two gca effects called the specific combining ability (sca) effect. The diallel analysis developed by Hayman (1954a) and Jinks (1954) provide a fairly reliable mechanism to properly understand the nature of gene action involved in the development of complex genetic characters having economic value. The type of gene action, allelic and non-allelic interactions involved in the inheritance of quantitative traits is indicated through component analysis showing distribution and proportion of dominant and recessive alleles among parents. In various diallel crosses, both additive and non-additive type of gene actions were reported to be involved in quantitative characters in wheat (Beyakin and Korobova, 1990; Chowdhry *et al*., 1992; Waldia *et al*., 1994; Farooq *et al*., 2011b; Singh *et al*., 2013a; Ram *et al*., 2014).

The GCA and SCA effects and their variances are very effective genetic parameters of direct utility to decide the next phase of the breeding programme, it also enables the plant breeder to decide about hybrid or pureline breeding, the selection of F_1's for a multiple crossing or a composite breeding programme and the possibility of employing appropriate selection techniques like modified mass selection, recurrent selection and reciprocal recurrent selection.

In the present study, an attempt has been made to understand the general combining ability (GCA) of the parents, specific combining ability (SCA) of hybrids and heritability patterns of morphological and physiological traits related to heat and drought tolerance considered for the development of high yielding cultivars in hexaploid wheat following Method 2 Model 1 of Griffing's method using seven parent half diallel and their derived F_1 generations. The Hayman's method, on the other hand, is used to estimate the gene action and other genetic parameters of the crop.

The results obtained under the present study have been discussed in the light of available literature.

5.2.1 Analysis of variance

The mean squares obtained from the analysis of variance for parents, hybrids and parent vs hybrids were significant for all morphological and physiological traits under normal and stress environment conditions in the present study (Table 4.6). Many workers including Gupta and Verma (2000b), Shah and Deora (2002), Nayeem *et al*. (2002), Dwidevi and Pawar (2004), and Ram *et al*. (2014) reported high variation for different traits in wheat. The significant differences in mean sum of squares indicated the large genetic variability for characters hence are amenable for selection.

5.2.2 Analysis of variance for combining ability

Analysis of variance for combining ability with respect to morphological and physiological traits is presented in Table 4.6, for both normal and stress environment conditions. The perusal of tables indicate that the variance due to GCA as well as SCA were highly significant for all the traits studied under both conditions. The variance for GCA were greater than the mean squares for SCA for all the traits which indicated that additive type of gene effects were more pronounced than those of non-additive ones. Similar results are reported by Sheikh and Singh (2000), Zalewski (2001), Mahmood and Chowdhry (2002), Kamaluddin (2007), Kulshreshtha and Singh (2011), Adel and Ali (2013) and Singh *et al*. (2013b).

5.2.3 General combining ability effects

General combining ability effects for morphological and physiological traits (Table 4.7) under normal and stress environment conditions indicated that certain lines/genotypes may contribute to high yields through individual yield components. For grain yield per plant, parents RGP18, PBW175 and DWR13 were found to be good general combiners under both normal and stress sown conditions. In addition, parents RGP18, DWR13 and DBW17, for days to 50% flowering, DWR17, RGP18 and DWR16 days to maturity, DWR13, RGP12 and DWR17 for plant height, DWR16 for number of tillers per plant, PBW175, DWR16 and DWR17 for number of grains per ear, DWR16 and DWR13 for 1000-grain weight, RGP1 and DWR17 for harvest index were found to be good combiners under both conditions.

For physiological traits, parents RGP12, RGP18 and DWR13 for relative leaf water content, PBW175, DWR13 and RGP18 for canopy temperature, DWR13, RGP18 and PBW175 for canopy temperature depression, RGP18 and DWR13 for drought susceptibility index, DWR13, DWR17, PBW175, RGP18 and DWR16 for germination stress index, DWR17, DWR13, DWR13 and PBW175 for seedling survivability were found to be good combiners under both normal and stress environment conditions.

