GENETIC ANALYSIS OF SPOT BLOTCH RESISTANCE, YIELD AND YIELD ATTRIBUTING TRAITS THROUGH INTERSPECIFIC (*Triticum dicoccum* (Schrank) Schulb × *Triticum durum* Desf.) HYBRIDIZATION IN TETRAPLOID WHEAT

Thesis submitted to the
University of Agricultural Sciences, Dharwad
in partial fulfillment of the requirements for the
Degree of

DOCTOR OF PHILOSOPHY

In

GENETICS AND PLANT BREEDING

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MARCH, 2010

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1. INTRODUCTION

Wheat (*Triticum* spp.) is a stuff of life and has been considered as the "versatile cereal food". It is also described as "king of cereals" for centuries and continues to retain this pride of place with its roots ramifying into the depths of human culture, wheat has an evolutionary history parallel with the history of human civilization itself. Actually the wheat plant is considered to have originated in the Mediterranean region. History reveals that, wheat cultivation converted men from hunters and gathers into farmers.

Wheat occupies second position next to rice among the all cultivated crops due to its feeding boon to mankind. It is grown across a wide range of environments around the world and has the broadest adaptation of all the crop species, more land is devoted world wide to the production of wheat than to any other crops. It is the number one food grain consumed directly by human beings and is estimated that more than 35 per cent of the world population depends on wheat (Borlaug, 1968 and Johnson *et al.,* 1978) as it supplies more nutrients particularly, essential amino acids than any other single crop (Ranum *et al.,* 1960). It contributes more calories and more protein to the world's diet than any other food crops. It also has relatively high content of niacin, thiamine and glutenin.

Wheat is a temperate crop, but still sustains well under wider agro climatic conditions. Major wheat production is concentrated between 30^0 and 60^0 N and 27^0 and 40^0 S latitudes (Nuttenson, 1955). It is still being grown beyond these limits successfully due to its wider adoptability of diverse species, which has lead to the harvesting of this crop in one or the other parts of the world through out the year.

In India three wheat species *viz.,* bread wheat (*Triticum aestivum* L.), macaroni wheat (*Triticum durum* def.) and dicoccum wheat [*Triticum dicoccum* (Schrank) (Schulb)] are being cultivated. Bread wheat occupies 80 per cent of the wheat area and is concentrated in North India. While cultivation of durum wheat is concentrated in Central and Peninsula India with 19 per cent of share. Remaining one per cent of wheat area is occupied by dicoccum wheat.

Wheat cultivation in Karnataka is unique wherein all three cultivated species *viz., Triticum aestivum*, *T. durum* and *T. dicoccum* are grown in typical hot tropical climate, characterized by prevalence of high temperatures during the crop growth. Wheat is one of the important rabi crops grown mainly in northern Karnataka both under rainfed and irrigated conditions (Mahantashivayogayya, 2002).

The statistics regarding spread of different wheat species in Karnataka indicate that semi dwarf bread wheat and durums dominate in irrigated area while dicoccum wheats dominate over bread wheat under rainfed and limited input conditions. The absence of bread wheat in such farming situations suggests that durum and emmer wheats are more adapted to higher temperatures and moisture stress conditions. Another specificity of both durum and dicoccum (emmer) wheats is their quality characters (Yenagi *et al.,* 1999).

Dicoccum wheat, a hulled wheat, commonly called by the name as "Jave, Sadaka, Samba, Khapli etc.,". In the world, cultivation of these wheats is only confined to few mountainous marginal areas of Italy. In India it is traditionally cultivated in Northern Karnataka, Southern Maharashtra, Sourashtra region of coastal Gujarat, Nilgiris and Palanihilly areas of Tamil Nadu and Telangan region in Andhra Pradesh (Mahantashivayogayya, 2002).

Dicoccum wheat differ from commercially available bread and durum wheats in cultivation practices. Due to its nutritional and therapeutic quality traits dicoccum wheats are preferred by many people. This wheat has a great demand in urban areas of central and southern India and also in Srilanka and Maldevas, but due to non availability of this wheat consumption is often confined to people of growing areas. Non-availability of free threshing varieties, lack of scientific techniques regarding dehulling of dicoccum wheat, value addition, reddish grain colour of the wheat are some of the constraints. In India, dicoccum wheat is mainly processed for preparation of semolina and used in preparation of several conventional dishes like godhi huggi, uppuma, sajjaka, madali, chapati, holige and also in preparation of pasta products like vermicelli (Reddy, 1996).

Scientific studies related to dicoccum wheat also reveals that they are nutritionally superior as compared to commercially available wheat with the high protein and dietary fibre contents (Bhuvaneshwari *et al.,* 1998). Dicoccum based products are more tasty and soft (Reddy, 1996) have high satiety value and a potential of backing, parboiling and popping quality. Products have low digestibility, low glycaemic value and it has been considered as a therapeutic food in the management of diabetes (Yenagi *et al.,* 1999), which is India's leading health problem.

With introduction of semi-dwarf dicoccum wheats, advent of irrigation facilities through major projects and consumers awareness towards quality importance of dicoccum wheat, the area under dicoccum wheat has been increasing. However, yield levels are not upto the expected levels possibly due to the susceptibility to important diseases like spot blotch leads to heavy loss in grain and fodder yield which again hinders its cultivation on large acreage. Losses due to this disease amounted to 19.6 per cent (Saari, 1998 and Sharma *et al.,* 2004). Spot blotch of wheat is caused by *Bipolaris sorokiniana* (Sacc) Shoem. [Syn. *Helminthosporium sativum* telomorph (*Cochliobolous sativus*)]. The disease becomes severe during grain filling stage and causes significant grain yield losses and grain quality deterioration. The effective and economic strategy to combat the spot blotch problem is to develop resistant cultivars. However, the availability of information on genetics of spot blotch resistance is scanty as revealed by available literature. Further, understanding the gene action of the spot blotch disease is of prime importance. Development of superior gene pool needs the genotypes with desired traits both qualitative and quantitative. But owing to their economic importance quantitative characters receive more attention. Greater yield and other economic traits are polygenic and quantitative in nature. To harness fixable genetic variation (*viz.,* additive, additive x additive) in the breeding material, it is worth while to decipher the total variation into its components. Several biometrical techniques are available to estimate the components of genetic variation. Of these, line x tester analysis provides nature of gene action as additive and dominance, combining ability effects and heterosis of the material used while generation mean analysis provides information on exact nature and magnitude of gene effects like additive, dominance and epistatic components.

Realizing the importance and need for such a comparative, study in tetroploid dicoccum wheat (dicoccum), the present investigation was under taken with the following objectives.

1. Screening and transfer of spot blotch resistance from *T. durum* to *T. dicoccum.*
2. Study of genetics of spot blotch resistance.
3. Study of inheritance of free threshability and grain pericarp colour.
4. Biochemical basis for spot blotch disease resistance and parental RAPD polymorphism for spot blotch resistance.

2. REVIEW OF LITERATURE

Dicoccum wheat being nutritionally superior compared to other wheats, has spot blotch as one of the major disease improvement for cultivation in irrigation project area due to high humidity. Resistance breeding is the economic and ecofriendly method to over come spot blotch disease. Previous studies conducted by different researchers on these various aspects are reviewed in this chapter under following headings.

2.1 Heterosis

2.2 Combining ability effects and variances

2.3 Genetics of spot blotch disease resistance in wheat

2.4 Genetics of Threshability and pericarp colour

2.5 Biochemical status of resistant and susceptible

2.6 Molecular diversity

2.1 Heterosis

Heterosis is the increased vigour or decreased vigour of F_1 over its mid parent. Heterobeltiosis is the other term used to indicate same phenomenon over better parent. The exploitation of heterosis in cultivated crop species is an important application of the science of genetics in agriculture and also a milestone in the history of plant breeding. Though it has played an important role in allogamous crops, commercial exploitation of heterosis in autogamous crop like wheat is limited by the difficulty in crossing, least pollen viability, high pollen weight, low seed set and high seed rate. The study of heterosis does not aim always at commercial exploitation of hybrid vigour but heterotic crosses are also likely to produce free breeding transgressive segregants. And also the extent of heterosis have a direct bearing in the breeding methodology adopted for varietal improvement. The review pertaining to the heterosis is presented in Table 1.

2.2 Combining ability effects and variances

Hybridization is the most potent technique for breaking yield barriers and evolving varieties having high yield potential. The selection of suitable parents is one of the most important steps in hybridization programme. Selection of the parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may not lead to expected degree of heterosis. Therefore, selection of potential parents, based on genetic information and knowledge of their combining ability is very important. The combining ability concept was first proposed by Sprague and Tatum (1942) in corn. According to them the general combining ability (gca) is the comparative ability of the line to combine with other crosses involving a parent from overall mean. Specific combining ability (sca) was defined as the deviation in the performance of general combining ability effects of parents involved in the crosses. A positive general combining ability (gca) indicates a parent that produces above average progeny, whereas parent with negative gca produces progeny that performs below average of the population. Specific combining ability can be either positive or negative and sca always refers to specific cross and never to particular parent by itself.

The most commonly used deigns for combining ability studies are line x tester (L x T) and diallel analysis. Combining ability analysis frequently used for testing the performance of parents in hybrid combinations. It is also useful in characterizing the nature and magnitude of gene action involved in controlling the quantitative traits.

The general and specific combining ability effects and variances obtained from a set of F_1s would enable a breeder to select desirable parents and crosses for each of the quantitative components separately. Sprague and Tatum (1942) from their results concluded that, the general combining ability was largely the results of additive gene action, while the specific combining ability was the result of the dominance, epistasis and genotypic environment interactions.

Review of literature on combining ability and gene action in wheat for different characters is presented in Table 2.

Table 1: Summary of review on heterosis of quantitative traits in wheat

Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
1	Days to flowering	8 x 8 diallel	-	-	11.8%	Budak (2001)
		-	-	-	Average negative	Esmail (2002)
		8 x 8 diallel	-	Negative significant	-	Singh and Singh (2003)
		8 commercial varieties and F_1s	-	-	Negative	Inamullah *et al.* (2006)
2	Days to maturity	8 x 8 diallel	-	Significant	-	Singh and Singh (2003)
		7 genotypes diallel	-	-	Significant	Sayed (2004)
		8 commercial varieties and F_1s	Negative	-	-	Inamullah *et al.* (2006)
3	Plant height	6 genotypes, diallel	-	-	Significant	Afiah and Sattar (1998)
		4 varieties, complete diallel	Negative	Negative	-	Kakar *et al.* (1999)
		8 genotypes, half diallel	-	-	Significant	Afiah *et al.* (2000)
		8 x 8 diallel	-	-	High	Budak (2001)
		F_1 and F_2 generations	-	-	Average	Esmail (2002)
		12 x 12 diallel	Positive	Positive	-	Mahantashivayogayya (2002)

Contd….

Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
		8 cultivars, diallel	Positive significant	Positive significant	-	Ashraf *et al.* (2004)
					Significant	Sayed and Moshref (2005)
		8 commercial varieties and F_1s	-	-	Negative	Inamullah *et al.* (2006)
		6 cultivars, 50 single crosses	-	Significant	-	Mahmood *et al.* (2006)
		15 F_1 single crosses	-	Negative significant	Negative significant	Fida Hussain *et al.* (2007)
4	Peduncle length	12 x 12 diallel	-	-	Significant positive	Mahantashivayogayya (2002)
		8 x 8 diallel	-	Significant	-	Singh and Singh (2003)
5	Spike length	4 varieties, complete diallel	-	-	Positive high	Kakar *et al.* (1999)
		8 genotypes, half diallel	-	-	Significant	Afiah *et al.* (2000)
		F_1 and F_2 generations	-	-	Average	Esmail (2002)
		35 x 4 line x tester	-	Positive	-	Hamada *et al.* (2002)
		12 x 12 diallel	Significant positive	Significant positive	-	Mahantashivayogayya (2002)
		8 x 8 diallel	-	Significant	-	Singh and Singh (2003)

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Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
		8 commercial varierties and F_1s	Maximum positive	Positive	-	Inamullah *et al.* (2006)
		60 cultivars, 50 single crosses	-	-	Significant	Mahmood *et al.* (2006)
		12 x 3, line x tester	-	-	Considerable	Ribadia *et al.* (2007)
		7 x 7 complete diallel	-	-	Positive	Bao *et al.* (2009)
6	Number of spikelets per spike	4 varieties, complete diallel	-	-	Low positive	Kakar *et al.* (1999)
		8 genotypes, half diallel	-	-	Non-significant	Afiah *et al.* (2000)
		F_1 and F_2 generations	-	-	Average	Esmail (2002)
		12 x 12 diallel	Significant positive	Significant positive	-	Mahantashivayogayya (2002)
		8 cultivars diallel	-	-	2.3%	Asharf *et al.* (2004)
		12 winter wheat cultivars, diallel	-	-	Positive	Nawracaa *et al.* (2004)
		11 winter wheat cultivars diallel	-	-	Low	Nawracaa *et al.* (2006)
		12 x 3, line x tester	-	-	Considerable	Rabadia *et al.* (2007)
		7 x 7 complete diallel	-	-	Positive	Bao *et al.* (2009)

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Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
7.	Grains per spike	4 varieties of wheat complete diallel	Positive	Positive	-	Kakar *et al.* (1999)
		8 bread wheat cultivars diallel	Positive significant	Positive significant	-	Ashraf *et al.* (2004)
		8 commercial variety, 28 F_1s	Positive	Positive	-	Inamullah *et al.* (2006)
		4x4 diallel cross	Positive significant	Positive significant	-	Akbar *et al.* (2007)
		8 wheat parents, 15 F1 single crosses	-	-	1.61-13.12%	Fida Hussain *et al.* (2007)
8	Number of tillers per plant	12 pure lines x 5 testers	-	Positive significant	-	Rajora (2000)
		8 cultivars diallel	Positive significant	Positive significant	61.90%	Ashraf *et al.* (2004)
		8 commercial varieties and F_1s	Positive	Positive	-	Inamullah *et al.* (2006)
		11 winter wheat diallel	-	-	Low	Nawracaa *et al.* (2006)
		15 F_1 single crosses	-	Positive significant	Positive significant	Fida Hussain *et al.* (2007)
		12 x 3 line x tester	-	-	Considerable	Ribadia *et al.* (2007)

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Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
9	Number of productive tillers per plant	Line x Tester bread wheat	-	Positive	-	Deshpande and Nayeem (1999)
		4 varieties complete diallel	-	-	Positive	Kakar *et al.* (1999)
		Wheat	-	Positive	-	Yadav and Narsinghani (2000)
		8 commercial varieties and F_1s	-	Positive	-	Inamullah *et al.* (2006)
		12 x 12 diallel	-	Positive significant	-	Mahantashivayogayya (2002)
10	Thousand grain weight	4 varieties, complete diallel	-	-	High positive	Kakar *et al.* (1999)
		Durum wheat half diallel	-	Positive significant	-	Saad (1999)
		8 genotypes, half diallel	-	-	Significant	Afiah *et al.* (2000)
		12 pure lines x 5 testers	-	Positive significant	-	Rajora (2000)
		-	-	-	Average	Esmail (2002)
		12 x 12 diallel	Significant positive	Significant positive	-	Mahantashivayogayya (2002)

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Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
		-	-	High	-	Hamada *et al.* (2002)
		-	-	-	Low positive	Nawracaa *et al.* (2003)
		8 x 8 diallel	-	Significant	-	Singh and Singh (2003)
		12 winter wheat, diallel	-	-	Low	Nawracaa *et al.* (2004)
		7 genotypes diallel	-	-	Positive significant	Sayed (2004)
		8 commercial varieties and F_1s	Positive	Positive	-	Inamullah *et al.* (2006)
		11 winter wheat cultivars diallel	-	-	Positive significant	Nawracca *et al.* (2006)
		4 x 4 diallel	-	-	Highly significant	Akbar *et al.* (2007)
		15 F_1 single crosses		Positive significant	-	Fida Hussain *et al.* (2007)
		7 x 7 complete diallel	-	Positive	-	Bao *et al.* (2009)
11	Yield per plant	5 genotypes, half diallel	-	-	Positive significant	Afiah (1997)
		6 genotypes, half diallel	High	-	-	El-Seidy and Hamada (1997)
		6 genotypes, diallel	-	-	Positive significant	Afiah and Sattar (1998)

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Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
		4 varieties complete diallel	-	-	Highest positive	Kakar *et al.* (1999)
		8 genotypes, half diallel	-	-	Significant	Afiah *et al.* (2000)
		12 pure lines x 5 testers	-	-	Positive significant	Rajora (2000)
		8 x 8 diallel	-	-	87%	Budak (2001)
		F_1 and F_2 generations	-	-	Average	Esmail (2002)
		35 x 4 line x testers	-	-	High significant	Hamada *et al.* (2002)
		8 x 8 diallel	-	Significant	74.4%	Singh and Singh (2003)
		8 cultivars diallel	-	-	High positive significant 126.64%	Ashraf *et al.* (2004)
		12 winter wheat cultivars diallel	-	-	Highest positive	Nawracaa *et al.* (2004)
		7 genotypes diallel	-	-	significant	Sayed (2004)
		6 genotypes half diallel	-	-	Positive significant	Hosary *et al.* (2005)
		5 genotypes, half diallel	-	Positive	-	Nour (2005b)
		-	-	-	Significant	Sayed and Moshref (2005)

Contd….

Sl. No.	Character	Material and methods	Heterosis		Heterosis	References
			Mid parent	Better parent		
		8 commercial varieties and F_1s	Positive	Positive	-	Inamullah *et al.* (2006)
		6 cultivars, 50 single crosses	Positive	Positive	29.77%	Mahmood *et al.* (2006)
		11 winter wheat cultivars diallel	-	-	Positive	Nawracaa *et al.* (2006)
		4 x 4 diallel	-	High significant	High	Akbar *et al.* (2007)
		15 F1 single crosses	-	Positive significant	Positive significant	Fida Hussain *et al.* (2007)
		12 x 3, line x tester	-	-	High	Ribadia *et al.* (2007)
		7 x 7 complete diallel	35.32%	29.92%	-	Bao *et al.* (2009)

Table 2: Summary of review of gene action and combining ability for quantitative HLB disease and quantitative traits in wheat

Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
1.	Days to flowering	5 genotypes	Half diallel	Additive x additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		10 lines, 2 testers	Line x tester	Additive	Significant	-	Pandey *et al.* (1999)
		12 lines, 5 testers	Line x tester	-	Highly significant	-	Rajora (2000)
		F1 and F2 generations	Diallel cross	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		35 lines, 4 testers	Line x tester	Non-additive	Significant	-	Hamada *et al.* (2002)
		10 lines, 5 testers	Line x tester	Additive	Significant	-	Lakshmikant and Gupta (2002)
		7 lines, 3 testers	Line x tester	Additive	Significant	-	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		10x 10 genotypes	Diallel	-	Highly significant	Significant	Mavi *et al.* (2003)
		8 lines, 3 testers	Line x tester	-	-	-	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	Highly significant	-	Singh and Singh (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004a)
		12 genotypes	Diallel	-	Significant	Significant	Mahantashivayogayya *et al.* (2004)

Contd…

Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		5 x 5 genotypes	Diallel	Additive	Significant	-	Siddique *et al.* (2004)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		5 genotypes	Crossed in all combinations	Additive	Significant	-	Malik *et al.* (2005)
		5 genotypes	Half diallel	-	Highly significant	Significant	Nour (2005b)
		10 genotypes	Diallel	Additive + non-additive	Significant	Highly significant	Srivastava (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)
		8 genotypes	Diallel	Additive	Significant	Significant	Hassan *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		6 genotypes	Half diallel	-	Significant	Significant	Ismail *et al.* (2006)
		11 lines, 4 testers	Line x tester	Additive	-	-	Vanpariya *et al.* (2006)
2.	Days to maturity	10 lines, 2 testers	Line x tester	Dominance	Significant	-	Pandey *et al.* (1999)
		10 x 10 genotypes	Diallel	-	Significant	Significant	Mavi *et al.* (2003)
		8 lines, 3 testers	Line x tester	-	Highly significant	-	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		10 genotypes	Crossed in all combinations except reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004a)
		5 x 5 genotypes	Diallel	Additive	Significant	Highly significant	Siddique *et al.* (2004)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		5 genotypes	Crossed in all combinations	Additive	-	-	Malik *et al.* (2005)
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		10 lines, 4 testers	Line x tester	Non-additive	-	-	Vanpariya *et al.* (2006)
3.	Plant height	5 genotypes	Half diallel	Additive x additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		10 lines, 2 testers	Line x tester	Additive	Significant	-	Pandey *et al.* (1999)
		12 lines, 5 testers	Line x tester	-	Highly significant	-	Rajora (2000)
		7 x 7 genotypes	Half diallel	Over dominance and partially dominant	Significant	Significant	Ivanovska *et al.* (2000)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		F1 and F2 generations	Diallel cross	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		10 lines, 5 testers	Line x tester	Additive	Significant	-	Lakshmikant and Gupta (2002)
		7 lines, 3 testers	Line x tester	Additive	Significant	-	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Additive + non-additive	Significant	Significant	Dhayal and Sastry (2003)
		4 genotypes	Crossed in all combinations except reciprocals	Additive	Significant	Significant	Meena and Sastry (2003)
		8 lines, 3 testers	Line x tester	-	Highly significant	-	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		33 hybrids	-	Additive	-	-	Soyalu and Sade (2003)
		5 x 10 genotypes	Complete diallel	Additive + non-additive	Highly significant	Highly significant	Wei *et al.* (2003)
		5 x 7 genotypes	p x q	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004a)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		10 genotypes	Crossed in all combinations except reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004)
		12 genotypes	Diallel	-	Significant	Significant	Mahantashivayogayya *et al.* (2004)
		5 x 5 genotypes	Diallel	Non-additive	-	Highly significant	Choudhary *et al.* (2005)
		5 genotypes	Crossed in all combinations	Additive	-	-	Malik *et al.* (2005)
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		8 genotypes	Half dialle	Additive	Significant	-	Dere and Yaldrm (2006)
		8 genotypes	Diallel	Additive	Significant	Significant	Hassan *et al.* (2006)
		9 genotypes	Diallel	Over dominance	Significant	-	Heidari *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		6 genotypes	Half diallel	Dominance	Significant	Significant	Ismail *et al.* (2006)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanpariya *et al.* (2006)
		4 genotypes	Complete diallel	Additive	-	-	Khan *et al.* (2007)
		12 lines, 3 testers	Line x tester	Non-additive	-	-	Ribadio *et al.* (2007)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
4.	Peduncle length	4 genotypes	Crossed in all combinations except reciprocals	Additive	Significant	Significant	Meena and Sastry (2003)
		5 x 5 genotypes	Diallel	Non-additive	-	Highly significant	Chowdhry *et al.* (2005)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanpariya *et al.* (2006)
5.	Spike length	5 genotypes	Half diallel	Additive x additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		10 lines, 2 testers	Line x tester	Additive	Significant	-	Pandey *et al.* (1999)
		F1 and F2 generations	Diallel cross	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		35 lines, 4 testers	Line x tester	Additive	Significant	-	Hamada *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		4 genotypes	Crossed in all combinations except reciprocals	Additive	Significant	Significant	Meena and Sastry (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		5 x 10 genotypes	Complete diallel	Additive + non-additive	Highly significant	Highly significant	Wei *et al.* (2003)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		5 x 7 genotypes	p x q	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004a)
		8 genotypes	Griffings complete diallele model II cross	Additive + Non-additive	Significant	Significant	Jin Bao *et al.* (2004b)
		12 genotypes	Diallel	-	Highly significant	Highly significant	Mahantashivayogayya *et al.* (2004)
		5 x 5 genotypes	Diallel	Additive	Significant	-	Chowdhry *et al.* (2005)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		10 genotypes	Diallel	Additive	Significant	Significant	Khedar *et al.* (2005)
		5 genotypes	Crossed in all combinations	Additive	-	-	Malik *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		8 genotypes	Half dialle	Additive	Significant	Significant	Dere and Yaldrm (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhayal and Dobariya (2006)
		8 genotypes	Diallel	Additive	Significant	Significant	Hassan *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		8 genotypes	Crossed in all combinations	Non-additive	Significant	Significant	Iqbal and Khan (2006a)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		6 genotypes	Half diallel	Dominance	Significant	Significant	Ismail *et al.* (2006)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanpariya *et al.* (2006)
		12 lines, 3 testers	Line x tester	Non-additive	-	-	Ribadio *et al.* (2007)
		8 genotypes	Half diallel	Additive	Significant	-	Tahmasebi *et al.* (2007)
6.	Number of tillers per plant	12 lines, 5 testers	Line x tester	-	Highly significant	-	Rajora *et al.* (1999)
		7 lines, 3 testers	Line x tester	Non-additive	-	Significant	Sing *et al.* (2002)
		10 genotypes	Crossed in all combinations	Additive + non-additive	Significant	Significant	Dhayal and Sastry (2003)
		10 x 10 genotypes	Diallel	-	Significant	Significant	Mavi *et al.* (2003)
		4 genotypes	Crossed in all combinations	Additive	Significant	Significant	Meena and Sastry (2003)
		8 lines, 3 testers	Line x tester	-	Highly significant	-	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		10 genotypes	Diallel	Additive	Significant	Significant	Joshi *et al.* (2004b)
		5 x 5 genotypes	Diallel	Additive	Significant	-	Siddique *et al.* (2004)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		10 genotypes	Diallel	Additive	Significant	Significant	Khedar *et al.* (2005)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		5 genotypes	Crossed in all combinations	Additive	-	-	Malik *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)
		8 genotypes	Half dialle	Non-additive	-	-	Dere and Yldrm (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhayal and Dobariya (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanpariya *et al.* (2006)
		4 genotypes	Complete diallel	Non-additive	-	-	Khan *et al.* (2007)
		12 lines, 3 testers	Line x tester	Non-additive	-	-	Ribadio *et al.* (2007)
		8 genotypes	Half diallel	Additive	Significant	-	Tahmasebi *et al.* (2007)
7.	Number of productive tillers per plant	5 genotypes	Half diallel	Additive + non-additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		12 genotypes	Diallel	-	Highly significant	Highly significant	Mahantashivayogayya *et al.* (2004)
		5 x 5 genotypes	Diallel	Additive	ghly significant	Highly significant	Chowdhry *et al.* (2005)
		10 genotypes	Diallel	Additive + non-additive	Highly significant	Highly significant	Srivastava (2005)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
8.	Number of spikelets per spike	5 genotypes	Half diallel	Additive + non-additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		10 lines, 2 testers	Line x tester	Additive	Significant	-	Pandey *et al.* (1999)
		12 lines, 5 testers	Line x tester	-	Significant	-	Rajora (2000)
		F1 and F2 generations	Diallel cross	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		35 lines, 4 testers	Line x tester	Additive	Significant	-	Hamada *et al.* (2002)
		7 lines, 3 testers	Line x tester	Non-additive	-	Significant	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	-	-	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Additive and non-additive	Significant	Significant	Dhayal and Sastry (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Additive and non-additive	Significant	Significant	Sharma *et al.* (2003)
		8 lines, 3 testers	Line x tester	-	Highly significant	-	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		5 x 10 genotypes	Complete diallel	Additive	Highly significant	Highly significant	Wei *et al.* (2003)
		5 x 7 genotypes	p x q	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004a)
		8 genotypes	Griffings complete diallel cross model II	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004b)
		10 genotypes	Crossed in all combinatiosn excluding reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004a)
		10 genotypes	Diellel	Additive	Significant	Significant	Joshi *et al.* (2004b)
		12 genotypes	Diallel	-	Highly significant	Highly significant	Mahantashivayogayya *et al.* (2004)
		6 x 6 genotypes	Diallel	Non-additive	Significant	Significant	Pareek and Garg (2004)
		5 x 5 genotypes	Diallel	Additive + non-additive	Significant	Highly significant	Siddique *et al.* (2004)
		5 genotypes	Crossed in all combinations	Additive	Significant	Significant	Awan *et al.* (2005)
		5 genotypes	Crossed in all combinations	Additive	Significant	-	Malik *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		-	-	Additive + non-additive	Highly significant	Highly significant	Saeed *et al.* (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)
		9 genotypes	Diallel	Partial dominance	Significant	Significant	Heidari *et al.* (2006)
		8 parents	Crossed in all combinations	Non-additive	Significant	Significant	Iqbal and Khan (2006a)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanppariya *et al.* (2006)
		12 lines, 3 testers	Line x tester	Non-additive	-	-	Ribadio *et al.* (2007)
9.	Number of grains per spike	5 genotypes	Half diallel	Additive x additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)
		5 genotypes	Diallel	Additive x additive	-	-	Nour (2005a)
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		10 genotypes	Diallel	Additive + non-additive	Highly significant	Highly significant	Srivastava (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)
		9 genotypes	Diallel	Partial dominance	Significant	Significant	Heidari *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		10 lines, 4 testers	Line x tester	Additive	-	-	Vanppariya *et al.* (2006)
		4 genotypes	Complete diallel	Additive	-	-	Khan *et al.* (2007)
		12 lines, 3 testers	Line x tester	Additive	-	-	Ribadio *et al.* (2007)
		8 genotypes	Half diallel	Partial dominance	Significant	-	Tahmasebi *et al.* (2007)
10.	1000 grain weight	5 genotypes	Half diallel	Additive x additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		10 lines, 2 testers	Line x tester	Additive	Significant	-	Pandey *et al.* (1999)
		12 lines, 5 testers	Line x tester	-	Highly significant	-	Rajora (2000)
		F1 and F2 generations	Diallel cross	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		35 lines, 4 testers	Line x tester	Non-additive	Significant	-	Hamada *et al.* (2002)
		7 lines, 3 testers	Line x tester	Additive	Significant	-	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	-	Highly significant	Singh *et al.* (2002)

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Sl. No.	Character	Material used	Methodology	Gene action	GCA	SCA	References
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		10 genotypes	Crossed in all combinations	Additive + non-additive	Significant	Significant	Dhayal and Sastry (2003)
		10x 10 genotypes	Diallel	-	Significant	Significant	Mavi *et al.* (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Over dominance	Significant	Significant	Sharma *et al.* (2003)
		8 lines, 3 testers	Line x tester	-	Highly significant	- Highly significant	Shoran *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		5 x 10 genotypes	Complete diallel	Additive + non-additive	Highly significant	Highly significant	Wei *et al.* (2003)
		5 x 7 genotypes	p x q	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004a)
		8 genotypes	Griffings complete diallel cross model II	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004b)
		10 genotypes	Crossed in all combinatiosn excluding reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004a)
		10 genotypes	Diellel	Additive	Significant	Significant	Joshi *et al.* (2004b)
		12 genotypes	Diallel	-	Highly significant	Highly significant	Mahantashivayogayya *et al.* (2004)

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Sl.	Character	Material used	Methodology	Gene action	GCA	SCA	References

No.							
		6 x 6 genotypes	Diallel	Non-additive	Significant	-	Pareek and Garg (2004)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Highly significant	Siddique *et al.* (2004)
		5 genotypes	Crossed in all combinations	Additive	Highly significant	Significant	Awan *et al.* (2005)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		10 genotypes	Diallel	Additive	Significant	Significant	Khedar *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		-	-	Non-additive	Highly significant	Highly significant	Saeed *et al.* (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		8 genotypes	Half dialle	Additive	Significant	-	Dere and Yldrm (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)
		9 genotypes	Diallel	Over dominance	Significant	-	Heidari *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		10 lines, 4 testers	Line x tester	Non-additive	-	-	Vanpariya *et al.* (2006)
		4 genotypes	Complete diallel	Non-additive	-	-	Khan *et al.* (2007)

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Sl.	Character	Material used	Methodology	Gene action	GCA	SCA	References

No.							
11	Grain yield per plant	5 genotypes	Half diallel	Additive + non-additive	Highly significant	Highly significant	Afiah *et al.* (1997)
		F1 and F2 generations	Diallel	Additive + non-additive	Highly significant	Highly significant	Esmail (2002)
		35 lines, 4 testers	Line x tester	Additive	Significant	-	Hamada *et al.* (2002)
		10 lines, 5 testers	Line x tester	Additive	Significant	-	Lakshmikant and Gupta (2002)
		7 lines, 3 testers	Line x tester	Additive	Significant	-	Singh *et al.* (2002)
		8 x 8 genotypes	Diallel	Additive	Highly significant	Highly significant	Ahmadi *et al.* (2003)
		10 genotypes	Crossed in all combinations	Additive + non-additive	Significant	Significant	Dhayal and Sastry (2003)
		10 genotypes	F1 and F2 generations	Additive	Significant	Significant	Joshi *et al.* (2003)
		10x 10 genotypes	Diallel	-	Significant	Significant	Mavi *et al.* (2003)
		10 genotypes	Crossed in all combinations except reciprocals	Overdominance	Significant	Significant	Sharma *et al.* (2003)
		20 lines, 4 testers	Line x tester	Over dominance	-	-	Singh and Singh (2003)
		11 lines, 4 testers	Line x tester	Non-additive	-	-	Singh *et al.* (2003)
		5 genotypes	Diallel	Non-additive	Significant	Significant	Soylu (2003)
		5 x 7 genotypes	p x q	Additive + non-additive	Significant	Significant	Jin Bao *et al.* (2004a)

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Sl.	Character	Material used	Methodology	Gene action	GCA	SCA	References

No.							
		10 genotypes	Crossed in all combinatiosn excluding reciprocals	Additive	Highly significant	Highly significant	Joshi *et al.* (2004a)
		12 genotypes	Diallel	-	Highly significant	Highly significant	Mahantashivayogayya *et al.* (2004)
		6 x 6 genotypes	Diallel	Non-additive	Highly significant	-	Pareek and Garg (2004)
		5 x 5 genotypes	Diallel	Non-additive	Highly significant	Highly significant	Siddique *et al.* (2004)
		5 genotypes	Crossed in all combinations	Additive	Highly significant	Significant	Awan *et al.* (2005)
		6 lines, 6 testers	Line x tester	Non-additive	Significant	Significant	Desai *et al.* (2005)
		10 genotypes	Diallel	Non-additive	Significant	Significant	Khedar *et al.* (2005)
		5 x 5 genotypes	Diallel	Non-additive	Significant	Significant	Nazir *et al.* (2005)
		5 genotypes	Diallel	Additive x additive	Significant	Significant	Nour (2005a)
		5 genotypes	Half diallel	-	Significant	Significant	Nour (2005b)
		-	-	Non-additive	Highly significant	Highly significant	Saud *et al.* (2005)
		10 genotypes	Diallel	Additive + non-additive	Highly significant	Highly significant	Srivastava (2005)
		6 genotypes	Half diallel	Additive	Significant	Significant	Darwish *et al.* (2006)
		11 lines, 3 testers	Line x tester	Additive + non-additive	Significant	Significant	Dhadhal and Dobariya (2006)

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Sl.	Character	Material used	Methodology	Gene action	GCA	SCA	References

No.							
		9 genotypes	Diallel	Over dominance	Significant	Significant	Heidari *et al.* (2006)
		8 x 8 genotypes	Half diallel	Additive	Significant	Significant	Inamullah *et al.* (2006)
		8 genotypes	Crossed in all combinations	Non-additive	Significant	Significant	Iqbal and Khan (2006a)
		8 genotypes	Crossed in all combinations	Additive	Highly significant	Highly significant	Iqbal and Khan (2006b)
		6 genotyles	Half diallel	Dominance	Significant	Significant	Ismail *et al.* (2006)
		10 lines, 4 testers	Line x tester	Non-additive	-	-	Vanpariya *et al.* (2006)
		4 genotypes	Complete diallel	Additive	-	-	Khan *et al.* (2007)
		12 lines, 3 testers	Line x tester	Non-additive	-	-	Ribadia *et al.* (2007)
		5 genotypes	Half diallel	Additive	Significant	Significant	Sayar *et al.* (2007)
		8 genotypes	Half diallel	Over dominance	Significant	Significant	Tahmasebi *et al.* (2007)
12	Helminthos-porium leaf blight resistance	9 parents	Half diallel	Additive and non-additive	Significant	Significant	Sharma *et al.* (2004)

2.3 Genetics of spot blotch resistance in wheat

Although spot blotch of wheat caused by *Bipolaris sorokiniana* (Sacc) (Syn *Helminthosporium sativum*) has been noticed in India as early as 1924 (Kulkarni, 1924) but it was not of much consequence till recently. The disease probability ranks close to leaf rust in destructiveness. For effective implementation of spot blotch (Helminthosporium leaf blight (HLB)) resistance, the inheritance pattern of Helminthosporium resistance has to be studied first. The investigations on genetics of spot blotch resistance are briefly reviewed under following paragraphs.

