ANALYSIS OF GENETIC DIVERSITY IN WHEAT

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By

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I. INTRODUCTION

Wheat, a cereal grass of the *Graminae* (*Poaceae*) family and of the genus *Triticum*, is the world's largest cereal crop. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade.

According to the earliest historic records, wheat was an important cultivated cereal in South-western Asia, its geographical centre of origin. Many wild species of *Triticum* are found in Lebanon, Syria, Northern Israel, Iraq and Eastern Turkey. Wheat was cultivated in ancient Greece and Egypt in pre-historic times. The central Asia, Near East, Mediterranean and Ethiopian regions are the world's most important centers of diversity of wheat and its related species (Kundu and Nagarajan, 1996; Perrino and Porcedu, 1990). Hindukush area is the centre of diversity of hexaploid wheat (Kundu and Nagarajan, 1996). The majority of the cultivated wheat varieties belongs to three main species of the genus *Triticum*. These are the hexaploid, *T. aestivum* L. (bread wheat), the tetraploid, *T. durum* Desf and the diploid, *T. dicoccum*. Schrank and *T. monococcum* Globally, *aestivum* wheat is most important species which covers 90 per cent of the area. Second popular wheat being durum wheat which covers about 9 per cent of the total area while *T. diccoum* wheat and *T. monococcum* wheat cover less than the one per cent of the total area.

The world acreage under wheat crop is 215.26 million ha with production of 584.76 million-tonnes with an average yield of 2717 kg per hectare. In India, wheat is the second most important crop after rice occupying 26.53 million ha, with production of 72.00 million tonnes with an average productivity of 2713 kg per hectare (Jagshorn and Mishra, 2005). Uttar Pradesh, Madhya Pradesh and Punjab are important states from the point of both area and production

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 the prevalence of high temperatures during the crop growth. The area under wheat is about 2.66 lakh ha with annual production of 2.50 lakh tonnes. The productivity is very low [988 kg per ha] as compared to national average of 2713 kg per ha (Jagshorn and Mishra, 2005). This is mainly due to the fact that large area of wheat (60 %) is grown under rainfed conditions and only a small part of the growing period experiences the cool climate. Very often the crop is exposed to terminal heat stress causing potential yield loss.

Wheat compares well with other cereals in nutritive value. It has good nutrition profile with 12.1 per cent protein, 1.8 per cent lipids, 1.8 per cent ash, 2.0 per cent reducing sugars, 6.7 per cent pentosans, 59.2 per cent starch, 70 per cent total carbohydrates and provides 314K cal/100g of food. It is also a good source of minerals and vitamins *viz*., calcium (37 mg/100g), iron (4.1 mg/100g), thiamine (0.45mg/100g), riboflavin (0.13mg/100g) and nicotinic acid (5.4mg/100mg) (Lorenz and Kulp, 1991).

Unlike other cereals, wheat contains a high amount of gluten, the protein that provides the elasticity necessary for excellent bread making. Hard wheat is high in protein (10-17%) and yields a flour rich in gluten, making it particularly suitable for yeast breads. The low-protein (6 to 10%) softer type yields flour lower in gluten and therefore, better suited for tender baked products, such as biscuits, pastries and cakes. *Triticum durum* wheat, although high in gluten, is not suitable for baking, but suitable for semolina, the basis for excellent pasta, such as spaghetti and macaroni preparation.

Yield being a complex character is a function of several component characters and their interaction with environment. Probing of structure of yield involves assessment of mutual relationship among various characters contributing to the yield. In this regard genotypic and phenotypic correlation reveals the degree of association between different characters and thus aid in selection to improve the yield and yield attributing characters simultaneously. Further, path coefficient analysis helps in partitioning of correlation coefficients into direct and indirect effects and in the assessment of relative contribution of each component character to the yield.

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. So, the knowledge of genetic diversity and relatedness in the

germplasm is a pre-requisite for crop improvement programmes. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes. So precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation would help to select parents for evolving superior varieties. For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme. In the present study, 169 released and unique genotypes were used for assessing the diversity considering yield as one of the important selection criterion.

Assessment of genetic diversity at the molecular level is more meaningful than at the phenotypic level as the later involves data on morphological traits which are environmental dependent. Though, they significantly contribute towards phenotypic variation but cannot be accurately phenotyped. So the study of polymorphism is best done at the level of arrangement of nucleotide bases in DNA, the primary source of all biological information. At this level, even seemingly identical accessions could display enormous differences, if only we could employ appropriate DNA profiling techniques. Besides, availability of virtually unlimited number of markers. Randomly Amplified Polymorphic DNA (RAPD) is one such method (Welsh and McClelland, 1990; Williams *et al*., 1990) of identifying polymorphism that can be used to elicit information on genetic differences among individuals of a population, between lines or germplasm accessions or any breeding material. RAPD technique is simple to operate and does not involve radioactive labelling.

Keeping these things in the view, an effort has been made in the present study to evaluate a set of wheat genotypes with the following objectives,

1. To estimate the variability, heritability and genetic advance for yield, yield components and quality traits
2. Correlation and path coefficient analysis
3. To assess genetic diversity through morphological traits and RAPD markers

II. REVIEW OF LITERATURE

A thorough understanding of the genetic diversity, extent of variation, genetic architecture of the plant and heritability of characters, among the genotypes would help in developing sound plant improvement programmes. Genetic variability is the gift of nature and it's fruitful utilization in any crop species calls for systematic collection, evaluation, description and grouping based on economic descriptors. A brief review of available information on the above aspects in wheat is presented in this section under the following headings.

2.1 Variability, heritability and genetic advance

2.2 Character association

2.3 Path analysis

2.4 Genetic diversity

2.5 Molecular diversity

2.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. The phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, it's magnitude on yield and it's component characters influences the selection strategies to be adopted by the breeders.

A comprehensive character wise review on phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (H) and genetic advance (GA) as per cent over mean is presented in Table 1.

2.2 CHARACTER ASSOCIATION

Grain yield is a complex trait, which is influenced by a number of contributing characters. The estimates of the inter relationship between grain yield and other yield attributes and among themselves would facilitate effective selection schemes to improve the yield. Thus, the review pertaining to the correlation between yield, yield contributing traits and among themselves in wheat is summarized in Table 2.

2.3 PATH ANALYSIS

Assuming yield is a contribution of several characters which are correlated among themselves and to the yield, path co-efficient analysis was developed (Wright, 1921; Dewey and Lu, 1959). Unlike the correlation coefficient which measures the extent of relationship, path coefficient measures the magnitude of direct and indirect contribution of the component characters to a complex character and it has been defined as a standardized, regression coefficient which splits the correlation coefficient into direct and indirect effects. The review of literature on contribution of different traits on yield is documented in Table 3.

2.4 GENETIC DIVERSITY

The assessment of genetic diversity using quantitative traits has been of prime importance in many contexts particularly in differentiating well defined populations. The germplasm in a self pollinated crop can be considered as a heterogeneous sets of groups, since each group being homozygous within itself. Selecting the parents for breeding programme in such crops is critical because, the success of such programme depends upon the segregants of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield.

To help the breeder in the process to identify the parents that nick better, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives. Among them, Mahalanobis's generalized distance occupy a unique place

Table 1. Review of literature on variability, heritability and genetic advance

Sl. No.	Material used for the study	H	GA	PCV	GCV	References
1	**Days to 50% flowering**					
1.	Durum wheat	97.7	28.68	-	14.8	Dixit (1990)
2.	F_3 population	High	-	-	-	Tiwari and Rawat (1993)
3.	6 x 6 diallel crosses	High	-	-	-	Senapathi *et al*. (1994)
4.	50 hill wheat along with standard varieties	49.44	3.09	3.04	2.13	Chaturvedi and Gupta (1995)
5.	44 diverse strains of spring wheat	87.6	5.3	2.9	2.7	Jagshoran (1995)
6.	9 generation from					
	HD2329 x Kalyansona	58.99	3.37	3.73	3.54	Jitendrakumar and Lutra (1995)
	HD2009 x Sonalika	74.17	3.65	1.87	1.61	
7.	1844 accessions of *T. monococcum*	-	-	High	High	Empilli *et al.* (1995)
8.	6 parents x their 15 F_1's of bread wheat	44.63	18.44	5.46	5.29	Singh *et al*. (1996)
9.	Inter varietal crosses of bread wheat	High	-	-	-	Nirmala and Jha (1998)
10.	52 Aegilops accessions	-	-	High	High	Zaharieva *et al.* (2003)
2	**Number of effective tillers per metre**					
1.	Durum wheat	Low	High	-	High	Shivkumar (1994)
2.	F_2 wheat lines	High	High	High	High	Raha and Ramgiru (1998)
3.	300 genotypes of bread and durum wheat	-	-	High	High	Sharma *et al*. (1998)
4.	F_2 wheat lines	High	High	High	High	Thakur *et al*. (1999)
7.	Late sown wheat genotypes	57.70	19.95	21.07	16.01	Mahesh *et al*. (2001)
8.	Durum wheat	98.84	42.94	-	-	Nayeem *et al.* (2003)

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Sl. No.	Material used for the study	H	GA	PCV	GCV	References
9.	Six cultivars/ liens of bread wheat	69.28-90.64	3.26-7.18	-	-	Ali-Firouzian *et al.* (2003)
3	**Plant height**					
1	Durum wheat	96.00	32.93	-	16.4	Dixit (1990)
2	11 parents and 9 F_1 hybrids	High	High	-	-	Mahamood and Shahd (1991)
3	40 strains	High	High	-	-	Mandal *et al*. (1991)
4	F_1 from diallel crosses	82.6	-	-	-	Pradanoric (1993)
5	F_2 generation of wheat	High	-	-	-	Collakua (1994)
6	44 diverse strain of spring wheat	63.5	10.51	8.04	6.40	Chaturvedi and Gupta (1995)
7	Wide range of lines and varieties	High	-	-	-	Dachev (1995)
8	1844 accessions of *T. monococcum*	-	-	High	High	Empilli *et al*. (1995)
9	50 hill wheat along with checks	95.1	23.3	11.9	11.0	Jag Shoran (1995)
10	6 parents and their 15 F_1's of bread wheat	41.66	80.00	9.12	8.64	Singh *et al*. (1996)
11	44 bread wheat lines	High	High	-	High	Shah (1998)
12	300 genotypes of bread and durum wheat	-	-	Low	Low	Sharma *et al*. (1998)
13	F_2's of 20 wheat crosses	High	-	-	-	Wang *et al*. (1998)
14	Semi-dwarf wheat	68.78	Moderate	-	-	Rebetzke (1999)
15	21 F_2 wheat lines	High	High	High	High	Thakur *et al*. (1999)
16	42 genetics stocks of durum wheat	High	-	-	-	Saiprasad and Pandy (2000)
17	50 bread wheat cultivars	-	-	High	High	Bergale *et al.* (2001)
18	50 wheat cultivars	High	High	High	High	Pawara *et al.* (2002)
19	52 Aegilops accessions	-	-	High	High	Zaharieva *et al.* (2003)
20	15 genotypes of foxtail millet	84.17	21.73	11.49	12.53	Muhammed and Hussain (2004)