Combining ability effects result indicated that the parent PBW175 showed significant GCA effects for grain yield per plant, number of grains per ear, relative water content, canopy temperature, canopy temperature depression, germination stress index and seedling survivability. Second parent DWR13 showed significant GCA effects for Grain yield per plant, days to 50% flowering, plant height, 1000-grain weight, relative water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability. Third parent RGP18 showed significant GCA effects Grain yield per plant, days to 50% flowering, days to maturity, relative water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability.

5.2.4. Specific combining ability effects

In self pollinated crops, SCA effects are not of much importance as they are mostly related to dominance gene effects and cannot be fixed in the end product inbred lines. However, if a cross combination exhibits high SCA effects as well as per se performance having at least one parent as good general combiner for a particular trait, it is expected that such a cross combination will lead to desirable transgressive segregants in later generations. Significant SCA effects of those combinations involving good x good combiners depicted the major role of additive type of gene effects, which is fixable. However, it can also be mentioned here that combinations of two good general combiners may not necessarily results in good segregants, but expectations are much more.

If the superior crosses involved both the parents having poor general combining ability for respective trait, very little gain is expected from these crosses, because the high SCA effects are due to dominance and epistatic gene effects which may not be accumulated through simple breeding procedures.

Keeping these facts in mind, superior crosses which had both high per se as well as SCA effects under both conditions were selected (Table 5.2). The crosses viz., PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP1, RGP12 x RGP18, RGP1 x DWR16, DWR16 x DWR13, RGP18 x DWR13 and DWR13 x DWR17 for grain yield per plant, yield contributing and physiological traits related to heat and drought tolerance were found desirable under both normal and late sown conditions. High yield cross combination PBW175 x RGP12 showed significant SCA effects for days to maturity, number of grains per ear, harvest index, canopy temperature, canopy temperature depression, drought susceptibility index and germination stress index; the cross PBW175 x RGP1 showed significant SCA effects for number of tillers per plant, 1000-grain weight, relative leaf water content, canopy temperature, canopy temperature depression, germination stress index and seedling survivability; the cross RGP12 x RGP1 showed significant SCA effects for days to 50% flowering, days to maturity, number of tillers per plant, harvest index, canopy temperature, canopy temperature depression, DSI,GSI and seedling survivability. The cross RGP12 x RGP18 showed significant SCA effects for days to maturity, plant height, canopy temperature, canopy temperature depression, drought susceptibility and germination stress index; the cross RGP1 x DWR16 showed significant SCA effects for plant height, number of grains per ear, germination stress index and seedling survivability; the cross DWR16 x DWR13 showed significant SCA effects for 1000 grain weight, relative leaf water content, canopy temperature, canopy temperature depression, germination stress index and seedling survivability; the cross RGP18 x DWR13 showed significant SCA effects for plant height, number of tillers, canopy temperature and drought susceptibility index; the cross DWR13 x DWR17 showed significant SCA effects for days to 50% flowering, number of tillers per plant, number of grain per ear, relative leaf water content, canopy temperature depression, drought susceptibility index and germination stress index under both normal and stress conditions. Therefore crosses viz., PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP18, RGP1 x DWR16, and DWR13 x DWR17 involved at least one parent as good general combiner indicated the superiority due to additive gene action. One cross combinations viz., RGP12 x RGP1 in which both parents are poor combiners indicated superiority due to non-additive type of gene action. Rest of the crosses viz., DWR16 x DWR13 and RGP18 x DWR13 had both parents as good general combiners. Similar results observed by Kakar *et al*. (1999), Sheikh and Singh (2000), Mahmood and Chowdhary (2002) and Singh *et al*. (2010).