The information on genetics of resistance to *Helminthosporium sativum* in barley was reported earlier by Griffee (1925) on the basis of correlations and concluded that there were at least three genetic factors responsible for mature plant reaction to *H. sativum*. Srivastava *et al.* (1971) first reported the studies on genetics of resistance to *H. sativum* in wheat. The mode of inheritance was studied in the F_1 and F_2 generations of four inter varietal crosses *viz.,* Sharbati Sonara x Agar local, Sharbati Sonara x Hyb. 65, E 4853 x Agra local and Sharbati Sonara x E. 4853. For scoring the plants, he used 0-4 scale. He concluded that resistance of Sharbati Sonara and E 4853 was due to two dominant complementary genes. These two sets of complementary genes are reported to be distinct from each other.

Adlakha *et al.* (1984) experimented in eight crosses involving four HLB resistant (HD 1927, E 5895, Motia and DT 188) and four HLB susceptible wheats (Kalyana sona, Sharbati sonara, HD 4500 and HD 4501). The disease was estimated on inoculated leaves seven days after inoculation, using a scale of 0-5. He reported that the resistance was dominant in the F_1 progenies and the F_2 indicated that resistance was conditioned by two dominant genes with complementary gene action in the cultivar Motia and in lines E 5895 and HD 1927 and by one dominant gene in line DT 188.

Singh *et al.* (1997) screened one hundred and five genotypes under artificial epiphytotic conditions against *H. sativum* for three crop years, following 0-9 scale (Saari and Prescott, 1975) and the disease intensity was recorded 10 days after the inoculation. Out of these, 16 genotypes were resistant, 21 moderately resistant, 48 moderately susceptible, 15 susceptible and 5 were highly susceptible. Further they studied F_2 segregation in crosses NI 8289 x U-262, CPAN 1910 x UP 262 and NI 8289 x HUW-234. In all the three crosses, they observed 1 resistant : 15 susceptible ratio and concluded that two duplicate recessive genes confer resistance to foliar blight of wheat caused by *H. sativum*.

Inheritance of resistance in wheat to *Cochliobolus sativus* (*Bipolaris sorokiniana*) causing spot blotch was reported by Singh *et al.* (2000). They studied mode of inheritance of resistance to the disease in F_1 and F_2 generations in intervarietal crosses using two resistant (VEE 'S' and HD 2206) and three susceptible varieties (HP 1633, K 8962 and Hork 'S') of spring wheat. They scored every plant using the double digit scale of Kumar *et al.* (1998). The results revealed that segregation in all the three crosses (R x S) followed a 1 resistant : 15 susceptible ratio. They concluded that the resistance is controlled by two pairs of complementary recessive genes.

Joshi *et al.* (2003) studied the genetics of leaf blight (*Bipolaris sorokokiniana*) resistance in durum wheat by crossing two resistant genotypes with two susceptible genotypes. The parents F_1, F_2 and F_3 generations from the four crosses were screened under artificial epiphytotic conditions. The results indicated that susceptibility is governed by two dominant genes with complementary effect. The resistant reaction expressed only when at least one of the two genes were in homozygous recessive from.

2.4 Genetics of threshability and pericarp colour

2.4.1 Threshability

Dicoccum wheats differ from other wheats *viz.,* bread and durum wheats for physical characteristics, nutritional and processing quality parameters. Non availability of free threshing varieties low yield and reddish grain colour are important constraints in cultivation and utilization. The loss incurred on dehulling can be recovered if free threshing dicoccum varieties are developed and consumer preference can improved by breeding for amber grained semi dwarf dicoccum wheat varieties.

A very significant sequence of changes in transition from the primitive to the cultivated forms of *Triticum* were those associated with seed dissemination. These included rachis fragility, spiklet articulation and glume tenacity or threshability. Of these, one that has been extensively investigated because of both its evolutionary significance and its importance in practical utilization of wheat grain, is that of the free threshing habit.

Mackey (1966) reported that a polygenic system is scattered through all three genomes that counteracts rachis brittleness and rough glumes.

Kerber and Rowland (1974) reported that the recessive allele tg as well as Q factor must be present for the expression of free threshing character in hexaploid wheat.

Hari and Giles (1980) reported that intact rachis of *Triticum monococcum* was controlled by two complementary recessive genes.

Mabal and Singh (1996) reported that the grain threshability in hull-less barley is controlled by two interacting pairs of dominant non-allelic genes (Th, Th1, Th2, Th,) with additive effects where free threshability is only conditioned by two recessive gene pairs (th1 th1, th2 th2).

Villareal *et al.* (1996) studied the inheritance of threshability in crosses of four non-free threshing synthetic hexaploid and two free threshing. The parents, thus F1s and individual F2 plant derived F3 progenies of crosses revealed that independently segregating loci with two dominant allele controlling threshability.

Chenn *et al.* (1999) reported that the hulled character of the Tibetean weed race was governed by a single dominant gene on the short arm of chromosome 2D. The hulled character gene may be identical to the gene Tg derived from *Aegilops tauschii*.

Luo *et al.* (2000) reported that a dominant allele at the Q locus on chromosome 5A is believed to be the principle factor responsible for free threshing with square head spike and non-fragile rachis in bread wheat. The spelt syndrome, resulting in pyramidal spike with the brittle rachis and hulled grain in *T. aestivum* is believed to be principally caused by 'q' allele.

2.4.2 Pericarp colour

Dicoccum wheat (*Triticum dicoccum*) has red grain colour and huisked seeds. The red grain colour, is the major constraints for consumer preference. Tomar *et al.* (2007) studied inheritance pattern of grain colour in F_1 hybrids developed by crossing *Triticum amplissifolium* and NI 5439 which are contrasting parents producing red and amber kernel colour, respectively. The F_1 hybrid produced red kernels indicating dominance over amber colour. The F2 sergegants of red and amber kernel colour fit well into the ratio of 3 red amber indicating that the character red colour in *T. amplissifolium* is governed by a single dominant gene. The monogenic inheritance was confirmed by the data recorded in BC_1 generation.

2.5 Biochemical status of resistant and susceptible genotypes

It is well known that, the disease resistance mechanism is a complex phenomenon and response to invasion by a disease causing organism, plant produces various kinds of reactions. During these processes, considerable changes take place in biochemical aspects like changes in concentration of sugars, phenols etc in plant tissues.

2.5.1 Sugars

Sugars are precursors for synthesis of phenols, photoalexins, lignins and callose. Hence, they play an important role in defense mechanism of plants. Horsfall and Diamond (1957) assigned a major role for sugars in disease resistance. In general, infection by some pathogens bring about lot of changes in respiratory pathway and photosynthesis which are vital processes in plants. This lead to wide fluctuations in sugar contents (Farkas and Kiraly, 1962, Kuc, 1966 and Klement and Goodman, 1967). The pathogen which disturbs photosynthetic activity either by mere injury to the photosynthetic organ or by directly affecting metabolic activity, certainly brings about changes in sugar content of plants. Reports on changes in sugar content during pathogenesis has been reviewed here under.

Kuprevica (1947) studied the physiology of the diseased plant in relation to parasitism. The sugar content of cell sap from leaves and stem of infected plants were

correspondingly less. The disease reaction has been correlated with the sugar level in different crop plants. Generally, high levels of total sugars, reducing sugars and non-reducing sugars in the host plant are stated to be responsible for disease resistance (Bateman and Millar, 1966 and Jayapal and Mahadevan, 1968).

Krog *et al.* (1961) found significant decrease in total sugar content especially the sucrose fraction in susceptible wheat plants infected with stem rust whereas resistant variety showed a light decrease in total sugar content.

Ramdayal and Joshi (1968) studied the post infection changes in sugar content of the leaf caused by *H. sativum* in barley and they reported that there was decrease in reducing, non-reducing and total sugars of infected leaves than that of healthy leaves. Reddy (1976) found that the *Dreshstera turcica* (Pass.) resistant sorghum variety contained consistently higher level of sugars than the susceptible variety through out the growth period.

Levy and Cohen (1984) found a negative correlation between sugar content in leaves and blight development cuased by *Exerohilum turcicum* (Pass) Leonard and Suggs in sweet corn.

Subramanyam *et al.* (1990) studied the influence of inoculation of *Drechslera hawaiiensis* (Bugnicourt) Subram and Jain on Biochemical parameters of wheat leaves. They found higher total and reducing sugar in resistant cultivars than in susceptible ones and further they observed that both the sugar content decreased after the disease development in both susceptible and resistant cultivars.

Total sugar content of resistant cultivar of maize to *Turcicum* blight was higher than the susceptible variety but it was reverse in case of reducing sugar. Due to infection there was sudden decrease in total sugar as well as reducing sugar in susceptible variety (Sharma *et al.,* 1992).

Kalappanavar and Hiremath (2000) reported that the multiple foliar disease resistant sorghum genotypes possessed higher content of sugar compared to susceptible ones.

Pradeep Kumar (2005) studied the changes in total sugars and reducing sugars, phenols content in barley leaves infected by *H. sativum* Pam., King and Bakker. He observed high amount of total sugar, reducing sugar and phenols in resistant genotypes as compared to susceptible genotypes. However, due to the infection, the total sugar, reducing sugar and phenols were decreased in al the genotypes but extent of decrease was more in susceptible genotypes than in resistant genotypes.

2.5.2 Phenols

Phenolic compounds are common constituents of many plants. They include simple phenols, coumarins, most flavenoids, certain amino acids, prosthetic groups of some enzymes, plant pigments and complex derivatives such as lignins. Phenolic substances are known to participate in a number of physiological processes which are essential for growth and development, such as oxidation-reduction reactions, lignifications and stimulation as well as inhibition of auxin activity.

Phenolic compounds occur in a variety of simple and complex forms. Simple phenols such as cinnamic, coumarin, caffeic, protocatechuic, chlorogenic and quinic acid exhibit antimicrobial activities.

Infection in certain diseases is characterized by increased synthesis of certain precursors of phenolic compounds and oxidation products of phenolics, such as quinones which exhibit more toxicity to microorganisms than their reduced forms.

Positive correlation between the amount of phenolic content and degree of resistance to plant disease has been evinced by several workers.

Newton and Anderson (1929) proposed the phenol hypothesis to explain resistance. They suggested that rust resistance in wheat is due to the liberation of phenolics in the host cells due to invasion of the fungus and that the phenols liberated kill the host cell and inhibit the growth of the pathogen. Owens (1953) suggested that the fungitoxic activity of these compounds could be due to a) binding of the quinone nucleus to –SH and NH_2 groups in the bacterial cell or b) disturbance of electron transport system.

It has been frequently observed that phenol accumulation takes place in all the infected plant tissues but more rapid accumulation of phenolics takes place in incompatible host pathogen complex than in the compatible ones (Kiraly and Farkas, 1962). Concentration of phenolic compounds is usually higher in resistant than in susceptible genotypes of different crop plants. Studies have also shown that qualitative and quantitative changes in these compounds occur after infection Luthra *et al*., 1988).

Kotireddy (1971) reported that rice cultivar resistant to *Pyricularia oryzae* Cav. contained more of total phenolics than the susceptible variety. Prasad *et al.* (1972) observed larger amount of total phenols and orthodihydroxy phenols in uninfected resistant rice varieties than in the susceptible plant extracts at all the sampling periods.

Mukherjee and Kundu (1973) reported that ten out of eighteen compounds, mostly of phenolic nature but with widely different structures, were highly antifungal against *H. oryzae*, *A. solani* and *Curvularia lunata* (Walker). Boedijin Tannic acid, penta chlorophenol, Picric acid and pyrogallol were found to be the promising inhibitors.

Vidyasekaran and Kandasamy (1971) reported that resistant leaves of finger millet varieties against *Helminthosporium tetramera* Mc. Kinney, contained more phenols than the susceptible leaves of the variety. Similar observations were also made by Sempio *et al.* 1975), while working with leaf rust of bean caused by *Uromyces phaseoli* var. *typica* (Reben) Wint. The leaves of rust resistant variety contained more phenols than susceptible variety.

Venkateshwaralu and Sirohi (1976) found that brown rust infection in wheat increased the phenol content considerably in susceptible varieties under normal day conditions and decreased under long day conditions.

Tripathi and Chiranjeevi (1977) observed more phenols in leaves of sorghum infected with zonate leaf spot as compared to healthy leaves both at 60 and 80 days after sowing.

Naik *et al.* (1981) observed more phenols in healthy leaves of sorghum than in the leaves infected with rust. Patil *et al.* (1981) while studying possible role of phenols in charcoal rot resistance in sorghum, observed higher quantity of phenols in tolerant than in susceptible ones.

The quantitative and qualitative estimation of total phenols and orthodihydroxy phenols determined in diseased and healthy leaves of different sorghum lines resistant, moderately resistant and highly susceptible to *Helminthosporium rostratum* Drechsler indicated higher concentration of total phenols and orthodihydroxy phenols in resistant line than that of moderately resistant and highly susceptible line (Singh and Chand, 1982).

Reddy (1984) working on quantitative changes in individual phenolic acid, in most infected groundnut leaves at different stages of development, found no qualitative changes in phenolic acids. However, he found an increased concentration of phenolic compounds due to infection. The quality of total phenols in roots of charcoal rot resistant variety (E 36-1) and in first internode was more than in root and in first internode of susceptible genotype CSH-6 (Anahosur and Naik, 1985).

Shree and Reddy (1986) reported that healthy hybrids (CSH-6 and CSH-148) resistant to *H. turcicum* contained comparatively large amounts of total phenols than the susceptible cultivars *viz*., Swarna and Neerujola.

Matho *et al.* (1987) analysed total phenolics, sugars and reducing sugars from alcoholic and aqueous extracts of resistant and susceptible rice varieties infected with bacterial blight pathogen. They observed the highest total phenol content (278.5 mg/100 g of fresh leaves) in IR-20, a resistant variety and the lowest (100 mg/100 g of fresh leaves) in Anand, the highly susceptible variety. The amount of phenolics and sugars present in the leaves of resistant varieties varied considerably but was always higher than the susceptible varieties.

Sharma *et al.* (1992) studied the biochemical relationship in resistant and susceptible cultivars of maize with Fusarium leaf blight disease. Biochemical analysis were done at 15 days interval after 30 days after sowing. Total sugars reduced in all the cultivars but the rate of reduction was more in susceptible than in resistant cultivars. The total phenolic content in healthy and diseased leaves was found non-significant. However, in the resistant cultivar, the

quantity of phenolics showed an increasing trend in response to infection indicating the post-infectionally formed phenolics which may play an important role in resistance.

Chandela *et al.* (1995) reported an increased content in the total phenolic acid in the resistant and intermediate resistant capsicum varieties following infection with *Phytophthora capsici* Leonian.

Kalappanavar (1996) observed higher content of phenols in multiple foliar disease resistant sorghum genotypes as compared to susceptible ones.

Neenamitter *et al.* (1997) reported in chickpea that phenol content decreased markedly in susceptible genotypes after inoculation with *Botrytis cinerea* Pers. Ex. Fr. than in resistant genotypes.

Sindhan *et al.* (1999) reported that the healthy leaves of resistant genotypes of mungbean contained higher amount of total phenol and ortho-dihydroxyphenol than susceptible ones.

Malli *et al.* (2002) observed more reduction in total phenols in susceptible genotypes than in resistant genotypes of mothbean following yellow mosaic virus infection.

2.6 Molecular diversity

Wheat is one of the most extensively studied crop species. The large genome size of wheat due to extensive regions of retrotransposon – type elements such that over 80 per cent of the genome consists of repetitive DNA sequence (Schulman *et al.,* 2004), the application of molecular techniques has been slow (Lagudh *et al.,* 2001 and Landgridge *et al.,* 2001). Many molecular markers are available to detect an adequate and useful polymorphism for the construction of molecular maps and consequently application of marker-assisted selection (MAS).

Recent advances in molecular techniques have led to the development of assays based on variation in DNA sequence, broadly referred to as DNA (or molecular) markers. DNA markers provide good resolution because, unlike most non-DNA-based markers (morphological, biochemical or physiological), they are unlimited in number, independent of environment, developmental stage and complex genetic interactions, frequently free of dominant and recessive effects and easy to score, analyse and interpret. Presently many kind of DNA based markers such as RFLP, RPAD, AFLP etc are available which detect polymorphism at the DNA level. The present study employed RAPD technique to assess genetic polymorphism. The major advantages of the RAPD technique is that, it does not need sequence information to start with. The polymorphism among genotypes can be detected by using random primers. Variation in the banding pattern of the amplification products occurs because of variation in the length of DNA sequences flanked by the primers.

An understanding of germplasm diversity and genetic relationship among breeding materials is an invaluable aid for crop improvement strategies.

Joshi and Nguyen (1993) used 40 RAPD primer pairs to study genetic diversity of 20 accessions of wild tetraploid durum wheat and 10 genotypes of cultivated tetraploid durum wheats selected from geographically diverse locations. They observed a higher level of polymorphism among different accessions.

Seven accessions of Tibetian wheat, 22 cultivars of common wheat and 17 lines of splet wheat used for RAPD analysis to assess the genetic diversity among within the texa RAPD polymorphism was found to be much higher within spelt wheat and the Tibetian wheat than within common wheat. The genetic diversity value between the Tibetian wheat and common wheat is lower than between Tibetian and Spelt wheat. The results of cluster analysis showed that 46 genotypes were distinctly classified into two groups. Group I included all European spelt wheat lines, while group II included all Chinese common wheat and the Tibetian wheat accessions (Sun *et al.,* 1998).

Fahima *et al.* (1999) conducted RAPD analysis on 100 genotypes of wild emmer wheat from 11 populations samples in Israel and Turkey using 10 primer pairs and concluded that natural selection causes adaptive RAPD ecogeographical differentiation. RAPD markers are useful for estimation of genetic diversity in wild emmer wheat and the identification of

suitable parents for the development of mapping populations for the tagging of agronomically important traits derived from wild wheat.

Ten primer pairs were used to study diversity of 15 accessions of 5 group of hexaploid wheat; common, spelta, mecha, vavilovii and semi wild wheat by Cao *et al.* (2000) and reported that, common wheat is most closely related to semi wild wheat follwed by spelta, vavilovii and mecha.

Barcaccia *et al.* (2002) reported the genetic diversity and relationships among 11 Italian local 17 RAPD marker loci. The proportion of genetic diversity was as high as 48 per cent among the local cultivars. Thus about 52 per cent of the total variation was within population. Local cultivars of emmer wheat found tube formed by a variable number of lines genetically distinguishable from each other and the vast majority of individuals over populations proved to be different multilocus genotypes.

Rajbir Yadav *et al.* (2002) conducted a study on genetic variability among 26 released varieties local cultivars of *Triticum durum* by using RAPD markers. A total of 4 series of primers were used to screen and 15 primers produced polymorphism. OPA-3 and OPP-6 were the most polymorphic primers. The varieties developed by the selection among the local race Bansi were grouped together. The highest degree of polymorphism was between the local land race Malraj with Motia and Jay. The clustering was clearly on the pattern of their parentage. The grouping of the gerplasm particularly the land races by RAPD markers can be used in developing the Indian durum wheat cultivars with wider genetic base.

Mandoulakani *et al.* (2003) used RAPD markers to evaluate genetic diversity among 28 Iranian wheat cultivars and advanced breeding lines. Among 50 decamer primers used eight showed polymorphism among the genotypes. Cluster analysis was alone by UPGMA method showed two main groups. Similarity coefficient raged from 0.40 to 0.91 with an average of 0.64. The greatest similarity was observed between Azadi and Khazar 1. The greatest genetic difference was observed between 7107 line number and Karaj 3.

RAPD markers were developed in a specific durum wheat population of 150 lines by Gocmen *et al.* (2003). Among 284 different primers screened for parent DNAs 13 produced the most polymorphic and clear bands. These 13 primers were selected and screened with the DNAs of 150 lines. They revealed a total number of 33 segregating loci. The preliminary results of this study could be used to a base for mapping economically important character loci of durum wheat by the development of other RAPDs.

Sun *et al.* (2003) studied on 35 spring wheat cultivars and lines with different levels of Fusarium resistance using 17 RAPD primer pairs and they reported that a collection of unrelated genotypes can be used to identify markers linked to an agronomically important traits as three RAPD markers, significantly associated with FHB were identified in this study.

3. MATERIAL AND METHODS

Relevant genetic material was generated at All India Coordinated Wheat Improvement Project, MARS, University of Agricultural Sciences, Dharwad and the evaluation of the material for spot blotch resistance and other traits experiments were conducted at ARS, Arabhavi, in accordance with the objectives of present investigation. Details are presented experimentwise.

3.1 Experiment 1: Heterosis, combining ability and gene action studies for Spot blotch disease resistance, yield and yield attributing traits using line x tester design

During the *rabi* season 2006, crossing was undertaken to generate F_1s at the fields located at Wheat Improvement Project, MARS, UAS, Dharwad for achieving set objectives. This experimental site is located between 15^0 – 26' N latitude and 75^0 - 07' E longitude and has altitude of 678 m above mean sea level. Dharwad comes under transition tract of Karnataka state. Further, the crop was raised at ARS, Arabhavi, which is located between 16^0 - 12' N Latitude and 74^0 - 54' E Longitude and has altitude of 640 m above mean sea level. The material included the lines, testers and F_1s. ARS, Arabhavi is the hot spot for spot blotch (Helminthosporium leaf blight) caused by *Bipolaris sorokiniana* (Saac.) Shoem (*Helminthosporium sativum* Pammel, King and Bakke Syn. *Cochliobolus sativus* and *Drechslera sorokiniana* (Saac) Subram and Jain).

3.1.1 Experimental material

The base material for the present study consisted of ten dicoccum wheat lines *viz*., L_1 – DDK-1025, L_2 – MACS2956, L_3 – NP200, L_4 – DDK1030, L_5 – MACS2947, L_6 – HW1095, L_7 – DDK1009, L_8 – DDK-1029, L_9 – DDK1028, L_{10} – MACS-2961 and four durum wheat testers *viz*., T_1 – NIDW295, T_2 – DWR185, T_3 – DWR1006, T_4 – DWR2006 (Table 3). These ten dicoccum lines and four testers were used for hybridization programme following the line × tester design at the fields of Wheat Improvement Project, MARS, UAS, Dharwad during *rabi* 2006-07 to generate F_1s. Further, the experimental material consisting of 54 entries *viz*., 10 lines, 4 testers and 40 hybrids (F_1s) were sown during *rabi* 2007-08 at Agricultural Research Station, Arabhavi, UAS, Dharwad.

3.1.2 Layout and Management

The experimental material consisting of 54 genotypes were laid out in randomized block design (RBD) with two replications. Each entry was sown in two rows of 1.0 m length per replication.

Half of the recommended dose (100:75:50 kg NPK/ha) of nitrogen along with the entire dose of phosphorus and potassium was applied at the time of sowing. The remaining 50 per cent of the nitrogen was top dressed at 30 days after sowing. The inoculum of spot blotch was sprayed to create the disease pressure. The crop was raised under irrigated condition. The crop stand, crop growth and the spot blotch disease development were satisfactory to screen for spot blotch disease resistance.

3.1.3 Recording of observations

In all the entries, five random plants were tagged in each replication for recording the observations. Mean of five plant observations was used for the statistical analysis. The procedure adopted for recording the observations for different characters is given below.

1. Days to flowering (DF)

The number of days taken from the date of sowing to the day on which the main ear comes out of flag leaf completely was recorded.

2. Days to maturity (DM)

The number of days taken from sowing to the date when all the ears of the plant turned to physiological maturity i.e., golden yellow colour was noted.

Table 3: The pedigree and reaction to spot blotch of parents

Lines	Pedigree	Reaction to spot blotch
DDK-1025	DDK-1030/DDK-1001/278-13	MS
MACS-2956	KRT5/*2/NP200	MS
NP-200	Sel Local of Rishi Valley	S
DDK-1030	DDK-1001/DDK-1019//MACS/2912	MS
MACS-2947	KRT5/*2/NP200	S
HW-1095	NP-200-20KR irradiated (200 Gray)	S
DDK-1009	NP-200*4/NP-200/ALTAR-84	S
DDK-1029	DDK-1012/HW-1093//276-15	MS
DDK-1028	DDK-1016/HW-1092//Kpdur local/DDK-1001	MS
MACS-2961	L.Khapli//Khapli/DWL5023	S
NIDW-295	BOOMER-33/PLATA-8	R
DWR-185	CPAN-6018/2*RAJ-1555	R
DWR-1006	DWL-5023/DON	R
DWR-2006	SULA/CREX //AAZ	R

MS - Moderately susceptible S – Susceptible R – Resistant

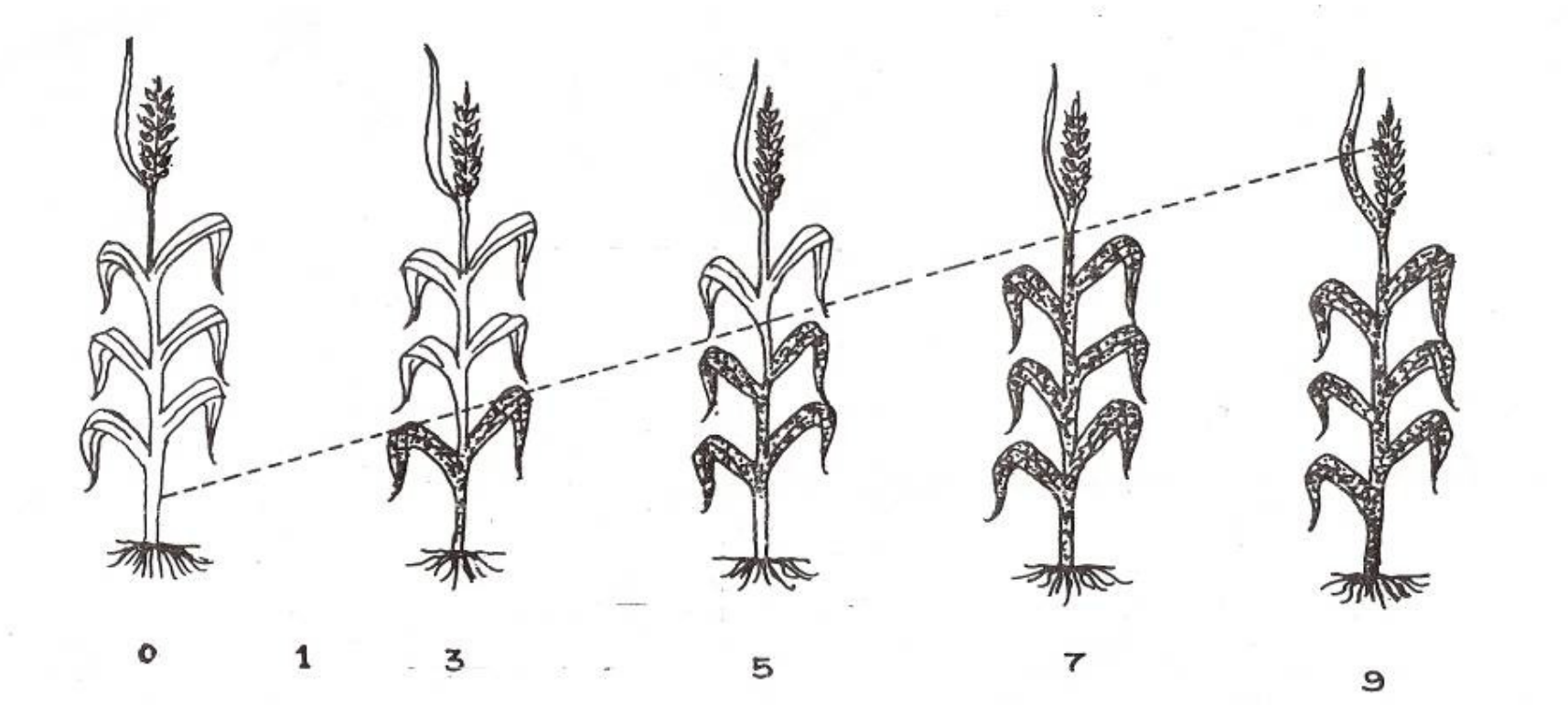


Fig. 1: Rating scale for spot blotch disease of wheat based on entire plant

3. Plant height (PH)

The plant height was measured in centimeters (cm) from the base of the plant or ground level to tip of the ear head of main tiller at the time of harvest.

4. Peduncle length (PL)

The length of peduncle of main culm was recorded in centimeters (cm) from the top most node to the base of the spike.

5. Spike length (SL)

Spike length of the main tiller from the base of the spike to the tip of the last spikelet excluding awns was recorded in centimeters (cm).

6. Number of tillers per plant (NTPP)

The total number of tillers was counted at the time of harvest.

7. Number of productive tillers per plant (NPTPP)

The number of tillers bearing ear heads was counted at the time of harvest.

8. Number of spikelets per spike (SPS)

The number of spikelets in the main spike were counted at the time of harvest and recorded.

9. Thousand grain weight (TGW)

Randomly selected 1000-grains were counted and weight was recorded in grams (g).

10. Number of grains per spike (GPS)

The number of grains in the main spike were counted and recorded.

11. Grain yield per plant (GYP)

The dried spikes per plant were threshed separately and weight was recorded in grams (g) per plant.

11. Threshability

It is tested by threshing the spike lets with hand either tough or loose at the time of threshing and recorded whether free threshable or non-free threshable.

12. Pericarp colour

The colour of the grain based upon the visual observations was recorded as red or amber coloured type.

13. Disease scoring for spot blotch (DS)

All the parents (lines and testers) and hybrids were tested against spot blotch blight under field conditions. The inoculum was sprayed to create disease pressure and the field was irrigated just after inoculation. The observations were recorded at two stages *viz*., 60 days after sowing (DS I) and 90 days after sowing (DS II). The disease intensity was recorded 10 days after the inoculation following 0 – 9 scale (Saari and Prescott 1975) (Fig. 1).

Scale

1 – 3	: Resistant
4	: Moderately resistant
5 – 6	: Moderately susceptible
7 – 8	: Susceptible
9	: Highly susceptible

3.1.4 Statistical analysis

Mean values of the plants selected at random in each entry in each replication were subjected for statistical analysis. The following statistical methods were adopted.

3.1.5 Analysis of variance for parents and hybrids

The replication mean of competitive plants in each parent and cross was utilized for statistical analysis and the variance due to different sources were worked out (Kempthorne, 1957).

Source	Degree of freedom	Mean sum of squares
Replications	(r-1)	
Treatments	(t-1)	
Parents	(p-1)	
Crosses	(mf-2)	
Parents Vs crosses	1	
Lines (females)	(f-1)	M_1
Testers (males)	(m-1)	M_2
Lines × testers	(f-1) (m-1)	M_3
Error	(t-1) (r-1)	M_4
Total	(tr-1)	

Where,

r = Number of replications

m = Number of male parents (testers)

f = Number of female parents (lines)

p = Total number of parents

t = Total number of treatments

3.1.6 Estimation of heterosis

Per cent heterosis of the derived F_1 over mid parent (MP), better parent (BP) and check hybrids was calculated as per the method of Turner (1953) and Hayes *et al*. (1955).

Recently released and notified variety DDK-1029 was considered for calculating standard heterosis for all the characters.

Heterosis for each trait was computed by using following formulae.

For better parent value (BP) for each character, superior value between the parents in each cross was taken.

3.1.7 Standard error of estimates

To compute the standard error (SE) of estimates of heterosis, mean squares due to error (M_4) from RBD analysis was considered.

$$\text{Per cent heterosis over mid parent (MP)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Where mid parent} = \frac{P1 + P2}{2}$$

$$\text{Per cent heterosis over better parent (BP)} = \frac{F_1 - BP}{BP} \times 100$$

$$\text{Per cent heterosis over check hybrid (CH)} = \frac{F_1 - CH}{CH} \times 100$$

For better parent value (BP) for each character, superior value between the parents in each cross was taken.

$$SE(MP) = \sqrt{\frac{3 \times M_4}{2 \times r}}$$ For testing heterosis over mid parent

$$SE(BP) = \sqrt{\frac{2 \times M_4}{r}}$$ For testing heterosis over better parent

$$SE(CH) = \sqrt{\frac{2 \times M_4}{R}}$$ For testing heterosis over checks

3.1.8 Estimation of average heterosis

The average heterosis (H) was calculated for each character by using following formula and is expressed as percentage.

$$H = \frac{\overline{F_1} - \overline{\text{Parents}}}{\overline{\text{Parents}}} \times 100$$

3.1.9 Combining ability analysis

Since the expected mean sum of squares are not available for the modified line x tester analysis, the mean of each replication for the eleven characters recorded for the

hybrids alone were subjected to analysis and the fresh mean sum of squares, along with the variance of general combining ability (GCA) of the parents and specific combining ability (SCA) of the hybrids were worked out based on the procedure developed by Kempthorne (1957).