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Sl. No.	Material used for the study	H	GA	PCV	GCV	References
4	**Peduncle length**					
1.	F_2 wheat generation	High	High	High	-	Dixit and Patil (1983)
2.	Wheat genotypes	High	-	-	-	Chaudhary *et al*. (1986)
3.	Wheat genotypes	High	-	-	-	Li (1989)
4.	6 parents and their 15 F_1's of bread wheat	26.26	20.89	3.73	3.63	Singh *et al*. (1996)
5.	300 genotypes of bread and durum wheat	-	-	Low	Low	Sharma *et al*. (1998)
5	**Days to maturity**					
1	Durum wheat	93.96	12.02	-	6.07	Dixit (1990)
2	47 tibetans wheat varieties	> 60%				Lu *et al*. (1991)
3	Intermating of F_2	High	High	High		Subhash *et al*. (1993)
4	50 genotypes of winder wheat	High	High	Low	Low	Jag Shoran (1995)
5	44 strains of breadwheat	Moderate		High	Low	Chaturvedi and Gupta (1995)
6	50 hill wheats along with std. varieties	57.10	0.70	0.99	0.50	Jagshoran (1995)
7	F_1s and their parents	High NS heritability				Wang and Weichun (1996)
8	F_1 of 15 crosses from 6 half diallels and their 6 parents	Lower				Hassan *et al*. (1996)
9	F_1, F_2, F_3, BC_1, BC_2, selfed BC_1, selfed BC_2	High	High			Dhanda and Sethi (1996)
10	6 parents and their 15 F_1's of bread wheat	26.26	20.89	3.73	3.63	Singh *et al*. (1996)
11	15 genotypes of foxtail millet	92.71	10.26	5.37	5.17	Muhammed and Hussain (2004)
6	**Spike length**					
1.	40 strains	High	High	-	-	Mandal *et al*. (1991)
2	21 genotypes	65	-	-	-	Zaheer Ahmed (1991)

Contd…

Sl. No.	Material used for the study	H	GA	PCV	GCV	References
3	F_1's from diallel	94	-	-	-	Prodanoric (1993)
4	Wide range of lines and varieties	High	-	-	-	Dachev (1995)
5	44 bread wheat lines	High	High	-	High	Shah (1998)
6	11 F_2 wheat lines	High	High	High	High	Thakur *et al*. (1999)
7	6 cultivars of bread wheat	49.93-66.05	1.28-2.25	-	-	Ali-Firouzian *et al*. (2003)
7	**Number of spikelets per spike**					
1	15 x 15 diallel crosses	7.8-49.5	-	-	-	Atate and Vitkare (1989)
2	6 generation from 3 cross	71.85-88.17	0.99-1.82	-	-	Pawar and Patil (1989)
3	11 parents and 9 F_2 population	High	High	-	-	Mahmood and Shahid (1991)
4	Wheat	87.09	2.95	8.12	7.58	Singh *et al*. (2001)
5	Late sown wheat	87.00	2.10	7.29	6.79	Mahesh *et al*. (2001)
8	**Grains per spike**					
1.	21 wheat genotypes	42	-	-	-	Zaheer Ahmad (1991)
2.	F_3 family from Giza 155 and west bread	High	-	-	-	Khiralla (1993)
3.	25 genotypes	73-91	27.53	17.97	15-45	Bahadur *et al*. (1994)
4.	F_5 generation	High	-	-	-	Collakua (1994)
5.	6 x 6 diallel	Moderate	-	-	-	Senapathi *et al*. (1994)
6.	50 hill wheat along with 3 checks	88.00	31.90	17.50	16.5	Jagshoran (1995)
7.	Generation from					
	HD2329 x Kalyanasona	68.15	3.36	7.19	6.81	Jitendra Kumar and Lutra (1995)
	HD2009 x Sonalika	41.11	2.29	14.02	9.07	
8.	F_2 wheat generation	High	Moderate	-	-	Ozkan *et al*. (1997)
9.	21 bread wheat varieties	Moderate	-	-	High	Uddin *et al*. (1997)
10.	Inter varietal crosses of bread wheat	Low	Low	Low	Low	Nirmala and Jha (1998)
11.	300 genotypes of bread and durum wheat	-	-	High	High	Sharma *et al*. (1998)
12.	25 wheat genotypes	High	High	High	High	Rama *et al*. (1999)
13.	F_2 population wheat cross in NC-1 design	High	-	-	-	Kamboj *et al*. (2000)

Sl. No.	Material used for the study	H	GA	PCV	GCV	References
	Contd…					*Contd…*
9	**1000 grain weight**					
1	11 parents and 9 F_2 population	High	High	-	-	Mahamood and Shahd (1991)
2	F_3 family from Giza 155 x West bread	High	-	-	-	Khiralla (1993)
3	1844 accessions of *T. monococcum*	-	-	High	High	Empilli *et al.* (1995)
4	6 parents and their 15 F_1's of bread wheat	28.81	2.22	8.79	1.33	Singh *et al*. (1996)
5	300 genotypes of bread and durum wheat	-	-	Moderate	Moderate	Sharma *et al*. (1998)
6	44 bread wheat lines	High	High	-	High	Shah (1998)
7	F_2's of 20 wheat crosses	High	-	-	-	Wang *et al*. (1998)
8	F_2 population of wheat intermediate cross in NC-1 design	Moderate	-	-	-	Kamboj *et al*. (2000)
9	50 bread wheat cultivars	-	-	High	High	Bergale *et al*. (2001)
10	52 Aegilops accessions	-	-	High	High	Zaharieva *et al.* (2003)
10	**Grain yield per plot**					
1.	Durum wheat	55.98	40.10	-	27.30	Dixit (1990)
2.	6 variety of half diallel	High	-	-	-	Khiralla *et al*. (1993)
3.	25 genotypes	39.31	18.23	22.51	14.11	Bahadur *et al*. (1994)
4.	F_5 generations	-	High	-	-	Collakua (1994)
5.	10 spring genotypes	Low	High	-	High	Liu and Ma (1994)
6.	6 x 5 diallel	Moderate	-	-	-	Senapathi *et al*. (1994)
7.	44 strains with Kaj3077 and K78 as checks	4.17	2.44	28.15	5.75	Chaturvedi and Gupta (1995)
8.	50 hill wheat along with 3 checks	82.50	58.90	34.60	-	Jagshoran (1995)
9.	6 parents and their 15 F_1's of bread wheat	7.47	1.93	14.19	12.54	Singh *et al*. (1996)
10.	F_2's of 20 wheat crosses	High	-	-	-	Wang *et al*. (1998)
11.	300 genotypes of bread and durum wheat	-	-	High	High	Sharma *et al*. (1998)

Sl. No.	Material used for the study	H	GA	PCV	GCV	References
12.	F_2 population of wheat cross in NC-1 design	High	-	-	-	Kamboj *et al*. (2000)
13.	50 bread wheat cultivars	-	-	High	High	Bergale *et al*. (2001)
11	**Protein content**					
1	44 strains of spring wheat with Raj 3077 and K_{68} checks	High	-	-	-	Chowdary and Gupta (1995)
2	42 genetic stocks of *Triticum durum*	High	-	-	-	Saiprasad and Pandey (2000)
3	Durum genotypes	95.83	1.67	6.72	6.58	Nayeem *et al*. (2003)

Table 2. Review of literature on correlation studies in wheat

Sl. No.	Material used for the study	Correlation with grain yield	References
1	**Days to 50% flowering**		
1	F_1 of crosses and parents	Positive and significant	Khan *et al*. (1999)
2	Advanced wheat lines	Negative	Narwal *et al*. (1999)
3	F_1 and F_2 generations of 5 half diallel crosses	Positive	Tammam *et al*. (2000)
4	F_6 and F_7 of triticale x wheat crosses	Negative	Gautam & Sethi (2002)
5.	76 genotypes of durum wheat	Positive	Nayeem *et al*. (2003)
2.	**Tillers per meter**		
1	Wheat genotypes	Positive	Saini *et al*. (1990)
2	*T. aestivum*	Positive	Dawari and Lutra (1991)
3	Bread wheat	Positive	Deshpande (1992)
4	257 land races of durum wheat	Significant positive	Al-Ajlouni and Jordat (1997)
5	Advanced wheat lines	Positive and significant	Narwal *et al*. (1999)
6	49 elite genotypes of wheat	Significant positive association with yield	Mahesh *et al*. (2001)
7.	4 wheat cultivars	Positive and significant	Jat and Dhakar (2003)
3.	**Plant height**		
1	Wheat	Positive	Szunics *et al*. (1982)
2	F_2 population of eight parent diallel crosses of wheat	Positive and significant	Bhullar (1984)
3	70 Ethiopian durum wheat genotypes	Strong positive	Getachew *et al*. (1993)
4	Winter x spring nursery	Positive and significant	Sharma *et al*. (1995)
5	15 F_2 populations from 6 x 6 half diallel	Significant	Abdel-Sabour *et al*. (1996)
6	F_1 of 15 crosses from 6 half diallels and their 6 parents	Significant	Hassan *et al*. (1996)
7	F_2 of crosses and parents	Positive & highly significant	Khan *et al*. (1999)

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Sl. No.	Material used for the study	Correlation with grain yield	References
8	200 genotypes of durum and dicoccum wheat	Significantly positive	Naik (2000)
9	16 wheat breeding lines	Strong negative	Mohammad Shahid *et al.* (2002)
4	**Peduncle length**		
1	200 genotypes of durum and dicoccuim wheat	Significantly negative under irrigated condition	Naik (2000)
2	F_6 and F_7 of triticale x wheat cross	Negative with spikes/plant, plant height, spikelets/ spike, days to maturity and heading	Gautam & Sethi (2002)
5	**Days to maturity**		
1	Wheat	Positive and significant	Jadhav (1994)
2	23 segregating population	Positive	Nirmala and Jha (1996)
6	**Spike length**		
1	*T. aestivum*	Positive	Dawari & Lutra (1991)
2	Bread wheat	Positive	Deshpande (1992)
3	15 F_1 population from 6 x 6 half diallel	Significant	Abdel-Sabour *et al*. (1996)
4	40 advanced F_8 lines of wheat along with 11 checks	Positive	Gupta *et al*. (1999)
5	Advanced wheat lines	Positive and significant	Narwal *et al*. (1999)
6	Three varieties of wheat planted under three dates of sowing with four nitrogen levels	Positive	Satish kumar *et al*. (2001)
7	50 hexaploid triticale	Positive	Reddy (2001)
8	F_6 and F_7 of triticale x wheat cross	Positive	Gautam & Sethi (2002)
9	40 F_1's	Strong and positive	Sudesh *et al*. (2002)
10	16 wheat breeding lines	Positive and significant	Mohammad Shahid *et al.* (2002)