5.2.5. Hayman's diallel analysis

To study the action of genes, genetic components and heritability Hayman Method (Hayman, 1954a) was used. Griffing and Hayman data analysis are often used together for complementary data interpretation. The analysis (either one or both) has been used for various crops such as wheat (Singh *et al*., 2003), barley (Kakani *et al*., 2007) and peas (Kalia and Sood, 2009). Diallel analysis and additive dominance models are the established mechanisms of conventional breeder to comprehend allelic and non-allelic gene action, nature and magnitude of genetic variance used by genotypes in specific combinations. Consequently, the use of genotypes with desirable genetic components is a continuous pre-requisite for synthesis of physiologically efficient and genetically superior genotypes showing promise for increased production per unit area under a given set of environments (Esmail *et al*., 1999; Khan *et al*., 2009; Khan and Hassan, 2011). All such endeavors need some genetic information and knowledge about the type of gene action involved in various agronomic and quality traits.

The diallel is based on certain assumptions. These assumptions of diallel cross analysis as given by Hayman (1954a) are:

a) Diploid segregation of chromosomes.
b) Homozygosity of parents.
c) Absence of reciprocal effects.
d) Absence of epistasis.
e) No multiple allelism.
f) Independent distribution of genes among parents.

To fulfill the assumptions such as absence of epistasis, no multiple allelism and independent assortment of genes, the data were tested through three scaling tests (regression analysis, t^2 test and array analysis of variance (Wr+Vr and Wr-Vr) to evaluate the adequacy of the additive-dominance model of the data. According to Mather and Jinks (1982) the regression coefficient is expected to be significantly different from zero and not from unity. Failure of this test means the presence of epistasis. If non-allelic interaction is present, Wr+Vr must change from array to array and similarly Wr-Vr will vary among arrays. Non-significant values of t^2 test confirm the presence of no non-allelic interaction and signify that genes are independent in their gene action for random association in genotypes. Failure of these three tests completely invalidates the additive-dominance model. Their further analysis was stopped, however, the genetic analysis was extended for those traits having sufficient variability and their Wr-Vr does not vary significantly from array at 0.01 probability levels. However, if even one test meets the assumptions, then the additive-dominance model is considered to be partially adequate. The direct and derived genetic components were computed according Hayman (1954a) and used by Hayman, (1958).

Illustration of genetic components of variance for morphological and physiological traits related to heat and drought tolerance in wheat

Data were analyzed using the Hayman approach as followed by Singh and Chaudhary (1979). From the data analysis, the genetic components of variation along with standard error and correlation coefficient were estimated for morphological and physiological traits related to heat and drought tolerance under normal and stress environment conditions (Table 4.11). Additive genotypic variance (D) was significant for all the traits under both normal and stress environment conditions except number of tillers per plant, number of grains per ear, 1000-grain weight, grain yield per plant and harvest index under stress environment condition. Dominance component (H_1) was also significant for all the traits under both normal and stress environment conditions. These results are in agreement with those obtained by Chowdhry *et al.* (1989), Abdel Nour *et al.* (2006) and Farooq *et al.* (2011a). Thus, the additive and dominance; both the variances were pre-dominance component governing the expression of grain yield, yield contributing and physiological traits related to heat and drought tolerance under both conditions.

Average degree of dominance in most of the cases confirmed over dominance for days to maturity, number of tillers per plant, number of grains per ear, 1000-grain weight, grain yield per plant, relative leaf water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability under both normal and stress environment conditions. Asif *et al.* (1999) and Chowdhry *et al.* (2002) reported over dominance for inheritance of grains per ear. Some researchers like Rahman *et al.* (2003), Heidari *et al.* (2006) and Farooq *et al.* (2010) also reported over dominance for inheritance of grain yield per plant and 1000-grain weight.

The magnitude of dominance values H_1 and H_2 was approximately equal to each other for traits like days to 50% flowering, days to maturity, number of tillers per plant, grain yield per plant, relative water content, canopy temperature and canopy temperature depression. Nazeer *et al.* 2011, Farooq *et al.* (2011a) and Zare-kohan and Heidari (2012) reported the similar results for days to 50% flowering, days to maturity, grain yield per plant and grains per ear in bread wheat. It confirms the existence of approximately equal proportion of positive and negative alleles in the parents to influence these traits.