3.1.10 ANOVA for combining ability

Source	Degrees of freedom	MSS	Expected mean sum of squares
Replications	(r-1)		
Crosses	(mf-1)		
Lines	(f-1)	M_1	σ^2 + r cov (FS)-2 cov (HS) + rm COV (HS)
Testers	(m-1)	M_2	σ^2 + r cov (FS)-2 cov (HS) + rm COV (HS)
Lines × testers	(m-1) (f-1)	M_3	σ^2 + r cov (FS)-2 cov (HS) + rm COV (HS)
Error	(r-1) (mf-1)	M_4	σ^2 + r cov (FS)-2 cov (HS) + rm COV (HS)
Total	(mfr-1)		

Where,

r = Number of replications

m = Number of male parents (testers)

f = Number of female parents (lines)

Cov (FS) = Covariance of full sibs

Cov (HS) = Covariance of half sibs

For the expectations of the mean sum of squares the following estimates were worked out.

$$\text{Cov (HS)} = \frac{(M_1 - M_3) + (M_2 - M_3)}{2r\,(m+f)}$$

$$\text{Cov (FS)} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r} + \frac{6r\text{Cov (HS)} - r\,(f+m)\,\text{Cov (HS)}}{3r}$$

Variance due to GCA = Cov (HS)

Variance due to SCA = Cov (FS) – 2 Cov (HS)

$$\text{GCA variance for lines} = \frac{(M_1 - M_3)}{Rm}$$

$$\text{GCA variance for testers} = \frac{(M_2 - M_3)}{Rf}$$

$$\text{SCA variance for hybrids} = \frac{(M_3 - M_4)}{R}$$

Where,

M_1 = Mean sum of squares due to females

M_2 = Mean sum of squares due to males

M_3 = Mean sum of squares due to females x males

M_4 = Mean sum of squares due to error

3.1.11 Estimation of combining ability effects

The model used to estimate gca and sca effects of ijk observations was

$$x_{ij} = \mu + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + e_{ijk},$$

Where,

μ = Population mean

gi = *gca* effect of i^{th} female parent

$\hat{g}_j$ = *gca* effect of j^{th} male parent

$\hat{s}_{ij}$ = *sca* effect of ij^{th} combination

$\hat{i}$ = Number of female parents

j = Number of male parents

k = Number of replications

e = Error

The individual effects were estimated as indicated below

$$\text{a. Lines : } \hat{g}_i = \frac{x_i}{mr} - \frac{x\ldots}{mrf}$$

Where,

x_i = total of i^{th} female parent over all male parents and replications

$$\text{b. Testers : } \hat{g}_j = \frac{x_j}{fr} - \frac{x...}{Mrf}$$

Where,

X_j = total of j^{th} male parent over all female parents and replications

$$\text{c. Specific combining ability effects} = s_{ij} = \hat{} \quad \frac{\times_{ij}}{r} - \frac{\times_{i..}}{mr} - \frac{\times_{j..}}{fr} - \frac{\times\ldots}{mfr}$$

Where,

X_{ij} = ij^{th} combination totaled over all the replications

The standard errors (SE) and critical differences (CD) pertaining to the *gca* effects of male and female parents and *sca* effects of different combinations were as follows.

$$\text{SE of gca for females} = \sqrt{\frac{M_4}{mr}} \; ; \; CD = SE \times \text{Table 't' for error df} \times \sqrt{2}$$

$$\text{SE of gca for males} = \sqrt{\frac{M_4}{fr}} \; ; \; CD = SE \times \text{Table 't' for error df} \times \sqrt{2}$$

$$\text{SE for sca} = \sqrt{\frac{M_4}{r}} \; ; \; CD = SE \times \text{Table 't' for error df} \times \sqrt{2}$$

3.1.12 Proportional contribution of lines, testers and their interaction

$$\text{Contribution of lines} = \frac{SS(l)}{SS(c)} \times 100$$

$$\text{Contribution of testers} = \frac{SS(t)}{SS\,(c)} \times 100$$

$$\text{Contribution of lines} \times \text{testers} = \frac{SS\,(l \times t)}{SS(c)} \times 100$$

Where,

SS (l)	= Sum of squares due to lines
SS (t)	= Sum of squares due to testers
SS (l × t)	= Sum of squares due to lines x testers
SS (C)	= Sum of squares due to crosses

3.2 Experiment 2: Genetics of spot blotch resistance, pericarp colour and threshability in tetraploid wheat

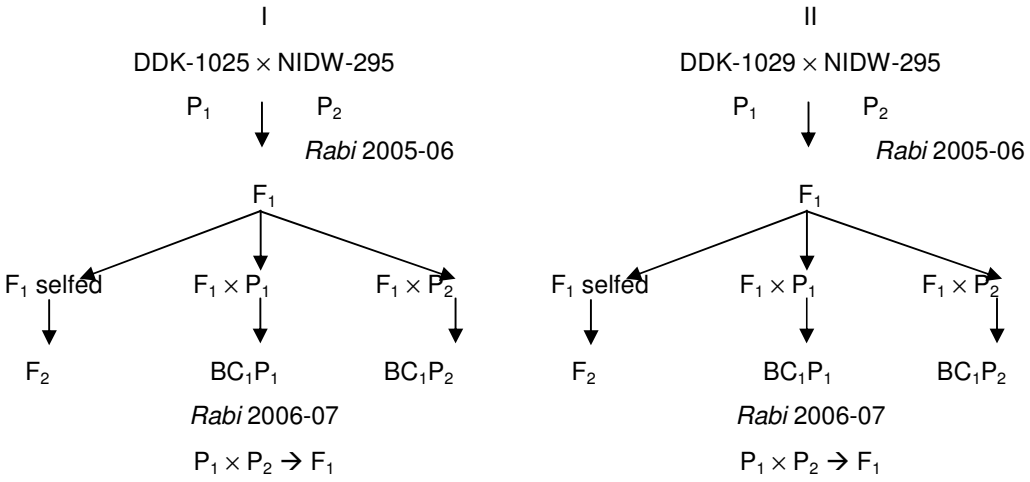
In order to investigate the genetics of resistance to spot blotch, threshability, pericarp colour, thousand grain weight and grain yield per plant, resistant (R) and susceptible (S) lines were crossed. Back crossing to both the parents was practiced. Segregating and non-segregating material was generated, which includes six generations *viz.*, P_1, P_2, F_1, F_2, BC_1P_1 (F_1 back crossed with P_1) and BC_1P_2 (F_1 back crossed with P_2). These six generations were evaluated under replicated trials and data obtained for various relevant traits was subjected for six generation mean analysis followed by Hayman (1958).

3.2.1 Development of experimental material

The base (parental) material for the present investigation consisted of two spot blotch susceptible dicoccum parents *viz*., DDK-1025 and DDK-1029 and one durum spot blotch resistant parent NIDW295. The dicoccum parents were crossed with durum parent separately to generate F_1s during *rabi* 2005-06 at the fields of Wheat Improvement Project, MARS, UAS, Dharwad. Emasculation of individual floret of susceptible parental plant was done from 8 am to 10 am and butter paper bag was used to cover the emasculated ear head. Next day from 10 am to 12 noon, the pollination was done with the resistant male source and again closed with butter paper bags properly to avoid contamination and labelled.

The true F_1s were identified based on ear head morphological characters during *rabi* 2006-07. The F_1 seeds collected in the earlier season were used to generate F_2s and backcrossing with both the parents separately during *rabi* 2006-07. Fresh cross of the susceptible and resistant parents was also done to generate F_1 seeds during *rabi* 2006-07.

The different generations developed for this experiment is as given below.



The seeds of all the six generations were collected and stored separately.

3.2.2 Experimental site

The main experiment was carried out during *rabi* 2007-08 at the fields of Agricultural Research Station, Arabhavi for achieving set objectives.

3.2.3 Experimental layout

At the fields of Agricultural Research Station, Arabhavi, the six generations *viz*., P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 of the two crosses were raised during *rabi* 2007 in the Randomized Block Design (RBD) with two replications. Each replication consisted of four rows of each parent, two rows of F_1s, 25 rows of F_2s and 15 rows of BC_1P_1 and BC_1P_2 of 1 m length.

The recommended agronomic practices were followed during the crop growth period. The spot blotch inoculum was sprayed to create the disease pressure. The crop was grown under irrigated conditions. The crop stand, crop growth and the spot blotch disease development were satisfactory to screen for spot blotch disease resistance.

3.2.4 Recording of observations

Five random plants of the parents P_1, P_2 and F_1s selected and all the individual plants of F_2, BC_1P_1 and BC_1P_2 generations were numbered in each replication and tagged. The observations were recorded on these plants and the data used for the statistical analysis. The procedure of recording observation is given below.

1. Disease scoring for Helminthosporium leaf blight (DS)

The selected plants were screened against Helminthosporium leaf blight at two stages *viz*., 60 days after sowing (DS I) and 90 days after sowing (DS II). The disease scale followed as given in Experiment I.

2. Threshability
3. Pericarp colour
4. Thousnand grain weight (TGW)
5. Grain yield per plant (GYP)

3.2.5 Statistical analysis

The details of statistical procedure adopted for analysis of six generations (*viz*., P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of the crosses on the nature and magnitude of various types of gene action controlling resistance to spot blotch and other characters are presented below.

3.2.6 Generation mean, variance and standard error of mean

Adequacy of scale must satisfy two conditions namely, additivity of gene effects in dependence of heritable components from non-heritable ones. The test of first condition provides information regarding absence or presence of gene interactions. The test of adequacy of scales is important because in most of the cases the estimations of additive and dominance components of variances are made assuming the absence of gene interaction. Mather (1949) and Hayman and Mather (1955) gave the following tests for scale effects.

3.2.7 Mather's scaling tests

The three quantities of scaling tests *viz*., A, B and C were calculated following the methods of Mather (1949) to detect the presence or absence of epistasis as detailed below.

$A = 2\,BC_1P_1 - P_1 - F_1$

$B = 2\,BC_1P_2 - P_2 - F_2$

$C = 4\,F_2 - 2\,F_1 - P_1 - P_2$

$D = 2\,F_2 - BC_1P_1 - BC_1P_2$

Where, P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 are the mean values of the respective generations. Significant deviation of A, B, C and D values from zero indicates presence of epistasis justifying the use of six parameter model.

Variance of means of the corresponding generations (squares of standard errors) were used to compute the variance of A, B, C and D as shown below.

$VA = 4V(BC_1P_1) + V(P_1) + V(F_1)$

$VB = 4V(BC_1P_2) + V(P_2) + V(F_1)$

$VC = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$

$VD = 4V(F_2) + V(BC_1P_1) + V(BC_1P_2)$

Where,

VA, *VB*, *VC* and *VD* are the variances of A, B, C and D, respectively. VP_1, VP_2, VF_1, VF_2, VBC_1P_1 and VBC_1P_2 are the variances of means of the respective generations.

The 't' values for each of these quantities were calculated to test their significance, as follows.

t (A) = A/SE (A)

t (B) = A/SE (B)

t (C) = A/SE (C)

t (D) = A/SE (D)

Where, standard error (SE) is the square root of respective variance.

SE (A) $=\sqrt{VA}$

SE (B) $=\sqrt{VB}$

SE (C) $=\sqrt{VC}$

SE (D) $=\sqrt{VD}$

The calculated values of 't' are compared with 1.96 and 2.575, which is a tabulated value of 't' at 5 per cent and 1 per cent level of significance.

The value of A, B, C and D should be equal to zero within the limits of their standard error. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. It is to be noted that,

a) D provides a test of largely of 'i' type of gene interaction (additive × additive)

b) C indicates 'l' (dominance × dominance) type of gene interaction.

c) Significance of C + D relates to 'i' (additive × additive) and 'l' (dominance × dominance) type of interaction.

d) 'j' (additive × dominance) type of interaction has no effect on C and D, but it affects A and B. A and B tests provide evidence on i, j and l of gene interactions.

3.2.8 Joint scaling test

In the Cavalli's (1952) joint scaling test genetic parameters *viz*., m, (d) and (h) are estimated from the observed means of three or more generations. When more than three generation means are available to estimate the above three parameter a weighed least-square analysis is employed which enables precise estimation of m, (d) and (h), such that deviations of observed form expected values are least. In this approach, reciprocals of variance of each of the means is used as a weight. Six equations from six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 would be available for estimation of *m*, [*d*] and [*h*] that are obtained by equating the observed family means to their expectations in terms of three genetic parameters as detailed below.

Generation	Weight	Coefficients			Observed generation mean
		m	[d]	[h]	
P_1	$1/VP_1$	1	-1	0	P_1
P_2	$1/VP_2$	1	1	0	P_2
F_1	$1/VF_1$	1	0	1	F_1
F_2	$1/VF_2$	1	0	0.5	F_2
BC_1P_1	$1/VBC_1P_1$	1	-0.5	0.5	BC_1P_1
BC_1P_2	$1/VBC_1P_2$	1	0.5	0.5	BC_1P_2

'P_2' is regarded as favourable parent and VP_2 = Variance of P_2/n.

The six equations and their weights are combined to get three simultaneous normal equations yielding weighted least squares estimates of the three parameters m, [d] and [h] as follows.

Each of the equation is multiplied through by the coefficient of m which it contains and by its weight and the six equations are then summed to get the first normal equation. The two further equations are obtained in the similar way using the coefficients of m, [d] and [h] and the weights as multiplier. The solution to these three simultaneous normal equations is obtained by way of matrix inversion, that is in the form of $M = J^{-1}S$.

Where,

M = Matrix of the estimations of the parameters *viz.*, m, [d] and [h]

J^{-1} = Inverse of the information matrix (J) and is a variance – covariance matrix

S = Column matrix obtained by multiplying respective observed values by coefficients and weight and is matrix of score.

By using the inversion matrix, the values of m, [d] and [h] were computed. The adequacy of the additive-dominance model was next tested by predicting the expected family means from the estimates of the three genetic parameters and comparing with the observed generation means with the help of chi-squares test. Significance of calculated chi-square values depicts the inadequacy of additive-dominance model and further analysis using Hayman's approach (1958) is required to cater for the possible non-allelic interaction effects.

3.2.9 Estimation of gene effects using six generation means

The generation means were analysed by the method suggested by Hayman (1958) to provide information on the inheritance of various traits. The generation means were used to estimated the six genetic parameters *viz.*, (m), (d), (h), (i), (j) and (l) of digenic interaction model representing F_2 mean, additive gene action, dominance genetic effect, additive × additive gene interaction effect, additive × dominance interaction effect and dominance × dominance gene effects, respectively assuming that no linkage and no higher order gene interaction exists. Considering the generation means as reference values, the above six genetic parameters were calculated following relationship between respective generation mean and genetic effects.

3.2.9.1 Components of generation means

$P_1 = m + (d) + (i)$

$P_2 = m - (d) + (i)$

$F_1 = m + (h) + (1)$

$F_2 = m + ½(h) + ¼(l)$

$BC_1P_1 = m + ½(d) + ½(h) + ¼(i) + ¼(j) + ¼(l)$

$BC_1P_2 = m - ½(d) + ½ (h) + ¼(i) + ¼(j) + ¼(l)$

Accordingly, by least squares computation method, the formulae for different gene effects are as follows.

3.2.9.2 Formulae for gene effects

m = Mean = F_2

d = Additive effect = $BC_1P_1 - BC_1P_2$

h = Dominance effect = $F_1 - 4F_2 - (½)P_1 - (½)P_2 + 2BC_1P_1 + 2\ BC_1P_2$

i = Additive × additive type of gene interaction = $2BC_1P_1 + 2BC_1P_2 - 4F_2$

j = Additive × dominance type of gene interaction = $BC_1P_1 - ½\ P_1 - BC_1P_2 - ½\ P_2$

l = Dominance × dominance type of gene interaction = $P_1 + P_2 + 2F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2$

The variance of these gene effects involving the variances of means of the generations were calculated as follows.

$Vm = V(F_2)$
$Vd = V(BC_1P_1) + V(BC_1P_2)$
$Vh = V(F_1) + 16V(F_2) + ¼V(P_1) + ¼V(P_2) + 4V(BC_1P_1) + 4V(BC_1P_2)$
$Vi = 4V(BC_1P_1) + 4V(BC_1P_2) + 16V(F_2)$
$Vj = V(BC_1P_1) + ¼V(P_1) + V(BC_1P_2) + ¼V(P_2)$
$Vl = V(P_1) + V(P_2) + 4V(F_1) + 16V(F_2) + 16V(BC_1P_1) + 16V(BC_1P_2)$

Where,

Vm = Variance of mean effect

Vd = Variance of additive effect

Vh = Variance of dominance effect

Vi = Variance of additive × additive interaction effect

Vj = Variance of additive × dominance interaction effect

Vl = Variance of dominance × dominance interaction effect

Square roots of the variance provided respective standard errors.

SE (*m*) = [*Vm*]½

SE (*d*) = [*Vd*]½

SE (*h*) = [*Vh*]½

SE (*i*) = [*Vi*]½

SE (*j*) = [*Vj*]½

SE (*l*) = [*Vl*]½

The standard errors were used to calculate the '*t*' values for testing significance of the corresponding variances.

t(*m*) = *m*/SE (*m*)

t(*d*) = *m*/SE (*d*)

t(*h*) = *m*/SE (*h*)

t(*i*) = *m*/SE (*i*)

t(*j*) = *m*/SE (*j*)

t(*l*) = *m*/SE (*l*)

3.3 Experiment 3: Biochemical basis of spot blotch disease resistance

3.3.1 Material

Four tetraploid wheat cultivars were selected for the study. Among the four entries, two entries *viz.,* NIDW 295 and DWR 185 were resistant durums and two entries *viz.,* DDK-1025 and DDK-1029 were susceptible dicoccums. At the two stages *viz.,* at 60 days after sowing (DAS) and at 90 days after sowing (DAS) total sugar and total phenol was estimated.

3.3.2 Materials used

Test tubes, conical flasks, pipettes, volumetric flasks, measuring cylinder, burette stand, test tube stand, glass rod, Whatman paper, tissue paper, squeeze bottle, cuvet and spectrophotometer.

3.3.3 Extraction of plant tissues in alcohol

Estimation of metabolites require their complete extraction from the tissues. The activities of the enzymes which synthesize and utilize them need to be stopped at once to get reliable values. Plant constituents possess different solvents. Though, water is the universal solvent, it does not penetrate the tissues quickly enough to stop enzymatic activity. In this context alcohol especially hot alcohol, is the choicest solvent for the extraction.

3.3.3.1 Reagent

Distilled ethanol (80%)

3.3.3.2 Procedure

One g of the tissue was weighed and made into small pieces and plunged immediately in boiling alcohol. Then it was cooled and passed through double layered muslin cloth. The pieces of the tissue was ground thoroughly in a mortar with pestle with hot alcohol. Again, it was passed through muslin cloth. The above procedure was repeated. The filtrates were pooled and filtered through Whatman No. 41 filter paper and made upto ten ml volume with alcohol. Then the extract was stored in a refrigerator at 4^0C. This alcoholic extract of the tissue contains reducing sugars, non-reducing sugars, phenols, ortho-dihydroxy phenols and amino acids which were estimated by further analysis.

3.3.4 Clarification of alcoholic extracts

Dark coloured alcohol extracts of the tissue create great problems in analytical procedure. The interference due to coloured plant pigments like chlorophyll, carotenes and xanthophylls is enormous which need to be eliminated prior to analysis. Heavy metal salts are therefore employed to tackle the problem excess, of which is precipitated by disodium hydrogen phosphate.

3.3.4.1 Reagents

Saturated solution of neutral lead acetate and saturated solution of disodium hydrogen phosphate.

3.3.4.2 Procedure

Two ml of saturated lead acetate solution was added drop-wise to ten ml of the coloured alcoholic extract with three ml of saturated solution of disodium hydrogen phosphate till the precipitation completed. The above solutions were mixed thoroughly and kept for overnight. Further, it was filtered through Whatman No. 41 filter paper and made upto 15 ml volume with 80 per cent alcohol and stored in a refrigerator at 4^0C.

3.3.5 Estimation of reducing sugar

The reducing sugar was estimated following Nelson's modification of Somogyi's method (Nelson, 1944).

3.3.5.1 Reagents

Alkaline copper reagent.

Solution A

Twenty five g of anhydrous sodium carbonate, 25 g of sodium potassium tartarate, 20 g of sodium bicarbonate and 200 g of sodium sulphate were dissolved in about 800 ml of distilled water and volume was made upto one litre.

Solution B

Fifteen g of copper sulphate was dissolved in distilled water and added one or two drops of concentrated sulphuric acid and made upto 100 ml volume with distilled water. Solutions A and B were mixed in 24:1 (v/v) proportion just before use.

Arsenomolybdate reagent

1. Twenty five g of ammonium molybdate was dissolved in 450 ml of distilled water. Twenty one ml of concentrated sulphuric acid was added and mixed with above solution.
2. Three g of sodium orthoarcenate was dissolved in 25 ml distilled water.

These above two solutions were mixed with stirring and placed in an incubator at 37^0C for 24-48 h. The reagent was stored in brown bottle.

3.3.5.2 Procedure

One ml of each sample (alcoholic extract) was pipetted to a test tube. To each one ml of extract, one ml of mixture of solution A and B was added. The test tubes were heated in a hot water bath for 20 min. The tubes were then cooled under a running tap water. After cooling one ml of arsenomolybdate reagent was added. The above solution was diluted to 15

ml after 15 min. The absorbance of the solution was measured in spectrophotometer at 500 nm. The amount of reducing sugar was determined by using standard curve prepared.

Acid hydrolysis of non-reducing sugar and its estimation as reducing sugar

Non-reducing sugar was first hydrolyzed with the help of diluted hydrochloric acid. Then the hydrolysate was neutralized and the reducing sugar was estimated by Nelson Somogyi's method.

Reagents

1. 0.1 and 1 N hydrochloric acid and 1 N sodium hydroxide
2. Phenolphthalein indicator solution in alcohol

Procedure

One ml of each alcohol extract was taken in a test tube and to it 1 N HCl was added. The test tubes were kept on hot water bath at 50^0C for 20 min. After cooling, one drop of indicator was added and mixed well. To this solution 1N sodium hydroxide was added drop-wise till the colour turns pink due to excess alkali. The excess alkali was reneutralized with 0.1 N hydrochloric acid till the solution became colourless. Then the volume was made upto five ml.

From the above five ml solution one ml was taken and reducing sugar present in the hydrolysate was estimated by nelson-Somogyi's method. The reducing sugar in the hydrolysate was a measure of total sugar. To get the quantity of non-reducing sugar, the quantity of reducing sugar was subtracted from this value and it was multiplied by a conversion factor of 0.95.

3.3.6 Estimation of total phenol

The total phenol present in plant samples was estimated following Folin-ciocalteau reagent method.

3.3.6.1 Reagents

1. Folin-ciocalteau reagent (FCR, 1%)
2. Sodium carbonate (2%)

3.3.6.2 Procedure

One ml of each alcoholic extract was taken in a test tube to which one ml of Folin-ciocalteau reagent followed by two ml of sodium carbonate solution (2%) were added. The tubes were shaken well and heated in a hot water bath for exactly one minute and then cooled under running tap water. The blue colour developed was diluted to 25 ml with water and its absorbance was read at 650 nm in spectrophotometer. The amount of phenols present in sample was calculated from a standard curve prepared from catechol.

3.4 Molecular characterization of spot blotch disease resistant and susceptible parents

3.4.1 Material

The base material for the present study consisted of one dicoccum variety (DDK 1001) which is susceptible to spot blotch and one durum variety (HD 4502) which is resistant to spot blotch.

3.4.2 Methodology

The DNA was extracted from the wheat genotypes by following CTAB extraction method (Saghai-Maroof *et al.,* 1984) with few modifications as described below.

1. Five grams of fresh young leaves from 10-12 days seedlings was taken. The sample was ground to fine powder in liquid nitrogen with precooled pastle and mortar.
2. The ground tissue was transferred to polypropylene tube containing 15 ml extraction buffer (2-3% w/v CTAB, 14M Nacl, 20mM EDTA, 100mM, Tris-Hcl pH-8; 0.03% □-

mercapto ethanol) pre-heated to 65^0C. Samples were incubated for 30 minutes with intermittent shaking at every 15 minutes.

3. Equal volume of chloroform-iso amyl alcohol (24:1 v/v) was added and gently agitated for 10 minutes to form an emulstion.
4. The tubes were centrifuged for 10 minutes at 6000 rpm at room temperature.
5. The supernatant was transferred to sterile tube and 10 ml of chilled isoproponol was added to each tube, mixed by inverting and incubated at 20^0C for 10 min.
6. The contents were centrifuged again for 20 minutes with 5000 rpm at 4^0C and the pellet was retained by discarding the supernatant.
7. The DNA pellet obtained was washed with 70 per cent ethanol and tubes were inverted on blotting paper to dry the pellet.
8. Later DNA was suspended in 50 □l TE (10 mM Tris Hcl, 1 mM EDTA) buffer and stored at -20^0C.

3.4.3 DNA quantity and quality estimation

The concentration of DNA was assessed spectrophotometrically and also by gel electrophoresis on 0.8 per cent agarose gel with known concentrations of uncut DNA.

To test the quality of DNA, samples were run on 0.8 per cent agarose gel in 1x TAE buffer and stained with ethidium bromide and checked for contamination by RNA (which usually runs ahead) and the DNA was evaluated by comparing it with a standard undigested DNA sample.

3.4.4 Optimization of polymerase chain reactions

3.4.4.1 Template DNA

The purified genomic DNA extracts (30 ng) spot blotch susceptible of (DDK 1001) and spot blotch resistant (HD 4502) wheat genotypes was used as template DNA per reaction.

3.4.4.2 Random primers

Commercial kit OPA, OPC, OPI series of decamer DNA primers were obtained from Operon Technologies Inc. Alamedos, USA and Oligo series from Sigma.Ind.

In order to findout specific primers 32 random decamer primers were used to screen the wheat genotypes. The sequences of the random primers given in Table 4.

3.4.4.3 dNTPs

The four individual dNTPs such as dATP, dGTP, dCTP and dTTP were obtained from M/s Bangalore Genei, Pvt. Ltd., Bangalore.

3.4.4.4 Taq DNA polymerase

Taq DNA polymerase (3 units per □l) and 10x Taq buffer were obtained from M/s Bangalore Genei, Pvt. Ltd., Bangalore.

3.4.4.5 Thermo cycler

Eppendorf was used for cyclic amplification of DNA.

Table 4: Sequences of primers used for parental RAPD polymorphism for spot blotch

Sl. No.		
1	A 02	TGCCGAGCTG
2	A 03	AGTCAGCCAC
3	A 05	AGGGGTCTTG
4	A 06	GGTCCCTGAC
5	A 07	GAAACGGGTG
6	A 08	GTGACGTAGG
7	A 09	GGGTAACGCC
8	A 10	GTGATCGCAG
9	A 11	CAATCGCCGT
10	A 12	TCGGCGATAG
11	A 13	CAGCACCCAC
12	A 14	TCTGTGCTGG
13	A 15	TTCCGAACCC
14	A 16	AGCCAGCGAA
15	A 17	GACCGCTTGT
16	A 18	AGGTGACCGT
17	A 19	CAAACGTCGG
18	A 20	GTTGCGATCC
19	OPC 05	GATGACCGCC
20	OPC 06	GAACGGACTC
21	OPC 08	TGGACCGGTG
22	OPC 10	TGTCTAAATG
23	OPI 20	ACCTGGACAC
24	OPI 20	GATGACCGCC
25	OPC 14	TGCTGTCCTG
26	Oligo 612	GCCTGGTGCC
27	Oligo 631	ATCCGTACGC
28	Oligo 685	ACCACTGGGC
29	Oligo 651	CATTGCTCG
30	Oligo 660	ATGGACAGGC
31	Oligo 678	TAGGGTCGGC
32	Oligo 688	GAGGCTGGGC

3.4.4.6 PCR mixture

The following reaction mixture was found to be optimum for PCR amplification.

Sl. No.	Components	Quantity (ml/reaction)
1	10x assay buffer with 15 mM $Mgcl_2$	2.5
2	dNTPs mix (2.5 mM each)	1.0
3	Primer (5 pM/□l)	1.0
4	Template (30 ng/□l)	1.0
5	Sterile distilled water	19.3
6	Taq DNA polymerase (3u/ml)	0.2

Except template, the master mix was equally distributed to PCR tubes (24 □l/tube) and later 1 □l of template DNA from the respective genotypes was added making the final volume of 25 □l.

3.4.5 The thermoprofile for PCR

The PCR amplification for RAPD analysis was performed according to Williams *et al.* (1990) with certain modifications. The optimum conditions of DNA amplifications were as follows.

Sl. No.	Step	Temperature (^{0}C)	Duration (min.)	Number of cycles
1	Denaturation	94	4	1
2	Denaturation	94	1	
3	Annealing	38	1	45
4	Extension	72	2	
5	Final extension	72	5	1
6	Hold	4	-	-

After the completion of the PCR, the products were stored at 4^0C until the gel electrophoresis was done.

3.4.6 Separation of amplified products on agarose gel electrophoresis

The amplified products from each tube along with 2 □1 of loading dye (bromophenol blue) were separated on 1.2 per cent agarose gel at 70 volts (< 5 volts per cm of gel) using 1x TAE buffer (pH 8.0) containing ethidium bromide (0.5 □g ml^{-1}). The gels were photographed using gel documentation system of ALFA Imager.

The amplified fragments were scored as '1' for the presence and '0' for the absence of a band and total number of fragments were calculated among two parents. The presence of band in one parent and absence in another parent was considered as polymorphic band. Finally the female (susceptible) specific or male (resistance) specific bands were noted.

4. EXPERIMENTAL RESULTS

The results of the experiments conducted are presented under the following headings.

4.1 Experiment 1: Heterosis, combining ability and gene action studies for spot blotch disease resistance, yield and attributing traits using line x tester design

4.1.1 Analysis of variance for parents and crosses (crosses)

The analysis of variance was carried out for 13 characters *viz*., disease scoring at 60 DAS, disease scoring at 90 DAS, days to flowering, days to maturity, plant height, peduncle length, spike length, spikelets per spike, grains per spike, number of tillers per plant, number of productive tillers per plant, thousand grain weight and yield per plant. The degrees of freedom and sum of squares are presented in Table 5. The differences among parents were significant for eight of the 13 characters studied. It was apparent that the 14 parents involved in the study comprising of both susceptible and resistant genotypes significantly differed for disease scoring at 60 DAS, days to flowering, days to maturity, number of tillers per plant, number of productive tillers per plant and thousand grain weight, spikelets per spike and grains per spike. While, the crosses also showed significant differences for characters *viz*., disease scoring at 60 DAS, 90 DAS, days to flowering, days to maturity, plant height, peduncle length, spike length and thousand grain weight. Similarly, parents Vs crosses also exhibited significant variances for disease scoring at 90 DAS, days to flowering, days to maturity, plant height, spike length and yield per plant.

In further partitioning of parental variation into its components, it was seen that the resistant males differed significantly for thousand grain weight, days to flowering and peduncle length. Similarly, susceptible females were significantly different for disease scoring at 60 DAS and days to maturity. Sum of squares due to the interaction component females Vs males were found significant for all the characters except plant height and yield per plant.

4.1.2 Magnitude of heterosis for different characters

Heterosis expressed in percentage was computed for eleven quantitative characters better parent (BP), mid parent (MP) and check DDK1029. The data on heterosis is presented character wise in Tables 6 to 18.

4.1.2.1 Disease scoring at 60 DAS (DS I)

Among female parents, 1 to 2 range was observed for helminthosporium leaf blight disease scoring at 60 DAS, whereas the crosses showed 1 to 3 range of disease score.

Among the 37 crosses that expressed positive heterosis over better parent, only 19 crosses had significant positive heterosis ranging from 0-200 per cent. Three crosses expressed negatively significant over better parent (Table 6) and ranged from -33.33 to -50.00 per cent (DDK 1025 x DWR 185 and HW 1095 x DWR 185).

The magnitude of mid parent heterosis ranged from -60.00 to 140.00 per cent. Positive heterosis over mid parent was expressed in 23 crosses, of which five were significant but only 4 crosses were significant. Negative heterosis was observed in 17 crosses and but only 4 crosses were significant. The highest positive hybrid vigour over mid parent (140.00) was observed in the cross NP200 × NIDW295, while the highest negative hybrid vigour over mid parent (-60.00) was seen in two crosses DDK1025 × DWR185 and HW1095 × DWR185.

Negative significant heterosis over the check DDK1029 was expressed in 20 crosses. While none of the crosses exhibited significant positive heterosis for disease score at 60 DAS.