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Sl. No.	Material used for the study	Correlation with grain yield	References
7	**Number of spikelets per spike**		
1	25 F_2 population of wheat under low fertility level	Significant	Yadav and Mishra (1992)
2	Wheat	Positive	Yadav and Mishra. (1992)
3	F_2 population of eight parent diallel crosses of wheat	Negative	Bhullar (1984)
4	Winter x Spring nursery	Positive and significant	Sharma *et al*. (1995)
5	15 F_2 populations from 6 x 6 half diallel	Significant	Abdel-Sabour *et al*. (1996)
6	F_1 of 15 crosses from 6 half diallels and their 6 parents	Significant	Hassan *et al*. (1996)
7	Isogenic population of wheat	Positive and significant	Jaglan *et al*. (1997)
8	F_2 of crosses and parents	Positive and highly significant	Khan and Bejwa (1999)
9	Wheat-Rye recombinant lines	Positive and significant	Yan-Zehong and Zheng-Youliang (1999)
10	200 genotypes of durum and dicoccum wheat	Significantly positive	Naik (2000)
11	50 hexaploid titicale	Positive	Reddy (2001)
12	Three wheat varieties planted under three dates of sowing with four nitrogen levels	Positive and significant	Satishkumar *et al*. (2001)
15	33 genotypes of wheat	Positive and significant	Singh *et al*. (2002)
16	40 F_1's of wheat	Strong and positive	Sudesh *et al*. (2002)

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SL. No	Material used for the study	Correlation with grain yield	References
8	**Grains per spike**		
1	32 bread wheat genotypes	Positive	Raut *et al*. (1995)
2	15 F_2 populations from 6 x 5 half diallel	Significant	Abdel-Sabour *et al*. (1996)
3	Wheat genotypes	Positive and significant	Paul and Ganguli (1996)
4	F_2 population derived from intercultivar crosses involving KAUZ "S" and 84 CZT04	Significant	Ozkan *et al*. (1997)
5	257 land races of durum wheat	Significant positive	Al-Ajlouni and Jaradat (1997)
6	Wheat genotypes	Significant	Wang *et al*. (1998)
7	22 common wheat cultivars	Positive	Dokuyucu and Akkaya (1999)
8	advanced wheat lines	Positive and significant	Narwal *et al*. (1999)
9	Pure line	Negative	Singh & Sharma (1999)
10	200 genotypes of durum & dicoccum wheat	Significantly positive	Naik (2000)
11	F_1 and F_2 generations of 5 half diallel crosses	Positive	Tammam *et al*. (2000)
12	Fifty bread wheat cultivars	Positive	Bergale *et al*. (2001)
13	F_6 and F_7 of triticale x wheat cross	Positive	Gautam & Sethi (2002)
9	**1000 grain weight**		
1	Pure line	Negative and significant	Yadav and Singh (1991) and Rao *et al*. (1993)
2	70 Ethiopian durum wheat genotypes	Strong positive	Getachew *et al*. (1993)
3	F_1 of 15 crosses from 6 half diallel and their 6 parents	Significant	Hassan *et al*. (1996)
4	15 F_2 populations from 6 x 6 half diallel	Significant	Abdel-Sabour *et al*. (1996)
5	Wheat genotypes	Positive and significant	Paul and Ganguli (1996)
6	257 land races of durum wheat	Significant positive	Al-Ajlouni and Jaradat (1997)

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SL. No	Material used for the study	Correlation with grain yield	References
7	22 common wheat cultivars	Positive and significant	Dokuyucu and Akkaya (1999)
8	F_1 of crosses and parents	Negative and significant	Khan *et al*. (1999)
9	Advanced wheat lines	Positive and significant	Narwal *et al*. (1999)
10	F_1 and F_2 generation of 5 half diallel crosses	Positive	Tammam *et al*. (2000)
11	F_6 and F_7 of triticale x wheat cross	Positive	Gautam and Sethi (2002)
12	76 genotypes of durum wheat	Positive	Nayeem *et al*. (2003)
13	4 wheat cultivars	Positive and significant	Jat and Dhakar (2003)
10	**Grain yield/plot**		
1	Pure line	Significant	Chaturvedi and Gupta (1995)
2	50 genotypes of winter wheat	Positively significant	Shorun (1995)
3	Wheat genotypes	Positive and significant	Paul and Ganguli (1996)
4	F_2 population derived from intercultivar crosses involving KAUZ "S" and 84 CZT04	Significant	Ozkan *et al*. (1997)
5	Wheat genotypes	Significant	Wang *et al*. (1998)
6	22 common wheat cultivars	Positive and significant	Dokuyucu and Akkaya (1999)
11	**Protein content**		
1	15 strains of wheat	Negative and non significant	Chowdary and Iqubal (1997)
2	42 genetic stocks of durum wheat	Low and negative	Saiprasad and Pandey (2000)

Table 3. Review of literature on path analysis for yield attributing traits on grain yield in wheat

Characters studied	Material used for the study	Effect on grain yield	References
Plant height	1. 44 strains of spring wheat	Direct positive	Chaturvedi and Gupta (1995)
	2. F_3 and F_4 genotypes of tetraploid wheat	Direct effect	Halloli (1997)
	3. 200 genotypes of durum and dicoccum wheat	Maximum indirect positive effect via total biomass and harvest index	Naik (2000)
Days to 50% flowering	1. 44 Strains of spring wheat	Direct positive	Chaturvedi and Gupta (1995)
	2. F_3 and F_4 genotypes of tetraploid wheat	Direct	Halloli (1997)
Number of tillers/meter	1. 44 strains of spring wheat	Direct positive	Chaturvedi and Gupta (1995)
	2. Advanced wheat lines	Positive and large direct effect	Narwal *et al*. (1999)
Spike length	1. Advanced wheat lines	Positive and large direct effect	Narwal *et al*. (1999)
Grains per spike	1. 15 F_1 hybrids and parents	Positive direct effect	Ibrahim (1994)
	2. 44 strains of spring	Positive direct effect	Chaturvedi and Gupta (1995)
	3. F_3 and F_4 genotypes of tetraploid wheat	Positive direct effect	Halloli (1997)
	4. Advanced wheat lines	Positive and large direct effect	Narwal *et al*. (1999)
	5. 22 common wheat cultivars	Direct via grain weight	Dokuyucu *et al*. (1999)
	6. 200 genotypes of durum and dicoccum wheat	Maximum indirect positive effect via total biomass and harvest index	Naik (2000)
1000 grain weight	1. Durum wheat	Positive direct effect	Deshmukh *et al*. (1990)
	2. 15 F_1 hybrids and parents	Positive direct effect	Ibrahim (1994)
	3. F_3 and F_4 genotypes of tetraploid wheat	Positive direct effect	Halloli (1997)
Grain yield/plot	1. Durum wheat	Direct positive effect	Ehdaie and Waines (1989)
	2. F_3 and F_4 genotypes of teraploid wheat	Positive direct effect	Halloli (1997)

and an efficient method to gauge the extent of diversity among genotypes, which quantify the difference among several quantitative traits. A summary of literature available on this aspect in wheat is presented below.

Genetic divergence study conducted by Lee and Kaltsikes (1973) in 10 durum wheat cultivars revealed no association between genetic divergence and geographic origin.

A total of 537 land races of winter wheat collected from 72 sites in Iran were evaluated for 12 yield components along with 3 local controls. The geographical sites were grouped into 5 climatic zones. Multivariate cluster analysis was carried out to categorize geographical sites as well as the ecogeographical sub-populations, based on plant characters. Character means for many characters in the sub-populations differed significantly from the main population. No specific pattern of variation among the regions was found due to ecogeographical variation (Vojdani *et al*., 1993).

Redhu *et al*. (1995) conducted genetic diversity study for nine quantitative characters in 121 indigenous and exotic varieties of wheat. The varieties were grouped into 27 clusters. Grouping of varieties in different clusters was not related to their geographical origin. Cluster means for different characters indicated the existence of large variability for plant height, peduncle length, number of grains per ear, 1000 grain weight and grain yield per plant.

Walia and Garg (1996) conducted cluster analysis in 405 pure breeding lines of *T. aestivum* for grain yield and it's associated traits. They observed 13 different clusters and the clustering pattern of the genotypes belonging to the same country revealed their distribution in more than one cluster showing non-parallelism between geographic and genetic diversity. Members of cluster IV and IX were highly diverse from each other and cluster VI had high mean values for grain yield, biological yield, number of tillers/unit area and harvest index.

Genetic divergence in 51 genotypes of spring wheat was studied by Gupta *et al*. (1996) and clustering was done using three different Tocher's values, *i.e*., 1060, 500 and 300. The genotypes were grouped into 7, 9 and 10 different clusters respectively. Linkage dendrogram and minimum spanning tree exhibited confirmity with the clustering pattern of D^2 statistic at Tocher's values 500 and 300.

Al-Ajlouni and Jaradat (1997) collected 257 land race genotypes of durum wheat from nine districts in Jordan and analysed to ascertain the amount of variation for 13 traits. Multivariate analysis by region revealed marked regional patterns and indicated that regions that have similar geographical and climatic similarity exhibit the same distribution patterns. The results suggested that Jordanian land races are rich sources of genetic variation and could be used in the reconstruction of a gene pool of germplasm for durum wheat improvement.

On the basis of non-hierarchical Euclidean cluster analysis, the 300 genotypes of bread and durum wheats from Indian and exotic collections were grouped into 16 clusters. Genotypes of heterogenous origin/place of release and of different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. This also suggested a lack of relationship between the genetic diversity and the ploidy level of genotypes (Sharma *et al*., 1998).

Bergale *et al*. (2001) studied genetic divergence among fifty bread wheat cultivars from India and Mexico for yield and yield components. The cultivars were grouped into 11 clusters. The presence of genotypes of different geographical origin in a single cluster suggest the possibility of existence of ancestral relationship among the cultivars. Cluster means revealed that plant height had the greatest contribution to genetic divergence.

Nimbalkar *et al*. (2002) conducted diversity analysis in 24 wheat cultivars for yield and yield contributing characters. The 24 cultivars grouped in to 12 clusters. The highest and lowest intracluster distance were observed in cluster III and I respectively. The intercluster distance was highest between cluster VII and cluster XII. Among the characters examined, the number of grains per spike, 1000-grain weight, grain weight per spike and number of productive tillers contributed considerably to the genetic divergence.

Dotlacil *et al*. (2000) conducted the cluster analysis in 120 accessions of European winter wheat land races and obsolete cultivars. Eight groups of cultivars were identified, one of them was represented by the check cultivars. Very specific clusters 7 and 8 were composed of 14 cultivars from six countries. Clustering has decreased the variability of cultivars within the clusters in most of evaluated characters, it was difficult to find a simple linkage between the geographic origin of cultivars and their appearance in particular clusters.

Molecular diversity

Zhang *et al*. (1996) studied genetic diversity of eighteen Chinese accessions of *Aegilops geniculata* using RAPD markers. Of 38 decamer primers used 17 produced polymorphic RAPDs among the 18 accessions of *A. geniculata*. By using genetic similarity coefficients they constructed the phenogram with UPGMA technique. The phenogram showed that RAPD data is useful in the measurement of genetic variation or similarity within a species. It also indicated that eight or nine accessions of the eighteen accessions could be selected to maintain at least 80 per cent of genetic variability of this collection.

Castagna *et al*. (1997) studied genetic variability among 49 accessions of *T. urartu* by RFLP and RAPD marker analysis and both the data sets were compared. One *T. timopheevii* accession and two accessions of *T. durum* and *T. aestivum* respectively were included to identify *T. urartu* accessions closely related to these polyploid wheats. 28 RFLP clones and 29 RAPD primers generated 451 and 155 polymorphic bands respectively. The three accessions from Armenia clustered together and were well separated from all other accessions, which showed less pronounced geographical patterns.