The value of F, which is the measure of relative frequency of dominant to recessive alleles in the parents were positive for days to 50% flowering, plant height, number of grains per ear, number of tillers per plant, grain yield per plant, harvest index, relative water content, canopy temperature, canopy temperature depression, drought susceptibility index and seedling survivability under both conditions implying that excess of dominant alleles was present in the parents for these traits under both conditions. The F value proved to be negative for days to maturity under normal conditions but for 1000-grain weight under stress environment condition implying the excess of recessive alleles for these traits in the respective environments.

The measurement of net dominance (h^2) was positive and significant for days to 50% flowering, days to maturity, plant height, number of grains per ear, 1000-grain weight and drought susceptibility index, but positive and non-significant for number of tillers per plant, grain yield per plant, harvest index, relative water content, canopy temperature, canopy temperature depression, germination stress index and seedling survivability indicated that the direction of dominance was towards a greater side and substantial contribution to dominance was due to heterogeneity of loci under both conditions.

The estimates of frequencies at non-additive loci can be obtained from $H_2/4H_1$. This ratio between the genes with positive and negative effects was less than expected theoretical of 0.25 for all the traits studied under both normal stress conditions confirmed the asymmetrical distribution of positive and negative alleles in the parents. Similar, findings were reported by Farooq *et al*. (2011a) and Zare-kohan and Heidari (2012).

The low values of number or group of genes that control the character and exhibited dominance (h_2/H_2) under both conditions indicated that there was at least one gene group for each trait. The ambidirectional dominance effect and the uncorrelated distribution of genes among the parents may be one of the causes for low estimates of this ratio (Mather and Jinks, 1971).

Narrow sense heritability (H_n) measures the magnitude of genotypic variation in the breeding material, which is mainly responsible for changing the genetic composition of the population via selection (Falconer, 1989; Dabholkar, 1992). Moreover, narrow sense heritability is directly proportional to additive variance and is maximum in additively controlled characters, and lower in non-additive genetic components. So, all the traits except canopy temperature depression and relative water content under both conditions, and days to 50% flowering, number of grains per ear, grain yield per plant and harvest index under stress environment condition coupled with significant additive variance showed moderate to high heritability values for these traits and prove the importance of additive gene action in the expression of these traits and could be useful in selection of elite genotypes from segregating material.

A high correlation (r) between parental measurement and parental order of dominance indicates that most of the dominant alleles act in one direction and recessive alleles in opposite direction (Hayman, 1954a). In the present study the correlations were found to be non-significant and positive in almost all the traits indicating recessive genes had positive effect and dominant genes were mostly negative.

Table 5.1: Three parents showing significant desirable gca effects for yield, yield contributing and physiological traits under both normal and stress sown conditions.

S.No.	Parents	Traits
1	PBW175	Grain yield per plant, number of grains per ear, canopy temperature, canopy temperature depression, germination stress index and seedling survivability.
2	DWR13	Grain yield per plant, days to 50% flowering, plant height, 1000-grain weight, relative water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability.
3	RGP18	Grain yield per plant, days to 50% flowering, days to maturity, relative water content, canopy temperature, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability.

Table 5.2: Eight cross combination showing significant desirable sca effects for yield, yield contributing and physiological traits under both normal and stress environment conditions and the general combiners involved in the respective crosses.

S.No.	Crosses	Traits	Combiners
1	PBW175 x RGP12	Grain yield per plant, days to maturity, number of grains per ear, harvest index, canopy temperature, canopy temperature depression, drought susceptibility index and germination stress index.	Good x Poor
2	PBW175 x RGP1	Grain yield per plant, number of tillers per plant, 1000-grain weight, relative leaf water content, canopy temperature canopy temperature depression, germination stress index and seedling survivability.	Good x Poor
3	RGP12 x RGP1	Grain yield per plant, days to 50% flowering, days to maturity, number of tillers per plant, harvest index, canopy temperature, canopy temperature depression, DSI,GSI and seedling survivability.	Poor x Poor
4	RGP12 x RGP18	Grain yield per plant, days to maturity, plant height, canopy temperature, canopy temperature depression, drought susceptibility and germination stress index.	Poor x Good
5	RGP1 x DWR16	Grain yield per plant, plant height, number of grains per ear, germination stress index and seedling survivability.	Poor x Good
6	DWR16 x DWR13	Grain yield per plant, 1000 grain weight, relative leaf water content, canopy temperature, canopy temperature depression, germination stress index and seedling survivability.	Good x Good
7	RGP18 x DWR13	Grain yield per plant, plant height, number of tillers, canopy temperature and drought susceptibility index.	Good x Good
8	DWR13 x DWR17	Grain yield per plant, days to 50% flowering, number of tillers per plant, number of grain per ear, relative leaf water content, canopy temperature depression, drought susceptibility index and germination stress index.	Good x Poor