Table 5: ANOVA for parents and hybrids

Source	df	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP
Replication/ location	1	0.2315	5.3333*	13.3704	0.0003	48.1482	212.8889**	1.3854	1.01389	4.0555	14.3310	31.2569	0.2269	64.9028
Parents	13	0.7582**	2.0357	29.7055**	13.3990**	64.4688	40.7545	1.7718	9.1082*	36.433*	72.4273**	72.5039**	1.6764**	71.6519
Females	9	0.4222**	1.6889	3.8056	3.5556*	39.4739	8.9646	1.0076	4.1312	16.525	34.0098	35.5569	0.7130	84.9331
Males	3	0.0200	1.1250	10.1667*	2.1250	138.6198	81.0804*	0.5616	0.1466	0.5866	9.4679	7.4912	2.0434**	34.1250
Female vs. males	1	5.7140**	7.8892*	321.4219**	135.8125**	66.9687	205.8838*	12.2806**	80.7852**	323.141**	606.524**	600.0654**	9.2546**	64.7024
Hybrids	39	0.6792**	2.3587*	53.3846**	13.7019**	269.6250*	112.4675*	5.9232**	3.3266	13.31	35.7283	30.4529	1.9809**	139.6199
Parents vs hybrids	1	0.1461	53.2149**	1276.359**	11.0625**	263.6250*	1.3906	13.9197**	0.0365	0.2539	57.4321	36.9839	74.4954	1284.688**
Error	53	0.1183	1.2201	3.4269	1.4717	54.6075	28.9577	1.1566	4.4177	17.671	17.6530	21.4423	0.3499	96.9904

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS DF – Days to flowering DM – Days to maturity
PH – Plant Height PL – Peduncle length SL – Spike length SPS – Spikelets per spike
GPS – Grains per spike NTPP – Number of tillers per plant NPTPP – Number of productive tillers per plant TGW – Thousand grain weight
GYP – Grain yield per plant * - Significant at 1% probability level ** - Significant at 5% probability level

Table 6: Magnitude of heterosis for disease score at 60 DAS (DS I)

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	50.00**	0.00	-25.00
2	DDK-1025 x DWR-185	-50.00**	-60.00**	-50.00**
3	DDK-1025 x DWR-1006	50.00**	0.00	-25.00
4	DDK-1025 x DWR-2006	0.00	-33.33	-50.00**
5	MACS-2956 x NIDW-295	0.00	-20.00	-50.00**
6	MACS-2956 x DWR-185	-33.33**	-55.56**	-50.00**
7	MACS-2956 x DWR-1006	50.00**	20.00	-25.00
8	MACS-2956 x DWR-2006	50.00**	20.00	-25.00
9	NP-200 x NIDW-295	200.00**	140.00**	-50.00**
10	NP-200 x DWR-185	33.33**	-11.11	0.00
11	NP-200 x DWR-1006	0.00	-20.00	-50.00**
12	NP-200 x DWR-2006	0.00	-20.00	-50.00**
13	DDK-1030 x NIDW-295	0.00	-33.33	-50.00**
14	DDK-1030 x DWR-185	0.00	-20.00	0.00
15	DDK-1030 x DWR-1006	0.00	-33.33	-50.00**
16	DDK-1030 x DWR-2006	0.00	33.33	0.00
17	MACS-2947 x NIDW-295	150.00**	66.67**	25.00
18	MACS-2947 x DWR-185	50.00**	20.00	-50.00**
19	MACS-2947 x DWR-1006	0.00	-33.33	-50.00**
20	MACS-2947 x DWR-2006	50.00**	0.00	-25.00
21	HW-1095 x NIDW-295	0.00	-33.33	-50.00**
22	HW-1095 x DWR-185	-50.00**	-60.00**	-50.00**
23	HW-1095 x DWR-1006	50.00**	0.00	-25.00
24	HW-1095 x DWR-2006	100.00**	33.33	0.00
25	DDK-1009 x NIDW-295	100.00**	100.00**	0.00
26	DDK-1009 x DWR-185	0.00	-50.00**	-50.00**
27	DDK-1009 x DWR-1006	0.00	0.00	-50.00**
28	DDK-1009 x DWR-2006	100.00**	100.00**	0.00
29	DDK-1029 x NIDW-295	100.00**	33.33	0.00
30	DDK-1029 x DWR-185	25.00**	0.00	25.00
31	DDK-1029 x DWR-1006	0.00	-33.33	-50.00**
32	DDK-1029 x DWR-2006	0.00	-33.33	-50.00**
33	DDK-1028 x NIDW-295	0.00	0.00	-50.00**
34	DDK-1028 x DWR-185	0.00	-50.00**	-50.00**
35	DDK-1028 x DWR-1006	0.00	0.00	-50.00**
36	DDK-1028 x DWR-2006	0.00	0.00	-50.00**
37	MACS-2961 x NIDW-295	50.00**	50.00	-25.00
38	MACS-2961 x DWR-185	10.00*	0.00	0.00
39	MACS-2961 x DWR-1006	50.00**	50.00	-25.00
40	MACS-2961 x DWR-2006	50.00**	50.00	-25.00

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 7: Magnitude of heterosis for disease score at 90 DAS (DS II)

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	10.00	-8.33	-26.67
2	DDK-1025 x DWR-185	-7.69	-11.11	-20.00
3	DDK-1025 x DWR-1006	0.00	-16.67	-33.33**
4	DDK-1025 x DWR-2006	-41.67*	-46.15**	-53.33**
5	MACS-2956 x NIDW-295	-30.00	-46.156**	-53.33**
6	MACS-2956 x DWR-185	-38.46*	-44.83**	-46.67**
7	MACS-2956 x DWR-1006	50.00*	15.38	0.00
8	MACS-2956 x DWR-2006	-33.33	-42.86**	-46.67**
9	NP-200 x NIDW-295	30.00	18.18	-13.33
10	NP-200 x DWR-185	-23.08	-20.00	-33.33*
11	NP-200 x DWR-1006	-10.00	-18.18	-40.00**
12	NP-200 x DWR-2006	-8.33	-8.33	-26.67
13	DDK-1030 x NIDW-295	10.00	-8.33	-26.67
14	DDK-1030 x DWR-185	-15.38	-18.52	-26.67
15	DDK-1030 x DWR-1006	10.00	-8.33	-13.33
16	DDK-1030 x DWR-2006	8.33	0.00	-20.00
17	MACS-2947 x NIDW-295	20.00	-4.00	-60.00**
18	MACS-2947 x DWR-185	-58.5**	-57.14**	-46.67**
19	MACS-2947 x DWR-1006	-20.00	-36.00*	-40.00**
20	MACS-2947 x DWR-2006	-25.00	-33.33*	-46.67
21	HW-1095 x NIDW-295	-20.00	-20.00	-33.33*
22	HW-1095 x DWR-185	0.00	-13.04	-46.67**
23	HW-1095 x DWR-1006	-20.00	-20.00	-60.00**
24	HW-1095 x DWR-2006	-40.00	-45.45*	-46.67**
25	DDK-1009 x NIDW-295	-10.00	-18.18	-40.00**
26	DDK-1009 x DWR-185	-41.67*	-44.00**	-53.33**
27	DDK-1009 x DWR-1006	-10.00	0.00	-26.67
28	DDK-1009 x DWR-2006	-25.00	-25.00	-40.00**
29	DDK-1029 x NIDW-295	-10.00	-28.00	-40.00**
30	DDK-1029 x DWR-185	0.00	-7.14	13.33
31	DDK-1029 x DWR-1006	-10.00	-28.00	-40.00**
32	DDK-1029 x DWR-2006	-8.33	-18.52	-26.67
33	DDK-1028 x NIDW-295	-20.00	-30.43	-46.67**
34	DDK-1028 x DWR-185	-41.5*	-46.15**	-53.33**
35	DDK-1028 x DWR-1006	-30.00	-39.13*	-53.33**
36	DDK-1028 x DWR-2006	-8.33	-12.00	-26.67
37	MACS-2961 x NIDW-295	-10.00	-28.00	-40.00**
38	MACS-2961 x DWR-185	0.00	-7.14	-13.33
39	MACS-2961 x DWR-1006	10.00	-12.00	-26.67
40	MACS-2961 x DWR-2006	-8.33	-18.52	-26.67

* - Significant at 1% probability level ** - Significant at 5% probability level

4.1.2.2 Disease score at 90 DAS (DS II)

The heterosis over better parent ranged from -41.67 (DDK1025 × DWR2006 and DDK1009 × DWR185) to 50.00 per cent (MACS2956 × DWR1026). A total of four crosses showed significant negative heterosis for better parent and one hybrid (MACS2956 × DWR1006) expressed significant positive heterosis (Table 7). The range of mid parent heterosis was from -57.14 (MACS2947 × DWR185) to 18.18 per cent (NP200 × NIDW295). Eleven crosses exhibited significant negative mid parent heterosis, whereas four crosses had positive heterosis but none of them were significant.

The range of standard heterosis over DDK1029 was from -60.00 (MACS2947 × NIDW295 and HW1095 × DWR1006) to 13.33 per cent (DDK1029 × DWR185). Twenty three crosses out of 40 exhibited significant negative heterosis over check DDK1029.

4.1.2.3 Days to flowering (DF)

The magnitude of heterosis for better parent with respect to days to flowering ranged from -15.22 (DDK 1030 × DWR 1006) to 18.11 per cent (DDK1028 × DWR185). A total of 21 crosses recorded significant negative heterosis and 8 crosses expressed significant positive heterosis. The mid parental heterosis ranged from -18.47 (DDK1030 × DWR1006) to 9.89 per cent (DDK1028 × DWR185).

Thirty crosses recorded significant negative heterosis and only three crosses showed significant positive mid parental heterosis (Table 8).

The heterosis over the check DDK1029 ranged from -22.00 (DDK1030 × DWR185 and DDK1030 × DWR1006) to 20.67 per cent (MACS2961 × DWR185). A total of 32 crosses showed significant negative heterosis and only one hybrid expressed significant positive heterosis over the check DDK1029.

4.1.2.4 Days to maturity (DM)

A total of 31 crosses recorded significant positive better parent heterosis with a range of -1.50 (NP 200 × DWR 2006, DDK1030 × DWR2006 and DDK1009 × DWR1006) to 10.20 per cent (HW1095 × NIDW295). Four crosses showed negative better parent heterosis but none of them were significant (Table 9).

The mid parent heterosis for days to maturity ranged from -3.67 (DDK1009 × DWR1006) to 6.67 per cent (HW1095 × NIDW295). A total of 22 crosses expressed significant positive heterosis while only five crosses showed significant negative heterosis.

The range of standard heterosis over the check DDK1029 was from -3.92 (DDK1030 × NIDW295) to 5.88 per cent (HW1095 × NIDW295 and HW1095 × DWR1006). A total of 16 and five crosses recorded significant positive and negative heterosis, respectively.

4.1.2.5 Plant height (cm) (PH)

The better parent heterosis ranged from -49.11 (MACS2961 × DWR2006) to 33.40 per cent (MACS2947 × DWR185) for plant height (Table 10). Out of 40 crosses only nine crosses recorded significant positive heterosis while one hybrid showed significant negative heterosis. Mid parental heterosis ranged from -52.10 (MACS2961 × DWR2006) to 26.75 per cent (MACS2947 × DWR185) with nine crosses and one hybrid with significant positive and negative mid parental heterosis, respectively.

The magnitude of standard heterosis over the check DDK1029 ranged from -47.24 (MACS2961 × DWR2006) to 32.39 per cent (MACS2947 × DWR185). For plant height, 11 crosses recorded significant positive and one hybrid negative heterosis over the check DDK1029.

4.1.2.6 Peduncle length (cm) (PL)

The better parent heterosis for peduncle length ranged from -78.45 (MACS2961 × DWR2006) to 42.28 per cent (DDK1029 × DWR1006). A total of five crosses expressed significant positive heterosis and one hybrid showed significant negative heterosis. The magnitude of midparent heterosis ranged from -81.38 (MACS2961 × DWR2006) to 30.03 per cent (DDK1029 × NIDW295). Out of 40 crosses, only one hybrid recorded significant positive

heterosis and three crosses recorded significant negative heterosis for the trait peduncle length (Table 11).

The heterosis over the check DDK1029 was ranged from -78.66 (MACS2961 × DWR2006) to 40.49 per cent (DDK1025 × DWR2006). Five crosses recorded significant positive heterosis and one hybrid recorded significant negative heterosis over the check DDK1029 for peduncle length.

4.1.2.7 Spike length (cm) (SL)

The magnitude of better parent heterosis for spike length ranged from -16.67 (MACS2961 × DWR1006) to 98.36 per cent (MACS2961 × DWR2006). Out of 40 crosses, only one hybrid recorded significant positive heterosis (Table 12). Sixteen crosses recorded negative heterosis for spike length but none of them were significant.

The mid parent heterosis ranged from -8.01 (MACS2961 × DWR1006) to 134.02 per cent (MACS2961 × DWR2006) for the spike length. A total of four crosses showed significant positive heterosis. Out of 40, six crosses expressed negative heterosis but none of them were significant.

The magnitude of standard heterosis over the check DDK1029 for the trait spike length was ranged from -10.67 (MACS2956 × DWR1006) to 115.55 per cent (MACS2961 × DWR2006). Only one hybrid expressed significant positive heterosis over the check DDK1029 and none of the crosses were recorded significant negative heterosis over the check DDK1029.

4.1.2.8 Number of spikelets per spike (SPS)

The range for the better parent heterosis was from -18.64 (DDK1030 × DWR2006) to 15.98 per cent (MACS2947 × DWR1006). Out of 40 crosses, only one expressed significant negative heterosis for the trait spikelets per spike. None of the crosses expressed significant positive heterosis (Table 13).

The magnitude of mid parental heterosis was ranged from -6.42 (MACS2956 × DWR1006) to 20.55 per cent (MACS2947 × DWR2006). Only two crosses expressed significant positive heterosis and none of the crosses recorded significant negative heterosis. The standard heterosis over the check DDK1029 was ranged from -18.22 (MACS2956 × DWR1006) to 5.14 per cent (MACS2947 × DWR1006). None of the crosses expressed significant heterosis (either positive or negative) for the trait spikelets per spike over the check DDK1029.

4.1.2.9 Number of grains per spike (GPS)

The magnitude of better parent heterosis ranged from -18.64 (DDK 1030 x DWR 2006) to 15.98 per cent (MACS 2947 x DWR 1006). Ten out of 40 crosses recorded positive better parent heterosis but none of them were significant. Mid parent heterosis ranged from -6.42 (MACS 2956 x DWR 1006) to 20.55 per cent (MACS 2947 x DWR 2006). Out of 40 crosses, 28 reported positive mid parent heterosis but only two (MACS 2947 x DWR 2006 and HW 1095 x DWR 2006) were positively significant (Table 14). The standard heterosis over check DDK 1029 was ranged from -18.22 (MACS 2956 x DWR 1006) to 5.14 per cent (MACS 2947 x DWR 1006). Nine crosses reported positive heterosis over the check DDK 1029. But none of them were significant. On the other hand ten crosses reported significant negative heterosis over the check DDK 1029.

4.1.2.10 Number of tillers per plant (NTPP)

The magnitude of better parent heterosis for number of tillers per plant ranged from -54.79 (DDK1009 × DWR2006) to 65.49 per cent (MACS2961 × DWR185). A total of five crosses expressed significant negative heterosis and only one hybrid expressed significant positive heterosis (Table 15).

The mid parent heterosis was ranged from -36.80 (DDK1009 × DWR2006) to 97.95 per cent (DDK 1030 × DWR1006). Out of 40 crosses, eight crosses expressed significant positive heterosis. While eight crosses showed negative heterosis but none of them were significant.

Table 8: Magnitude of heterosis for days to flowering

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-7.52**	-10.55**	-18.00**
2	DDK-1025 x DWR-185	-4.72	-10.04**	-19.33**
3	DDK-1025 x DWR-1006	-10.14**	-11.43**	-17.33**
4	DDK-1025 x DWR-2006	-5.30	-8.76**	-16.67**
5	MACS-2956 x NIDW-295	-3.01	-7.53**	-14.00**
6	MACS-2956 x DWR-185	-1.57	-8.42**	-16.67**
7	MACS-2956 x DWR-1006	-13.77**	-16.20**	-20.67**
8	MACS-2956 x DWR-2006	-10.61**	-15.11**	-21.33**
9	NP-200 x NIDW-295	-9.77**	-15.19**	-20.00**
10	NP-200 x DWR-185	-2.36	-10.47**	-17.33**
11	NP-200 x DWR-1006	-9.42**	-13.19**	-16.67**
12	NP-200 x DWR-2006	-9.85**	-15.60**	-20.67**
13	DDK-1030 x NIDW-295	-7.52**	-12.77**	-18.00**
14	DDK-1030 x DWR-185	-7.87**	-15.22**	-22.00**
15	DDK-1030 x DWR-1006	-15.22**	-18.47**	-22.00**
16	DDK-1030 x DWR-2006	-10.61**	-16.01**	-21.33**
17	MACS-2947 x NIDW-295	-10.53**	-16.20**	-20.67**
18	MACS-2947 x DWR-185	-1.57	-10.07**	-16.67**
19	MACS-2947 x DWR-1006	5.80*	1.04	-2.67
20	MACS-2947 x DWR-2006	-9.09**	-15.19**	-20.00**
21	HW-1095 x NIDW-295	12.78**	7.53**	0.00
22	HW-1095 x DWR-185	16.54**	8.42**	-1.33
23	HW-1095 x DWR-1006	6.52*	3.52	-2.00
24	HW-1095 x DWR-2006	0.00	-5.04*	-12.00**
25	DDK-1009 x NIDW-295	6.02*	1.08	-6.00
26	DDK-1009 x DWR-185	3.94	-3.30	-12.00**
27	DDK-1009 x DWR-1006	-11.59**	-14.08**	-18.67**
28	DDK-1009 x DWR-2006	-6.82*	-11.51**	-18.00**
29	DDK-1029 x NIDW-295	-9.02**	-14.49**	-19.33**
30	DDK-1029 x DWR-185	-5.51	-13.36**	-20.00**
31	DDK-1029 x DWR-1006	-8.70**	-12.50**	-16.00**
32	DDK-1029 x DWR-2006	-4.55	-10.64**	-16.00**
33	DDK-1028 x NIDW-295	9.02**	3.94	-3.33
34	DDK-1028 x DWR-185	18.11**	9.89**	0.00
35	DDK-1028 x DWR-1006	-0.72	-3.52	-8.67**
36	DDK-1028 x DWR-2006	-9.09**	-13.67**	-20.00**
37	MACS-2961 x NIDW-295	-8.27**	-13.48**	-18.67**
38	MACS-2961 x DWR-185	-6.30*	-13.77**	20.67**
39	MACS-2961 x DWR-1006	-11.59**	-14.98**	-18.67**
40	MACS-2961 x DWR-2006	6.82*	0.36	-6.00*

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 9: Magnitude of heterosis for days to maturity

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	4.08**	0.25	0.00
2	DDK-1025 x DWR-185	3.55**	0.00	0.00
3	DDK-1025 x DWR-1006	2.50*	-0.24	0.49
4	DDK-1025 x DWR-2006	2.50*	-0.24	0.49
5	MACS-2956 x NIDW-295	6.12**	4.00**	1.96
6	MACS-2956 x DWR-185	4.57**	2.74*	0.98
7	MACS-2956 x DWR-1006	0.50	-0.50	-1.47
8	MACS-2956 x DWR-2006	1.50	0.50	-0.49
9	NP-200 x NIDW-295	7.65**	4.46**	3.43**
10	NP-200 x DWR-185	6.60**	3.70**	2.94*
11	NP-200 x DWR-1006	-0.50	-2.45*	-2.45*
12	NP-200 x DWR-2006	-1.50	-3.43**	-3.43**
13	DDK-1030 x NIDW-295	0.00	-2.97**	-3.92**
14	DDK-1030 x DWR-185	6.60**	3.70**	2.94*
15	DDK-1030 x DWR-1006	1.50	-0.49	-0.49
16	DDK-1030 x DWR-2006	-1.50	-3.43**	-3.43**
17	MACS-2947 x NIDW-295	8.16**	3.92**	3.92**
18	MACS-2947 x DWR-185	7.11**	3.18**	3.43**
19	MACS-2947 x DWR-1006	7.00**	3.88**	4.90**
20	MACS-2947 x DWR-2006	5.50**	2.43*	3.43**
21	HW-1095 x NIDW-295	10.20**	6.67**	5.88**
22	HW-1095 x DWR-185	5.58**	2.46*	1.96
23	HW-1095 x DWR-1006	8.00**	5.62**	5.88**
24	HW-1095 x DWR-2006	7.00**	4.65**	4.90**
25	DDK-1009 x NIDW-295	6.63**	3.21**	2.45*
26	DDK-1009 x DWR-185	2.03*	-0.99	-1.47
27	DDK-1009 x DWR-1006	-1.50	-3.67**	-3.43**
28	DDK-1009 x DWR-2006	2.50*	0.24	0.49
29	DDK-1029 x NIDW-295	4.08**	2.00	0.00
30	DDK-1029 x DWR-185	3.05	1.25	-0.49
31	DDK-1029 x DWR-1006	3.50**	2.48*	1.47
32	DDK-1029 x DWR-2006	5.50**	4.46**	3.43**
33	DDK-1028 x NIDW-295	6.12**	2.72**	1.96
34	DDK-1028 x DWR-185	8.12**	4.93**	4.41**
35	DDK-1028 x DWR-1006	4.50**	2.20*	2.45*
36	DDK-1028 x DWR-2006	4.00**	1.71	1.96
37	MACS-2961 x NIDW-295	6.12**	3.48**	1.96
38	MACS-2961 x DWR-185	6.09**	3.72**	2.45*
39	MACS-2961 x DWR-1006	2.50*	0.99	0.49
40	MACS-2961 x DWR-2006	4.50**	2.96**	2.45*

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 10: Magnitude of heterosis for plant height

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	16.10	8.21	15.24
2	DDK-1025 x DWR-185	27.76**	19.06**	26.79**
3	DDK-1025 x DWR-1006	2.84	2.11	16.97
4	DDK-1025 x DWR-2006	5.35	4.03	19.82*
5	MACS-2956 x NIDW-295	3.06	1.74	2.29
6	MACS-2956 x DWR-185	6.14	4.78	5.34
7	MACS-2956 x DWR-1006	11.14	4.20	13.17
8	MACS-2956 x DWR-2006	0.11	-6.67	1.94
9	NP-200 x NIDW-295	16.15	15.32*	15.27
10	NP-200 x DWR-185	1.85	1.12	1.08
11	NP-200 x DWR-1006	15.56	7.70	16.36
12	NP-200 x DWR-2006	8.53	0.57	9.27
13	DDK-1030 x NIDW-295	18.72*	15.66*	17.83*
14	DDK-1030 x DWR-185	0.83	-1.7	0.07
15	DDK-1030 x DWR-1006	13.86	8.23	18.97**
16	DDK-1030 x DWR-2006	-3.82	-9.09	0.51
17	MACS-2947 x NIDW-295	7.95	2.58	7.14
18	MACS-2947 x DWR-185	33.40**	26.75**	32.39**
19	MACS-2947 x DWR-1006	-0.49	-3.02	9.11
20	MACS-2947 x DWR-2006	11.23	7.79	21.95*
21	HW-1095 x NIDW-295	4.01	3.70	3.32
22	HW-1095 x DWR-185	-6.78	-7.05	-7.48
23	HW-1095 x DWR-1006	3.57	-3.91	3.40
24	HW-1095 x DWR-2006	-2.26	-9.84	-2.42
25	DDK-1009 x NIDW-295	5.29	3.67	1.34
26	DDK-1009 x DWR-185	25.44**	23.52**	20.73*
27	DDK-1009 x DWR-1006	28.48**	16.86*	23.65**
28	DDK-1009 x DWR-2006	20.40*	8.88	15.88
29	DDK-1029 x NIDW-295	23.80**	23.34**	22.88*
30	DDK-1029 x DWR-185	7.60	7.19	6.78
31	DDK-1029 x DWR-1006	-4.74	-11.73	-4.94
32	DDK-1029 x DWR-2006	1.99	-5.84	1.99
33	DDK-1028 x NIDW-295	12.65	8.79	11.81
34	DDK-1028 x DWR-185	-0.33	-3.75	-1.09
35	DDK-1028 x DWR-1006	-7.50	-11.29	-1.69
36	DDK-1028 x DWR-2006	-6.57	-10.90	-0.69
37	MACS-2961 x NIDW-295	18.24*	15.67*	17.36*
38	MACS-2961 x DWR-185	25.66**	22.92**	24.71**
39	MACS-2961 x DWR-1006	13.23	7.18	17.38*
40	MACS-2961 x DWR-2006	-49.11**	-52.10**	-47.24**

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 11: Magnitude of heterosis for peduncle length

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	18.22	16.03	24.86
2	DDK-1025 x DWR-185	22.86	21.98	32.72*
3	DDK-1025 x DWR-1006	10.69	-3.52	21.31
4	DDK-1025 x DWR-2006	28.19*	17.19	40.49**
5	MACS-2956 x NIDW-295	2.35	-0.09	3.06
6	MACS-2956 x DWR-185	6.97	3.21	7.69
7	MACS-2956 x DWR-1006	17.77	-2.23	18.58
8	MACS-2956 x DWR-2006	-6.21	-18.19	-5.57
9	NP-200 x NIDW-295	2.81	2.47	7.88
10	NP-200 x DWR-185	-15.26	-16.49	-11.08
11	NP-200 x DWR-1006	11.64	-5.07	17.14
12	NP-200 x DWR-2006	1.73	-9.19	6.75
13	DDK-1030 x NIDW-295	16.75	15.31	23.32
14	DDK-1030 x DWR-185	-10.08	-10.18	-2.87
15	DDK-1030 x DWR-1006	9.70	-5.04	18.77
16	DDK-1030 x DWR-2006	-1.32	-10.39	6.84
17	MACS-2947 x NIDW-295	5.87	2.22	11.82
18	MACS-2947 x DWR-185	22.99	20.12	32.86*
19	MACS-2947 x DWR-1006	-0.56	-11.75	12.54
20	MACS-2947 x DWR-2006	4.87	-2.46	18.69
21	HW-1095 x NIDW-295	-10.03	-10.45	-5.84
22	HW-1095 x DWR-185	-10.46	-11.87	-6.28
23	HW-1095 x DWR-1006	6.97	-9.18	11.96
24	HW-1095 x DWR-2006	-26.34	-34.34	-22.91
25	DDK-1009 x NIDW-295	0.54	-4.11	-3.20
26	DDK-1009 x DWR-185	32.61*	24.99	27.67
27	DDK-1009 x DWR-1006	42.28**	15.05	36.99*
28	DDK-1009 x DWR-2006	32.09*	12.32	27.18
29	DDK-1029 x NIDW-295	33.68*	30.03*	33.68*
30	DDK-1029 x DWR-185	3.27	-0.72	3.28
31	DDK-1029 x DWR-1006	-7.75	-23.72*	-7.74
32	DDK-1029 x DWR-2006	-0.83	-13.83	-0.83
33	DDK-1028 x NIDW-295	2.53	-0.57	8.30
34	DDK-1028 x DWR-185	-13.12	-14.77	-6.15
35	DDK-1028 x DWR-1006	-7.38	-18.19	3.94
36	DDK-1028 x DWR-2006	-18.31	-24.37*	-8.35
37	MACS-2961 x NIDW-295	15.43	11.68	14.25
38	MACS-2961 x DWR-185	28.79	23.17	27.48
39	MACS-2961 x DWR-1006	16.29	-4.42	15.11
40	MACS-2961 x DWR-2006	-78.45**	-81.38**	-78.66**

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 12: Magnitude of heterosis for spike length

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-2.24	11.31	1.67
2	DDK-1025 x DWR-185	-4.27	5.04	-0.44
3	DDK-1025 x DWR-1006	-8.12	-0.58	-4.44
4	DDK-1025 x DWR-2006	-0.75	14.98	3.22
5	MACS-2956 x NIDW-295	3.25	11.44	-4.78
6	MACS-2956 x DWR-185	2.05	5.88	-5.89
7	MACS-2956 x DWR-1006	-3.13	-0.99	-10.67
8	MACS-2956 x DWR-2006	-1.81	7.95	-9.44
9	NP-200 x NIDW-295	-9.69	2.50	-6.78
10	NP-200 x DWR-185	-10.55	-2.18	-7.67
11	NP-200 x DWR-1006	-13.02	-6.21	-10.22
12	NP-200 x DWR-2006	-7.10	7.27	-4.11
13	DDK-1030 x NIDW-295	5.18	14.76	-0.67
14	DDK-1030 x DWR-185	9.18	14.57	3.11
15	DDK-1030 x DWR-1006	10.35	14.11	4.22
16	DDK-1030 x DWR-2006	4.59	16.21	-1.22
17	MACS-2947 x NIDW-295	22.36	25.64*	1.56
18	MACS-2947 x DWR-185	20.52	22.35	3.11
19	MACS-2947 x DWR-1006	23.80	27.58*	9.22
20	MACS-2947 x DWR-2006	28.25	34.27*	6.44
21	HW-1095 x NIDW-295	17.84	27.54	9.33
22	HW-1095 x DWR-185	7.54	11.90	-0.22
23	HW-1095 x DWR-1006	5.51	8.16	-2.11
24	HW-1095 x DWR-2006	12.10	23.56	4.00
25	DDK-1009 x NIDW-295	7.63	19.17	5.00
26	DDK-1009 x DWR-185	0.34	6.92	-2.11
27	DDK-1009 x DWR-1006	2.16	7.30	-0.33
28	DDK-1009 x DWR-2006	1.82	14.76	-0.67
29	DDK-1029 x NIDW-295	2.33	14.55	2.33
30	DDK-1029 x DWR-185	8.44	16.89	8.44
31	DDK-1029 x DWR-1006	-4.33	1.65	-4.33
32	DDK-1029 x DWR-2006	5.22	19.87	5.22
33	DDK-1028 x NIDW-295	-0.62	14.54	6.33
34	DDK-1028 x DWR-185	-8.10	2.14	-1.67
35	DDK-1028 x DWR-1006	-0.57	8.99	6.33
36	DDK-1028 x DWR-2006	0.52	17.83	7.56
37	MACS-2961 x NIDW-295	-8.69	5.93	-0.78
38	MACS-2961 x DWR-185	-12.78	-2.40	-5.22
39	MACS-2961 x DWR-1006	-16.67	-8.01	-9.44
40	MACS-2961 x DWR-2006	98.36**	134.02**	115.55**

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 13: Magnitude of heterosis for number of spikelets per spike

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-11.31	-1.51	-8.41
2	DDK-1025 x DWR-185	-14.48	-4.79	-11.68
3	DDK-1025 x DWR-1006	-15.38	-5.79	-12.62
4	DDK-1025 x DWR-2006	-8.14	3.57	-5.14
5	MACS-2956 x NIDW-295	-6.57	-1.33	-13.55
6	MACS-2956 x DWR-185	-3.54	2.14	-10.75
7	MACS-2956 x DWR-1006	-11.62	-6.42	-18.22
8	MACS-2956 x DWR-2006	-1.52	5.69	-8.88
9	NP-200 x NIDW-295	-11.47	-2.28	-9.81
10	NP-200 x DWR-185	-15.14	-6.09	-13.55
11	NP-200 x DWR-1006	-16.97	-.12	-15.42
12	NP-200 x DWR-2006	-6.88	4.37	-5.14
13	DDK-1030 x NIDW-295	-13.98	-1.69	-5.14
14	DDK-1030 x DWR-185	-11.02	1.94	-1.87
15	DDK-1030 x DWR-1006	-14.41	-1.94	-5.61
16	DDK-1030 x DWR-2006	-18.64*	5.65	-10.28
17	MACS-2947 x NIDW-295	5.15	9.97	-4.67
18	MACS-2947 x DWR-185	8.25	13.51	-1.87
19	MACS-2947 x DWR-1006	15.98	21.62	5.14
20	MACS-2947 x DWR-2006	13.40	20.55*	2.80
21	HW-1095 x NIDW-295	12.76	18.50	3.27
22	HW-1095 x DWR-185	-1.02	4.30	-9.35
23	HW-1095 x DWR-1006	0.51	5.91	-7.94
24	HW-1095 x DWR-2006	12.76	20.44*	3.27
25	DDK-1009 x NIDW-295	4.95	11.87	-0.93
26	DDK-1009 x DWR-185	-1.98	4.76	-7.48
27	DDK-1009 x DWR-1006	-1.98	4.76	-7.48
28	DDK-1009 x DWR-2006	-5.94	1.88	-11.21
29	DDK-1029 x NIDW-295	-8.41	0.26	-8.41
30	DDK-1029 x DWR-185	2.80	12.82	2.80
31	DDK-1029 x DWR-1006	-1.40	8.21	-1.40
32	DDK-1029 x DWR-2006	0.47	11.69	0.47
33	DDK-1028 x NIDW-295	-8.37	2.97	-2.80
34	DDK-1028 x DWR-185	-3.96	8.19	1.87
35	DDK-1028 x DWR-1006	-2.05	10.35	3.92
36	DDK-1028 x DWR-2006	-1.76	12.06	4.21
37	MACS-2961 x NIDW-295	-5.91	4.28	-3.27
38	MACS-2961 x DWR-185	-12.73	-3.03	-10.28
39	MACS-2961 x DWR-1006	-9.09	1.01	-6.54
40	MACS-2961 x DWR-2006	-7.27	4.35	-4.67

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 14: Magnitude of heterosis for number of grains per spike

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-5.00	-1.51	-8.41
2	DDK-1025 x DWR-185	-6.40	-4.79	-11.68*
3	DDK-1025 x DWR-1006	-6.80	-5.79	-12.62*
4	DDK-1025 x DWR-2006	-3.60	3.57	-5.14
5	MACS-2956 x NIDW-295	-6.57	-1.33	-13.55**
6	MACS-2956 x DWR-185	-3.54	2.14	-10.75*
7	MACS-2956 x DWR-1006	-11.62	-6.42	-18.22**
8	MACS-2956 x DWR-2006	-1.52	5.69	-8.88
9	NP-200 x NIDW-295	-11.47	-2.28	-9.81
10	NP-200 x DWR-185	-15.14	-6.09	-13.55**
11	NP-200 x DWR-1006	-16.97	-8.12	-15.42**
12	NP-200 x DWR-2006	-6.88	4.37	-5.14
13	DDK-1030 x NIDW-295	-13.98	-1.69	-5.14
14	DDK-1030 x DWR-185	-11.02	1.94	-1.87
15	DDK-1030 x DWR-1006	-14.41	-1.94	-5.61
16	DDK-1030 x DWR-2006	-18.64**	-5.65	-10.28*
17	MACS-2947 x NIDW-295	5.15	9.97	-4.67
18	MACS-2947 x DWR-185	8.25	13.51	-1.87
19	MACS-2947 x DWR-1006	15.98	21.62	5.14
20	MACS-2947 x DWR-2006	13.40	20.55*	2.80
21	HW-1095 x NIDW-295	12.76	18.50	3.27
22	HW-1095 x DWR-185	-1.02	4.30	-9.35
23	HW-1095 x DWR-1006	0.51	5.91	-7.94
24	HW-1095 x DWR-2006	12.76	20.44*	3.27
25	DDK-1009 x NIDW-295	4.95	11.87	-0.93
26	DDK-1009 x DWR-185	-1.98	4.76	-7.48
27	DDK-1009 x DWR-1006	-1.98	4.76	-7.48
28	DDK-1009 x DWR-2006	-5.94	1.88	-11.21*
29	DDK-1029 x NIDW-295	-8.41	0.26	-8.41
30	DDK-1029 x DWR-185	2.80	12.82	2.80
31	DDK-1029 x DWR-1006	-1.40	8.21	-1.40
32	DDK-1029 x DWR-2006	0.47	11.69	0.47
33	DDK-1028 x NIDW-295	-8.37	2.97	-2.80
34	DDK-1028 x DWR-185	-3.96	8.19	1.87
35	DDK-1028 x DWR-1006	-2.05	10.35	3.90
36	DDK-1028 x DWR-2006	-1.76	12.06	4.21
37	MACS-2961 x NIDW-295	-5.91	4.28	-3.71
38	MACS-2961 x DWR-185	-12.73	-3.03	-10.28*
39	MACS-2961 x DWR-1006	-9.09	1.01	-6.54
40	MACS-2961 x DWR-2006	-7.27	4.35	-4.67

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 15: Magnitude of heterosis for number of tillers per plant

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-51.16*	-36.36	-38.24
2	DDK-1025 x DWR-185	-42.33*	-21.77	-27.06
3	DDK-1025 x DWR-1006	-19.53	23.35	1.76
4	DDK-1025 x DWR-2006	-0.47	44.59	25.88
5	MACS-2956 x NIDW-295	-38.76*	-15.28	-7.06
6	MACS-2956 x DWR-185	-9.69	29.44	37.06
7	MACS-2956 x DWR-1006	-25.58	18.70	12.94
8	MACS-2956 x DWR-2006	8.91	65.78**	65.29**
9	NP-200 x NIDW-295	-27.97	0.00	10.59
10	NP-200 x DWR-185	-18.77	16.80	24.71
11	NP-200 x DWR-1006	-42.53*	-8.12	-11.76
12	NP-200 x DWR-2006	-30.27	6.43	7.06
13	DDK-1030 x NIDW-295	18.54	44.03	24.12
14	DDK-1030 x DWR-185	-19.66	2.14	-15.88
15	DDK-1030 x DWR-1006	35.39	97.95**	41.76
16	DDK-1030 x DWR-2006	10.67	52.12	15.88
17	MACS-2947 x NIDW-295	-6.53	18.47	9.41
18	MACS-2947 x DWR-185	12.06	48.17	31.18
19	MACS-2947 x DWR-1006	12.56	69.38*	31.77
20	MACS-2947 x DWR-2006	-9.05	29.29	6.47
21	HW-1095 x NIDW-295	11.89	38.00	21.77
22	HW-1095 x DWR-185	16.49	50.17	26.76
23	HW-1095 x DWR-1006	6.49	57.29	15.88
24	HW-1095 x DWR-2006	13.92	58.46*	24.00
25	DDK-1009 x NIDW-295	-9.04	12.87	0.59
26	DDK-1009 x DWR-185	-35.11	-15.86	-28.23
27	DDK-1009 x DWR-1006	-9.04	34.91	0.59
28	DDK-1009 x DWR-2006	-54.79*	-36.80	-50.00
29	DDK-1029 x NIDW-295	-8.24	9.47	-8.23
30	DDK-1029 x DWR-185	-10.59	11.76	-10.59
31	DDK-1029 x DWR-1006	-2.35	40.98	-2.35
32	DDK-1029 x DWR-2006	11.18	50.60	11.18
33	DDK-1028 x NIDW-295	16.08	28.68	-2.35
34	DDK-1028 x DWR-185	-35.91	-25.18	-46.12
35	DDK-1028 x DWR-1006	31.68	80.62*	10.76
36	DDK-1028 x DWR-2006	52.45	94.64**	28.23
37	MACS-2961 x NIDW-295	-9.86	-0.39	-24.71
38	MACS-2961 x DWR-185	65.49*	92.62**	38.23
39	MACS-2961 x DWR-1006	7.75	47.47	-10.00
40	MACS-2961 x DWR-2006	43.66	82.96*	20.00

* - Significant at 1% probability level ** - Significant at 5% probability level

The standard heterosis over the check DDK1029 was ranged from -50.00 (DDK1009 × DWR2006) to 65.29 per cent (MACS2956 × DWR2006). Only one hybrid (MACS2956 × DWR2006) expressed significant positive heterosis and none of the crosses expressed significant negative heterosis.