Okuno *et al*. (1998) conducted RAPD analysis in 112 accessions of *Aegilops tauschii* (DD genome), *A. cylindrica* (CCDD), *A. crossa* (DDMM), *A. biuncialis* (UUMM) and *A. triuncialis* (UUCC) collected from the central Asia and north Caucasia. The control Asian accessions of *Aegilops* species were more diverse than the accessions from north Causasia. *A. tauschii* and *A. cylindrica* from north Caucasia were genetically uniform. Association between altitudal variation of *Aegilops* species and variability of RAPD markers was not found.

Seven accessions of the Tibetian wheat, 22 cultivars of common wheat and 17 lines of spelt wheat were used for RAPD analysis to assess the genetic diversity among and 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 that 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 (Qixin sun *et al*., 1998).

Bered *et al*. (2002) evaluated 54 wheat genotypes from different origins and area based on the use of RAPD markers. Of 100 primers screened, 20 produced scorable bands, which generated 91 bands. The average genetic similarity, value among all genotype pairs was 0.88, showing large genetic relationship in the wheat germplasm evaluated. The dendogram clustered the genotypes into nine groups and showed efficiency in identifying genetic variability.

Barcaccia *et al*. (2002) reported the genetic diversity and relationships among 11 Italian local cultivars of emmer wheat are assessed with 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 to be 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 Malraraj with Motia and Jay. The clustering was clearly on the pattern of their

parentage. The grouping of the germplasm 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 done by UPGMA method showed two main groups. Similarity coefficient ranged 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 as a base for mapping economically important character loci of durum wheat by the development of other RAPDs.

III. MATERIAL AND METHODS

The present experiment was conducted during *rabi* 2004-05. The details of the materials used and techniques adopted during the course of investigation are described in this chapter.

3.1 EXPERIMENT-I

3.1.1 Location and experimental site

The present investigation was carried out at the fields located at Wheat Improvement Project, Main Agricultural Research Station, Dharwad. The experimental site is located between 15°-26° N latitude and 76”07’ E longitude and has altitude of 678 m above mean sea level. It comes under transition tract of Karnataka state.

3.1.2 Experimental material

The experimental material of the study comprised of 169 wheat genotypes. This material includes 143 *aestivum* wheat (*Tritium aestivum*), 22 durum wheat (*T. durum*) genotypes, three *dicoccum* (*T. dicoccum)* and one *Triticale*. The details of these genotypes are provided in Table 4.

3.1.3 Experimental layout

The experiment was laid out in Simple lattice Design with two replications. Each genotype in each replication was grown in a plot of 3 rows of 2 meter length each with a spacing of 23 cm between rows. The crop was provided with protective irrigations.

3.1.4 Recording of observations

Observations on yield and yield attributing characters were recorded. In each plot, five random plants were tagged to record these observations. By taking the average, the mean value for the treatment was computed. The characters studied and techniques adopted to record the observations are given below.

3.1.4.1 Days to 50 per cent flowering

The number of days taken from the date of sowing to the day on which the main ear comes out of the flag leaf completely in 50 per cent of the plants was taken.

3.1.4.2 Days to maturity

Number of days taken from the date of sowing to the time when more than 75 per cent of the spikes on the plots turned golden yellow was recorded.

3.1.4.3 Plant height (cm)

The plant height was measured from bottom of the plant *i.e.*, from soil level to the base of the spike in centimeter.

3.1.4.4 Peduncle length (cm)

Length of the peduncle of the main culm was recorded in centimeter from the top most node to the base of the spike.

3.1.4.5 Number of productive tillers per meter

The number of tillers bearing ear heads were counted at the time of harvest per meter length of each row.

Table 4 : List of genotypes used in the study

Sl. No.	Genotypes	Species	Pedigree
1	AJANTA	*T.aestivum*	PW5/Y53
2	AKW 1071 (PURNA)	*T.aestivum*	VEE/3/FLN/ACC//ANA
3	BIJAGA YELLOW	*T. durum*	M. Local/Gaza
4	BW 11 (PURBALI	*T.aestivum*	KVZ/TI/TITO
5	C 306	*T.aestivum*	RGN/CSK-3//2* C591/3/C21/N14//C281
6	CHHOTI LERMA	*T.aestivum*	L.R.(SIB)*HUA.R
7	CPAN 1676 (ROHINI)	*T.aestivum*	BON//CNO/SN64/3/KAL/BEB
8	CPAN 1796	*T.aestivum*	NAPO/TOB'S'//8156/3/KAL/BB
9	DBW 14	*T.aestivum*	RAJ 3765/PBW343
10	DDK 1001	*T. dicoccum*	Local dicoccum 4*// local dicoccum/RAJ 1555
11	DDK 1009 (GANGA)	*T. dicoccum*	NP200*4//MP200/ALTAR-84
12	DL 153-2 (KUNDAN)	*T.aestivum*	Tanori 71/NP 890
13	DL 784-3 (VAISHALI)	*T.aestivum*	KAL*4/TR380 0.27*4/3 AG/3/HD 2281
14	DL 803-3 (KANCHAN)	*T.aestivum*	HUW-202-K7537/mutant of HD2160
15	DT 46	*Triticale*	JNIT 140/DTS/1209
16	DWR 16 (KEERTHI)	*T.aestivum*	SKA/70B
17	DWR 39 (PRAGATI)	*T.aestivum*	LR64/2* SN64//S308
18	DWR 137 (KIRAN)	*T. durum*	BJGY//206
19	DWR 162	*T.aestivum*	KVZ/BUHO//KAL/BB
20	DWR 185	*T. durum*	CPAL-6018/2*RAJ1555
21	DWR 195 (ANURADHA)	*T.aestivum*	BOMARA-105-7
22	DWR 1006	*T. durum*	SULA/CREX//AAZ
23	GW 273	*T.aestivum*	CPAN-2084/VW205
24	GW 322	*T.aestivum*	PBW-173/GW-196
25	GW 405	*T.aestivum*	MACS2340/IWP5070
26	GW 496 (GUJARAT WHEAT)	*T.aestivum*	HD2285/4/CNO/NO//CC/INIA 66/3/KAL/BB
27	GW 503	*T.aestivum*	CPAN 1582/J142
28	GW 1139	*T.durum*	H41-3(HD1962*(E4870*K65))
29	HB 208	*T.aestivum*	SPO/MTA//MQ/2* RNW//3/BJ'S'/P14/KT54B
30	HD 1982 (JANAK)	*T.aestivum*	YT54/N10B//HD845
31	HD 2009 (ARJUN)	*T.aestivum*	LR64A/NAI60
32	HD 2135 (NILGIRI)	*T.aestivum*	CPAL2009/HD2329
33	HD 2428	*T.aestivum*	HD 1949/HD2160
34	HD 2501	*T.aestivum*	HD2189/HD2160
35	HD 2643 (GANGA)	*T.aestivum*	VE'S'/HD2407/HD2329
36	HD 2687 (SHRESHTH)	*T.aestivum*	CPAN 2009/HD2329
37	HD 2733	*T.aestivum*	ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA
38	HD 2781 (ADITYA)	*T.aestivum*	BOW/C306//C591/HW2004
39	HD 2824	*T.aestivum*	PTO-1/CNO79/PRL/GAA/3/HD1951
40	HD 2833	*T.aestivum*	PBW226/HW1042//HD2285
41	HD 4672 (MALVA RATNA)	*T. durum*	BIJAGA RED/PBW34//ALTAR84
42	HDR77	*T.aestivum*	PTZ/2*HD2204

Sl. No.	Genotypes	Species	Pedigree
43	HI 977	*T.aestivum*	GLL/AUST1161 0.157//CNO/NO/3/Y50E/3*KAL
44	HI 1077 (MANGLA)	*T.aestivum*	Galo/Aust 11-61 0.157//CNO/NO/KAL/BB
45	HI 1500 (AMRITA)	*T.aestivum*	HW2002*2//STREMTALLI/PNC5
46	HI 8381 (MALVASHRI)	*T. durum*	JO 69 'S'/AA 'S'/FGO 'S'
47	HI 8498 (MALAV SHAKTI)	*T. durum*	CR"S"-GS'S'/A-9-30-1///RAJ911
48	HP 1633 (SONALI)	*T.aestivum*	TH*6/TF//6*SK/*
49	HP 1731 (RAJ LAKSHMI)	*T.aestivum*	Lara/Parula/Tonichi
50	HP 1744 (RAJESHWARI)	*T.aestivum*	CNO/PRI//CHILENO/GERUDA
51	HP 1761 (JAGDISH)	*T.aestivum*	RL6010/6INIA66//3*KAUZ
52	HS 375	*T.aestivum*	BB/G11/CJ71/3TA EST//KAL/BB
53	HS 420 (9SHIVALIK)	*T.aestivum*	KAJ3302//CMH73A-49/3*79
54	HS 1097-17 (GIRIJA)	*T.aestivum*	CJ60/3/SPO/MTA//MQ/2*RNW
55	HS 1138-6-4 (SHAILAJA)	*T.aestivum*	PJ 'S'/P14//KT54B/3/SKA
56	HUW 12 (MALVIYA 12)	*T.aestivum*	NP876/CIANO 66
57	HUW 55 (MALVIYA 55)	*T.aestivum*	E4870/HD 1982//INDA 66/HD 2189
58	HUW 206 (MALVIYA 206)	*T.aestivum*	KVZ/BUHO//KAL/BB
59	HUW 213	*T.aestivum*	NORTEBO/MOTI//HD 2160
60	HUW 234	*T.aestivum*	HUW12/SPRW//HUW12
61	HUW 318 (MALVIYA WHEAT)	*T.aestivum*	HUW206//KAL/MUS
62	HUW 468 (MALVIYA WHEAT)	*T.aestivum*	CPAN-1962/TONI..LIRA'S'/PRL'S'
63	HUW 533	*T.aestivum*	UNNATH C 306/HUW 81// 8027
64	HW 517	*T.aestivum*	BB-CC/CIANO 'S'*//NO 66-PI62
65	HW 657	*T.aestivum*	TIMGALEN */K65
66	HW 741	*T.aestivum*	BB/CC/3/CNO/NO//PI 'S'
67	HW 1085 (BHAWANI)	*T.aestivum*	UNNATHALYANSONA*2//CPAN3057
68	HW 2004 (AMAR)	*T.aestivum*	C306*/7TR380-14*7/3AG14
69	HW 2045	*T.aestivum*	HD 2402*6 /SUNSTAR*6/C-80-1
70	HYB 65	*T.aestivum*	GW-AUS/115
71	J-1-7	*T. aestivum*	SELECTION FROM J1
72	JNK-4W-184 (JAIRAJ)	*T.durum*	(T.PALO-YAGULUTE)(PITELE-2-B-W)
73	K 68	*T.aestivum*	NP773/K13
74	K 852	*T.aestivum*	SELECTION FROM S 308
75	K 7410 (K-POORVI)	*T.aestivum*	K860 'S'/KAL
76	K 8020 (TRIVENI)	*T.aestivum*	KAL/HD1982
77	K 8027 (MAGHAR)	*T.aestivum*	NP875/4/N10B/Y53//Y50/3/KT55B/5/2*K852
78	K 8804	*T.aestivum*	BEE/WLWL711
79	K 8962 (INDRA)	*T.aestivum*	K860;S/PV80//HT2160
80	K 9006 (UJIYAR)	*T.aestivum*	K8101/K68
81	K 9107 (DEWA)	*T.aestivum*	K8101/K68
82	K 9465 (GOMTI)	*T.aestivum*	K 68
83	K 9644	*T.aestivum*	HD 2402/K8305
84	KALYANSONA	*T.aestivum*	P 'J' 'S'/GB55