Table 5.3: showing reduced percent for morphological and physiological traits in heat and drought stress environment.

S.No.	Traits	Mean normal	Mean stress	Reduced %age
1	Days to 50% flowering	110.10	91.89	-16.53
2	Days to maturity	146.72	127.81	-12.88
3	Plant height	87.71	81.80	-6.73
4	Number of tillers per plant	9.70	5.19	-46.49
5	Number of grains per ear	39.59	35.11	-11.31
6	Grain yield per plant	11.01	6.41	-41.78
7	1000- grain weight	39.49	29.10	-26.31
8	Harvest index	31.41	25.79	-17.89
9	Relative leaf water content	62.31	49.19	-21.05
10	Canopy temperature	24.23	27.67	14.19
11	Canopy temperature depression	3.41	1.25	-63.34

CHAPTER-VI

SUMMARY AND CONCLUSION

The present study entitled "Characterizing diversity for heat and drought related traits in hexaploid wheat (*Triticum aestivum* L.)" was carried out with a view to evaluate wheat genotypes for different morphological and physiological traits related to heat and drought tolerance as well as to study the combining ability of parents for various morphological and physiological traits by crossing the genotypes in half diallel fashion and evaluating their progenies under normal and stress environment conditions, that can be used in future breeding programme.

The experimental material of the present study comprised twenty true breeding lines of hexaploid wheat received from ICARDA, Syria (Table 3.1), and were raised in the field at the Research Farm of Division of Plant Breeding and Genetics during *Rabi* 2014-15, in a randomized block design with three replication under normal and stress environment conditions. Each entry was planted in three rows of 1m each, with plant-to-plant and row-to-row distance of 10 and 25 cm, respectively. Of these, the best seven heat and drought tolerant lines (PBW-175, RGP1, RGP12, RGP18, DWR13, DWR16 and DWR17) were used as parents to develop the experimental material for half diallel mating design. Seeds of 21 F_1's along with their parents were sown during *Rabi* 2015-16 in a randomized block design with three replication under normal and stress environment conditions. Recommended cultural/management practices were followed for raising the wheat crop. Five competitive plants were randomly selected from each entry for recording data of different characters on various growth stages. The traits studied included morphological traits viz., days to 50% flowering, days to maturity, plant height, number of tillers per plants, number of grains per ear, 1000-grain weight, grain yield per plant, harvest index, and physiological traits viz., relative leaf water content, canopy temperature (grain filling stage), canopy temperature depression (grain filling stage), drought susceptibility index, germination stress index and seedling survivability under normal and stress environment conditions. The summarized findings of the present study are as under:-

The extent of variability, heritability and genetic advance as percent of mean in the genotypes of wheat was studied for morphological and physiological traits viz., days to 50% flowering, days to maturity, plant height, number of tillers per plants, number of grains per ear, 1000-grain weight, grain yield per plant and harvest index, and physiological traits viz., relative leaf water content, number of tillers per plants, canopy temperature (grain filling stage), canopy temperature depression (grain filling stage), drought susceptibility index, germination stress index and seedling survivability under normal and stress sown conditions.

Analysis of variance revealed that genotypes differed significantly among themselves for all the traits. The genetic variability was high for most of the morphological characters, whereas the physiological characters showed moderate level of genetic variability under both conditions; studies on variation genotypic and phenotypic revealed that overall phenotypic variance was higher in magnitude than corresponding genotypic variation for most of the characters in both environments. Germination stress index, seedling survivability, relative leaf water content and harvest index had high estimates of phenotypic variance.