4.1.2.11 Number of productive tillers per plant (NPTPP)

The range for better parent heterosis for number of productive tillers per plant (Table 16) was ranged from -56.80 (DDK1009 × DWR2006) to 70.29 per cent (MACS2961 × DWR185). Four crosses out of fourty recorded significant negative heterosis and one hybrid recorded significant positive heterosis.

The mid parent heterosis was ranged from -35.98 (DDK1025 × NIDW295) to 96.40 per cent (DDK1028 × DWR2006). A total of six crosses recorded significant positive heterosis and none of the crosses showed significant negative heterosis.

The heterosis over the check DDK1029 was ranged from -47.85 (DDK1009 × DWR2006) to 47.85 per cent (DDK1030 × DWR1006). None of the crosses recorded significant either positive or negative heterosis for the trait.

4.1.2.12 Thousand grain weight (g) (TGW)

The parent with high thousand grain weight was considered as better parent. The magnitude of better parent heterosis for thousand grain weight was ranged from -14.38 (MACS2961 × DWR185) to 43.29 per cent (NP200 × DWR1006). A total of 17 crosses recorded significant positive heterosis and one significant negative heterosis (Table 17).

The mid parent heterosis was ranged from -2.50 (DDK1009 × NIDW295) to 49.31 per cent (NP200 × DWR1006) and twenty seven crosses recorded significant positive heterosis and none of the crosses recorded significant negative heterosis for the trait thousand grain weight.

The standard heterosis over the check DDK1029 was ranged from 2.98 (DDK1028 × DWR1006) to 51.12 per cent (NP200 × DWR1006). Out of 40 crosses, 34 expressed significant positive heterosis over the check DDK1029 and none of the crosses recorded negative heterosis.

4.1.2.13 Grain yield per plant (g) (GYP)

Among male and female parent of hybrid, a high yielding parent was considered as better parent.

Significant positive hybrid vigour over better parent was observed in two crosses. The heterosis ranged from -27.22 (DDK1029 × DWR2006) to 193.42 per cent (DDK1030 × DWR1006) over the better parent (Table 18).

Nine out of 40 crosses manifested significant positive heterosis over the mid parent for grain yield per plant. Four crosses manifested negative heterosis over mid parent but none of them were significant. The mid parent heterosis was ranged from -24.59 (DDK1029 × DWR2006) to 256.80 per cent (DDK1030 × DWR1006).

The hybrid vigour over the check DDK1029 ranged from -21.77 (DDK1029 × DWR2006) to 225.17 per cent (HW1095 × DWR185). Out of 40, 38 crosses showed positive heterosis over the check, of which only five were significant. Only two crosses manifested negative heterosis but both were non-significant over the check DDK1029.

A total of 29 crosses showed positive heterosis over all the three cases, better parent, mid parent and check DDK1029. The crosses MACS2956 × NIDW295 and DDK1030 × DWR1006 showed significant positive heterosis in all the three cases.

4.1.3 Combining ability and gene action

Analysis of variance for combining ability for all the traits studied was computed and presented in Table 19.

Table 16: Magnitude of heterosis for number of productive tillers per plant

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-51.16*	-35.98	-35.38
2	DDK-1025 x DWR-185	-42.33	-21.77	-23.93
3	DDK-1025 x DWR-1006	-20.93	19.09	4.29
4	DDK-1025 x DWR-2006	-0.47	44.59	31.29
5	MACS-2956 x NIDW-295	-38.28*	-14.36	-3.07
6	MACS-2956 x DWR-185	-8.98	30.17	42.94
7	MACS-2956 x DWR-1006	-25.00	17.61	17.79
8	MACS-2956 x DWR-2006	-29.69	6.82	10.43
9	NP-200 x NIDW-295	-27.24	1.08	14.72
10	NP-200 x DWR-185	-18.68	16.43	28.22
11	NP-200 x DWR-1006	-42.41*	-9.62	-9.20
12	NP-200 x DWR-2006	-29.18	7.69	11.66
13	DDK-1030 x NIDW-295	18.54	45.02	29.45
14	DDK-1030 x DWR-185	-20.22	1.43	-12.88
15	DDK-1030 x DWR-1006	35.39	93.96**	47.85
16	DDK-1030 x DWR-2006	8.99	49.81	19.02
17	MACS-2947 x NIDW-295	-3.63	21.57	14.11
18	MACS-2947 x DWR-185	15.54	51.19	36.81
19	MACS-2947 x DWR-1006	16.06	70.02*	37.42
20	MACS-2947 x DWR-2006	-7.77	29.93	9.20
21	HW-1095 x NIDW-295	-4.17	25.84	26.99
22	HW-1095 x DWR-185	-0.23	35.53	32.21
23	HW-1095 x DWR-1006	-8.80	37.52	20.86
24	HW-1095 x DWR-2006	-2.31	42.09	29.45
25	DDK-1009 x NIDW-295	-7.07	15.15	4.91
26	DDK-1009 x DWR-185	-33.70	-14.69	-25.15
27	DDK-1009 x DWR-1006	-7.07	34.38	4.91
28	DDK-1009 x DWR-2006	-53.80*	-35.85	-47.85
29	DDK-1029 x NIDW-295	-4.29	13.04	-4.29
30	DDK-1029 x DWR-185	-6.75	14.72	-6.75
31	DDK-1029 x DWR-1006	1.84	42.18	1.84
32	DDK-1029 x DWR-2006	15.95	54.92	15.95
33	DDK-1028 x NIDW-295	17.73	30.71	1.84
34	DDK-1028 x DWR-185	-35.11	-24.69	-43.86
35	DDK-1028 x DWR-1006	33.33	77.78*	15.34
36	DDK-1028 x DWR-2006	54.61	96.40*	33.74
37	MACS-2961 x NIDW-295	-7.25	1.99	-21.47
38	MACS-2961 x DWR-185	70.29*	95.83**	44.17
39	MACS-2961 x DWR-1006	10.87	46.76	-6.14
40	MACS-2961 x DWR-2006	47.83	86.30*	25.15

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 17: Magnitude of heterosis for thousand grain weight

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	25.11**	37.18**	44.66**
2	DDK-1025 x DWR-185	16.10**	32.57**	47.15**
3	DDK-1025 x DWR-1006	38.64**	39.85**	34.37**
4	DDK-1025 x DWR-2006	27.41**	40.94**	50.25**
5	MACS-2956 x NIDW-295	16.68*	23.40**	34.99**
6	MACS-2956 x DWR-185	16.39**	28.42**	47.64**
7	MACS-2956 x DWR-1006	32.51**	36.54**	36.60**
8	MACS-2956 x DWR-2006	-5.58	0.79	11.41
9	NP-200 x NIDW-295	13.52*	18.74**	31.27**
10	NP-200 x DWR-185	-0.20	8.97	26.55**
11	NP-200 x DWR-1006	43.29**	49.31**	51.12**
12	NP-200 x DWR-2006	12.62*	18.91**	32.75**
13	DDK-1030 x NIDW-295	21.19**	31.64**	40.20**
14	DDK-1030 x DWR-185	-6.16	6.20	18.98*
15	DDK-1030 x DWR-1006	33.16**	33.38**	29.53**
16	DDK-1030 x DWR-2006	5.89	16.06**	24.94**
17	MACS-2947 x NIDW-295	0.21	5.03	15.88*
18	MACS-2947 x DWR-185	-3.91	5.11	21.84**
19	MACS-2947 x DWR-1006	29.89**	35.07**	36.35**
20	MACS-2947 x DWR-2006	10.63	17.03**	30.52**
21	HW-1095 x NIDW-295	-0.21	5.35	15.39*
22	HW-1095 x DWR-185	6.02	16.79**	34.49**
23	HW-1095 x DWR-1006	14.04	17.71**	17.99*
24	HW-1095 x DWR-2006	-5.10	1.12	11.91
25	DDK-1009 x NIDW-295	-7.89	-2.50	6.58
26	DDK-1009 x DWR-185	8.17	19.45**	37.22**
27	DDK-1009 x DWR-1006	27.68**	31.45**	31.39**
28	DDK-1009 x DWR-2006	8.94	16.38**	28.41**
29	DDK-1029 x NIDW-295	3.00	10.47	19.11*
30	DDK-1029 x DWR-185	-7.78	3.12	16.87*-
31	DDK-1029 x DWR-1006	22.21**	24.09**	22.21**
32	DDK-1029 x DWR-2006	-1.63	6.46	16.01*
33	DDK-1028 x NIDW-295	14.06*	33.42**	31.89**
34	DDK-1028 x DWR-185	-6.95	12.98*	17.99*
35	DDK-1028 x DWR-1006	6.14	14.97*	2.98
36	DDK-1028 x DWR-2006	-4.63	12.47	12.53
37	MACS-2961 x NIDW-295	3.70	16.03*	19.85**
38	MACS-2961 x DWR-185	-14.38*	-0.34	8.56
39	MACS-2961 x DWR-1006	27.64**	31.64**	23.82**
40	MACS-2961 x DWR-2006	2.74	15.94*	21.09**

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 18: Magnitude of heterosis for grain yield per plant

Sl. No.	Crosses	Better parent	Mid parent	Check DDK-1029
1	DDK-1025 x NIDW-295	-22.92	-5.11	57.82
2	DDK-1025 x DWR-185	-5.98	16.94	92.52
3	DDK-1025 x DWR-1006	35.55	104.51*	177.55*
4	DDK-1025 x DWR-2006	11.96	46.84	129.25
5	MACS-2956 x NIDW-295	124.47*	162.93**	187.07**
6	MACS-2956 x DWR-185	8.74	25.95	35.37
7	MACS-2956 x DWR-1006	87.97	116.45**	70.07
8	MACS-2956 x DWR-2006	-7.59	0.34	-0.68
9	NP-200 x NIDW-295	45.21	70.09	85.71
10	NP-200 x DWR-185	31.15	51.90	63.26
11	NP-200 x DWR-1006	127.82	162.34*	106.12
12	NP-200 x DWR-2006	70.25	84.88	82.99
13	DDK-1030 x NIDW-295	68.62	86.47	115.65
14	DDK-1030 x DWR-185	43.72	57.01	78.91
15	DDK-1030 x DWR-1006	193.42**	256.80**	203.40**
16	DDK-1030 x DWR-2006	68.99	72.26	81.63
17	MACS-2947 x NIDW-295	101.06	107.12*	157.14*
18	MACS-2947 x DWR-185	-3.28	-1.67	20.41
19	MACS-2947 x DWR-1006	53.11	97.09	84.35
20	MACS-2947 x DWR-2006	91.53	102.39*	130.61
21	HW-1095 x NIDW-295	-7.74	12.99	86.39
22	HW-1095 x DWR-185	60.94	99.17*	225.17**
23	HW-1095 x DWR-1006	-17.17	24.56	67.35
24	HW-1095 x DWR-2006	-25.25	-2.42	51.02
25	DDK-1009 x NIDW-295	34.65	51.28	120.75
26	DDK-1009 x DWR-185	3.94	18.16	70.41
27	DDK-1009 x DWR-1006	0.00	42.18	63.95
28	DDK-1009 x DWR-2006	-12.03	6.27	44.22
29	DDK-1029 x NIDW-295	12.23	25.97	43.54
30	DDK-1029 x DWR-185	21.31	34.55	51.02
31	DDK-1029 x DWR-1006	-7.14	11.43	-7.14
32	DDK-1029 x DWR-2006	-27.22	-24.59	-21.77
33	DDK-1028 x NIDW-295	-13.30	-3.55	10.88
34	DDK-1028 x DWR-185	9.29	20.12	36.05
35	DDK-1028 x DWR-1006	68.67	104.03*	72.11
36	DDK-1028 x DWR-2006	27.85	31.17	37.42
37	MACS-2961 x NIDW-295	0.00	4.16	27.89
38	MACS-2961 x DWR-185	42.62	46.63	77.55
39	MACS-2961 x DWR-1006	54.08	11.44	2.72
40	MACS-2961 x DWR-2006	32.28	26.28	42.18

* - Significant at 1% probability level ** - Significant at 5% probability level

Table 19: ANOVA for combining ability

Source	Df	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP
Replication/ location	1	0.1125	1.5125	4.5250	0.0004	335.3000*	24.0250	0.1602	6.2188	31.7938	59.5094	0.2156	43.0500	24.875
Females	9	0.6514**	2.9292	125.0139**	31.0833**	281.5208**	147.392**	5.2421**	8.6341*	51.8389	40.8885	4.0929**	217.8398	34.537
Males	3	0.9125	0.07918	25.8167	5.2250	306.7458**	138.339**	7.4192**	1.8042	31.0010	15.0848	0.54467	83.0313	7.217
Female x male	27	0.6625**	2.4218	32.5713**	8.8499**	260.6648**	97.9514	5.9839**	1.7266	30.8834	28.6821	1.4363**	119.8342	6.905
Error	39	0.1381	1.4356	4.0565	1.6795	56.9169	22.2217	1.1565	3.8127	19.9917	23.6204	0.4076	125.6005	15.25

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS DF – Days to flowering DM – Days to maturity
PH – Plant Height PL – Peduncle length SL – Spike length SPS – Spikelets per spike
GPS – Grains per spike NTPP – Number of tillers per plant NPTPP – Number of productive tillers per plant TGW – Thousand grain weight
GYP – Grain yield per plant * - Significant at 1% probability level ** - Significant at 5% probability level

The ANOVA indicated that the gca effect for females was highly significant for seven traits *viz.,* DS I, DF, DM, PH, PL, SL, NPTPP and for SPS. The gca effect due to male parents was highly significant for only three traits *viz.,* PH, PL and SL. Specific combining ability effect for the crosses was highly significant ($p<0.01$) for six traits *viz.,* DS I, DF, DM, PH, SL and NPTPP.

4.1.4 General combining ability effects

The character wise general combining ability effects (gca) of ten susceptible and four resistant parents are presented in Table 20.

The gca effects for disease scoring at 60 DAS ranged from -0.49 in DDK1028 to 0.51 in MACS2947. Eight parents manifested positive gca effects and six showed negative gca effects. Among females, DDK1028, DDK1025 and MACS2956 showed highly significant and negative gca effects. Whereas, NACS2956 recorded significant negative and positive gca effects MACS2947 and NP200. Among males, NIDW295 and DWR185 recorded highly significant positive gca effect and DWR1006 recorded highly significant gca effect in negative direction.

The gca effect for disease scoring at 90 DAS ranged from -0.86 in HW1095 to 0.89 in DDK1030. Among females, one parent (DDK1030) showed significant positive gca effect and two parents (HW1095 and DDK1028) showed significant negative gca effect. However, none of the male parents recorded significant gca effects either positive or negative direction.

The maximum negative gca effect observed was -4.39 in DDK1030, while maximum positive gca effect observed was 8.36 in HW1095 for days to flowering (Table 20). Among females, seven parents recorded highly significant gca effects, of which two were in positive direction. Among males, NIDW295 recorded significant positive gca effect and DWR2006 recorded highly significant negative gca effect.

For days to maturity, the gca effect ranged from -2.59 (DDK1030) to 3.41 (HW1095). Among females, eight parents expressed highly significant gca effects, of which three were in positive direction. Among males, two parents *viz*., NIDW295 and DWR1006 expressed significant positive and negative gca effects, respectively.

The maximum negative gca effect observed was -8.38 in HW1095, while the maximum positive gca effect was 9.26 in DDK1025 for plant height. Among females DDK1025, MACS2947 and DDK1009 showed significant gca effects in positive direction, whereas HW1095, DDK1009, DDK1028 and MACS2961 showed significant negative gca effects for plant height. Among males, only one parent (DWR2006) expressed highly significant negative gca effect.

The gca effect for peduncle length was ranged from -5.32 in HW1095 to 7.60 in DDK1025. Among females, four parents recorded significant gca effects in positive direction. The female parents HW1095 and DDK1028 expressed significant gca effect in negative direction. Among males, DDK1006 recorded highly significant positive gca effect.

For spike length, the gca effect ranged from -0.94 in MACS2956 to 2.01 in MACS2961. Three parents among females expressed highly significant gca effect of which two were in negative. Among males DWR2006 and DWR1006 recorded significant negative gca effects.

For spikelets per spike the gca effect was ranged from -1.59 in MACS2956 to 1.54 in DDK1028. Among females, four parents recorded significant two parents gca effects of which one parent showed gca effect in negative direction. Among males none of the parents expressed significant gca effect for spikelets per spike.

The gca effect for grains per spike ranged from -3.18 (MACS 2956) to 3.09 (DDK 1028). Among females, five parents recorded positive gca effects, in which MACS 2947 and DDK 1028 recorded significant positive gca effects. Among males none of the parents recorded significant positive gca effects.

The gca effect for number of tillers per plant was ranged from -4.39 in DDK1009 to 3.49 in MACS 2956. Four parents among females recorded significant gca effects.

Table 20: Estimation of general combining ability effects of different susceptible lines and resistant testers for spot blotch disease yield and yield attributing traits in tetraploid wheat

	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP
Susceptible lines													
DDK-1025	-0.24*	0.14	-2.14**	-1.09**	9.26**	7.60**	-0.25	-0.87	-1.73	-2.71*	-2.49	1.42**	5.55
MACS-2956	-0.24*	-0.11	-2.39**	-1.09**	-2.79	-1.07	-0.94**	-1.59**	-3.18**	3.49**	1.26	0.49**	-0.52
NP-200	0.26*	0.51	-2.76**	-1.21**	1.35	-1.35	-0.89**	-1.19*	-2.38*	0.19	0.33	0.71**	1.18
DDK-1030	0.01	0.89*	-4.39**	-2.59**	0.36	0.95	-0.12	-0.07	-0.13	1.69	1.88	0.15	6.38*
MACS-2947	0.51**	-0.49	-0.01	2.66**	7.49**	3.66*	0.21	1.23*	2.47*	2.24	2.46	-0.03	3.18
HW-1095	-0.11	-0.86*	8.36**	3.41**	-8.38**	-5.32**	0.00	0.58	1.17	2.65*	2.94**	-0.54**	4.55
DDK-1009	0.01	-0.36	0.99	-1.84**	5.56*	4.81**	-0.20	-0.29	-0.58	-4.39**	-4.09	-0.06	-0.25
DDK-1029	0.14	0.39	-2.14**	-0.21	-1.94	-0.65	0.02	0.81	1.62	-1.54	-1.24	-0.65**	-8.84**
DDK-1028	-0.49**	-0.74*	5.24**	1.41**	-5.88*	-3.43*	0.17	1.54**	3.09**	-1.51	-1.23	-0.83**	-5.50
MACS-2961	0.14	0.64	-0.76	0.54	-5.05*	-5.21**	2.01**	-0.17	-0.33	-0.11	0.18	-0.66**	-5.72
S.E for GCA	0.11	0.35	0.58	0.37	2.18	1.36	0.31	0.56	1.13	1.29	1.40	0.18	3.24
Resistant testers													
NIDW-295	0.16**	-0.01	0.89*	0.46*	2.16	1.06	-0.13	0.01	0.02	-1.35	-1.07	-0.05	1.88
DWR-185	0.16**	-0.01	0.29	0.41	1.72	0.60	-0.32	-0.17	-0.34	-0.60	-0.35	0.09	-0.21
DWR-1006	-0.29**	0.09	0.49	-0.54*	1.99	2.16**	-0.44*	-0.26	-0.51	0.44	0.68	0.16	1.11
DWR-2006	-0.04	-0.06	-1.66**	-0.34	-5.87**	-3.82	0.89**	0.42	0.84	1.51*	0.73	-0.21	-2.77
S.E for GCA	0.06	0.2	0.34	0.22	1.26	0.79	0.18	0.33	0.65	0.75	0.81	0.11	1.87

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS DF – Days to flowering DM – Days to maturity
PH – Plant Height PL – Peduncle length SL – Spike length SPS – Spikelets per spike
GPS – Grains per spike NTPP – Number of tillers per plant NPTPP – Number of productive tillers per plant TGW – Thousand grain weight
GYP – Grain yield per plant * - Significant at 1% probability level ** - Significant at 5% probability level

For number of productive tillers per plant, the gca effect ranged from -4.09 in DDK1009 to 2.94 in HW1095. Among female parents, DDK1009 recorded significant negative and HW1095 recorded significant positive gca effects. For this trait also, none of the male parents recorded significant gca effects.

The gca effect for thousand grain weight was ranged from -0.83 in DDK1028 to 1.42 in DDK1025. In seven female parents highly significant gca effects were observed of which in three were positive. However, none of the male parents expressed significant gca effects for thousand grain weight.

For yield per plant, the gca effect was ranged from -8.84 in DDK1029 to 6.38 in DDK1030. The two female parents DDK1030 and DDK1029 expressed significant positive and negative sca effects, respectively. As in five above characters, none of the male parents expressed significant gca effect for this character.

None of the parents studied showed positive gca effect for all the characters. HW1095 recorded significant gca effect for four characters. Out of 12 characters studied, for three characters DDK1025 and DDK1028 expressed significant gca effects. The male parent NIDW295 expressed significant gca effect for three characters.

The specific combining ability effect of different cross combinations are given in Table 21.

In 50 per cent of the crosses, the sca effects were negative for disease scoring at 60 DAS. The sca effect for disease scoring at 60 DAS was highest in cross NP200 × NIDW295 (1.09) followed by the cross MACS2947 × DWR185 (0.84). Among 40 crosses, eight crosses recorded significant positive sca effects, on the contrary 13 crosses recorded significant sca effects in negative direction.

For disease scoring at 90 DAS, the sca effect varied from -1.44 (DDK1025 × DWR2006) to 2.66 (MACS2956 × DWR1006). Four crosses recorded significant positive sca effects and three crosses recorded significant but negative sca effects for this trait.

The sca effect for days to flowering was ranged from -7.34 (DDK1028 × DWR2006) to 9.16 (MACS2961 × DWR2006). A total of 21 crosses showed negative sca effect of which in nine crosses recorded significant sca effect in negative direction. Among the rest 19 crosses which showed positive sca effect, five and three crosses, respectively recorded highly significant and significant positive sca effect.

For days to maturity, the sca effect varied from -3.29 (NP200 × DWR2006) to 3.84 (DDK1030 × DWR185). In 50 per cent of the crosses, the sca effects were negative for days to maturity. Seven crosses and recorded significant and positive sca effects. On the contrary, seven crosses showed highly significant negative sca effects.

The sca range for the plant height was -37.36 (MACS2961 × DWR2006) to 16.90 (MACS2961 × DWR185). A total of 16 crosses expressed negative sca effects for plant height, of which seven were significant, respectively. Five crosses expressed highly significant and two crosses expressed significant and positive sca effects.

For the peduncle length, the sca effect varied from -22.70 (MACS2961 × DWR2006) to 11.35 (MACS2961 × DWR188). Out of 40 crosses, 22 crosses recorded positive sca effects, of which six showed highly significant and sca effects. Out of 18 crosses, which showed negative sca effects, five crosses were significant.

The sca effect for spike length was ranged from -2.66 (MACS2961 × DWR1006) to 7.25 (MACS2961 × DWR2006). Twenty two crosses expressed positive sca effect but only one hybrid was significant. Out of 18 crosses which expressed negative sca effects, four showed significant sca effect for spike length.

For the trait spikelets per spike in 25 crosses, the sca effect was positive and in 16 it was negative. The sca effect ranged from -1.46 (DDK1029 × NIDW295) to 1.28 (MACS2947 × DWR1006). None of the hybrid expressed significant sca effect for this trait.

Table 21: Estimation of specific combining ability effects of crosses in tetraploid wheat for spot blotch disease yield and component traits

Crosses	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP
DDK-1025 x NIDW-295	0.09	0.51	-1.01	-0.71	-6.00	-2.87	0.28	0.22	0.43	-3.55	-3.76	0.09	-10.18
DDK-1025 x DWR-185	-0.41*	1.01	-1.41	-0.66	4.37	0.45	0.28	-0.30	-0.61	-2.40	-2.58	0.15	-2.99
DDK-1025 x DWR-1006	0.54**	-0.09	-0.11	0.79	-4.34	-5.26*	0.04	-0.42	-0.84	1.46	0.99	-0.95**	8.19
DDK-1025 x DWR-2006	-0.21	-1.44*	2.54*	0.59	5.97	7.68**	-0.60	0.51	1.01	4.49	5.34*	0.70	4.97
MACS-2956 x NIDW-295	-0.41*	-1.24*	2.24*	1.29	-5.08	-2.11	0.39	-0.16	-0.32	-4.45	-2.21	0.24	14.90*
MACS-2956 x DWR-185	-0.41*	-0.74	0.84	0.34	-2.02	0.04	0.49	0.62	1.24	2.30	4.57	1.11**	-5.31
MACS-2956 x DWR-1006	0.54**	2.66**	-2.36*	-1.21	4.45	2.42	0.17	-0.89	-1.79	-2.84	-0.56	0.15	-1.53
MACS-2956 x DWR-2006	0.29	-0.69	-0.71	-0.41	2.65	-0.36	-1.05	0.43	0.86	4.99*	-1.81	-1.50**	-8.06
NP-200 x NIDW-295	1.09	1.14	-1.89	2.91**	1.96	-0.08	0.16	0.24	0.48	1.85	1.62	-0.29	-1.70
NP-200 x DWR-185	0.09	-0.36	0.71	2.46**	-9.82*	-6.49**	0.28	-0.38	-0.76	3.50	3.10	-0.81*	-2.91
NP-200 x DWR-1006	-0.46*	-0.96	1.01	-2.09**	3.05	2.18	0.17	-0.69	-1.39	-3.74	-4.03	1.10**	2.07
NP-200 x DWR-2006	-0.71**	0.19	0.16	-3.29**	4.81	4.39	-0.62	0.83	1.66	-1.61	-0.68	0.00	2.54
DDK-1030 x NIDW-295	-0.66**	-0.24	1.24	-3.21**	5.13	3.22	-0.06	0.12	0.23	2.65	2.47	1.00**	-2.50
DDK-1030 x DWR-185	0.34	-0.24	-1.16	3.84**	-9.70*	-5.81*	0.48	1.00	1.99	-4.90*	-5.15*	-0.85*	-5.81
DDK-1030 x DWR-1006	-0.21	-0.34	-1.36	1.29	6.30	0.47	0.70	0.28	0.56	3.86	3.72	-0.07	11.17
DDK-1030 x DWR-2006	0.54**	0.81	1.29	-1.91**	-1.73	2.12	-1.13*	-1.39	-2.79	-1.61	-1.03	-0.07	-2.86
MACS-2947 x NIDW-295	0.34	1.64**	-5.14	-0.46	-11.19**	-3.66	-0.19	-1.08	-2.17	-0.40	-0.61	-0.78*	6.80
MACS-2947 x DWR-185	0.84**	-1.36*	-1.54**	-0.91	10.95**	4.44	0.15	-0.30	-0.61	2.55	2.37	-0.44	-11.21
MACS-2947 x DWR-1006	-0.71**	-0.46	8.76	1.54*	-9.33*	-4.50	0.81	1.28	2.56	1.61	1.44	0.66*	-3.13
MACS-2947 x DWR-2006	-0.46*	0.19	-2.09**	-0.16	9.57*	3.71	-0.77	0.11	0.21	-3.76	-3.21	0.56	7.54

Contd…

Crosses	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP
HW-1095 x NIDW-295	-0.54**	0.01	1.99*	0.79	1.32	-1.09	0.72	1.27	2.53	1.29	1.01	-0.32	-4.98
HW-1095 x DWR-185	-0.54**	1.01	1.59	-3.16**	-7.45	-0.78	0.06	-1.25	-2.51	1.39	1.14	1.08**	17.51**
HW-1095 x DWR-1006	0.41*	-0.09	0.89	1.79**	1.64	4.26	0.00	-0.87	-1.74	-1.50	-1.74	-0.32	-7.01
HW-1095 x DWR-2006	0.66**	-0.94	-4.46**	0.59	4.49	-2.40	-0.78	0.86	1.71	-1.19	-0.40	-0.44	-5.53
DDK-1009 x NIDW-295	0.34	0.01	4.86**	2.54**	-14.25**	-10.26**	0.53	1.24	2.48	4.73*	4.44	-1.51**	4.87
DDK-1009 x DWR-185	-0.66**	-0.99	0.96	-1.41*	2.86	1.40	0.09	0.02	0.04	-0.93	-1.18	0.82*	-0.44
DDK-1009 x DWR-1006	-0.21	0.91	-4.24**	-2.46*	5.11	3.22	0.37	0.11	0.21	2.93	2.69	0.28	-2.71
DDK-1009 x DWR-2006	0.54**	0.06	-1.59	1.34	6.28	5.64*	-1.00	-1.37	-2.74	-6.73**	-5.96*	0.42	-1.73
DDK-1029 x NIDW-295	0.21	-0.74	-2.01	-1.59	11.77**	8.59	0.07	-1.46	-2.92	0.38	0.09	0.09	2.11
DDK-1029 x DWR-185	0.71**	1.26*	-1.91	-2.04*	-1.63	-1.98**	0.82	1.12	2.24	-0.78	-1.03	-0.22	5.30
DDK-1029 x DWR-1006	-0.34	-0.84	0.89	0.91	-11.98**	-7.55	-0.21	0.31	0.61	-0.42	-0.66	0.13	-4.57
DDK-1029 x DWR-2006	-0.59**	0.31	3.04**	2.71*	1.84	0.95	-0.69	0.03	0.06	0.82	1.59	0.00	-2.84
DDK-1028 x NIDW-295	-0.16	-0.11	2.61*	-1.21	6.20	2.15	0.28	-0.99	-1.99	1.35	1.08	1.30**	-6.03
DDK-1028 x DWR-185	-0.16	-0.61	5.71**	1.34	-4.45	-2.62	-0.25	0.19	0.37	-6.83**	-7.09	0.04	-0.24
DDK-1028 x DWR-1006	0.29	-0.71	-0.99	0.29	-5.23	-0.53	0.60	0.71	1.42	1.79	1.53	-1.24**	3.74
DDK-1028 x DWR-2006	0.04	1.44*	-7.34**	-0.41	3.48	1.00	-0.63	0.10	0.19	3.69	4.48	-0.10	2.52
MACS-2961 x NIDW-295	-0.29	-0.99	-2.89**	-0.34	10.14*	6.09*	-2.20**	0.62	1.23	-3.85	-4.13	0.17	-3.30
MACS-2961 x DWR-185	0.21	1.01	-3.79**	0.21	16.90**	11.35**	-2.40**	-0.70	-1.41	6.10*	5.85*	-0.88	6.09
MACS-2961 x DWR-1006	0.16	-0.09	-2.49*	-0.84	10.33**	5.30*	-2.66**	0.18	0.36	-3.14	-3.38	0.27	-6.23
MACS-2961 x DWR-2006	-0.09	0.06	9.16**	0.96	-37.36**	-22.74	7.25**	-0.09	-0.19	0.89	1.67	0.44	3.44
S.E for SCA	0.19	0.60	1.01	0.65	3.77	2.36	0.54	0.98	1.95	2.24	2.43	0.32	5.60

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS DF – Days to flowering DM – Days to maturity
PH – Plant Height PL – Peduncle length SL – Spike length SPS – Spikelets per spike
GPS – Grains per spike NTPP – Number of tillers per plant NPTPP – Number of productive tillers per plant TGW – Thousand grain weight
GYP – Grain yield per plant * - Significant at 1% probability level ** - Significant at 5% probability level

The sca effect for grains per spike ranged from -2.92 (DDK 1029 x NIDW 295) to 2.56 (MACS 2947 x DWR 1006). Twenty crosses recorded positive sca effects but none of them were significant.

For number of tillers per plant, the sca effect varied from -6.83 (DDK1028 × DWR185) to 6.10 (MACS2961 × DWR185). Out of 40 crosses, 21 recorded positive sca effects of which three were significant. Among the rest 19, two crosses recorded highly significant and one recorded significant sca effects.

The sca effect for number of productive tillers per plant varied from -5.96 (DDK1009 × DWR2006) to 5.85 (MACS2961 × DWR185). In 50 per cent of the crosses, the sca effects were positive of which only two crosses recorded significant sca effects.

For the trait thousand grain weight, the sca effect varied from -1.51 (DDK1009 × NIDW295) to 1.30 (DDK1028 × NIDW295). Out of 40 crosses, 23 crosses recorded positive sca effects and four were highly significant and three were significant. The rest of 17 crosses showed negative sca effects and five and two crosses recorded highly significant and significant sca effects, respectively.

The sca effects for yield per plant ranged from -11.21 (MACS2947 × DWR185) to 17.51 (HW1095 × DWR185). Sixteen crosses showed positive sca effects only two were significant.

4.1.5 Gene action

As summarized in Table 22 variance due to GCA was less that of SCA for all the characters studied except for yield per plant. Hence, the ratio of GCA variance to SCA variance for all the traits except for yield per plant, was less than unity. Additive genetic variance was higher than dominance variance in yield per plant. In the rest of the traits studied, dominance variance was higher than additive variance.

4.1.6 Threshability and pericarp colour

All the dicoccum parents are non free threshing with red pericap colour whereas, durum parents were free threshing and amber grained. All the F_1s reported free threshability and red grain colour (Table 23).

4.2 Experiment 2: Genetics of spot blotch pericarp colour and threshability in tetraploid wheat

4.2.1 Genetics of spot blotch resistance in tetraploid wheat

Helminthosporium leaf blight (spot blotch) of wheat caused by *Bipolaris sorokiniana* is one of the major diseases that limits wheat production. Resistance breeding thus, requires understanding of inheritance pattern of resistance to this disease. In this context, an attempt was made to know the inheritance of resistance to spot blotch through generation mean analysis.

For this, two susceptible parents (DDK-1025 and DDK-1029) were crossed to a resistant parent (NIDW-295) and six generations, *viz.,* P_1, P_2, F_1, F_1, BC_1P_1 and BC_1P_2 were produced. These segregating (F_2, BC_1P_1 and BC_1P_2) and non-segregating (P_1, P_2 and F_1) generations were evaluated at a time and data on characters determining resistance and yield was generated. The data was subjected for scaling tests (Mather, 1949) and six generation mean analysis (Hayman, 1958) in order to study inheritance pattern of resistance to spot blotch. The results obtained are described under the following heads.