Contd…

Sl. No.	Genotypes	Species	Pedigree
85	KHARCHIA 65	*T.aestivum*	KHARCHIA 65/ WL711
86	KRL 1-4	*T.aestivum*	KHLC/WL711
87	KRL-19	*T.aestivum*	PBW255/KRL 1-4
88	KSML 3	*T.aestivum*	NA
89	LERMA RAJO	*T.aestivum*	Y50/N10B//L52/3/2*LR
90	LOK 1	*T.aestivum*	S308/S331
91	MACS 1967	*T.durum*	Gulab/CPAN1471
92	MACS 2496	*T.aestivum*	VEERY #5
93	MACS 2694	*T.durum*	MEXICAL*RAJ 1555* MACS 2130
94	MACS 2846	*T.durum*	CPAN 6079/MACS 2340
95	MLKS 11	*T.aestivum*	NA
96	MOTIA (BANSI 168)	*T.aestivum*	SEL.LOCAL BANSI
97	N59	*T.durum*	Gaza/Motie
98	NI 917	*T.aestivum*	C591*/CHARTER (EX-73)
99	NI 5439	*T.aestivum*	REP80/3*NP710
100	NI 5643	*T.aestivum*	NEW THATCH/NI 284-5
101	NI 5749	*T.durum*	G-4-48*N59
102	NIAW 34	*T.aestivum*	CNO79/PRL 'S'
103	NIDW 15	*T.durum*	DOM 50
104	NIDW 295	*T.aestivum*	BOOMER 33/ PLATA 8
105	NP 884	*T.aestivum*	E1913 * NP755
106	NW 1012	*T.aestivum*	PARANA#2//JUP/BJY 'S'/31VEE#5
107	NW 1014	*T.aestivum*	HAHN 'S'
108	NW 2036	*T.aestivum*	BOW/CROW/BUC/PVN
109	PBN 51	*T.aestivum*	BUC 'S'/FLK 'S'
110	PBN 142 ((KAILASH)	*T.aestivum*	(HD 2189*NI 917)* NI 917
111	PBW 65	*T.aestivum*	USA255/K816/3/WL202
112	PBW 343	*T.aestivum*	ND/1945//KAL//BB/3/YACO 'S'/4/VEE #5 'S'
113	PBW 373	*T.aestivum*	ND/VG/944//KAL/BB/3/YACO 'S'/4/VEE# 5 'S'
114	PBW 396	*T.aestivum*	CNO67/MFD//MON 'S'/3/SERI
115	PBW 443	*T.aestivum*	PBW 304/CPAN 1922
116	PBW 502	*T.aestivum*	WH485/PBW 343//RAJ/1482
117	PDW 215	*T.durum*	RAJ 911//AA 'S'/D#2E/3/DWNL5002
118	PDW 233	*T.durum*	YAV 'S'/TEN 'S'
119	RAJ 821	*T.aestivum*	NP875/HD (M) 1508
120	RAJ 911	*T.durum*	V-0229 (CIMMAYAT)
121	RAJ 1482	*T.aestivum*	COCORIT/RAJ 911
122	RAJ 1555	*T.durum*	COCORIT/RAJ911
123	RAJ 3765	*T.aestivum*	HD2402/VL631
124	RAJ 4037	*T.durum*	DL 788-2/RAJ 3717
125	SAFED LERMA	*T.aestivum*	Y50/N10B//L52/3/3/*LR
126	SAGARIKA	*T.aestivum*	NP 798/KAL
127	SHARBATI SONORA	*T.aestivum*	AMBER MUTANT OF S64
128	SKAML 1	*T.aestivum*	NA
129	SONAK	*T.aestivum*	II54.388/AN/3/YT54/N10B/LR

Sl. No.	Genotypes	Species	Pedigree
130	SONALIKA	*T.aestivum*	II54.388/AN/3/YT54/N10B//LR
131	SONORA 64	*T.aestivum*	YT54/N10B//2*Y54
132	UP 301	*T.aestivum*	L.R.*SON.64
133	UP 368	*T.aestivum*	LR64*SON.64
134	UP 1109	*T.aestivum*	UP262/UP368
135	UP 2003	*T.aestivum*	BB/2*7C
136	UP 2113	*T.aestivum*	UP 346/WG 377
137	UP 2121	*T.aestivum*	UP 366/SONAKA 68
138	UP 2338	*T.aestivum*	UP368/VL421//UP262
139	UP 2382	*T.aestivum*	CPAN 2004/HD 2204
140	UTKALIKA	*T.aestivum*	DG 65/C304//FAO1061-68R
141	VINATA (N 8223)	*T.aestivum*	C306/H65(SELECTION OF N-112)
142	VL 401	*T.aestivum*	FKN/N10B
143	VL 804	*T.aestivum*	CPAN 3018/CPAN 3004/PBW65
144	VL 829	*T.aestivum*	IBWSN/CPAN2099
145	VL 832	*T.aestivum*	PBW 65/CPAN3031
146	WH 147	*T.aestivum*	E4870/C286/C273/4/S339/PV18
147	WH 533	*T.aestivum*	VEE#5
148	WH 542	*T.aestivum*	JUP/BJY ‘S’//URES
149	WH 896	*T.durum*	STN ‘S’/WH852
150	WH 711	*T.aestivum*	ALD ‘S’HUAC//HD 2285/3/HFW-17
151	PBW 524	*T.aestivum*	NA
152	JAY	*T.dicoccum*	Motia/KPH (DM)
153	K 53	*T.aestivum*	SEL.LOCAL OF JHANSI
154	K 65	*T.aestivum*	C591/NP773
155	MONDHYA 3-2	*T.aestivum*	SEL.LOCAL MONDHYA
156	NP 165	*T.aestivum*	NP4/FR
157	NP 718	*T.aestivum*	NP710 ‘S’
158	NP 737	*T.aestivum*	CHNW/NP111
159	NP 745	*T.aestivum*	NP710 ‘S’
160	NP 760	*T.aestivum*	NP710 ‘S’
161	NP 761	*T.aestivum*	NP710 ‘S’
162	NP 771	*T.aestivum*	NP710 ‘S’
163	NP 823	*T.aestivum*	NP165/C5/NP799/NP770
164	NP 824	*T.aestivum*	WIS245 ‘S’/NP165/NP770/3/C518/NP165
165	NP 825	*T.aestivum*	NP824 ‘S’
166	NP 836	*T.aestivum*	INDUCED AWNWD AWNWD MUTANT NP 799
167	NP 890	*T.aestivum*	GAZA(DR)/2*C281
168	RIDLEY	*T.aestivum*	NABAWA/HARDFEDERATION
169	VIJAY	*T.durum*	Motia/KHAPLI (DM)

3.1.4.6 Spike length (cm)

The average spike length of five plants on the main culm from the base of the spike to the top of the last spikelet excluding awns was recorded in centimeter.

3.1.4.7 Number of spikelets per spike

Total number of spikelets on main spike of all five plants were counted at the time of maturity and average was recorded.

3.1.4.8 Number of grains per spike

Total number of grains in the main spike were counted at the time of harvest and recorded.

3.1.4.9 1000 grain weight (g)

Total of 1000 grains in each entry was taken and weight was recorded in grams.

3.1.4.10 Protein content

The protein content was analyzed by non-destructive method using Infratec 1241 grain analyzer.

3.1.4.11 Grain yield (g/plot)

Total dry weight of grains harvested from all 3 rows was taken as grain yield per plot and expressed as grams per plot.

3.2 STATISTICAL ANALYSIS

The statistical analysis of the data on individual character was carried out on the mean values over two replications. The statistical methods adopted were as follows.

i) General mean (X) = $\dfrac{\text{Sum of observations of all the plants for each genotype}}{\text{Number of plants}}$

ii) Range = The minimum and maximum values for each trait within population

iii) Coefficient of variation (CV%) = $\dfrac{\sigma_p}{\bar{X}} \times 100$

Where,

σ_p = Phenotypic standard deviation

3.2.1 Analysis of variance (ANOVA)

The analysis of variance (ANOVA) for all characters was carried out separately.

The structure of ANOVA

Source of variation	d.f.	M.S.S.	Expected values of M.S.S.
Replication (r)	r-1	M_1	-
Genotypes (g)	g-1	M_2	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1) (g-1)	M_3	σ_e^2
Total	(rg-1)	$M_1 + M_2 + M_3$	-

Where, r = number of replications

g = number of genotypes

3.2.2 Estimation of genetic parameters

In order to assess and quantify the genetic variability among the genotypes for the characters under study, the following parameters were estimated.

3.2.2.1 Estimation of variance components

Phenotypic and genotypic variances were estimated using the following formula,

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS (genotypes) - MSS (error)}}{\text{Number of replications}} = \frac{M_2 - M_3}{r}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \text{MSS error} = \frac{M_2 - M_3}{r} + M_3$$

3.2.2.2 Genotypic and phenotypic coefficient of variation

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

1. Genotypic coefficient of variability (GCV)

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

2. Phenotypic coefficient of variability (PCV)

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

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

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

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973). It is as follows

0-10% : Low

10-20% : Moderate

20% and above : High

3.2.2.3 Heritability

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage.

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

The heritability was categorized as low, moderate and high as given by Robinson *et al.* (1949).

0-30% : Low

30-60% : Moderate

60% and above : High

3.2.2.4 Genetic Advance (GA)

The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated by using the following formula.

Genetic Advance (GA) = $ih^2 \sigma_p$

Where, i = Intensity of selection

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

The value of i was taken as 2.06 assuming 5% selection intensity.

3.2.2.5 Genetic Advance over mean (GAM)

Genetic advance over mean was estimated using the following formula

$$\text{GAM } (\%) = \frac{GA}{\bar{X}} \times 100$$

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al*. (1955).

It is as follows.

0-10% : Low

10-20% : Moderate

20% and above : High

3.2.2.6 Association and path analysis

a) Association studies

The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components.