Studies on phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) revealed that most of characters showed moderate to high value of PCV and GCV. Apart from showing moderate to high values of PCV and GCV, the traits like number of grains per ear, number of tillers per plant, 1000-grain weight, grain yield per plant, canopy temperature depression, drought susceptibility index, germination stress index and seedling survivability also showed high values of heritability and genetic advance under both normal and stress environment conditions. Hence these traits are considered as most effective for selection.

It can be concluded from this study that the mean performance of the test wheat cultivars was different under heat and drought stress. The heat and drought tolerance superiority of RGP18 , DWR13, DWR16, PBW175, and RGP12 cultivars under heat and drought stress conditions could be associated with their higher yielding, days to 50% flowering, days to maturity, plant height, number of tillers per plants, number of grains per ear, 1000-grain weight, yield per plant and harvest index, and physiological traits viz., relative leaf water content, number of effective tillers per plants, canopy temperature(grain filling stage), canopy temperature depression (grain filling stage), drought susceptibility index, germination stress index and seedling survivability. The other possible mechanism(s) for heat and drought tolerance of the superior cultivars could not be excluded.

The correlation coefficients among grain yield, yield contributing and physiological traits related to heat and drought tolerance revealed positive and significant correlation of yield per plant with days to maturity, number of tillers per plant, number of grains per ear, 1000-grain weight, harvest index, relative water content and canopy temperature depression indicating that each of these traits contribute equally to yield per plant under heat stress in wheat. Whereas, the yield per plant showed negative and significant correlation with canopy temperature and drought susceptibility index. Thus, it can be concluded from the present study that canopy temperature depression, days to maturity, number of grains per ear, number of tillers per plant, 1000-grain weight, harvest index and relative water content can be used as indirect selection tools for breeding of high yield varieties of wheat under heat and drought stress.

Analysis of variance in half diallel revealed that both GCA and SCA variances were important for all traits under both normal and stress sown conditions. The variance for GCA were greater than the mean squares for SCA for all the traits which indicated that additive type of gene effects were more pronounced than those of non-additive ones.

Among the seven parents (PBW175, RGP12, RGP1, RGP18, DWR13, DWR16 and DWR17) in half diallel cross, three parents viz., RGP18, DWR13 and PBW175 showed significant GCA effects for yield, yield contributing and physiological traits under both normal and stress environment conditions.

Crosses viz., PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP18, RGP1 x DWR16, and DWR13 x DWR17 (one parent as good general combiner); RGP12 x RGP1 in which both parents are poor combiners (both parents are poor combiners) and DWR16 x DWR13 and RGP18 x DWR13 (both parents as good general combiners), were found to be desirable crosses for grain yield per plant, yield contributing and physiological traits related to heat and drought tolerance under both normal and stress environment conditions and can be used in the future breeding programme. These cross combinations showing desirable SCA effects for grain yield per plant, yield contributing and physiological traits associated to heat and drought tolerance and produce transgressive segregants in succeeding generations, which can be selected and improved for increasing yield under heat and drought stress environments.

The genetic component analysis revealed that both additive (D) and dominant components (H_1 and H_2) were equally important in genetic manifestation of all the traits under both conditions, however, the magnitude of dominance components (H_1 and H_2) was greater than additive component for all the traits under study except number of tillers per plant, reflecting preponderance of non-additive gene action in these traits in half diallel conditions under both conditions. The difference in both values of H_1 and H_2 for most of the traits suggested asymmetric distribution of dominance and recessive alleles among parents.

Positive and significant/non-significant value of 'F' suggested that most of the traits were governed by dominant gene action and these alleles were also in increasing order as reflected by higher values of 'h^2' under both normal and stress environment conditions.

Average degree of dominance $(H_1/D)^{1/2}$, being greater than unity for most of the traits reflecting involvement of over-dominance type of gene action for these traits under both conditions.