1. Generation means

Mean values along with standard error of six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of crosses DDK-1025 x NIDW-295 and DDK-1029 x NIDW-295 in respect to disease score at 2 stages (DS I and DS II), thousand grain weight and yield per plant have been tabulated in Table 24 and 25, respectively and presented character wise in the following paragraphs.

Table 22: Genetic components of variance for quantitative characters in wheat

Sl. No.	Characters	Per cent contribution			GCA Var	S CA Var	GCA Var/SCA Var	Var (A) F=1	Var (D) F=1	Var (A)/ Var (D)
		Lines	Testers	Crosses						
1.	Disease score at 60 DAS	0.00	0.01	0.26	0.0085	0.28	0.03	0.02	0.26	0.076
2.	Disease score at 90 DAS	0.06	-0.12	0.49	0.006	0.36	0.016	0.13	0.49	0.27
3.	Days to flowering	11.56	-0.34	14.26	3.06	20.38	0.15	6.12	14.26	0.43
4.	Days to maturity	2.78	-0.18	3.59	0.66	4.91	0.13	1.33	3.59	0.37
5.	Plant height (cm)	2.61	2.30	101.87	2.39	106.65	0.02	4.78	101.87	0.047
6.	Peduncle length (cm)	6.18	2.02	37.86	3.21	44.28	0.07	6.42	37.86	0.17
7.	Spike length (cm)	-0.09	0.07	2.41	0.025	2.46	0.01	0.05	2.41	0.02
8.	Spikelets per spike	0.86	0.00	-1.04	0.25	0.54	0.46	0.50	1.04	0.48
9.	Grains per spike	3.45	0.02	-4.17	0.99	2.17	0.46	2.00	4.17	0.48
10.	Number of tillers per plant	2.62	0.01	5.45	0.75	6.95	0.11	1.51	5.45	0.28
11.	Number of productive tillers per plant	1.53	-0.68	2.53	0.05	2.43	0.02	0.13	2.53	0.04
12.	Thousand grain weight	0.33	-0.04	0.51	0.063	0.64	0.1	0.13	0.51	0.25
13.	Grain yield per plant	12.55	-1.84	-2.88	2.19	1.49	1.47	4.37	2.88	1.52

Var (A) – Additive variance
Var (D) – Dominance variance

Table 23: Morphological characterization of parents and F_1s for free threshability and pericarp colour

Parents/crosses	Threshability	Pericarp colour	Parents/crosses	Threshability	Pericarp colour	Parents/crosses	Threshability	Pericarp colour
DDK-1025	NF	R	MACS-2956 x NIDW-295	F	R	HW-1095 x DWR-1006	F	R
MACS-2956	NF	R	MACS-2956 x DWR-185	F	R	HW-1095 x DWR-2006	F	R
NP_200	NF	R	MACS-2956 x DWR-1006	F	R	DDK-1009 x NIDW-295	F	R
DDK-1030	NF	R	MACS-2956 x DWR-2006	F	R	DDK-1009 x DWR-185	F	R
MACS-2947	NF	R	NP-200 x NIDW-295	F	R	DDK-1009 x DWR-1006	F	R
HW-1095	NF	R	NP-200 x DWR-185	F	R	DDK-1009 x DWR-2006	F	R
DDK-1009	NF	R	NP-200 x DWR-1006	F	R	DDK-1029 x NIDW-295	F	R
DDK-1029	NF	R	NP-200 x DWR-2006	F	R	DDK-1029 x DWR-185	F	R
DDK-1028	NF	R	DDK-1030 x NIDW-295	F	R	DDK-1029 x DWR-1006	F	R
MACS-2961	NF	R	DDK-1030 x DWR-185	F	R	DDK-1029 x DWR-2006	F	R
NIDW-295	F	A	DDK-1030 x DWR-1006	F	R	DDK-1028 x NIDW-295	F	R
DWR-185	F	A	DDK-1030 x DWR-2006	F	R	DDK-1028 x DWR-185	F	R
DWR-1006	F	A	MACS-2947 x NIDW-295	F	R	DDK-1028 x DWR-1006	F	R
DWR-2006	F	A	MACS-2947 x DWR-185	F	R	DDK-1028 x DWR-2006	F	R
DDK-1025 x NIDW-295	F	R	MACS-2947 x DWR-1006	F	R	MACS-2961 x NIDW-295	F	R
DDK-1025 x DWR-185	F	R	MACS-2947 x DWR-2006	F	R	MACS-2961 x DWR-185	F	R
DDK-1025 x DWR-1006	F	R	HW-1095 x NIDW-295	F	R	MACS-2961 x DWR-1006	F	R
DDK-1025 x DWR-2006	F	R	HW-1095 x DWR-185	F	R	MACS-2961 x DWR-2006	F	R

NF – Non free threshable F – Free threshable R – Red perocarp colour A – Amber pericarp colour

A. DDK-1025 x NIDW-295

a. Disease score at 60 DAS (DS I)

Mean disease score at 60 DAS for spot blotch in the parents varied from 3.30 (P_2) to 3.70 (P_1). Lowest disease score at 60 DAS for spot blotch was observed for F_1 generation (1.60) and highest score for F_2 generation (3.98) (Table 24).

b. Disease score at 90 DAS (DS II)

Wide range of variability was observed for spot blotch disease score at 90 DAS among six generations. The resistant parent (P_2) recorded lowest score (5.20) at 90 DAS and resistant parent (P_1) recorded highest score (8.00) at 90 DAS among six generations. Among segregating generations, BC1P2 recorded lowest (6.35) disease score followed by F_2 generation (6.65) and BC1P1 generation with disease score 7.35 (Table 24).

c. Thousand grain weight (TGW)

In the present study, highest thousand grain weight was observed in F_1 generation (49.73 g) followed by BC_1P_2 (49.35 g), BC_1P_1 (4.428 g) and F_2 (46.94 g) generations. Among parents, P_2 recorded highest (44.07 g) thousand grain weight and P_1 recorded 43.33 g for thousand grain weight (Table 24).

d. Grain yield per plant (GYP)

BC_1P_1 generation showed highest mean value for grain yield per plant (28.95 g) followed by F_1 generation (26.80g). Susceptible parent P_1 expressed highest mean yield levels (23.40 g) compared to resistant parent P_2 (16.70 g). BC_1P_2 and F_2 generations displayed moderate yield levels (24.60 and 25.92 g, respectively) (Table 24).

B. DDK-1029 x NIDW-295

a. Disease score at 90 DAS (DS I)

Mean disease score at 60 DAS for spot blotch in the cross DDK-1029 x NIDW-295 varied from 1.20 (F_1) to 3.50 (P_1) generation (Table 25). Resistant parent P_2 recorded 2.20 diseased score. Among segregating generations, BC_1P_1 generation recorded highest (3.17) disease score followed by BC_1P_1 (2.90) and F_2 generation (2.48).

b. Disease score at 90 DAS (DS II)

Lowest mean disease score at 90 DAS was recorded for F_1 generation (4.20). Among parents, resistant parent P_2 recorded 5.30 and susceptible parent P_1 recorded 8.10 mean disease score at 90 DAS. F_2 generation recorded highest (5.78) mean disease score at 90 DAS among segregating generations followed by BC_1P_2 (5.50) and BC_1P_1 (5.08) generation (Table 25).

c. Thousand grain weight (TGW)

BC_1P_2 generation recorded highest thousand grain weight (48.20 g) followed by F_2 generation with 46.86 g mean thousand grain weight (Table 25). Among parents P_2 expressed highest mean thousand grain weight (46.79 g) followed by P_1 (42.62 g). F_1 and BC_1P_1 generations exhibited moderate mean thousand grain weight of 44.25g and 44.46 g, respectively.

d. Grain yield per plant (GYP)

As for the above character, BC_1P_2 exhibited highest (30.20 g) mean grain yield per plant (Table 25). While, P_2 exhibited lowest means grain yield per plant (14.40). The susceptible parent P_1 recorded 23.60 g mean grain yield per plant. The rest generations, *viz.,* F_1, F_2 and BC_1P_1 recorded 19.10, 24.40 and 25.83 g mean grain yield per plant, respectively.

2 Scaling tests

Segregating and non-segregating generations of the cross DDK-1025 x NIDW-295 and DDK-1029 x NIDW-295 were studied in respect of four traits for scaling tests. This was done to test the adequacy of simple additive dominance model in genetic control of the traits. Further, 't' test was conducted with respect to four parameters A, B, C and D of scaling test.

Table 24: Mean and SE in different generations for disease scoring, thousand grain weight and grain yield per plant (g) in the crosses DDK-1025 x NIDW-295

Characters	P_1 (DDK1025)		P_2 (NIDW295)		F_1		F_2		BC_1P_1		BC_1P_2	
	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm
DSI	3.70	0.22	3.30	0.20	1.60	0.29	3.98	0.15	3.60	0.37	3.45	0.28
DSII	8.00	0.16	5.20	0.12	6.20	0.25	6.65	0.17	6.35	0.42	7.35	0.28
TGW	43.33	1.01	44.07	1.06	49.73	1.96	46.94	0.67	48.42	1.81	49.38	1.93
GYP	23.40	4.56	16.70	1.98	26.80	4.39	25.92	1.42	28.95	3.39	24.60	2.15

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS
TGW – Thousand grain weight GYP – Grain yield per plant

In the present study in the cross DDK-1025 x NIDW-295 for only two traits *viz.,* DS I and DS II, calculated 't' values were found to be larger than table value at both 5 and 1 per cent significance levels (Table 26). In the cross DDK-1029 x NIDW-295 for three traits out of four *viz.,* DS I, DS II and grain yield per plant, calculated 't' values were larger than the table 't' values. This implies that additive and dominance effects of genes (simple additive dominance model) are not satisfactory to explain the inheritance of these characters.

Hence, presence of digenic or higher order non-allelic interaction for two traits in DDK-1025 x NIDW-295 and three traits in DDK-1029 x NIDW-295 was indicated. It was found necessary to incorporate parameters specifying non-allelic gene interaction effects as explained by Hayman (1958) in six parameter model.

3 Six generation mean analysis to estimate gene effects

Hayman's six parameter model (1958) was followed to estimate interaction effects. Mean values of the six generations, *viz.,* P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 were used to estimate various genetic parameters. The parameters estimated were mean effect (m), additive effect (d), dominance effect (h), additive x additive (i),additive x dominance effect (j) and dominance x dominance effect (l).

The results obtained are presented in Table 26 and 27 character wise as below.

a. Disease score at 60 DAS (DS I)

In both the crosses DDK-1025 x NIDW-295 and DDK-1029 x NIDW-295, the mean effect for the trait was positive and significant. While, the dominance gene action (h) was negative and significant in the cross DDK-1025 x NIDW-295. In the second cross, DDK-1029 x NIDW-295, significant epistatic effects were also noticed. The magnitude of additive x additive effect (i) was positively significant. Whereas, dominance x dominance effect (l) was highest and negatively significant. The similar signs in (h) and (l) components in the cross DDK1025 $\times$ NIDW295 and it was duplicate in the cross DDK1029 $\times$ NIDW 295 indicate the presence of complementary nature of epistasis (Table 26).

b. Disease score at 90 DAS (DS II)

As in the above character, the mean effect was positive and highly significant in both the crosses (Table 26). In the cross DDK-1025 x NIDW-295, significant and negative epistatic effect was noticed. The additive x dominance effect (j) was highest and negative. Further, the estimates of (h) and (l) were positive and negative, respectively. This infers duplicate nature of gene interaction operating for the trait.

In the cross DDK-1029 x NIDW-295, the magnitude of dominance effect (h) was found highly significant in negative direction for the trait. Among the interaction effects, additive x dominance (j) effect recorded highly significant negative value and found to be predominant in genetic control of the trait. For this trait, opposite signs of (h) and (l) infer the duplicate type of gene interaction in this cross.

c. Thousand grain weight (TGW)

In the cross DDK 1025 x NIDW 295, the magnitude of dominance (h) effect was found significant in positive direction for the trait thousand grain weight (Table 27). Among the interaction effects, dominance x dominance (l) effect was highly significant and negative and found to be predominant in genetic control of the trait. For this trait, opposite signs of (h) and (l) infer the duplicate type of gene interaction in this cross. In the cross DDK 1029 x NIDW 295, only mean was found highly significant and none of the gene effects were significant.

d. Grain yield per plant (GYP)

In the cross, DDK-1029 x NIDW-295, the mean effect was positive and significant (Table 27). In the F_2 generation of DDK 1025 x NIDW 295, 11 segregants exhibited disease score less than 4 and grain yield per plant of 39 to 60 g. Two F_2 segregants registered spot blotch disease score of 7 and grain yield per plant of 47 and 50 g. In BC_1P_1 (F_1 x DDK 1025) 7 segregants showed disease score less than 4 and grain yield per plant of 43-62 g. Twelve segregants of BC_1P_2 (F_1 x NIDW 295) generation reported disease score less than 5 and grain yield per plant of 38 to 59 g.

Table 25: Mean and SE in different generations for disease scoring, thousand grain weight and grain yield per plant (g) in the crosses DDK-1029 x NIDW-295

Characters	P_1 (DDK1025)		P_2 (NIDW295)		F_1		F_2		BC_1P_1		BC_1P_2	
	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm	Mean	SEm
DSI	3.50	0.32	2.20	0.20	1.20	0.12	2.48	0.09	3.17	0.25	2.90	0.32
DSII	8.10	0.10	5.30	0.16	4.20	0.14	5.78	0.11	5.08	0.33	5.50	0.48
TGW	42.64	1.23	46.79	0.53	44.25	2.36	46.86	0.47	44.46	2.06	48.20	1.14
GYP	23.60	4.52	14.40	1.46	19.10	2.81	24.40	1.00	25.83	4.21	30.20	5.56

DS I – Disease score at 60 DAS DS II – Disease score at 90 DAS
TGW – Thousand grain weight GYP – Grain yield per plant

Table 26: Scaling tests and estimation of gene effects for disease scoring at 2 stages

Scale	DS I		DS II	
	DDK-1025 x NIDW-295	DDK-1029 x NIDW-295	DDK-1025 x NIDW-295	DDK-1029 x NIDW-295
a) Scaling tests				
a	1.90 ± 0.82	1.63* ± 0.61	-1.50 ± 0.89	-2.13** ± 0.68
b	2.00** ± 0.67	2.40** ± 0.67	3.30** ± 0.62	1.50 ± 0.98
c	5.7091** ± 0.88	1.84** ± 0.57	0.99 ± 0.87	1.34* ± 0.54
d	0.9045 ± 0.55	-1.09* ± 0.44	-0.40 ± 0.60	0.99 ± 0.62
b) Gene effects				
m	3.98** ± 0.149	2.48** ± 0.086	6.65** ± 0.17	5.78** ± 0.11
d	0.15 ± 0.465	0.27 ± 0.405	-1.00 ± 0.50	-0.42 ± 0.58
h	-0.37** ± 1.12	0.55 ± 0.909	0.41 ± 1.24	-4.47** ± 1.25
i	-0.18 ± 1.104	2.19* ± 0.88	0.81 ± 1.21	-1.97 ± 1.23
j	-0.50 ± 0.489	-0.38 ± 0.447	-2.40** ± 0.51	-1.82** ± 0.59
l	-0.21 ± 2.06	-6.23** ± 1.72	-2.61 ± 2.19	2.61 ± 2.38

DS I – Disease score at 60 DAS
DS II – Disease score at 90DAS
* - Significant at 1% probability level
** - Significant at 5% probability level

Table 27: Scaling tests and estimation of gene effects for thousand grain weight and grain yield per plant

Scale	Thousand grain weight		Grain yield per plant	
	DDK-1025 x NIDW-295	DDK-1029 x NIDW-295	DDK-1025 x NIDW-295	DDK-1029 x NIDW-295
a) Scaling tests				
a	3.78 ± 4.23	2.05 ± 4.89	7.70 ± 9.27	8.97 ± 9.97
b	4.91 ± 4.45	5.37 ± 3.32	5.70 ± 6.45	26.90* ± 11.57
c	0.90 ± 4.97	9.55 ± 5.26	9.98 ± 11.58	21.39* ± 8.37
d	-3.89 ± 2.95	1.06 ± 2.53	-1.71 ± 4.92	-7.84 ± 7.26
b) Gene effects				
m	46.94** ± 0.66	46.86** ± 0.47	25.92** ± 1.42	24.39** ± 0.99
d	-0.93 ± 2.64	-3.74 ± 2.37	4.35 ± 4.01	-4.37 ± 6.97
h	13.81* ± 6.27	-2.59 ± 5.62	10.17 ± 11.06	14.58 ± 14.97
i	7.78 ± 5.91	-2.13 ± 5.06	3.42 ± 9.84	14.48 ± 14.51
j	-0.56 ± 2.74	-1.66 ± 2.44	1.00 ± 4.72	-8.97 ± 7.37
l	-16.47** ± 11.67	-5.29 ± 10.77	-16.82 ± 19.79	-50.34 ± 29.14

DS I – Disease score at 60 DAS
DS II – Disease score at 90DAS
* - Significant at 1% probability level
** - Significant at 5% probability level

In the F_2 generation of the cross DDK 1029 x NIDW 295, eight segregants reported the lower spot blotch disease score i.e., less than score 5 during second stage with the grain yield per plant of 45 to 65 g. Six F_2 segregants registered higher grain yield per plant *i.e.*, 55 to 70 g and the disease severity was 5-7. In BC_1P_1 (F_1 x DDK 1029) generation 10 segregants exhibited lower disease scores with high grain yield per plant. Similarly in BC_1P_2 (F_1 NIDW 295) 13 segregants registered lower spot blotch disease score and high grain yield per plant.

4.2.2 Genetics of threshability and pericarp colour in tetraploid wheat

In order to study inheritance pattern of threshability and pericarp colour, the non-segregating (P_1, P_2 and F_1) and segregating (F_2, BC_1P_1 and BC_1P_2) generations of two crosses *viz.,* DDK-1025 x NIDW-295 and DDK-1029 x NIDW-295 were evaluated on individual plant basis.

For the trait threshability, all the six generations were screened and categorized as free threshable and non-free threshable. For pericarp colour, all the plants of six generations were classified as red and amber pericarp colour. These observations recorded for individual plants were pooled and utilized for determining the total number of free threshable and non-free threshable for threshability trait and red and amber for pericarp colour in P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 generations.

Further, chi-square method was followed in order to test goodness of fit and establish gene relationship. The results obtained are explained below.

4.2.2.1 Threshability

In the cross DDK-1025 x NDIW-295 (Table 28), it is clear that the parent DDK-1025 (P_1) was found to be non-free threshable. All the 10 plants of F_1 generation were categorized as free threshable.

In case of F_2 population, out of 225 plants scored, 164 plants were registered as free threshable and 61 plants were found to be non-free threshable. Further, these observations displayed a good fit to the monogenic ratio of 3:1 for free threshability verses non-free threshability as indicated by low chi-square value of 0.535 (Table 27). Among the back cross generations, out of 105 plants screened in $BC1P_1$ (F_1 x DDK-1025), 50 free threshable plants were recorded. The data was found to be in good fit with expected ratio of 1:1 for free threshable : non-free threshable with the calculated chi-square value of 0.238. The back cross results further confirmed the F_2 monogenic F : NF ratio of 3:1. In case of BC_1P_2 (F_1 x NIDW-295), out of 108 plants observed, 106 fall under free threshable and 2 under non-free threshable category, which was in conformity with expected F:NF ratio of 1:0.

In another cross, DDK-1029 x NIDW-295 and DDK-1029 (P_1) recorded non-free threshability and NIDW-295 (P_2) recorded free threshability. The F_1 generation also showed free threshability (Table 28).

Further, all the plants of segregating generations were observed for threshability trait. Out of 210 F_2 plants observed, 160 plants categorized as free threshable and 50 as non-free threshable. These observations displayed a good fit to the monogenic F_2 ratio of 3:1 for free threshable to non-free threshable, as it is indicated by low chi-square value of 0.158 (Table 29). A total of 110 $BC1P_1$ (F_1 x DDK-1029) plants were observed in the cross DDK-1029 x NIDW-295 and 58 plants were categorized as free threshable and 52 plants as non-free threshable. Again this data was also found to be in good fit with expected ratio of 1:1 (F:NF) with the calculated chi-square value of 0.327 which is less than tabe chi-square value of 5.99 at 5 per cent with 2 degrees of freedom.

Out of 100 plants observed in BC_1P_2 (F_1 x NIDW-295) generation, which is a test cross, 96 plants categorized four free threshable and as non-free threshable. This was in conformity with expected F :NF ratio of 1:0 with the calculated chi-square value (0.16) less than table chi-square value.

All these results in both the crosses *viz.,* F_2 ratio of 3:1, back cross generations ratio viz., BC_1P_1 ratio of 1:1 and BC_1P_2 ratio of 1:0 (F:NF) depicted that the trait non-free threshability is controlled by single recessive gene and free threshability is dominant over non-free threshability in F_1.

Table 28: Reaction of parents, F_1, F_2 and back cross generations of *T. dicoccum x durum* cross for threshability

Cross : DDK-1025 x NIDW-295

Generation	Free threshable	Non-free threshable	Total
P_1 (DDK1025)	0	10	10
P_2 (NIDW295)	10	0	10
F_1	10	0	10
F_2	164	61	225
BC_1P_1 (F1 × DD1025)	50	55	105
BC_1P_2 (F1 × NIDW295)	108	0	108

Cross : DDK-1029 x NIDW-295

Generation	Free threshable	Non-free threshable	Total
P_1 (DDK1029)	0	10	10
P_2 (NIDW295)	10	0	0
F_1	10	0	10
F_2	160	50	210
BC_1P_1 (F1 × DD1029)	58	52	110
BC_1P_2 (F1 × NIDW295)	100	0	100

4.2.2.2 Pericarp colour

In the cross DDK-1025 x NIDW-295, the parent DDK-1025 was observed to be red pericarp colour and another parent NIDW-295 recorded amber pericarp colour. The F_1 generation was classified under red pericarp colour (Table 30).

Out of 225 F_2 plants, 166 plants showed red pericarp colour and 59 plants showed amber pericarp colour. The chi-square test depicted that the F_2 observations follow a good fit to the ratio of 3:1 red pericarp colour to amber pericarp colour with low chi-square value of 0.1792 (Table 31). In the back cross generations, a total of 105 plants were observed for pericarp colour in BC_1P_1 (F_1 x DDK-1025) and all plants recorded red pericarp colour following the expected ratio of 1:0 for red : amber pericarp colour. In $BC1P_2$ (F_1 x NIDW-295) generation. 56 plants out of 108, recorded red pericarp colour and 52 recorded amber pericarp colour. The test cross result was found to be in good fit with expected ratio of 1:1 for red : amber pericarp colour which further confirmed the F_2 monogenic red : amber ratio of 3:1.

In the second cross DDK-1029 x NIDW-295, P_1 (DDK-1029) showed red pericarp colour, while P_2 (NIDW295) showed amber pericarp colour and the F_1 plants recorded red pericarp colour (Table 30).

In F_2 generation, 210 plants were observed for the trait pericarp colour out of which 155 plants classified as red and 55 plants as amber pericarp colour (Table 30). After the test of goodness of fit with chi-square method, the observations displayed a good fit to the monogenic ratio of 3:1 for red : amber pericarp colour with low chi-square value of 0.158 (Table 31). Among the back cross generations, out of 110 plants screened in $BC1P_1$ (F_1 x DDK-1029), 105 plants with red pericarp colour and 5 plants with amber pericarp colour were recorded. The data was found to be in good fit with expected ratio of 1:0 for red : amber pericarp colour. In case of $BC1P_2$ (F_1 x NIDW-295), 100 plants were observed for pericarp colour and 47 plants showed red and 53 plants showed amber pericarp colour. This back cross ($BC1P_2$) generation results were found good fit with expected ratio of 1:1 red : amber pericarp colour with low chi-square value of 0.360 (Table 31). The back cross results further confirmed the F_2 monogenic, red : amber pericarp colour ratio of 3:1.

For the trait pericarp colour, in both the crosses, the results of F_2 with ratio of 3:1, back cross (BC1 P_1) with the ratio of 1:0 and test cross (BC1 P_2) with ratio of 1:1 (Red : amber) concluded that the trait pericarp colour is controlled by single gene. Finally red pericarp colour is dominant over amber pericarp colour in F_1 generation.

In the cross DDK 1025 x NIDW 295, 18 F2, 7 BC1P1 and 12 BC1P2 segregants were identified with lower spot blotch disease scores and high grain yield per plant. Similarly in the cross DDK 1029 x NIDW 295, 14 F2, 10 BC1P1 and 13 BC1P2 segregants were reported with lower spot blotch disease scores and higher grain yield per plant.

4.3 Experiment 3: Biochemical basis of spot blotch disease resistance

Infection of pathogen brings about lot of changes in respiratory path way and photosynthesis which are the important vital processes taking place inside the plant leading to wider fluctuations in biochemical components. This inturn alters the resistance of the host.

4.3.1 Total sugar

The amount of total sugar in resistant as well as susceptible wheat genotypes decreased as the age of the crop advanced (Table 32). At 60 DAS, the resistant genotypes NIDW 295 recorded maximum (14.54 mg/g dry weight) total sugar content followed by DWR 185 (14.19 mg/g dry weight). At 90 DAS, the same genotype NIDW 295 (11.43 mg/g dry weight) recorded maximum total sugar followed by DWR 185 (11.2 mg/g dry weight). Among susceptible genotypes, DDK 1029 recorded 12.30 mg/g dry weight of sugar and DDK 1025 recorded 11.48 mg/g dry weight of total sugar. The total sugar content of susceptible genotypes also reduced at 90 DAS and recorded lowest total sugar contents. It is found that there was significant decrease in the total sugar content from 60 to 90 DAS.

Table 29: Test of significance of segregation ratios for threshability in *T. dicoccum x T. durum* cross of wheat

Cross : DDK-1025 x NIDW-295

Generation	Observed		Total	Expected		Expected ratio		Chi-square value (χ^2)	Table Chi-square value at 5% with 2 df
	F	NF		F	NF	F	NF		
F_2	164	61	225	168.75	56.25	3	1	0.535	
BC_1P_1	50	55	105	52.5	52.5	1	1	0.238	5.99
BC_1P_2	106	2	108	54	54	1	0	0.037	

NF - Non free threshable BC_1P_1 – Back cross generation 1 with parent 1 (DDK-1025)
F - Free threshable BC_1P_2 – Back cross generation 1 with parent 2 (NIDW-295)

Cross : DDK-1029 x NIDW-295

Generation	Observed		Total	Expected		Expected ratio		Chi-square value (χ^2)	Table Chi-square value at 5% with 2 df
	F	NF		F	NF	F	F		
F_2	160	50	210	157.5	52.5	3	1	0.158	
BC_1P_1	58	52	110	55	55	1	1	0.327	5.99
BC_1P_2	96	4	100	100	0	1	0	0.16	

NF - Non free threshable BC_1P_1 – Back cross generation 1 with parent 1 (DDK-1025)
F - Free threshable BC_1P_2 – Back cross generation 1 with parent 2 (NIDW-295)

Table 30: Reaction of parents, F_1, F_2 and back cross generations of *T. dicoccum x durum* cross for pericarp colour

Cross : DDK-1025 x NIDW-295

Generation	Red pericarp colour	Amber pericarp colour	Total
P_1 (DDK1025)	10	0	10
P_2 (NIDW295)	0	10	10
F_1	10	0	10
F_2	166	59	225
BC_1P_1 (F1 × DD1025)	105	0	105
BC_1P_2 (F1 × NIDW295)	56	52	108

Cross : DDK-1029 x NIDW-295

Generation	Red pericarp colour	Amber pericarp colour	Total
P_1 (DDK1029)	10	0	10
P_2 (NIDW295)	0	10	10
F_1	10	0	10
F_2	155	55	210
BC_1P_1 (F1 × DD1029)	110	0	110
BC_1P_2 (F1 × NIDW295)	47	53	100

Table 31: Test of significance of segregation ratios for pericarp colour in *T. dicoccum x T. durum* cross

Cross : DDK-1025 x NIDW-295

Generation	Observed for		Total	Expected for		Expected ratio		Chi-square value (χ^2)	Table Chi-square value at 5% with 2 df
	Red	Amber		Red	Amber	Red	Amber		
F_2	166	59	225	168.75	56.25	3	1	0.1792	
BC_1P_1	105	0	105	105	0	1	0	-	5.99
BC_1P_2	56	52	108	54	54	1	1	0.1481	

BC_1P_1 – Back cross generation 1 with parent 1 (DDK-1025)
BC_1P_2 – Back cross generation 1 with parent 2 (NIDW-295)

Cross : DDK-1029 x NIDW-295

Generation	Observed		Total	Expected		Expected ratio		Chi-square value (χ^2)	Table Chi-square value at 5% with 2 df
	Red	Amber		Red	Amber	Red	Amber		
F_2	155	55	210	157.5	52.5	3	1	0.158	
BC_1P_1	105	5	110	110	0	1	0	-	5.99
BC_1P_2	47	53	100	50	50	1	1	0.36	

BC_1P_1 – Back cross generation 1 with parent 1 (DDK-1025)
BC_1P_2 – Back cross generation 1 with parent 2 (NIDW-295)

4.3.2 Total phenol

The total phenol content among different genotypes and stages of crop growth varied significantly (Table 32). At 60 DAS, the total phenol content was significantly more in the resistant genotype DWR 185 (2.02 mg/g dry weight) as compared to other resistant genotype NIDW 295 (1.98 mg/g dry weight).The similar trend was also noticed in 90 DAS *i.e.*, DWR 185 recorded highest total phenol (1.62 mg/g dry weight) compared to NIDW 295 (1.57 mg/g dry weight). Among susceptible lines DDK 1025 recorded highest total phenol (1.53 mg/g dry weight) compared to DDK 1029 (1.49 mg/g dry weight). Between resistant and susceptible genotypes between 60 to 90 DAS, there was significant decrease in the total phenol content.

4.4 Experiment 4: Molecular characterization of spot blotch disease resistant and susceptible parents

For assessment of parental polymorphism, total 32 random decamer primers (Operon Technologies Ltd.) to screen parents *viz.,* DDK 1001 (susceptible to spot blotch) and HD 4502 (resistant to spot blotch) (Table 33). Out of 32 primers screened, 4 primers *viz.,* OPA 03, OPA 06, OPA 19 and OPC 10 were not amplified. Maximum number of amplicons (14) produced by OPA 17 and lowest number of amplicons (2) produced by OPA 07 and oligo 615 (Table 32).

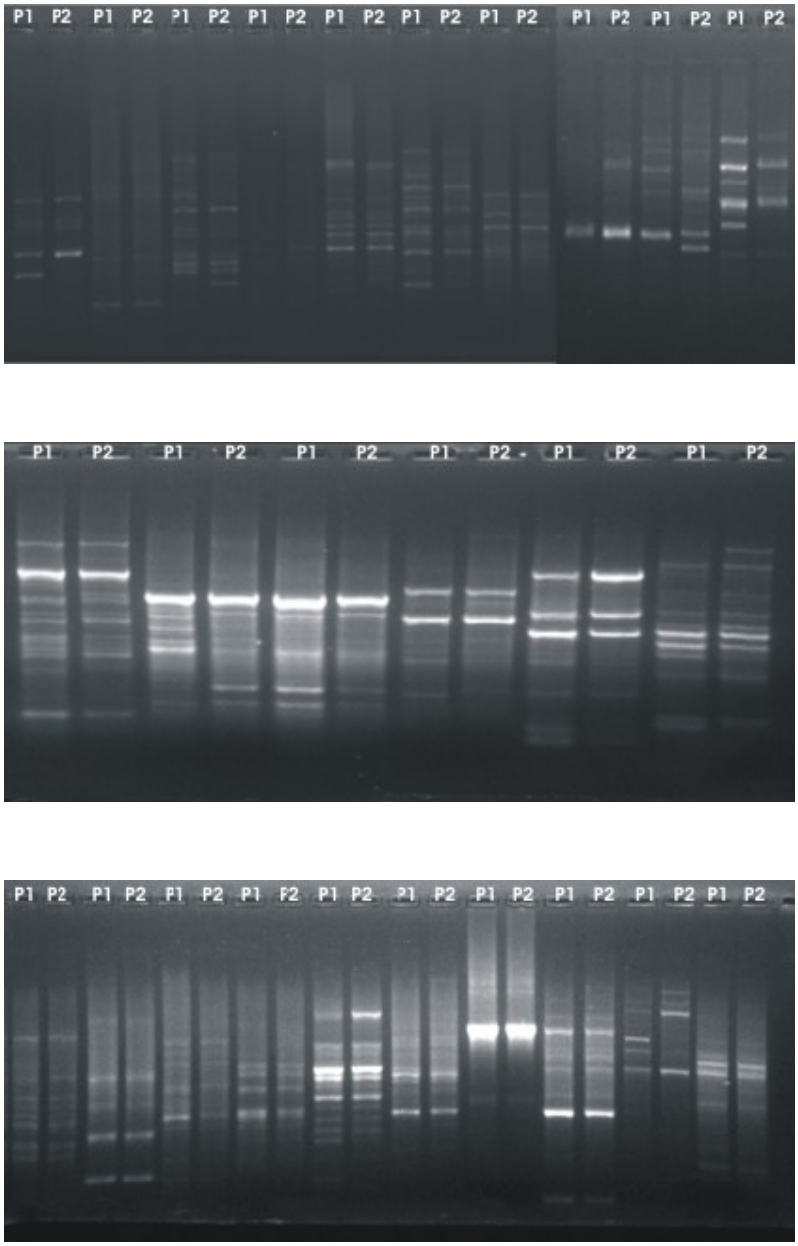
Overall 181 fragments were produced by 28 primers indicating average 6.46 fragments per primers. Out of total 181 fragments, 14 were polymorphic with overall 7.73 per cent polymorphism. Out of 28 amplified primers, 12 were polymorphic. Maximum polymorphism was indicated by OPA 7 primer (50%) and lowest polymorphism was shown by OPA 17 primers (7.14%). Out of 28 oligos, 5 primers developed 7 female parent specific fragments and 7 primers produced 7 male parent specific fragments (Table 33). Further, these polymorphic primers will be used for screening entire mapping population for mapping and tagging of spot blotch disease resistance (Plate 1).