Genotypic and phenotypic correlations were calculated by using the formula given by Weber and Moorthy (1952).

$$r_p = \frac{Cov_p\,(XY)}{\sqrt{\sigma^2_p\,(X)\;\sigma^2_p\,(Y)}}$$

$$r_g = \frac{Cov_g\,(XY)}{\sqrt{\sigma^2_g\,(X)\;\sigma^2_g\,(Y)}}$$

Where,

r_g = Genotypic correlation

r_p = Phenotypic correlation

$Cov_p(XY)$ = Genotypic covariance between the characters 'x' and 'y'

$\sigma^2_p\,(X)$ and $\sigma^2_p\,(Y)$ = Phenotypic covariance between the characters 'x' and 'y'

Estimates of correlation coefficients were compared against r-values given in Fisher and Yates (1963) table at (n-2) df at the probability levels of 0.05 and 0.01 to test their significance.

b) Path analysis

Path coefficient analysis was carried out for each population separately by using the correlation coefficients to know the direct and indirect effects of the six components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations, which express the basic relationship between correlations and path coefficients. The equations were as follows

$$r_1y = P_1y + r_{12}\,P_2y + r_{13}\,P_3y + \ldots\ldots\ldots + r_{1\,11}\,P_{11}y$$

$$r_2y = r_{21}P_1y + P_2y + r_{23}\,P_3y + \ldots\ldots\ldots + r_{2\,11}P_{11}y$$

$$r_3y = r_{31}P_1y + r_{23}\,P_2y + P_3y + \ldots\ldots\ldots + r_{3\,11}P_{11}y$$

...

...

$$r_{11}y = r_{1\,11}P_1y + r_{2\,11}P_2y + r_{3\,11}P_3y + \ldots\ldots\ldots r_{10\,11}P_{10\,11} + P_{11}y$$

Where, r_1y to $r_{11}y$ denote the correlation coefficients between independent characters 1 to 11 and dependent character 'y', r_{11} to $r_{10\,11}$ denote the correlation coefficients between all possible combinations of independent characters. P_1y to $P_{11}y$ denote the direct effects of characters 1 to 11 on character y.

Genetic diversity analysis

Multivariate analysis using D^2 statistics

Mahalanobis (1936) D^2 – statistic was used for assessing the genetic divergence between genotypes.

The generalized distance between any two populations is defined as,

$$D^2 = \Sigma \quad \Sigma\,(\lambda^{ij}) \sum_{i=1}^{p} \delta_i \sum_{j=1}^{p} \delta_j$$

Where,

λ^{ij} = The reciprocal matrix to the common dispersion matrix

δ_i = The difference between the two mean values of the two populations for ith character ($\mu i1 - \mu i2$)

δ_j = The difference between the mean values of the two populations for the jth character ($\mu j1 - \mu j2$)

μ = Vector mean values for all the characters

The formula for the estimation of distance, D^2 from samples:

$$D^2p = d^1 S^{-1} d$$

Where,

D^2p = Square of the distance considering P variables.

$d = (X_1i - X_2i)$

X = Vector of mean values of all the characters

S^{-1} = inverse of variance covariance matrix

Formula for computation of D^2 values, which requires inversion of the matrix, becomes complicated especially when the numbers of variables under consideration are large. Therefore, the original correlated unstandardized variables (Xi) were transformed to standardized uncorrelated variables (Yi) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two population i.e., D^2i.

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula,

$$D^2 = \Sigma (\bar{Y}_{1i} - \bar{Y}_{2i})^2$$

Where,

$\bar{Y}_{1i}$ = Vector of transformed mean values, for first genotype

$\bar{Y}_{2i}$ = Vector of transformed mean values, for second genotype

The square root of the D^2 values gives the generalized distance (D) between the two populations. The D^2 values were arranged in a matrix form. The significance of D^2 values between any two populations was tested using the following formula,

$$F = \frac{(n_1 + n_2 - p - 1)}{(n1 + n_2 - 2)\, P} \times \frac{(n_1\, n_2)\, D^2}{(n1 + n_2)}$$

This computed F was compared with table F value at 5 per cent and 1 per cent levels of significance with P(number of characters) and $(n_1 + n_2 - p - 1)$ degrees of freedom.

Determination of population constellation

All the $n(n - 1)/2$ D^2 values were considered for determining the population constellation. This was realized by using Tocher's method as described by Rao (1952). The criterion used in clustering by this is that any two varieties belonging to the same cluster, should at least, in average, show a smaller D^2 value than those belonging to different clusters. As per the device it was to start with two closely associated population and find a third population, which had the smallest average D^2 from these two. Similarly, the fourth was chosen to have a smallest average D^2 from the first three and so on. The permissible increase in D^2 values for clustering into the same group was fixed approximately nearer the maximum D^2 value shown by a population to the nearest population. This procedure was continued till D^2 values of all the pairs of genotypes were exhausted. After the formation of the clusters inter and intra group distance was calculated. The square root of the average D^2 values obtained from the above represents the distance (D) between and within clusters.

3.3 EXPERIMENT II: ASSESSMENT OF MORPHOLOGICAL AND MOLECULAR DIVERSITY

Materials

The base material for the present study consisted of Thirty seven wheat genotypes. Among them two genotypes belong to *T. dicoccum,* seven genotypes were *Triticum durum* while 28 genotypes belongs to *Triticum aestivum* species.

Sl. No.	Genotypes	Species	Sl. No.	Genotypes	Species
1	BIJAGA YELLOW	*T. durum*	20	MLKS 11	*T.aestium*
2	DDK 1001	*T. dicoccum*	21	N 59	*T.durum*
3	DDK 1009	*T. dicoccum*	22	NI 5439	*T.aestium*
4	DWR 162	*T. aestivum*	23	PBN 51	*T.aestium*
5	DWR 1006	*T. durum*	24	PBN 142	*T.aestium*
6	HD 1982	*T. aestivum*	25	PBW 373	*T.aestium*
7	HD 2009	*T. aestivum*	26	RAJ 911	*T.durum*
8	HD 2135	*T. aestivum*	27	RAJ 1555	*T. durum*
9	HP 1633	*T. aestivum*	28	SAFED LERMA	*T.aestium*
10	HS 420	*T. aestivum*	29	SHARABATI SONARA	*T.aestium*
11	HUW 12	*T. aestivum*	30	SONAK	*T.aestium*
12	HW 517	*T. aestivum*	31	SONALIKA	*T.aestium*
13	HW 1085	*T. aestivum*	32	SONARA 64	*T.aestium*
14	HYV 65	*T. aestivum*	33	UP 301	*T.aestium*
15	J-1-7	*T. aestivum*	34	VL 401	*T.aestium*
16	K 68	*T. aestivum*	35	VL 829	*T.aestium*
17	K 852	*T. aestivum*	36	WH 147	*T.aestium*
18	MACS 2694	*T. durum*	37	RIDLEY	*T.aestium*
19	MACS 2846	*T.durum*			

METHODOLOGY

DNA extraction

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% β-mercapto ethanol) pre-heated to 65℃. 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 emulsion.

4. The tubes were centrifuged for 10 minutes at 6000 rpm at room temperature.
5. The supernatant was transferred to sterile tuber and 10 ml of chilled isoproponol was added to each tube, mixed by inverting and incubated at -20℃ for 10 min.
6. The contents were centrifuged again for 20 minutes with 5000 rpm at 4℃ 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 µl TE (10 mM Tris Hcl, 1 mM EDTA) buffer and stored at -20℃.

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.

Optimization of polymerase chain reactions

Template DNA

The purified genomic DNA extracts (30 ng) of wheat genotypes was used as template DNA per reaction.

Random primers

Commercial kit OPA and OPP of decamer DNA primers were obtained from Operon technologies Inc. Alamedos, USA.

dNTPs

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

Taq DNA polymerase

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

Thermo cycler

Primus 96 plus supplied by MWG AG Biotech, Auzinger Strasse TA, Eberiberg, Germany was used for cyclic amplification of DNA.

PCR mixture

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

Sl. No.	Components	Quantity (µl/reaction)
1.	10x assay buffer with 15 mM	2.0
2.	dNTPs mix (2.5 mM each)	1.6
3.	Primer (5 pM/µl)	2.0
4.	Template (30 ng/µl)	1.0

5.	Mg Cl_2	0.5
6.	Sterile distilled water	0.33
7.	Taq DNA polymerase (3u/µl)	12.57

Except template, the master mix was equally distributed to PCR tubes (19 µl/tube) and later 1 µl of template DNA from the respective genotypes was added making the final volume of 20 µl.

The thermoprofile for PCR

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

Sl. No.	Step	Temperature (°C)	Duration (min)	Number of cycles
1.	Denaturation	94	5	1
2.	Denaturation	94	1	
3.	Annealing	38	1	37
4.	Extension	72	2	
5.	Final extension	72	10	1
6.	Hold (stmya)	4	-	-

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

Separation of amplified products on agarose gel electrophoresis

The amplified products from each tube along with 2 ml of loading dye (bromophenol blue) were separated on 1.4 per cent agarose gel at 70 volts (<5 volts per cm 7 gel) using 1x TAE buffer (pH 8.0) containing ethidium bromide (0.5 µg ml^{-1}). Lambda DNA ECORI/Hind III double digest was used as DNA molecular weight marker. The gels were photographed using gel documentation system of Hero lab EASY, Germany.

Scoring the amplified fragments

The amplified fragments were scored as '1' for the presence and '0' for the absence of a band generating the 0 and 1 matrix and per cent polymorphism was calculated by using the following formula.

$$\text{Per cent polymorphism} = \frac{\text{Number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

Analysis of the profile of the amplified fragments

Pair wise genetic similarities (Sij) between genotypes were estimated by DICE similarity coefficient. Clustering was done using the symmetric matrix of similarity coefficient and clusters obtained based on unweighted pair group arithmetic mean (UPGMA) using SHAN module of NTSYS-PC version 2.0 (Rohlf, 1998), the similarity measurements were converted to genetic distance measurements as (1-SM) X 100 (Spooner *et al*., 1996).

IV. EXPERIMENTAL RESULTS

A field experiment comprising of 169 wheat genotypes was laid out in a simple lattice design with all recommended agronomic practices during *rabi* 2004. The extent of genetic variability, association between yield and yield components, path analysis, genetic diversity was studied. An attempt to study the molecular diversity was also made in 37 genotypes. The results of the present investigation are presented under the following headings.

4.1 Genetic variability, heritability and genetic advance

4.2 Character association

4.3 Path analysis

4.4 Genetic diversity

4.5 Morphological and molecular diversity

4.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The analysis of variance for 11 characters was carried out to partition the total variance due to genotypes and other sources. The variance due to known and unknown causes were worked out using the method suggested by Choudhary and Prasad (1967) and Lush (1949).

Analysis of variance revealed highly significant differences among entries in respect of all the characters studied. The mean sum of squares of all the 11 characters studied is presented in table 5. The mean performance of these genotypes for various characters is presented in Appendix I. Range, mean, phenotypic and genotypic coefficient of variation, heritability estimates and predicted genetic advance as per cent of mean for characters studied are presented in Table 6.

4.1.1 Days to 50 per cent flowering

The variability observed for days to 50 per cent flowering was high, as reflected by its wide range from 41 days (HD 2833) to 69.5 days (WH 147) with an average value of 55.6 days. PCV and GCV were moderate being 11.0 per cent and 10.9 per cent, respectively. The magnitude of heritability estimated was very high (97.8%) with high expected genetic advance (GAM) of 22.2 as per cent of mean.

4.1.2 Days to maturity

Days to maturity ranged from 67 days (MOTIA, PBW 396, SHARBATI SONARA, SKAML 1, VL 401 and NP 761) to 116.5 days (WH 896). The average value for the trait was 94.4 days. The PCV and GCV values were moderate (14.7% and 14.6%, respectively). High heritability estimate of 99.5 per cent was recorded with high (30.1%) expected GAM.