Low to moderate narrow sense heritability (H_n) estimates are observed in almost all traits under both normal and stress environment conditions.

FUTURE LINE OF WORK

The heat and drought tolerant wheat genotypes viz., PBW175, RGP18, RGP12, DWR13, and DWR16 and heat susceptible genotypes viz., RGP1 and DWR17 identified in the present study can be used in the development of mapping populations for identification of QTLs/genes for terminal heat and drought stress associated traits. Also, positive and significant correlation of yield per plant with days to maturity, 1000-grain weight, harvest index, relative water content, and canopy temperature depression suggested that these traits can be effectively used as indirect selection tools for breeding of high yield varieties of wheat under heat and drought stress.

In half diallel, best cross combinations viz., PBW175 x RGP12, PBW175 x RGP1, RGP12 x RGP18, RGP1 x DWR16, DWR16 x DWR13, RGP18 x DWR13 and DWR13 x DWR17 having one of the parent or both parents as good general combiners for grain yield per plant, yield contributing and physiological traits associated to heat and drought tolerance can be further utilized in breeding programmes due to fixable type of gene action as these cross combinations showed high SCA under both conditions.

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Appendix I: Mean performance of 20 hexaploid wheat genotypes for different morphological and physiological traits under normal (N) and stress (S) environments during *Rabi* 2014-2015.

Genotypes	**Days to 50% flowering (days)**		**Days to maturity (days)**		**Plant height (cm)**		**No. of tillers per plant**		**No. of grains/ ear**		**Grain yield per plant (g)**		**1000-grain weight (g)**	
Environment	N	S	N	S	N	S	N	S	N	S	N	S	N	S
PBW 175	108	88	147	124	97	89	12.6	3.1	49	38	13.6	8.2	47.2	37.5
RGP 1	106	90	148	133	74	78	8.0	4.8	31	26	8.7	6.1	33.1	21.5
RGP 2	113	96	146	132	90	82	8.2	5.8	35	38	12.0	8.0	40.2	21.5
RGP 3	112	93	146	124	87	85	9.9	5.2	35	33	10.3	6.7	36.4	24.4
RGP 7	109	94	147	127	87	80	9.0	4.2	35	32	10.0	5.8	37.8	23.8
RGP 11	109	92	148	130	88	74	8.3	5.3	49	41	11.5	7.8	37.8	28.7
RGP 12	105	91	144	128	74	66	10.4	8.7	39	42	8.8	4.2	44.6	27.2
RGP 15	109	93	147	129	96	82	10.6	4.2	30	32	11.2	6.1	41.1	29.7
RGP 16	111	93	147	132	92	85	8.3	5.2	37	31	10.7	5.7	38.4	30.8
RGP 18	105	80	144	116	93	85	11.8	3.7	40	29	13.8	10.4	45.6	30.3
DWR 1	112	89	147	134	89	83	8.8	3.9	39	35	10.4	4.9	38.9	31.9
DWR 13	111	78	145	112	97	92	10.8	4.2	33	35	13.3	9.7	46.4	32.1
DWR 16	112	99	150	132	76	83	13.6	9.3	43	42	14.7	9.8	33.1	35.1
DWR 17	114	98	150	135	89	92	9.5	7.5	52	37	8.9	4.2	41.3	28.0
DWR 18	112	92	145	132	89	80	8.1	6.4	31	39	9.0	4.2	37.7	29.6
PBW 644	113	96	148	132	88	79	9.5	3.3	55	33	13.3	5.0	36.6	29.2
PBW 550	109	92	146	129	94	76	10.9	4.8	36	32	9.2	5.2	35.4	28.5
DBW 14	108	95	147	128	86	82	8.6	4.7	37	33	10.4	5.0	46.7	32.2
HD 3043	113	97	145	130	88	80	9.8	5.0	33	36	10.8	6.7	35.4	30.2
RAJ 3765	112	92	147	128	82	83	8.0	4.6	53	39	9.4	4.6	37.8	29.3
Mean	**110.10**	**91.89**	**146.72**	**127.81**	**87.71**	**81.80**	**9.70**	**5.19**	**39.59**	**35.11**	**11.01**	**6.41**	**39.49**	**29.10**
C.D. 5%	0.23	0.73	0.85	0.43	2.32	5.16	0.40	1.41	2.80	6.60	3.27	1.35	2.13	3.98
C.V.	0.45	0.50	0.27	0.03	3.45	467	0.60	1.91	1.68	8.64	15.19	13.51	11.83	7.10