Table 32: Total sugar content and total phenol content in resistant durum susceptible dcoccum genotypes as influenced by spot blotch

Genotypes	Total sugar content mg/g dry weight	Total phenol content mg/g dry weight
NIDW 295 (60 DAS)	14.54	1.98
DWR 185 (60 DAS)	14.19	2.02
DDK 1025 (60 DAS)	11.48	1.53
DDK 1029 (60 DAS)	12.30	1.49
NIDW 295 (90 DAS)	11.43	1.57
DWR 185 (90 DAS)	11.20	1.62
DDK 1025 (90 DAS)	9.01	1.22
DDK 1029 (90 DAS)	9.00	1.30
S.D.	2.05	0.29
S.E.	0.73	0.10
CD at 5% CD at 1%	2.43 3.60	0.33 0.49

Table 33: Parental polymorphism using RAPD

Sl. No.	Primer	No. of fragments	Poly morphic (%)	Poly morphism	Female (susceptible) specific	Male (resistant) specific
1	OPA 02	8	0	0	-	-
2	OPA 03	-	-	-	-	-
3	OPA 05	3	0	0	-	-
4	OPA 06	-	-	-	-	-
5	OPA 07	2	1	50	-	✓
6	OPA 08	4	0	0	-	-
7	OPA 09	7	1	14.29	✓	-
8	OPA 10	10	1	10	-	✓
9	OPA 11	7	1	14.29	-	✓
10	OPA 12	7	2	28.57	✓✓	-
11	OPA 13	6	0	0	-	-
12	OPA 14	6	0	0	-	-
13	OPA 15	10	1	10	-	✓
14	OPA 16	8	1	12.5	-	✓
15	OPA 17	14	1	7.14	✓	-
16	OPA 18	3	0	0	-	-
17	OPA 19	-	-	-	-	-
18	OPA 20	10	0	0	-	-
19	OPC 05	7	1	14.29	-	✓
20	OPC 06	5	0	0	-	-
21	OPC 08	5	0	0	-	-
22	OPC 10	-	-	-	-	-
23	OPC 14	5	0	0	-	-
24	OPI 01	8	0	0	-	-
25	OPI 20	7	1	14.29	-	✓
26	OPI 612	5	0	0	-	-
27	Oligo 631	11	1	9.09	✓	-
28	Oligo 661	4	0	0	-	-
29	Oligo 615	2	0	0	-	-
30	Oligo 660	6	0	0	-	-
31	Oligo 678	6	2	33.33	✓✓	-
32	Oligo 688	5	0	0	-	-
	Total	**181**	**14**	**-**	**7**	**7**



P1 – DDK1001 (Susceptible) P2 – HD4502 (Resistant)

Plate 1: Molecular characterization of spot blotch disease resistance and susceptible parents using RAPD

5. DISCUSSION

Dicoccum wheat (*Triticum dicoccum* Schrank Schulb) a hulled wheat, commonly called by different names *viz.,* "Jave, Khapli, Samba, Sadaka, Kavada" etc., wheat, is grown in a typical hot tropical climate, characterized by the prevalence of high mean daily temperature during the crop growth period affecting GS_1 and GS_3 phase. Dicoccum wheat is considered to be nutritionally and therapeutically superior as compared to commercially available bread and durum wheats with high protein and dietary fiber content. Spot blotch (Helminthosporium leaf blight (HLB)) caused by *Bipolaris sorokiniana* (*Helminthosporium sativum*) is one of the major disease that limits the cultivation of dicoccum wheat. Spot blotch affects all parts of the plant resulting in severe yield losses. Chemical control of the disease alone is ineffective hence an integrated approach is suggested. Even if chemical control is recommended in large scale the cost of cultivation becomes high. Therefore, the alternative strategy to combat the disease is to breed for genetic resistance.

Not much work has been carried out in dicoccum wheat with respect to spot blotch resistance. The reason being this species cultivated in isolated areas with less acerage to search for resistance source to the disease, the wild relative of dicoccum wheat *viz.,* the land races of *Triticum dicoccoides* and other related species are to be screened under epiphytotic conditions. Since, most of the land races of *T. dicoccoides* and other species were winter types, the flowering and the seed setting is a major problem at tropical conditions like Dharwad. More over these wild land races are brittle in nature with tough glumes and transferring resistance to spot blotch is time consuming job which need more resources. The alternative would be to search the source of resistance among the cultivated species cross compatible to dicoccum wheat. Since, durum wheats are evolved from dicoccum wheats, these wheats are similar to dicoccum wheat except brittleness with tough glumes and red grain colour. While, the grain quality of dicoccum wheat is superior with respect to protein content, protein quality, dietary fiber content etc.

It is also easy to transfer spot blotch disease resistance from these durum wheats where the source of resistance to this disease is easily available. This is mainly because the crop improvement in this species has been undertaken at different laboratory since long and many durum wheat varieties having released in India, most of which are resistant to spot blotch.

Work on spot blotch resistance in India has been carried out by Adlakha *et al.* (1994), Singh *et al.* (1997), Singh *et al.* (2000), Joshi *et al.* (2003), Ragiba *et al.* (2004) etc. in bread wheat. But in tetrapliod wheat the information on genetics of spot blotch resistance is inexhaustive. Under such circumstances the first and foremost important objective is to understand the genetics of spot blotch resistance. In this regard, keeping the objective in view, the present investigation was undertaken to study.

i. The genetics of spot blotch resistance in tetraploid wheat using two mating designs *viz.,* line x tester and six generation mean analysis.

ii. To obtain genetic information (relative magnitude of additive and non-additive gene effects for different economic traits) existing in the genetic material as obtained by line x tester design.

iii. To understand the pattern of inheritance for threshability and pericarp colour.

iv. Biochemical basis of spot blotch.

v. Molecular characterization of spot blotch disease resistant and susceptible parents.

The results are discussed experiment wise under following sub headings.

5.1 Experiment 1: Heterosis, combining ability and gene action studies for Spot blotch disease resistance, yield and yield attributing traits using line x tester design

5.1.1 Heterosis

One of the main objectives of genetic analysis is to know the gene action operating in the genotype, which inturn is an indication of the possibility of exploiting available heterotic advantage in a crop under study. The information on heterosis would provide an indication of potentiality of that cross for isolating productive segregants in later generations of segregation. Although heterosis breeding was originally meant for cross pollinated crops, there is sufficient evidence that, it can also be exploited in a number of self pollinated crops including wheat. But commercial exploitation of heterosis in wheat has still been impossible.

The term hererosis was first coined by Shull (1914) and the modern concept of cross vigour (heterosis) came with the work of Shull (1948). He defined hererosis as the superiority of F_1 cross over both of its parents in terms of yield or some other economical trait. Heterosis is manifested as increase in vigour, size, growth rate, yield, decrease in disease etc. It can be best explained as superiority or inferiority of the cross to both the parents. Heterosis is often estimated over the average of the two parents (mid parent) and called as average heterosis. More generally, heterosis is estimated over the superior parent and is referred to as heterobeltiosis.

For the present study, per cent heterosis over mid parent, better parent as well as heterosis over the recently notified best available check variety DDK1029, were calculated for spot blotch disease resistance, yield and other component characters and proportion of the crosses showing heterosis in desirable direction (positive/negative) with respect to each trait was studied.

5.1.1.1 Disease scoring at 60 and 90 DAS

Heterosis for disease would be favourable when it is in the negative direction, as the disease undesired phenomenon. Among the crosses, the cross *viz.,* NP200 x NIDW295 recorded highest heterosis over better parent, mid parent and best check DDK 1029 for disease score at 60 DAS. At 90 DAS, MACS 2956 x DWR 1006 was the cross with highest heterosis. The genes responsible for durable resistance might have extended the resistance for the disease till the attainment of physiological maturity.

5.1.1.2 Days to flowering

Heterosis for maturing traits such as days to flowering and maturity should be in the negative direction, because earliness is required in many aspects as early maturing genotypes can avoid stresses including terminal drought, heat and spot blotch disease.

Heterosis over better parent revealed 21 crosses to be effective towards earliness out of 40 crosses. This result is in conformity with the previous findings of Singh and Singh (2003) in which they found negative significant heterosis in 8 x 8 diallel crosses for the trait days to flowering. More proportion of crosses (75%) showed significant desirable heterosis over mid parent, while 77.5 per cent of the crosses showed desirable standard heterosis over the check DDK1029.

Highest heterobeltiosis and mid parental heterosis in desirable direction was evidenced by the cross DDK 1030 x DWR 1006 and standard heterosis by the cross DDK 1030 x DWR 1006 and DDK 1030 x DWR 185. Similar kind of useful negative heterosis for the trait was reported by Esmail (2002) and Inamullah *et al.* (2006) in the crosses.

5.1.1.3 Days to maturity

Crop duration is an important component while effecting selection pressure. Early genotypes and crosses are more advantageous compared to late types to escape biotic and abiotic stresses *viz.,* disease, heat, moisture etc.

In the present study only 10 per cent of the crosses registered heterobeltiosis in the desirable direction but none of them were significant in desirable direction. Singh and Singh (2003) reported significant better parent heterosis in the crosses of 8 x 8 diallel crosses and Sayed (2004) also reported significant hererosis. As many as only five crosses each showed significant mid parental and standard heterosis over DDK 1029 in desired direction. These results are in conformity with the results of Inamullah *et al.* (2006) in the material of 8 commercial varieties and F_1s for the traits days to maturity.

The cross HW 1095 x NIDW 295 recorded highest heterosis over better parent, mid parent and economic hererosis. The top five crosses which showed early maturity compared to others are DDK 1030 x NIDW 295, NP200 x DWR 2006, DDK 1030 x DWR 2006, DDK 1009 x DWR 185 and NP 200 x DWR 1006 (Table 34).

5.1.1.4 Plant height (cm)

The estimates of heterosis for the trait plant height indicated that there were as many as nine crosses showed positive significant better parent and mid parent heterosis. Also only one cross showed negative heterobeltiosis and heterosis over mid parent. Several earlier workers Afiah and Sattar (1998), Afiah *et al.* (2000) Budak (2001), Mahantashivayogayya (2002), Ashraf *et al.* (2004) and Mahmood *et al.* (2006) also reported significant positive heterosis in plant height. Similarly Kakar *et al.* (1999), Inamullah *et al.* (2006) and Fida Hussain *et al.* (2007) reported significant negative heterosis for the trait plant height. Kamat (1996) and Naik (2000) suggested that whether tallness or dwarfness is desirable is matter of debate. Woyessa (2002) from his experiments concluded that heterosis in the negative direction is better opted for plant height as the trait plant height indirectly affected the grain yield negatively via days to maturity, number of tillers per plant, number of spikes per meter square, grains per spike and test weight. The top five crosses based on per se performance for plant height were MACS 2961 x DWR 2006, HW 1095 x DWR 185, DDK 1029 x DWR 1006, DDK 1028 x DWR 1006 and DDK 1028 x DWR 185 (Table 34).

5.1.1.5 Peduncle length (cm)

Among the 40 crosses, only one cross exhibited significant better parent heterosis as well as heterosis over check and three crosses over the mid parent in desired direction.

The cross MACS 2961 x DWR 2006 exhibited highest heterosis over better parent, mid parent as well as over the check DDK 1029 in the desired direction. This cross MACS 2961 x DWR 2006 ranks first in the list of top five crosses for yield and yield attributing traits based on per se performance for the trait plant height as well as peduncle length (Table 34).

The top five crosses in desired direction were MACS 2961 x DWR 2006, NP200 x DWR 185, DDK 1028 x DWR 2006, DDK 1029 x DWR 1006 and HW1095 x DWR 185 (Table 34).

Mahantashivayogayya (2002) and Singh and Singh (2003) also reported significant heterosis for the trait peduncle length.

5.1.1.6 Spike length (cm)

Spike length can be taken as one of the best selection criteria to improve the yield (Hanchinal *et al.,* 1994). An appreciably higher level of hererosis was evidenced in the present study for spike length. Only one cross registered significant positive heterobeltiosis and standard heterosis and four crosses showed significant positive mid parent hererosis. The cross MACS 2961 x DWR 2006 recorded highest heterosis over better parent, mid parent as well as over the check DDK 1029.

Singh and Singh (2003), Inamullah *et al.* (2006), Ribadia *et al.* (2007) and Bao *et al.* (2009) reported positive significant heterosis for this trait. The mean performance of top five crosses with respect to spike length ranged from 9.57 cm to 9.84 cm. These five crosses were HW 1095 x DWR 185, DDK 1029 x DWR 185, DDK 1028 x DWR 2006, MACS 2947 x DWR 2006, DDK1028 x NIDW 295 and DDK1028 x DWR 1006 (Table 34).

5.1.1.7 Number of spikelets per spike (SPS)

Number of spikelets per spike is also an important yield contributing character in dicoccum wheat. For this trait none of the crosses showed significant positive heterosis over better parent. Two crosses recorded significant positive mid parent heterosis. Several other reports of Kakar *et al.* (1999), Nawracaa *et al.* (2006) and Ribadia *et al.* (2007) also reported positive but lower levels of heterosis for spikelets per spike. The maximum spikelets per spike was manifested by MACS 2947 x DWR 1006 with mean performance of 22.50 spikelets per spike.

The crosses MACS 2947 x DWR 1006, DDK 1028 x DWR 2006, DDK 1028 x DWR 1006, HW1095 x NIDW 295 and HW1095 x DWR 2006, MACS 2947 x DWR 2006 and DDK

1029 x DWR 185 were among the top performers for number of spikelets per spike (Table 34).

5.1.1.8 Number of grains per spike (GPS)

Out of 40, ten crosses reported positive heterosis but none of them were significant for the trait number of grains per spike. Only two crosses reported significant mid parent heterosis. Kakar *et al.* (1999) and Inamullah *et al.* (2006) also reported only positive heterosis for this trait. Based on the per se performance the crosses MACS 2947 × DWR 1006, DDK 1028 × DWR 2006, DDK 1028 × DWR 1006, HW 1095 × NIDW 295 and HW 1095 × DWR 2006, MACS 2947 × DWR 2006 and DDK 1029 × DWR 185 were top performing crosses for number of grains per spike (Table 34)

5.1.1.9 Number of tillers per plant

Only one and eight crosses displayed positive significant heterobeltiosis and mid parent heterosis, respectively for number of tillers per plant. This was also reported by Rajora (2000), Ashraf *et al.* (2004), Inamullah *et al.* (2006) and Fida Hussain *et al.* (2007). Among the fourty crosses, the top five crosses based on per se per performance (Table 34) were MACS 2956 x DWR 2006, DDK 1030 x DWR 1006, MACS 2961 x DWR 185, MACS 2956 x DWR 185 and MACS 2947 x DWR 1006 with 28.10 as the maximum number of tillers per plant.

5.1.1.10 Number of productive tillers per plant

Out of 40 crosses only one cross *viz.,* MACS 2961 x DWR 185 registered significant and positive heterobeltiosis. As many as six crosses recorded significant heterosis over mid parent in desired direction. The cross MACS 2961 x DWR 185 showed highest better parent heterosis among fourty, is one among the top five crosses with high mean number of productive tillers per plant. The positive heterosis for the triat was also reported by Deshpande and Nayeem (1999), Kakar *et al.* (1999), Yadav and Narsinghani (2000), Mahantashivayogayya (2002) and Inamullah *et al.* (2006). The crosses DDK 1030 x DWR 1006, MACS 2961 x DWR 185, MACS 2956 x DWR 185, MACS 2947 x DWR 1006 and MACS 2947 x DWR 185 were among the top performers for number of productive tillers per plant (Table 34).

5.1.1.11 Thousand grain weight

Thousand grain weight is one of the prime characters considered to improve the per se performance of the crosses and varieties in wheat. Generally the spot blotch disease greatly affects the crop during grain filling stage and as a consequence of which the thousand grain weight also gets reduced. Sharma *et al.* (1997) reported that the AUDPC of spot blotch disease negatively correlated with 1000 kernel weight. Therefore, any genotype or cross which show consistently better mean value may be considered as tolerant type.

As many as 17 crosses out of 40 showed consistent significant positive heterosis over better parent and 20 crosses recorded significant positive mid parent heterosis for the trait thousand grain weight. Thirty four crosses registered positive significant heterosis over the check DDK 1029. Many earlier workers *viz.,* Saad (1999), Afiah *et al.* (2000), Rajora (2000), Singh and Singh (2003), Sayed (2004), Nawracaa *et al.* (2006), Akbar *et al.* (2007), Fida Hussain *et al.* (2007) and Bao *et al.* (2009) reported significant positive heterosis for the trait. It is always desirable to decide about the potentiality of the cross by considering the per se performance along with the heterotic value, due to obvious reasons that generally heterosis might result when a high performing parent is crossed with a poor performing parent, though mean performance of such crosses will not be any where near the better or best parent used in the study. The crosses NP 200 x DWR 1006 was not only the top per se performer, but also reported highest heterosis over better parent, mid parent as well as over check DDK 1029. The other top crosses based on per se performance were DDK 1025 x DWR 1006, MACS 2956 x DWR 185, DDK 1025 x DWR 185 and DDK 1025 x NIDW 295 (Table 34).

Table 34: Parental combinations and sca effects of the top crosses exhibiting desirable *per se* performance with respect to yield and yield attributing traits in wheat

Crosses		*Per se* performance	sca effects	Crosses with gca status of parents
Days to maturity	DDK-1030 x NIDW-295	95-100 days	-3.21	H x L
	NP-200 x DWR-2006		-3.29	H x H
	DDK-1030 x DWR-2006		-1.91	H x H
	DDK-1009 x DWR-185		-1.41	H x M
	NP-200 x DWR-1006		-2.09	H x M
Plant height (cm)	MACS-2961 x DWR-2006	45.35	-37.36	H x H
	HW-1095 x DWR-185	79.53	-7.45	H x M
	DDK-1029 x DWR-1006	81.71	-11.98	M x M
	DDK-1028 x DWR-1006	84.51	-5.23	H x M
	DDK-1028 x DWR-185	85.02	-4.45	H x M
Peduncle length (cm)	MACS-2961 x DWR-2006	7.74	-22.74	H x M
	NP-200 x DWR-185	32.26	-6.49	M x M
	DDK-1028 x DWR-2006	33.26	1.00	H x M
	DDK-1029 x DWR-1006	33.47	-7.55	M x L
	HW-1095 x DWR-185	34.00	-0.78	H x M
Spike length (cm)	HW-1095 x DWR-185	9.84	0.72	M x M
	DDK-1029 x DWR-185	9.76	0.82	M x M
	DDK-1028 x DWR-2006	9.68	-0.63	M x H
	MACS-2947 x DWR-2006	9.58	-0.77	M x H
	DDK-1028 x NIDW-295 and DDK-1028 x DWR-1006	9.57	0.28 0.60	M x M M x L
Spikelets per spike	MACS-2947 x DWR-1006	22.50	1.28	H x M
	DDK-1028 x DWR-2006	22.30	0.10	H x M
	DDK-1028 x DWR-1006	22.24	0.71	H x M
	HW-1095 x NIDW-295 and HW-1095 x DWR-2006	22.10	1.27 0.86	M x M M x M
	MACS-2947 x DWR-2006 and DDK-1029 x DWR-185	22.00	0.11 1.12	H x M M x M

Contd…

Crosses		*Per se* performance	sca effects	Crosses with gca status of parents
Grains per spike	MACS-2947 x DWR-1006	45.00	2.56	H x M
	DDK-1028 x DWR-2006	46.00	0.19	H x M
	DDK-1028 x DWR-1006	44.47	1.42	H x M
	HW-1095 x NIDW-295 and HW-1095 x DWR-2006	44.20	2.53 1.71	M x M M x M
	MACS-2947 x DWR-2006 and DDK-1029 x DWR-185	44.00	0.21 2.24	H x M M x M
Number of tillers per plant	MACS-2956 x DWR-2006	28.10	4.99	H x H
	DDK-1030 x DWR-1006	24.10	3.86	M x M
	MACS-2961 x DWR-185	23.50	6.10	M x M
	MACS-2956 x DWR-185	23.30	2.30	H x M
	MACS-2947 x DWR-1006	22.40	1.61	M x M
Number of productive tiller per plant	DDK-1030 x DWR-1006	24.10	3.72	M x M
	MCAS-2961 x DWR-185	23.50	5.85	M x M
	MAS-2956 x DWR-185	23.30	4.57	M x M
	MACS-2947 x DWR-1006	22.40	1.44	M x M
	MACS-2947 x DWR-185	22.30	2.37	M x M
Thousand grain weight (g)	NP-200 x DWR-1006	12.18	1.10	H x M
	DDK-1025 x DWR-1006	12.11	0.70	H x M
	MACS-2956 x DWR-185	11.90	1.11	H x M
	DDK-1025 x DWR-185	11.86	0.15	H x M
	DDK-1025 x NIDW-295	11.66	0.09	H x M
Grain Grain yield per plant (g)	HW-1095 x DWR-185	47.80	17.51	M x M
	DDK-1030 x DWR-1006	44.60	11.17	H x M
	MACS-2956 x NIDW-295	42.20	14.90	M x M
	DDK-1025 x DWR-1006	40.80	8.19	M x M
	MACS-2947 x NIDW-295	37.80	6.80	M x M

5.1.1.12 Grain yield per plant

Grain yield is the most important character in which breeder invariably interested to improve. It is a complex quantitative character influenced directly or indirectly by many componental traits. It is also being influenced by the environmental conditions which posses problems in selecting genetically potential plants. Therefore, most of the times, breeders have to exercise caution while selecting for this trait. Many a times, the higher expression is due to manipulation of the local microclimatic conditions, which may not be heritable. Compared to other quantitative traits, grain yield per plant witnessed very high magnitude of heterosis. The relative heterosis ranged from -27.22 to 193.42 per cent for the trait.In the present study, only two and seven crosses displayed significant positive heterosis over better parent and mid parent respectively. As many as five crosses recorded significant positive heterosis over the check DDK 1029.

Many early researcher *viz.,* Budak (2001), Hamada *et al.* (2002), Singh and Singh (2003), Ashraf *et al.* (2004), Nawracaa *et al.* (2004), Sayed (2004), Hosary *et al.* (2005), Sayed and Moshref (2005), Akbar *et al.* (2007), Fida Hussain *et al.* (2007), Ribadia *et al.* (2007) and Bao *et al.* (2009) reported significant wide range of heterosis for grain yield per plant.

The cross DDK 1030 x DWR 1006 reported highest heterosis over better parent and mid parent with the per cent heterosis of 193.42 per cent and 256.80 per cent respectively. This cross is one among the top five crosses based on per se performance. This cross showed 187.07 per cent heterosis over check DDK 1029. The crosses MACS 2956 x NIDW 295 and DDK 1030 x DWR 1006 showed significant positive heterosis over better parent, mid parent and over check DDK 1029. The cross HW 1095 x DWR 185 showed highest standard heterosis of 225.17 per cent and is top performer for the trait grain yield per plant with the mean of 47.80 g. The top five crosses exhibited not only the high per se performance but also exhibited significant positive heterosis.

The present investigation revealed that maximum heterosis was observed for grain yield per plant. However, all the crosses showing heterosis for grain yield per plant were not heterotic for all other component characters and also different characters did not manifest heterosis equally.

These findings support the view point of Singh and Konda (1969) and Singh and Singh (1970) who also found that heterosis in a complex character like yield can be registered by heterosis in single or several characters. However, Williams (1959), Adams and Durate (1961) and Adams (1967) were of opinion that heterosis in a complex character is attained through component character interaction when hybrid parents differ reciprocally in different components.

5.1.2 Analysis of variance for combining ability

The ratio of the additive and non-additive variance, which is to be considered in order to decide the predominance of the kind of genetic variance for a given character. If the ratio of the additive to non-additive variance is more than unity, it indicates the major role of additive gene action in controlling the expression of character whereas, less than unity indicates the importance of non-additive variance. There was more non-additive variance for all the characters except for the yield per plant. Under such situations where non-additive variance is predominant, simple selection will not be of any use to fix the higher expression observed in these characters. Predominance of additive genetic variance for grain yield implied that simple selection measures would bring about desired improvement and self pollination behaviour of tetraploid wheat will provide the basis for predominance of additive genetic variance for quantitative trait like grain yield.

5.1.3 General combining ability effects

5.1.3.1 Disease

In respect of disease scores at 60 DAS i.e., first stage (DS I), significant negative gca effects were observed for lines DDK 1025, MACS 2956 and DDK 1028 and a tester DWR-1006. Crosses involving these parents are expected to exhibit lower disease scores. At first stage of disease score, thirteen crosses exhibited significant negative sca effects. The crosses NP 200 x DWR 2006 and MACS 2947 x DWR 1006 exhibited highest sca effects.

Nevertheless, higher magnitude of sca variance obtained in the present investigation revealed preponderance of non-additive gene action for the trait.

In the present study for disease score at 90 DAS i.e., second stage (DS II), only two parents namely HW-1095 and DDK1028 recorded negative significant gca effects. As many as three crosses recorded negative significant sca effects for the trait. At this stage also sca variance was higher than gca variance, indicating the predominance of non-additive gene action controlling the trait.

5.1.3.2 Days to flowering

In the study, the ratio of gca variance to sca variance was lesser than unity. This indicates that non-additive type of gene action plays a major role in controlling the trait. Hamada *et al.* (2002) and Desai *et al.* (2005) noticed predominance of non-additive gene action for the trait. Among the parents, five lines viz., DDK 1030, NP 200, MACS 2956, DDK 1025 and DDK 1029 and one tester DWR 2006 found to be best general combiners with significantly negative gca effects for days to flowering. The parents HW 1095, DDK 1028 and NIDW 295 were proved to be poor general combiners for the trait. With regard to sca effects, nine crosses proved to be superior. These results are in conformity with the reports of Desai et al. (2005), Darwish et al. (2006), Hassan et al., (2006) and Ismail et al., (2006).

5.1.3.3 Days to maturity

Prominence of gca variance over sca variance was observed for the trait days to maturity and the ratio of gca variance to the sca variance less than unity obtained in the present study suggested predominance of non-additive gene action for the trait. The findings of Pandey *et al.* (1999), Desai *et al.* (2005) and Vanpariya *et al.* (2006) were supportive of this observation. Contrarily, presence of additive effects was reported by Joshi *et al.* (2004a), Siddique *et al.* (2004), Malik *et al.* (2005) and Inamullah *et al.* (2006).

The six parents *viz.,* DDK 1030, DDK 1009, NP 200, DDK 1025, MACS 2956 and DWR 1006 were reported as best general combiners with the significant negative gca effects for days to maturity. As many as nine crosses were recorded as best specific, combiners based on their sca effects. Similarly, Mavi *et al.* (2003), Joshi *et al.* (2004a), Nour (2005b), Dhadhal and Dobariya (2006) and Inamullah *et al.* (2006) reported the significant gca and sca effects in wheat. From the Table 34, it is clear that the top five crosses recorded for days to maturity which showed maturity in 95 to 100 days had atleast one of the parent as best general combiner for the trait.

5.1.4 Plant height (cm)

Analysis of data for combining ability revealed that sca variance was found to be prominent. This points the non-additive effects to be relatively more important for the trait. The findings of Singh *et al.* (2003), Choudhary *et al.* (2005), Ismail *et al.* (2006) and Ribadia *et al.* (2007) were in confirmity with the above results. Further, parents *viz.,* HW1095, DDK 1028, DWR 2006 and MACS 2961 considered to be best general combiners based on gca values. In the evaluation of crosses, seven cross combinations were promising based on significant negative sca effects.

The cross MACS 2961 x DWR 2006 reported to have highest sca effects compared to other crosses and both of its parents are good general combiners with significant sca effects. This cross ranks first among top five crosses based on per se performance for plant height (Table 34).

5.1.5 Panicle length (cm)

Combining ability studies revealed that the ratio of gca variance to sca variance was less than unity depicting the importance of non-additive gene action for peduncle length. The studies undertaken by Choudhary *et al.* (2005) in 5 x 5 diallel cross also confirmed high sca effects and non-additive type of gene action controlling the trait. Among the parents, HW 1095, MACS 2961 and DDK 1028 were found to be good general combiners with highly significant negative gca values. Six crosses reported as good specific combiners with highly significant negative sca effects.

The crosses MACS 2961 x DWR 2006, DDK 1029 x DWR 1006 and NP 200 x DWR 185, not only reported good sca effects but also had high per se values for peduncle length.

5.1.6 Spike length (cm)

The ratio of gca variance to sca variance was lesser than unity for the trait spike length. This revealed preponderance of non-additive gene action and hence heterosis phenomena for spike length character can be further exploited from the material generated. Similar behaviour of non-additive gene action with pronounced sca variance for plant height was on record (Chowdhary *et al.,* 2005, Singh *et al.,* 2003, Desai *et al.,* 2005, Nazir *et al.,* 2005, Iqbal and Khan, 2006a and Ribadia *et al.,* 2007).

With respect to general combining ability, among the parents, one line namely MACS 2961 and one tester DWR 2006 were found to be best combiners for spike length. These above lines could be further used in breeding programme for improvement in spike length. The parents MACS 2956, NP 200 and DWR 1006 proved to be inferior for general combining ability for the trait. With regard to sca effects, the crosses MACS 2961 x DWR 2006 proved to be superior. This cross had both the parents with significantly higher gca effect for spike length.

5.1.7 Number of spikelets per spike

In the present study, for the trait number of spikelets per spike, the ratio of gca variance to sca variance was less than unity. This depicts that non-additive type of gene action playes a major role in controlling the trait. Pandey *et al.* (1999), Hamada *et al.* (2002), Singh *et al.* (2002), Ahmadi *et al.* (2003), Wei *et al.* (2003), Joshi *et al.* (2004a), Awan *et al.* (2005), Malik *et al.* (2005), Darwish *et al.* (2006) and Vanpariya *et al.* (2006) also recorded high gca effects for number of spikelets per spike. Singh *et al.* (2002a), Singh *et al.* (2003), Pareek and Garg (2004), Nazir *et al.* (2005), Iqbal and Khan (2006a) and Ribadia *et al.* (2007) noticed predominance of non-additive gene action for the trait.

None of the crosses exhibited significant sca effects for the trait. The parents DDK 1028 and MACS 2947 displayed significant gca effects for the trait. The parents MACS 2956 and NP 200 were found to be poor general combiners as they showed negative significant gca effects. Alternatively, crosses from high x medium combination for gca effects, like MACS 2947 x DWR 1006 also displayed highest per se values.

5.1.8 Number of grains per spike

For the trait grains per spike, the ratio of gca variance to sca variance was lesser than unity showing predominance of non-additive gene action controlling the trait. Desai *et al.* (2005) and Nazir *et al.* (2005) reported the non-additive gene action controlling the trait. The parents MACS 2947 and DDK-1028 recorded significantly effects in desired direction on gca. None of the crosses reported significant sca effects for the trait. But the crosses MCAS 2947 $\times$ DWR 1006 reported high positive sca value and is listed first in the list of top per se performance for grains per spike.

5.1.9 Number of tillers per plant

Analysis of data for combining ability revealed the predominance of sca variance. This depicted non-additive effects to be relatively more important for the trait. The findings of Singh *et al.* (2002), Singh *et al.* (2003), Desai *et al.* (2005), Nazir *et al.* (2005), Dere and Yaldrm (2006), Khan *et al.* (2007) and Ribadia *et al.* (2007) were in confirmity with the above results. Further, parents considered to be best combiners, namely MACS 2956 and DWR 2006 based on gca values. The cross involving these two parents possessed greater per se values. This indicated positive and strong relationship between gca status of parents and per se performance of the cross for the trait. In the evaluation of crosses, the cross combinations MACS 2961 x DWR 185, MACS 2956 x DWR 2006 and DDK 1009 x NIDW 295 were promising based on sca effects.

It is interesting to note that the crosses MACS 2961 x DWR 185 and DDK 1009 x NIDW 295 behaved as good specific combiners while the parents of these crosses expressed non-significant gca effects. This confirmed prevalence of non-additive gene effects in such crosses. Similar results were obtained by Singh *et al.* (2002a) in the crosses developed by crossing 7 lines and 3 testers.

5.1.10 Number of productive tillers per plant

In the present investigation, it is clear that non-additive type of gene action plays a major role in controlling the trait number of productive tillers per plant as the ratio of gca variance to sca variance was less than unity. Rajora and Maheshwari (1996) also recorded predominance of non-additive gene action for the trait.

With respect to gca effects, only one parent HW 1095 among fourteen parents recorded significant gca effect for number of productive tillers per plant. Two crosses namely MACS 2961 x DWR 185 and DDK 1025 x DWR 2006 exhibited significant sca effects for the trait.

5.1.11 Thousand grain weight

As many as three parents showed positive and significant gca effects namely, DDK1025, NP200, MACS 2956 and proved as best general combiners for thousand grain weight. With respect to sca effects seven crosses exhibited highly significant positive sca effects. Similar kind of results were reported by Afiah *et al.* (1997) Esmail (2002), Ahmadi *et al.* (2003), Shoran *et al.* (2003), Wei *et al.* (2003), Joshi *et al.* (2004a) and Mahantashivayogayya *et al.* (2004).

All the top five crosses listed in Table 34 based on per se performance had the gca status of parents as high x medium. The cross DDK 1028 x NIDW 295 was the best specific combiner with higher sca effects. But none of its parents showed significant gca effects.

As reported by earlier workers Hamada *et al.* (2002) Singh *et al.* (2003), Pareek and Garg (2004), Siddique *et al.* (2004), Desai *et al.* (2005), Nazir *et al.* (2005), Soud *et al.* (2005), Vanpariya *et al.* (2006) and Khan *et al.* (2007), in this study also there was predominance of non-additive gene action for the trait as the ratio of gca variance to sca variance is less than unity.

5.1.12 Number of grain yield per plant

From the investigation, it is clear that the magnitude of gca variance was higher than sca variance. This revealed predominance of additive gene action for grain yield per plant. Similar kind of observations were made by Hamada *et al.* (2002), Lakshmikant and Gupta (2002), Singh *et al.* (2002), Ahmad *et al.* (2003), Joshi *et al.* (2003), Joshi *et al.* (2004), Awan *et al.* (2005), Darwish *et al.* (2006), Inamullah *et al.* (2006), Iqbal and Khan (2006b), Khan *et al.* (2007) and Sayar *et al.* (2007).

In the present study, the magnitude and direction of gca effects points to DDK 1030 as an excellent general combiner along with high (per se) mean. The crosses HW 1095 x DWR 185 and MACS 2956 x NIDW 295 recorded as good specific combiner as they reported higher sca effects for the trait grain yield per plant. These two crosses were listed among the top five crosses based on per se performance. Significant gca and sca effects were also reported earlier by many workers.

5.1.12 Methods for working out pooled scores of gca for disease, yield and yield attributing traits

Yield is considered as a complex character dependent on interaction effect of number of componental traits. So, in order to achieve improvement in yield levels it is first necessary to bring improvement in the yield influencing traits.

Further, the basic need to study line x tester, would be to assess the true potential of parents involving so that genetically superior parents may be utilized in crossization. Therefore, even though gca effects for yield help for distinguishing parents, working out pooled score for gca effects will be more reliable in deciding the true genetic potentiality of the parents.

Two different methods, namely, simple pooled method and per cent gca method have been worked out in different crops (Patnaik, 2000).

5.1.13 Simple pooled gca method

In this method, significant gca effect in desired direction is given score of +1 and -1 score to gca significance in undesirable direction (Arunachalam and Bandyopadhyay, 1979). These values are added over different yield attributing traits to arrive at pooled score of gca effects. The main disadvantage existing with this system is that all parents with significant gca effects in desirable direction will get the same score (+1) for all the characters. Hence, it is not possible to assess the genetic differences existing among the genotypes of this crop which get a score of +1 for a particular character.

Therefore, it becomes very important to develop a system of working out pooled scores of gca by utilizing the actual gca values and also ensuring quantification of differences in gca effects among parental genotypes.