4.1.3 Plant height

The mean plant height was 80.7 cm with a range of 55 cm (PBN 51) to 113 cm (NP 165). The PCV (14.8%) and GCV (14.5%) values were moderate. The trait had a high heritability of 95.6 per cent and high expected GAM (29.1%).

4.1.4 Peduncle length

The peduncle length exhibited a wider variation, which ranged from 19.2 cm (WH 711) to 40.5 cm (CPAN 1796) with overall mean of 29.7cm. The trait revealed moderate PCV (15.6%) and GCV (14.6%) values. The heritability recorded was high (86.8%) with high GAM (27.9%).

Table 5. Mean sum of squares for 11 characters in wheat genotypes

Characters	RMSS	GMSS	EMSS
Days to 50% flowering	90.56	74.33**	0.84
Days to maturity	227	382.97**	0.87
Plant height(cm)	1.25	278.38**	6.21
Peduncel length(cm)	0.22	40.26**	2.84
Number of productive tillers/mt	1259	1413.59**	45.49
Spike length(cm)	1.23	3.8**	0.19
Number of spikelets / spike	7.08	11.18**	1.27
Number of grains / spike	88.59	93.74**	8.2
1000 grain weight(g)	0.25	39**	8.02
Protein content	9.77	2.69**	0.37
Grain yield per plot	286288	78079.61**	9723.9

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

Table 6. Genetic variability parameters in wheat genotypes

Characters	Mean	Range	GCV	PCV	h^2 (%)	GAM (%)
Days to 50% flowering	55.60	41-69.50	10.90	11.03	97.80	22.21
Days to maturity	94.44	67-116.50	14.64	14.67	99.50	30.08
Plant height(cm)	80.74	55-113	14.45	14.77	95.60	29.11
Peduncle length(cm)	29.73	19.17-40.50	14.55	15.62	86.80	27.92
Number of productive tillers/mt	157.17	96-213.35	16.64	17.18	93.80	33.19
Spike length(cm)	9.14	6.09-12.60	14.72	15.46	90.60	28.88
Number of spikelets / spike	18.33	12.66-26.33	12.15	13.61	79.60	22.31
Number of grains / spike	37.53	23.83-61.00	17.42	19.02	83.90	32.88
1000 grain weight (g)	42.39	30.99-56.04	9.29	11.44	65.90	15.52
Protein content	15.02	12.25-17.7	7.17	8.23	76.00	12.92
Grain yield per plot	887.52	360-1635	20.83	23.61	77.90	37.86

4.1.5 Number of productive tillers per meter length

Number of productive tillers per meter estimated showed a wide variation, which ranged from 96 (CPAN 1676) to 213.4 (MACS 2496) and mean value for this trait was 157.2. The PCV (17.2%) and GCV (16.6%) were moderate for this trait. The heritability estimate was high (93.8%) with high GAM (33.2%).

4.1.6 Spike length

A range of 6.1 cm (HI 8498) to 12.6 cm (HD 2824) was observed for spike length. With the mean value of 9.1 cm. The moderate PCV and GCV values of 15.5 per cent and 14.7 per cent, respectively were exhibited for this trait. The heritability observed was 90.6 per cent with high genetic advance of 28.9 as per cent of mean.

4.1.7 Number of spikelets per spike

Number of spikelets per spike ranged from 12.7 (DL 784-3) to 26.3 (DDK 1009) with a mean of 18.3. This trait exhibited moderate PCV and GCV value (13.6 and 12.2, respectively). It had high heritability of 79.6 per cent with high GAM (22.31%).

4.1.8 Number of grains per spike

Number of grains per spike ranged from 23.8 (K 9465) to 61 (RAJ 821) with a mean of 37.5. Moderate PCV (19.0%) and GCV (17.4%) values were recorded for this trait with high heritability value of (83.9%). Genetic advance as per cent mean was also high (32.9%) for this trait.

4.1.9 1000-grain weight

The average 1000-grain weight was 42.4 g and it ranged from 31 g (NI 917) to 56.0 g (HB 208). The PCV and GCV values for this trait were moderate and low (11.4 and 9.3, respectively). Heritability was high (65.9%) with moderate expected GAM (15.5%).

4.1.10 Protein content

The variation of 12.3 per cent (DWR 185) to 17.7 per cent (NI 917). With a mean of 15 per cent low PCV (8.2%) and GCV (7.2%) were recorded for protein content. This trait exhibited high heritability value (76%) with the moderate value of Genetic advance as per cent mean (12.9%).

4.1.11 Grain yield per plot

Wider variation of 360 (NP 825) to 1635 g (DWR-195) with over all mean of 887.5 g. High PCV (23.6%) and GCV (20.8%) was observed for grain yield per plot, with overall mean of 537g. Heritability was high (77.9%) with high GAM of 37.9 per cent.

4.2 CHARACTER ASSOCIATION

4.2.1 Yield vs. yield components

From the Table 7 and 8, it was observed that grain yield per plot exhibited significant and positive genotypic correlation (0.17) with days to 50 per cent flowering. At both genotypic and phenotypic level seed yield per plot showed significant correlation with plant height, peduncle length and protein content in negative direction.

4.2.2 Association among yield components

Days to 50 per cent flowering exerted highly significant association with days to maturity (0.794, 0.788), number of spikelets per spike (0.445 ,0.408) and significant correlation with spike length (0.183, 0.173) in positive direction, at both genotypic and

Table 7. Phenotypic correlation coefficient among yield, yield components and protein content in wheat

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	1.000	0.788**	-0.128	-0.170*	-0.227**	0.173*	0.408**	0.138	0.063	-0.086	0.146
X2		1.000	0.001	-0.131	-0.182*	0.235**	0.370**	0.108	0.061	-0.006	0.041
X3			1.000	0.477**	0.088	0.001	-0.113	0.040	0.167*	0.166*	-0.250**
X4				1.000	0.100	-0.217**	-0.249**	-0.157*	0.143	-0.098	-0.160
X5					1.000	0.056	-0.018	-0.081	0.015	0.083	0.078
X6						1.000	0.312**	0.096	-0.131	0.065	0.008
X7							1.000	0.257**	-0.120	0.027	0.124
X8								1.000	-0.139	0.041	0.020
X9									1.000	-0.137	0.094
X10										1.000	-0.330**
X11											1.000

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

X1-Days to 50% flowering
X2-Days to maturity
X3-Plant height
X4-Peduncle length
X5-Productive tillers per meter length
X6-Spikelength
X7-Number of Spikelets per spike
X8-Number of Grains per spike
X9-1000grain weight
X10-Protien content
X11-Yield per plot

Table 8. Genotypic correlation coefficient among yield, yield components and protein content in wheat

	X_1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	1.000	0.794**	-0.131	-0.188*	-0.240**	0.183*	0.445**	0.154*	0.089	-0.104	0.169*
X2		1.000	0.000	-0.140	-0.189*	0.245**	0.409**	0.118	0.077	-0.011	0.044
X3			1.000	0.527**	0.095	-0.004	-0.137	0.061	0.210**	0.184*	-0.295**
X4				1.000	0.103	-0.241**	-0.306**	-0.188*	0.188*	-0.145	-0.195*
X5					1.000	0.053	-0.028	-0.102	0.012	0.092	0.087
X6						1.000	0.374**	0.106	-0.187*	0.077	-0.008
X7							1.000	0.300**	-0.154*	0.012	0.136
X8								1.000	-0.184*	0.054	0.027
X9									1.000	-0.174*	0.096
X10										1.000	-0.381**
X11											1.000

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

X1-Days to 50% flowering
X2-Days to maturity
X3-Plant height
X4-Peduncle length
X5-Productive tillers per meter length
X6-Spikelength
X7-Number of Spikelets per spike
X8- Number of Grains per spike
X9-1000grain weight
X10-Protien content
X11-Yield per plot

Table 9. Phenotypic path of different yield components and protein content on grain yield in wheat

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	rp
X1	**0.166**	-0.088	0.018	0.021	-0.034	-0.004	0.031	0.002	0.006	0.027	0.146
X2	0.131	**-0.111**	0.000	0.016	-0.027	-0.005	0.028	0.002	0.006	0.002	0.041
X3	-0.021	0.000	**-0.141**	-0.058	0.013	0.000	-0.009	0.001	0.016	-0.052	-0.250**
X4	-0.028	0.015	-0.067	**-0.122**	0.015	0.005	-0.019	-0.003	0.014	0.031	-0.160*
X5	-0.038	0.020	-0.012	-0.012	**0.149**	-0.001	-0.001	-0.001	0.001	-0.026	0.078
X6	0.029	-0.026	0.000	0.026	0.008	**-0.022**	0.024	0.002	-0.012	-0.020	0.008
X7	0.068	-0.041	0.016	0.030	-0.003	-0.007	**0.076**	0.004	-0.011	-0.009	0.124
X8	0.023	-0.012	-0.006	0.019	-0.012	-0.002	0.020	**0.016**	-0.013	-0.013	0.020
X9	0.010	-0.007	-0.024	-0.017	0.002	0.003	-0.009	-0.002	**0.095**	0.043	0.094
X10	-0.014	0.001	-0.023	0.012	0.012	-0.001	0.002	0.001	-0.013	**-0.313**	-0.330**

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

Residue 0.789

X1-Days to 50% flowering
X2-Days to maturity
X3-Plant height
X4-Peduncle length
X5-Productive tillers per meter length
X6-Spikelength
X7-Number of Spikelets per spike
X8- Number of Grains per spike
X9-1000grain weight
X10-Protien content
Rp-Phenotypic correlation with yield

Table 10. Genotypic path of different yield components and protein content on grain yield in wheat

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	rg
X1	**0.193**	-0.102	0.018	0.034	-0.043	-0.008	0.027	0.005	0.008	0.038	0.169*
X2	0.153	**-0.128**	0.000	0.025	-0.034	-0.011	0.024	0.003	0.007	0.004	0.044
X3	-0.025	0.000	**-0.139**	-0.094	0.017	0.000	-0.008	0.002	0.020	-0.067	-0.295**
X4	-0.036	0.018	-0.073	**-0.179**	0.019	0.011	-0.018	-0.006	0.017	0.052	-0.195*
X5	-0.046	0.024	-0.013	-0.018	**0.179**	-0.002	-0.002	-0.003	0.001	-0.033	0.087
X6	0.035	-0.031	0.001	0.043	0.010	**-0.045**	0.022	0.003	-0.017	-0.028	-0.008
X7	0.086	-0.052	0.019	0.055	-0.005	-0.017	**0.060**	0.009	-0.014	-0.004	0.136
X8	0.030	-0.015	-0.008	0.034	-0.018	-0.005	0.018	**0.029**	-0.017	-0.020	0.027
X9	0.017	-0.010	-0.029	-0.034	0.002	0.008	-0.009	-0.005	**0.093**	0.063	0.096
X10	-0.020	0.001	-0.026	0.026	0.016	-0.003	0.001	0.002	-0.016	**-0.362**	-0.381**

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

Residue 0.725

X1-Days to 50% flowering
X2-Days to maturity
X3-Plant height
X4-Peduncle length
X5-Productive tillers per meter length
X6-Spikelength
X7-Number of Spikelets per spike
X8--Number of Grains per spike
X9-1000grain weight
X10-Protien content
Rg- genotypic correlation with yield

phenotypic levels respectively, and has shown positive significant correlation with number of grains per spike (0.154) at genotypic level only. This trait revealed negative and highly significant association with productive tillers per meter length (-0.24, -0.227) and significant correlation with peduncle length (-0.188, -0.17) at both genotypic and phenotypic level.