Contd……

Genotypes	**Harvest index (%)**		**Relative leaf water content (%)**		**Canopy temperature ^{0}C (grain filing)**		**Canopy temperature depression ^{0}C (grain filing)**		**Drought susceptibility index**		**Germination stress index (%)**		**Seedling survivability (%)**	
Environment	N	S	N	S	N	S	N	S	N	S	N	S	N	S
PBW 175	26	16	72	51	23.4	26.2	4.1	3.5	-	-0.69	-	41	-	75
RGP 1	24	16	55	52	24.8	26.3	1.8	-0.3	-	1.99	-	36	-	46
RGP 2	29	26	60	50	24.3	27.4	2.8	1.7	-	0.50	-	37	-	64
RGP 3	33	29	58	49	24.6	28.2	3.0	2.1	-	0.38	-	55	-	68
RGP 7	32	29	58	47	24.2	27.4	3.6	1.1	-	0.15	-	67	-	59
RGP 11	34	28	62	49	24.4	27.3	4.0	-0.2	-	-0.02	-	50	-	72
RGP 12	27	25	73	51	25.0	28.8	4.5	3.6	-	-0.08	-	69	-	74
RGP 15	27	27	56	49	23.7	28.6	2.7	1.1	-	0.22	-	53	-	67
RGP 16	28	20	56	49	24.6	27.8	3.1	0.7	-	0.33	-	38	-	69
RGP 18	31	33	73	64	22.8	25.7	5.1	3.6	-	-0.95	-	70	-	76
DWR 1	34	26	66	48	24.7	28.5	2.6	1.7	-	-0.15	-	55	-	49
DWR 13	37	33	73	43	23.3	26.0	6.5	0.3	-	-1.89	-	72	-	78
DWR 16	29	29	70	53	23.2	28.8	2.7	3.1	-	-0.95	-	71	-	74
DWR 17	35	28	55	43	26.0	29.1	1.8	-0.5	-	2.85	-	36	-	47
DWR 18	31	22	53	49	24.3	28.8	3.6	1.7	-	0.35	-	54	-	73
PBW 644	31	28	62	48	23.7	28.5	2.3	0.8	-	0.23	-	42	-	71
PBW 550	39	25	62	48	25.3	28.6	4.0	0.4	-	0.18	-	55	-	68
DBW 14	33	26	67	47	24.3	28.4	3.6	1.2	-	0.25	-	65	-	68
HD 3043	36	19	55	47	24.6	28.2	3.0	0.8	-	0.12	-	47	-	61
RAJ 3765	34	31	60	48	24.6	27.2	3.6	0.9	-	0.95	-	62	-	71
Mean	**31.41**	**25.79**	**62.31**	**49.19**	**24.23**	**27.67**	**3.41**	**1.25**	**-**	**0.19**	**-**	**53.80**	**-**	**65.92**
C.D. 1%	1.60	2.62	5.21	4.92	0.03	1.54	0.70	0.16	-	1.08	-	16.79	-	13.99
C.V.	6.32	8.99	4.76	3.51	2.57	3.18	2.73	3.34	-	36.26	-	16.99	-	12.00

CERTIFICATE-IV

Certified that all the necessary corrections as suggested by the external examiner and the Advisory Committee have been duly incorporated in the thesis entitled **"Characterizing diversity for heat and drought related traits in hexaploid Wheat (*Triticum aestivum* L.)"** submitted by **Mr. Sunil Singh Kotwal,** Registration No. **J-14-M-369.**

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