5.1.14 Per cent gca method

If the actual gca values are added across characters to arrive at pooled score, it will have a practical problem with respect to differences in unit of measurement of each character. The unit of measurement of each character is different and due to this the magnitude of mean values for different characters will be varying. But, always higher mean values for a character do not truly reflect the importance of the character. If raw values of gca effects are added across the characters then relatively less important character with higher per se gca effects influences the pooled score most, as against the important character with low per se gca values. This would be rather misleading if parents were selected based on such poled scores. To overcome this disadvantage raw gca values to be converted into per cent gca valies (Patil, 1995).

In per cent gca method, gca effects of parents for each character is converted into per cent values by comparing with respective F_1 means. Then individual per cent gca values are pooled to get pooled gca score. Patnaik (2000) also followed per cent gca method in deciding relative importance of parents involved in diallel study in *hirsutum* cotton.

Thus, following this method minute differences in gca values among the parents are focused. Further, the problem arising due to differences in unit of measurement associated with the type of character concerned giving comparatively higher and lower per se gca values are also overcome.

The results obtained in two methods are compared and discussed as below.

In the present study, differences were found in the ranking between simple pooled gca method and per cent gca method of evaluation of pooled scores for disease, yield and yield related traits. In simple pooled gca method, fourteen parents ranked 1 to 7 ranks are 2 to 3 parents shared same rank (Table 35). The parent DWR 2006 ranked first and four parents shared second rank namely DDK 1030, HW 1095, DDK 1028 and MACS 2961.

Further, based on per se performance of F_1 crosses for all the traits in per cent gca method the overall ranking of first five parents in descending order were MACS 2947, DDK 1030, NP 200, HW 1095 and DDK 1025 (Table 36). Among lines MACS 2947 and among testers NIDW 295 were found to be best combining for disease, yield and yield related triats with the highest per cent gca scores.

5.1.15 Threshability and pericarp colour

The caryopsis of non free threshing wheat are closely invested in the spikelet by tough thick tenacious glumes that are not readily detached with pressure and vigours rubbing. On the other hand, only slight rubbing or threshing action is required to separate the glume from the spikelet of free thesing wheat to release the kernel enclosed between the lemma and palea. The glume tenacity is classified as easy as threshing as that of *T. aestivum*. In this study dicoccum parents have brittle rachis and tough glumes and are non free threshing with red pericap colour whereas, durum parents were free threshing and amber grained as they have non brittle rachis and easy threshing glumes as that of *T. aestivum*. Generally dicoccum wheats are not preferred by consumers due to its husked seed nature and red grain colour. The husked grains are governed by ‘q’ and necked grain trait by ‘Q’ which is located on chromosome five of genome A (Morris and Sears, 1967). Here the non free threshing types are governed by recessive gene ‘q’ and the red grain colour is dominant over amber.

Table 35: Simple pooled gca score for disease, yield and important yield attributing traits in L x T crosses of tetraploid wheat

Sl. No.	Parents	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP	Pooled score	GCA status	Overall rank
Susceptible lines (dicoccum)																	
1	DDK-1025	+1	0	+1	+1	-1	-1	0	0	0	-1	0	1	0	1	High	3
2	MACS-2956	+1	0	+1	+1	0	0	-1	-1	-1	1	0	1	0	1	High	3
3	$NP_2$00	0	0	+1	+1	0	0	-1	-1	-1	0	0	1	0	0	Low	4
4	DDK-1030	0	-1	+1	+1	0	0	0	0	0	0	0	0	0	2	High	2
5	MACS-2947	-1	0	0	-1	-1	-1	0	1	1	0	0	0	0	-2	Low	6
6	HW-1095	0	+1	-1	-1	+1	+1	0	0	0	1	1	-1	0	2	High	2
7	DDK-1009	0	0	0	+1	-1	-1	0	0	0	-1	-1	0	0	-3	Low	7
8	DDK-1029	0	0	+1	0	0	0	0	0	0	0	0	-1	-1	0	Low	4
9	DDK-1028	+1	+1	-1	-1	+1	+1	0	+1	1	0	0	-1	0	2	High	2
10	MACS-2961	0	0	0	+1	+1	1	0	0	0	0	0	-1	0	2	High	2
Resistant testers (durum)																	
1	NIDW-295	0	0	-1	-1	0	0	0	0	0	0	0	0	0	-2	Low	6
2	DWR-185	-1	0	0	0	0	0	0	0	0	0	0	0	0	-1	Low	5
3	DWR-1006	+1	0	0	+1	0	-1	-1	0	0	0	0	0	0	0	Low	4
4	DWR-2006	0	0	+1	0	+1	0	1	0	0	1	0	0	0	4	High	1

DS I – Disease score at 60 DAS
DS II – Disease score at 90 DAS
DF – Days to flowering
DM – Days to maturity
PH – Plant Height
PL – Peduncle length
SL – Spike length
SPS – Spikelets per spike
GPS – Grains per spike
NTPP – Number of tillers per plant
NPTPP – Number of productive tillers per plant
TGW – Thousand grain weight
GYP – Grain yield per plant

Table 36: Per cent gca method for disease, yield and important yield attributing traits in L x T crosses of tetraploud wheat

Sl. No.	Parents	DSI	DSII	DF	DM	PH	PL	SL	SPS	GPS	NTPP	NPTPP	TGW	GYP	Pooled score	Lines	Testers	Overall
Susceptible lines (dicoccum)																		
1	DDK-1025	-16.11	2.88	-3.36	-1.05	9.89	19.24	-2.70	-4.30	-4.27	-14.96	-13.98	13.92	21.39	6.58	5	-	6
2	MACS-2956	-16.11	-2.26	-3.75	-1.05	-2.98	-2.71	-10.16	-7.86	-7.85	19.27	7.07	4.80	-2.00	-25.58	7	-	11
3	NP_200	17.45	10.49	-4.33	-1.17	1.44	-3.42	-9.62	-5.88	-5.88	1.05	1.85	6.96	4.55	13.49	4	-	4
4	DDK-1030	0.67	18.30	-6.89	-2.51	0.38	2.40	-1.30	-0.35	-0.32	9.33	10.56	1.47	24.59	56.35	2	-	2
5	MACS-2947	34.23	-10.08	-0.02	2.57	8.00	9.26	2.27	6.08	6.10	12.37	13.81	-0.29	12.25	96.56	1	-	1
6	HW-1095	-7.38	-17.69	13.11	3.30	-8.95	-13.46	0.00	2.87	2.89	14.63	16.51	-5.29	17.53	18.06	3	-	3
7	DDK-1009	0.67	-7.40	1.55	-1.78	5.94	12.17	-2.16	-1.43	-1.43	-24.24	-22.96	-0.59	-0.96	-42.63	9	-	13
8	DDK-1029	9.40	8.02	-3.36	-0.20	-2.07	-1.65	0.22	4.00	4.00	-8.50	-6.96	-6.37	-34.07	-37.55	8	-	12
9	DDK-1028	-32.89	-15.22	8.22	1.36	-6.28	-8.68	1.84	7.61	7.63	-8.34	-6.91	-8.14	-21.19	-80.98	10	-	14
10	MACS-2961	9.40	13.16	-1.19	0.52	-5.39	-13.19	21.73	-0.84	-0.82	-0.61	1.01	-6.47	-22.04	-4.73	6	-	8
Resistant testers (durum)																		
1	NIDW-295	10.74	-0.21	1.40	0.45	2.31	2.68	-1.41	0.05	-0.05	-7.45	-6.01	-0.49	7.24	9.25	-	1	5
2	DWR-185	10.74	-0.21	0.45	0.40	1.84	1.52	-3.46	-0.84	-0.84	-3.31	-1.97	0.88	-0.81	4.40	-	2	7
3	DWR-1006	-19.46	1.85	0.77	-0.52	2.13	5.47	-4.76	-1.28	-1.26	2.43	3.82	1.57	4.28	-4.98	-	3	9
4	DWR-2006	-2.68	-1.23	-2.60	-0.33	-6.27	-9.67	9.62	2.08	2.08	8.34	4.10	-2.06	-10.67	-9.31	-	4	10
	F_1 mean	1.49	4.86	63.76	103.34	93.64	39.51	9.25	20.24	40.45	18.11	17.81	10.2	25.95				

DS I – Disease score at 60 DAS
DS II – Disease score at 90 DAS
DF – Days to flowering
DM – Days to maturity
PH – Plant Height
PL – Peduncle length
SL – Spike length
SPS – Spikelets per spike
GPS – Grains per spike
NTPP – Number of tillers per plant
NPTPP – Number of productive tillers per plant
TGW – Thousand grain weight
GYP – Grain yield per plant

5.2 Experiment 2: Genetics of spot blotch resistance, pericarp colour and threshability in tetraploid wheat

5.2.1 Genetics of spot blotch resistance tetraploid wheat

Spot blotch caused by *Bipolaris sorokiniana* (Sacc.) Sheom. (Syn. *Helminthosporium sativum* telomorph *Cochliobolous sativus*) has been important and a major wheat disease world wide, particularly in warmer growing areas characterized by an average temperature in the coolest month above 17^0C (Dubin and Bimb, 1991, Dubin and Van Ginkel, 1991, Duveiller and Gilchrist, 1994, Saari, 1998, Dubin and Duveiller, 2000 and Duveiller, 2002). Increase in temperature coupled with high relative humidity favor the outbreak of the disease (Dubin and Rajaram, 1996 and Ragiba *et al.,* 2004). Symptoms developed necrosis and associated chlorosis of the leaves resulting in reduction of photosynthetic area and premature senescence (Neema and Joshi, 1971 and Zillinsky, 1983). The disease becomes especially severe during grain filling stage (Joshi and Chand, 2002) and causes significant grain yield losses (Sharma *et al.,* 1997). Root infections can be so severe that infected plants dry out without producing any seed. Under favourable conditions, spikelets may be affected, causing grain shriveling. At the stage of three quarters of the inflorescence emerged and it weather conditions are conductive *i.e.,* continuous rain for 5-6 days followed by warmer temperatures (day average of 20-30^0C), disease epidemic can develop very rapidly (Mehta, 1998). Fungal infection accelerates leaf senescence at later growth stages (Degne and Oerke, 1985). The disease effects all plant parts and may cause to 100 per cent yield losses (Mehta, 1993 and Ragiba *et al.,* 2004).

In wheat among reports have indicated that the spot blotch cause substantial grain yield loss to the extent of 19.6 per cent, which some times vary depending upon the temperature and relative humidity. In India major concentration for breeding wheat varieties has been given to brown and stem rust resistance in central and peninsular India, stripe and brown rust resistance in North Western India and brown rust in North Eastern India. While in all these wheat growing regions specific wheat breeding programmes for spot blotch resistance have not been under taken. Hence, presently available cultivated wheat varieties possess very low to moderate level of tolerance to this disease (Saari, 1998 and Sharma *et al.,* 2004). Prophylactic and curative mesrures for the control of this disease can not be implemented under Indian conditions due to small farm holding coupled with economic constraints (Razzaque and Hossain, 1991).

In view of the huge wheat acreage attacked by spot blotch, even a marginal reduction in disease may be of significance for wheat growing areas, especially those in developing countries.

The best strategy to address the spot blotch problem is to develop resistant cultivars although this may take considerable time. However, to do so, the genetics of resistance in improved genotypes must be further understood.

Previous studies have reported the resistance to spot blotch in wheat and barley (*Hordeum vulgare* L.) to be qualitatively (Adlakha *et al.,* 1984, Sharma and Bhatta, 1999, Singh *et al.,* 2000, Srivastava *et al*.., 1971 and Wil Cox Son *et al.,* 1990), as well as quantitatively (Kutcher *et al.,* 1994, Sharma *et al.,* 1997 and Velzquez Cruz, 1994) inherited. For qualitative inheritance one, two or three recessive or dominant genes with epistatis were involved in imparting resistance.

Since, dicoccum wheat is being cultivated in the marginal areas of Southern hill zone, peninsular India and coastal regions of Southern, the crop improvement prorgamme in dicoccum wheat is being concentrated in these regions. While developing the semi dwarf dicoccum wheat varieties, the mani objectives was yield and grain quality improvement along with stem rust resistance. The least propriety was on spot blotch resistance. Hence, all the available cultivars processes very low to moderate tolerance to this disease.

Keeping all the above issues into consideration the present study was undertaken to elucidate the genetic control of spot blotch resistance, pericarp colour and threshability by following six generation mean analysis. In two separate crosses by taking two susceptible dicoccum wheat varieties *viz.,* DDK 1025 and DDK 1029 and one resistant durum wheat variety *viz.,* NIDW 295.

The results obtained are discussed as below.

Inheritance of spot blotch resistance

In the present study DDK 1025 and DDK 1029 used as susceptible parents and were crossed to NIDW 295 separately and six generations (P_1, P_2, F_1, F_2, BP_1 and BP_2) were produced. Absolute resistance was not been observed in the present investigation. So, quantitative analysis based on additive and non-additive gene effects using six generation means was considered appropriate to describe inheritance of characters determining resistance or susceptibility as below.

5.2.2 Disease score at 60 DAS (DSI)

In the cross DDK 1025 x NIDW 295, mean of F_1 generation for disease score at 60 DAS was lower and lower than the resistant parental value indicating negative over dominance for the trait which is desired one. Gene effects revealed that dominance component (h) was negative and highly significant which is again desirable. Further, comparatively higher magnitude of dominance component (h) than additive component (d) revealed its predominance for genetic control of the trait. The (h) and (l) components obtained same signs showing prevalence of complementary epistasis in this cross for disease scoring at 60 DAS.

In the second cross DDK 1029 x NIDW 295, F_1 generation means for this traits was lower and tended more towards resistant parent. In this cross also F_1 mean value was lower than resistant parent indicating over dominance for the traits as in first cross. Although both additive and non-additive components were non significant based on estimation of gene effects, dominance component (h) was relatively higher than the additive (d) component. The magnitidue of dominance x dominance (l) effects was highest compared to other parameters. It was therefore clear that non-allelic interactions like dominance x dominance effects played an important role in the inheritance of resistance to disease at 60 DAS. The dominance (h) and dominance x dominance (l) effects were showing opposite significant indicating that epistatis governing resistance in the cross DDK 1029 x NIDW 295 at 60 DAS was due to duplicate genes.

5.2.3 Disease scoring at 90 DAS (DS II)

Further, at the second stage of disease score i.e., disease score at 90 DAS (DSII), in the cross DDK 1025 x NIDW 295,F_1 mean value(6.20) was more tended towards resistant parent NIDW-295 (5.20) than susceptible parent DDK 1025 (8.00). This indicated dominance of resistance was evident for the trait. Here also, both the additive and dominance components were non-significant but additive (d) component is relatively higher than dominance (h) component. The magnitude of additive x dominance (j) effect was highest among all parameters, indicating non-allelic interaction like additive x dominance effect played an important role in the inheritance of the triat in cross DDK 1025 x NIDW 295. The dominance (h) and dominance x dominance (l) obtained opposite signs showing prevalence of duplicate gene action governing resistance at 90 DAS.

The F_1 mean values in the cross DDK 1029 x NIDW 295 for disease score at 90 DAS (DS II) was lower than resistant parent NIDW 295 indicating over dominance of resistance for disease spread was evident. Based on the estimation of gene effects for disease score at 90 DAS (DS II), dominance (h) gene action was found to be important for genetic control of the trait. The magnitude of additive x dominance (j) effects was highest compared to other parameters indicating non-allelic interaction like additive x dominance effect played important role in the inheritance of resistance to disease spread. Here also, the opposite signs of dominance (h) and dominance x dominance (l) effects revealed that epistasis governing resistance in this cross was due to duplicate genes.

The information on resistance to spot blotch in wheat is very scarce. The studies so far carried out are on bread wheat and to some extent the durum wheat. No report is available so far with respect to dicoccum wheat. In bread wheat the studies for the inheritance of resistance to this disease are a many times contradictory to each other. Srivastava *et al.* (1971) observed that resistance is governed by two non-allelic complimentary genes, where as Narula and Srivastava (1971) and Singh *et al.* (1997) found that it is governed by two duplicate recessive genes. Singh *et al.* (2000) reported resistance is controlled by two pairs of

complementary recessive genes. Adlakha *et al.* (1994) depicted that resistance is dominant and is governed either by one or two genes in different genotypes. The report of Joshi *et al.* (2003) depicts that susceptibility is governed by two dominant genes with complementary effect. Ragiba *et al.*(2004) reported that two recessive genes were responsible for imparting resistance to spot blotch.

Wilcoxson *et al.* (1990) reported that resistance to spot blotch in barley (*Hordeum vulgare* L.) lines was conditioned by one or two genes. Kutcher *et al.* (1994) reported that resistance to spot blotch in two barley crosses was quantitatively inherited.

5.2.4 Genetics of threshability and pericarp colour in tetraploid wheat

5.2.4.1 Threshability

Generally dicoccum wheats are not preferred by the consumers due to its husked seed nature. The husked grains (non-free-threshing) are governed by the genetic locus 'q' and naked grains trait by 'Q' which is located of chromosome five of genome A (Morris and Sears, 1967). Here in the crosses of non-free threshing dicoccum and free threshing durum the non-free threshing types are governed by the recessive gene. The results of the present study was supported by the reports of Luo *et al.* (2000) who reported that dominant allel at Q locus on chromosome 5A is believed to be the principle factor responsible for free threshing in bread wheat.

5.2.4.2 Pericarp colour

Cultivated dicoccum (*Triticum dicoccum* Schrank, Schulb) being highly self pollinated crop has inherent problem of epistatic interactions and linkage of desirable and undesirable characters, which inherit as a blocks of genes through generations. In this crop, seed yield has undesirable linkage with red grain colour and husked seeds. Preference for grain colour in Indian sub continent is different from rest of the world as in this part of the world wheat is mainly used for chapatti/roti preparations for which the whole wheat is milled to get whole wheat flour from small mills, while in rest of the world wheat flour obtained from the roller flour mills and are used for food preparations such as bread and bakery products. Hence grain colour does not find any complaints by the consumers. But in India amber grain colour is much preferred before dicoccum wheat was mainly used for the preparation of Upama, pasta, etc. But because of the health consciousness, this wheat is being used for the chapatti preparations. Also because of the development of dicoccum wheat varieties such as DDK-1025 which is suitable for the preparation of bread and bakery products, consumer are very particular about the colour of the bakery products also. In view of the grain quality of dicoccum wheats with respect to high protein content, better quality of gluten protein, high dietary fibre content, this wheat is preferred by non insulin dependent diabetic subjects for the management of diabetes. Hence, there is need to develop dicoccum wheat with amber grain colour without affecting the quality.

Overall the pericarp colour red or amber would be considered as a qualitative trait having monogenic or oligogenic inheritance showing gene for gene relationship because multigene families could also be primarily regarded as Mendelian genes with duplicate espistasis, displaying of single gene preducts individually. In the present study, it was found that based on F_1 phenotype, red pericarp colour is dominant over amber. Tomar *et al*. (2007) also reported the monogenic inheritance of kernel colour and red grain colour is dominant over amber. Amber grain colour is governed by recessive genes and ones, the amber grained lines are if identified further their stability will be easy. Hence, identifying the genes governing amber pericarp colour through qualitative approach helps for effective selection of amber pericarp coloured lines, so that these lines could be directly used to develop amber grain coloured dicoccum varieties.

In the cross DDK 1025 x NIDW 295, 18 F2, 7 BC1P1 and 12 BC1P2 segregants were identified with lower spot blotch disease scores and high grain yield per plant. Similarly in the cross DDK 1029 x NIDW 295, 14 F2, 10 BC1P1 and 13 BC1P2 segregants were reported with lower spot blotch disease scores and higher grain yield per plant.

5.3 Experiment 3: Biochemical basis of spot blotch disease resistance

In recent years, it is becoming increasingly evident that several natural and induced defence mechanisms operate in host plants against different diseases. One such defence mechanism is the presence of certain compounds inhibitory to the pathogen. Sometimes, the host plant is induced to synthesize these compounds on infection. Analysis of biochemicals in selected resistant and susceptible genotypes was carried out at two different stages to understand their role in resistance or susceptibility to spot blotch in wheat genotypes.

In general, the infection by some pathogens brings changes in respiratory pathway and photosynthesis which are the vital process taking place inside the plant leading to wide fluctuations in sugars (Farkas and Kiraly, 1962, Klement and Goodman, 1967, Bateman and Miller, 1966, Jayapal and Mahadevan, 1968, and Prasad *et al.,* 1972). The disease reaction has been correlated with the sugar level in different crop plants. Generally, high levels of total sugars, in the host plant are stated to be responsible for disease resistance.

Difference in sugar level at 60 DAS between resistant and susceptible genotypes was due to inherent character of the genotypes as there was less disease development in all the genotypes especially in susceptible genotypes. Subsequently, the gap widened with respect to sugar content as well as disease development between resistant and susceptible genotypes. In susceptible genotypes, disease development was more whereas, the mean sugar content was reduced at later stages of the crop growth.

This indicated the utilization of these sugars by the invaded pathogens for their nutrition. Such nutritional utilization of sugars by the invading pathogens has been reported earlier also (Krog *et al.,* 1961 and Thind *et al.,* 1977).

In the present investigation, the resistant genotypes of wheat (NIDW 295 and DWR 185) exhibited more amount of mean total sugar as compared to susceptible genotypes during the growth *i.e*., 60 and 90 DAS. Further, observations revealed that there was reduction in total sugars due to infection and these results are in conformity with the reports of Ramdayal and Joshi (1968) in barley against leaf spot pathogen, Mandokhot *et al.* (1979) and Levy and Cohen (1984) in case of maize against *Turcicum* blight and Subramanyam *et al.* (1990) in wheat against *Exerohilum hawaiiensis*.

Sugars act as precursor for synthesis of phenolics, phytoalexins, lignin and cellulose which play an important role in defence mechanism of plants against invading pathogens. In the present study also resistant genotypes recorded higher sugars and these results corroborate the findings of Tripathi and Chiranjeevi (1977), Naik *et al.* (1981) and Basarkar *et al.* (1988) in various disease resistant sorghum genotypes. Overall, high sugar content in resistant wheat genotypes may be responsible for lower development of the helminthosporium leaf blight.

Among all the biochemical components of different hosts, phenols stand out as most important components in imparting resistance to several plant diseases.

In the present investigation, resistant genotypes *viz.,* NIDW 295 and DWR 185 recorded high amount of phenols than susceptible ones both at 60 DAS and 90 DAS. The high phenolic content in resistant genotypes may be due to more sugar as it acts as precursor for synthesis of phenolics. This is in agreement with the findings of Prabhu *et al.* (1984) who reported that the total phenolics were more in callus tissues of sorghum genotypes which were resistant to downy mildew. Further, they had attributed the disease resistance to the capacity of plant to accumulate phenols at a faster rate.

The phenolic content in different genotypes significantly decreased with increase in age of the plant. However, the amount of phenolic content was significantly more in resistant genotypes compared to susceptible ones. The results are in line with the findings of Malli *et al.* (2002), who reported that there was more reduction in total phenols in susceptible genotypes than in resistant genotypes of moth bean following yellow mosaic virus infection. In contrast to this, Naik *et al.* (1981) reported that the rust resistant sorghum genotypes recorded higher phenols as the age of the crop increased and similarly that of Harmas and Terba (1984) who reported high phenolic content in resistant barley and wheat genotypes against brown rust. Kalappanavar and Hiremath (2000) reported higher phenolic content in

multiple foliar disease resistant sorghum genotypes than susceptible ones. Phenols directly or indirectly interfere with several metabolic systems of organisms. Based on these findings, it could be concluded that rapid accumulation of phenolic compounds occur in incompatible (resistant) host pathogen interactions than the compatible (susceptible) ones.

5.4 Experiment 4: Molecular characterization of spot blotch disease resistant and susceptible parents

Genetic variation is a pre-requisite for any crop improvement programme to be successful. Classifying the germplasm accessions/cultivars solely based on a few discrete morphological characterstics may not provide an accurate indication of the genetic divergence among cultivars, species and other study groups.

Presently, many kinds DNA based molecular markers such as RFLP, RAPD and AFLP etc. are available which detect polymorphism at the DNA level. The present study employed RAPD technique to assess genetic polymorphism. The major advantages of the RAPD techniques is that, it does not need sequence information to start with. The polymorphism among genotypes can be detected by using random primers. Variation in the banding pattern of the amplification products occurs because of variation in the length of DNA sequences flanked by the primers.

The present study utilized 32 RAPD primers and two parents *viz.,* DDK 1001 susceptible to spot blotch and HD4502 resistant to spot blotch. The primers produced average of 6.46 fragments per primer and 7.73 pre cent polymorphism.

Twelve primers were polymorphic. Polymorphism based on RAPD has been reported among genotypes of wheat by many early workers such as Sun *et al.* (1998), Fahima *et al.* (1998), Rajbir Yadav *et al.* (2002) and Sun *et al.* (2003). Five primers developed seven female parent specific fragments and seven primers produced seven male specific fragments. Further, these polymorphic primers will be used for screening entire mapping population for mapping and tagging of spot blotch disease resistance.

Future line of work

1. The traits those expressed predominance of additive gene action can be exploited by applying simple selection schemes in later segregating generations.
2. The magnitude and direction of gca effects points to DDK1030 as a excellent general combiner along with high per se value and the crosses HW1095 $\times$ DWR185 and MACS2956 $\times$ NIDW295 recorded as good specific combiner for the trait grain yield per plant.
3. Based on per cent gca method, MACS2947 and NIDW295 were found to be best general combiners for spot blotch disease, yield and yield related traits.
4. Based on the magnitude of sca effects of crosses, some crosses are identified as promising for each character separately, which is used further in the breeding programme are likely to yield desirable genotypes with better performance for those respective characters such genotypes inturn can be used in combination breeding programme for the improvement of yield as well as spot blotch resistance.
5. The preliminary information about the genetics of spot blotch disease resistance was developed and it is governed by duplicate epistasis. Some of the sergeants identified with lower spot blotch disease scores and high grain yield per plant.
6. The information obtained on genetics of spot blotch resistance, threshability and pericarp colour will be useful to develop the free threshable amber grained dicoccum varieties and promising crosses/segregants identified in the present study should be carried forward.
7. The polymorphic RAPD primers identified in the present study disease can be further used to screen the mapping population and tagging resistance or susceptibility to spot blotch for use in effective marker assisted selection programmes.

6. SUMMARY AND CONCLUSIONS

Dicoccum wheat commonly called as Jave or Khapli wheat is nutritionally superior compared to other wheats *viz.,* bread and durum wheat. Helimenthosporium leaf blight (spot blotch) caused by *Bipolaris sorokiniana* (Syn. *Helminthosporium sativum*) is one of the major disease that limits dicoccum wheat production. Development of resistant cultivars is most effective economic strategy to combat the spot blotch problem. Dicoccum wheat has red grain colour and husked seeds, which are also the major constraints for consumer preference. But inexhaustive information on genetics of spot blotch resistance threshability and pericarp colour lead the present investigation with foremost important objective to understand the genetics of spot blotch resistance, threshability and pericarp colour.

Experiment 1: Heterosis, combining ability and gene action studies for spot blotch disease resistance, yield and attributing traits using line x tester design

The material for this investigation comprised of ten dicoccum lines showing susceptibility to spot blotch and four durum testers showing resistance to spot blotch crossed in line x tester deign. The lines were DDK 1025, MACS 2956, NP 200, DDK 1030, MACS 2947, HW 1095, DDK 1009, DDK 1029, DDK 1028 and MACS 2961, while testers were NIDW 295, DWR 185, DWR 1006 and DWR 2006. Parents as well as 40 F1s were evaluated during *rabi* 2007-08 at Agricultural Research Station, Arabhavi, University of Agricultural Sciences, Dharwad which is the hot spot for Helminthosporium leaf blight. The experimental results are summarized below.

1. Analysis of variance for parents and hybrids was carried out for all the characters. The differences among parents were significant for eight characters *viz.,* disease scoring at 60 DAS (DSI), days to flowering days to maturity, number of tillers per plant, number of productive tillers per plant, thousand grain weight, spikelets per spike and grains per spike. The hybrids showed significant variation for disease scoring at 60 DAS (DS I), disease scoring at 90 DAS (DS II), days to flowering, days to maturity, plant height, peduncle length, spike length and thousand grain weight.
2. The magnitude of herterosis was high for disease scoring at 60 DAS, disease scoring at 60 DAS, plant height, peduncle length, spike length, number of tillers per plant, number of productive tillers per plant and grain yield per plant. Grain yield per plant recorded highest heterosis among all traits. Further, the magnitude of heterosis was generally less for days to flowering, days to maturity, spikelets per spike, grains per spike and thousand grain weight.
3. Analysis of variance for combining ability indicated that SCA variance was higher than GCA variance for all the traits under study except for grain yield per plant. All the characters except grain yield per plant showed preponderance of non-additive variance.
4. On the basis of simple pooled gca scores, the gca effects of the parental genotypes were scored over all the characters and MACS 2956, DDK 1030, HW 1095, DDK 1028, MACS 2961 and DWR 2006 found to be good combiners. Based on per cent gca method the first top five good combiners in descending order were MCAS 2947, DDK 1030, NP 200, HW 1095 and DDK 1025. Among lines MACS 2947 and among testers NIDW 295 found to be best combining for disease yield and yield related traits.
5. Very few crosses exhibited significant sca effects under desired direction. In general, the magnitude of sca effects was less for all the characters. None of the female parents expressed consistent performance with all the male parents and *vice versa*.

Based on the *per se* performance, top five crosses were identified for some of the important traits including yield per plant. As indicated by the magnitude of sca effects of the hybrids, some hybrids were identified as promising for each character separately which if used further in the breeding programme are likely to yield desirable genotypes with better performance for those respective characters. Such genotypes in turn can be used in combination breeding programme for the improvement of yield as well as spot blotch resistance.

Yield is considered as an ultimate character of relevance and interest to the breeder. In the present study, the magnitude and direction of gca effects points to DDK 1030 as excellent general combiner along with high (*per se*) mean. The top five crosses recorded not only high per se performance but also exhibited positive heterosis.

Experiment 2 : Genetics of Helminthosporium leaf blight resistance, pericarp colour and threshability in tetraploid wheat.

In the present study two susceptible dicoccum parents DDK 1025 and DDK 1029 were crossed to resistant durum NIDW 295 separately and six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) were produced. The six generations were evaluated during *rabi* 2007-08 at ARS, Arabhavi.

The experimental results are summarized below

1. In the crosses DDK 1025 x NIDW 295, mean of F1 generation for spot blotch disease score was lower than resistant parent NIDW 295, indicating overdominance for the trait. Predominance of dominance component (h) was observed in the genetic control of the trait. Prevalence of complementary espistasis was observed for disease resistance at first stage. Similarly in the second cross DDK 1029 x NIDW 295, F1 mean disease score was lower than resistant parent revealed presence of overdominant gene action. In this case non-allelic interactions like dominance x dominance effects was predominant in inheritance of resistance at DS I. The epistasis governing resistance in this cross at DS I was due to duplicate genes.
2. The disease score at 90 DAS (DS II) in the cross DDK 1025 x NIDW 295, F1 mean value tended towards resistant parent. The additive (d) component was found relatively higher than dominant (h) component and the additive x dominance (j) effect was predominant epistasis governing the trait DS II. The opposite signs of dominance (h) and dominance x dominance (l) effect revealed prevalence of duplicate gene action governing resistance at 90 DAS. In the second cross, DDK 1029 x NIDW 295, over dominance was lower than resistant parent NIDW 295. The estimation of gene effects for disease score at 90 DAS (DS II) predicted dominance gene action was important for genetic control of the trait. As the magnitude of additive x dominance (j) effects was highest indicating its importance in governing the resistance at second stage (DS II). As in first cross, epistasis governing the resistance in DDK 1025 x NIDW 295 was due to duplicate genes.
3. In the cross DDK 1025 x NIDW 295, 18 F2, 7 BC1P1 and 12 BC1P2 segregants were identified with lower spot blotch disease scores and high grain yield per plant. Similarly in the cross DDK 1029 x NIDW 295, 14 F2, 10 BC1P1 and 13 BC1P2 segregants were reported with lower spot blotch disease scores and higher grain yield per plant.
4. With respect to pericarp colour qualitative analysis based on chi-square method revealed that red pericarp colour is governed by single dominant gene and red pericarp colour is dominant over amber pericarp colour.
5. Qualitative analysis based on chi-square method revealed that free threshability is dominant over non-free threshability.

Experiment 3 : Biochemical basis of disease resistance

In the biochemical studies, it has indicated that resistant genotypes (NIDW 295 and DWR 185) recorded high amount of total sugar and phenols as compared to susceptible ones (DDK 1025 and DDK 1029). However, as the crop growth advanced, there was increase incidence and the total sugars and phenols were decreased in all genotypes, but the extent of decrease was maximum in susceptible genotypes than in resistant genotype.

Experiment 4: Molecular characterization of spot blotch disease resistant and susceptible parents

In the molecular parental RAPD polymorphism, 12 primers were polymorphic, five were female parent specific and seven were male parent specific.

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GENETIC ANALYSIS OF SPOT BLOTCH RESISTANCE, YIELD AND YIELD ATTRIBUTING TRAITS THROUGH INTERSPECIFIC (*Triticum dicoccum* (Schrank) Schulb × *Triticum durum* Desf.) HYBRIDIZATION IN TETRAPLOID WHEAT

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ABSTRACT

Dicoccum wheat (*Triticum dicoccum* (Schrank) Schulb) is nutritionally superior compared to other wheats. Development of resistant cultivars against spot blotch caused by *Bipolaris sorokiniana* is of prime requirement since it is the major disease that limits wheat production. Red grain colour, husked seed also interferes with consumer preference. So to understand the genetics behind spot blotch resistance, pericarp colour and threshability, line x tester and six generation mean analysis was done. Line x tester analysis was done using ten susceptible dicoccum lines and four resistant durum testers. Six generation mean analysis was done in two crosses involving two susceptible dicoccums (DDK-1025 and DDK-1029) and one resistant durum (NIDW-295).

In line x tester analysis of variance for parents and hybrids for agronomic traits were found significant for eight traits including disease scoring at 60 and 90 DAS.

Grain yield/plant recorded highest heterosis and except for grain yield/plant all the traits reported SCA variance higher than GCA variance showing predominance of non-additive gene action. The top five crosses recorded, high *per se* performance and positive heterosis.

Six generation mean analysis indicated that disease score for spot blotch in F_1 generation was lower than resistant parent (NIDW-295), indicating over dominance for the trait. Predominance of dominance component (h) and complementary epistasis was observed for spot blotch resistance. In the cross DDK-1025 x NIDW-295, $18F_2$, $7BC_1P_1$ and $12BC_1P_2$ segregants and in cross DDK-1029 x NIDW-295, $14F_2$, $10BC_1P_1$ and $13BC_1P_2$ segregants were reported with lower spot blotch disease and higher grain yield per plant.

Pericarp colour and threshability is governed by single genes independently. Red pericarp is dominant over amber and free-threshability is dominant over non-free threshability. The biochemical studies revealed that total sugar and phenols are also positively associated with disease resistance. In the molecular parental RAPD polymorphism twelve primers were polymorphic.