Highly significant and positive correlation was noticed for days to maturity with spike length (0.245, 0.235) and number of spikelets per spike (0.409, 0.37) at both genotypic and phenotypic levels. This trait had significant association with productive tillers per meter length (-0.189, -0.182) in negative direction. The association of plant height was found to be highly significant and positive with peduncle length (0.527, 0.477) and significant association with protein content (0.184, 0.166) at both genotypic and phenotypic levels. A highly significant correlation with 1000-grain weight at genotypic level (0.21) and significant correlation (0.167) at phenotypic level in positive direction exhibited by plant height.

Peduncle length revealed positive significant correlation with 1000 grain weight (0.188) at genotypic level. This trait exhibited highly significant negative association with spike length (-0.241,-0.217), number of spikelets per spike (-0.306,-0.249) and negative significant association with number of grains per spike (-0.188,-0.157) at both genotypic and phenotypic levels.

At both phenotypic and genotypic levels, spike length revealed highly significant positive association with spikelets per spike (0.312, 0.374) and negatively significant association with 1000-grain weight (-0.187) at genotypic level.

Spikelets per spike exhibited highly significant association with number of grains per spike (0.300, 0.257) in positive direction at both genotypic and phenotypic levels and it had shown negative significant association with 1000 grain weight at genotypic level.

The association was found to be negatively significant for number of grains per spike with 1000 grain weight (-0.184) at genotypic level. Negative significant correlation was noticed for 1000-grain weight with protein content.

4.3 PATH ANALYSIS

4.3.1 Direct effects

Table 9 and 10 indicate it was observed that, at both genotypic and phenotypic levels days to 50 per cent flowering (0.19, 0.17), productive tillers per meter length (0.18, 0.15), 1000 grain weight (0.09, 0.1),number of spikelets per spike (0.06, 0.08), and number of grains per spike (0.03, 0.02) exhibited direct positive effects on seed yield per plot. Days to maturity (-0.13, 0.1), plant height (-0.14, -0.1), spike length, (-0.05, -0.02), peduncle length (-0.18,-0.12) and protein content (-0.36, -0.31) exhibited direct negative effects on grain yield per plot.

4.3.2 Indirect effects

At both genotypic and phenotypic levels indirect effect of days to 50 per cent flowering was moderate and positive via peduncle length (0.03, 0.02) and protein content (0.03, 0.03) whereas negative indirect effect exhibited through days to maturity (-0.10, -0.09) on grain yield per plot and productive tillers per meter length (-0.04, -0.03).

Days to maturity exhibited moderate positive indirect effect via peduncle length (0.03, 0.02) followed by number of spikelets per spike (0.02, 0.03) and moderate negative indirect effect through number of productive tillers per meter length (-0.03, -0.03) at both genotypic and phenotypic levels respectively on grain yield per plot.

Plant height at both genotypic and phenotypic levels exhibited moderate indirect negative effect through peduncle length (-0.09, -0.06) and protein content (-0.07, -0.05), respectively.

Indirect effect of peduncle length on grain yield per plot was positive and moderate via protein content (0.05, 0.03) and moderate and negative via plant height (-0.07, -0.07) at genotypic and phenotypic levels, respectively.

At both genotypic and phenotypic levels indirect effect exhibited by number of productive tillers per meter length on grain yield per plot was positive and moderate via days to maturity (0.02, 0.02) and it was negative via days to 50 per cent flowering (-0.05, -0.04).

4.4 GENETIC DIVERSITY

4.4.1 Relative contribution of different traits towards diversity

Difference in proportion of contribution of each character to total diversity was observed and are presented in Table 11. Days to 50 per cent flowering (ranked first 2156 times out of 14196 total number of combinations) contributed 15.19 per cent to divergence of genotypes. This was followed by number of spikelets per spike (14.29%), grain yield per plot (14.18%), productive tillers per meter length (11.78%), plant height (11.16%), 1000 grain weight (10.97%), number of grains per spike (5.35%), protein content (4.64%), peduncle length (4.25%), days to maturity (4.13%), and spike length (4.07%).

4.4.2 Group constellation

Twelve clusters were formed by grouping all the 169 genotypes in such a way that genotypes within each cluster had smaller D^2 value than those in other clusters. Cluster pattern revealed that, cluster III was largest consisting of 28 genotypes, followed by cluster II, IV, V, VI and VII with 26 genotypes, while the cluster I had six genotypes. The remaining clusters VIII, IX, X, XI, and XII were solitary (Table 12).

Cluster I, II and III included genotypes belonging to both species *T. aestivum* and *T. durum,* cluster I was with one *durum* and five *aestivum* species, cluster II was with three *durum* and 23 *aestivum* species and cluster III was constituting four *durum* and 24 *aestivum* species.. Cluster IV, VI and VII comprised of genotypes belonging to all three species, where cluster IV constituted one dicoccum, four durum and 21 *aestivum* species. Cluster IV with one *dicoccum,* five *durum* and 20 *aestivum* species and cluster VII with one *dicoccum* two *durum* and 23 *aestivum* species. In the remaining five solitary clusters, three clusters namely cluster IX, XI and XII comprised of genotypes belonging to *T. aestivum* species. The cluster X had *Triticale* and the cluster VIII with genotype belonging to *T. durum* species.

4.4.3 Cluster means

The cluster means in respect of 11 characters and overall character wise scores across the 12 clusters are presented in Table 13.

When observed for early flowering habit, genotype Kalyansona in the cluster XII was early flowering with mean number of days to 50 per cent flowering being 50 days, and with number of days to maturity of 83 days, indicating genotypes of this cluster have characteristic early maturing habit. While solitary cluster VIII with genotype HI-8381 genotype exhibited late flowering (69 days) and genotype HI 8381 exhibited late maturity (107 days) habit, with lower protein content and higher grain yield per plot (995 g). With respect to grain yield per plot cluster VIII was followed by cluster XII and it was closely followed by cluster VII. Cluster IX with single genotype showed taller plant type (88 cm), with lower peduncle length (24.5cm) and higher number of spikelets per spike (18.5).With respect to productive tillers per meter, spike length and protein content cluster IX with genotype NP 737 had higher mean value (166.35, 11.59 cm and 16.85% respectively).Higher value for number of grains per spike (40.10) was, observed in cluster IV.

Based on cluster means, characters were scored as the character with the higher magnitude in the desired direction was given the first rank. Hence the cluster with least over all score across 11 characters secured the first rank and the cluster with the highest score of 90 secured the 11^{th} rank (Table 13) .The cluster II with over all score of 55 across the 11 characters gets first rank followed by cluster IV, VI and VIII.

Table 11. Per cent contribution of different traits towards total diversity

Source	Times ranked first	Contribution %
Days to 50% flowering	2156	15.19
Days to maturity	586	4.13
Plant height	1584	11.16
Peduncle length	603	4.25
Productive tillers per meter length	1672	11.78
Spike length	578	4.07
Spikelets per spike	2029	14.29
Grains per spike	759	5.35
1000-grain weight	1558	10.97
Protein content	658	4.64
Yield per plot	2013	14.18

Table 12. Clustering pattern of wheat genotypes

Cluster	Genotypes
1st	AJANTA*, AKW1071*, BIJAGA YELLOW+, BW11*, C 306*, CHHOTI LERMA*
2nd	NIAW 34*, UP 301*, NW2036*, HW 741*, UP 2338*, MOTIA*, WH711*, GW 322*, RAJ 911+, VL 829*, SAGARIKA*, NP165*, HS 1097-17*, DWR 137+, HD 1982*, K 8804*, NP 771*, DL 153-2*, JNK-4W-184+, HDR 27*, RIDLEY*, LOK 1*, HUW 234*, PBW 114*, HP 1633*, HD2687*
3rd	PBW 524*, NP 718*, PBW 443*, N59+, PBN 51*, RAJ 1482*, SHARBATI SONARA*, MACS 1967+, K8962*, VL 832*, UP 368*, HW 1085*, HUW 318*, K68*, HS 1138-6-4*, NP 823*, NIDW 15+, GW 405*, UP 2382*, VIJAY+, HI 977*, HD 2009*, DL 784-3*, CPAN 1676*, DWR 162*, HP 1731*, HD 2733*, KARCHIA 65*
4th	PBW 373*, SAFED LERMA*, NP761*, RAJ 821*, MONDHYA 3-2*, HW 657*, MLKS 11*, SONARA 64*, WH 896+, NP 890*, VL 804*, HD 4672+, HS 420*, NI 5749+, K 8027*, LERMA ROJO*, HD 2643*, J-1-7*, GW 273*, K 9644*, DDK 1009#, NW 1014*, HUW 213*, DWR 39*, UP 2121*, HI 8498+
5th	NI 5439*, PDW 215+, HW 2045*, K9107*, HD 2428*, UP 2003*, PBW 65*, VINATA*, K 53*, NP 825*, SONAK*, RAJ 3765*, NP 884*, WH 533*, NP 745*, HD 2824*, DWR 195*, DBW 14*, HUW 65*, HI 1500*, MACS 2694+, HUW 533*, HP 1761*, GW 503*, K7410*, KRL-19*,
6th	WH 542*, NP 836*, K 65*, NI 5643*, VL 401*, RAJ 4037+, HW 517*, HD 2501*, GW 1139+, K 9465*, KSML 3*, HYV 65*, MACS 2846+, DDK 1001#, UP2113*, HUW 206*, K 8020*, HD 2833*, HS 375*, SONALIKA*, PDW 233+, DWR 1006+, NP 760*, NW 1012*, DWR 16*, PBW 343*
7TH	HD 2135*, HI 1077*, DWR 185+, GW 496*, CPAN 1796*, K 852*, HUW 12*, HUW 468*, NIDW 295*, HD 2781*, HP 1744*, KRL 1-4*, RAJ 1555+, SKAML 1*, UP 1109*, NI 917*, WH 147*, NP 824*, JAY#, K 9006*, MACS 2496*, PBW 502*, UTKALIKA*, DL 803-3*, HW 2004*, PBN 142*,
8TH	HI 8381+
9TH	NP 737*
10TH	DT 46
11TH	HB 208*
12TH	KALYANA SONA*

* - *T. aestivum* + - *T. durum* # - *T. dicoccum*

Table 13. Cluster means for 11 characters in wheat

Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	Over all score	Rank
I	60.75 (11)	105.25 (11)	73.55 (3)	32.61 (11)	143.88 (9)	10.20 (2)	17.36 (11)	35.75 (9)	41.79 (8)	14.93 (8)	880.00 (7)	90	11
II	54.58 (4)	90.77 (4)	82.66 (10)	29.87 (8)	163.92 (2)	9.03 (6)	18.58 (4)	36.57 (7)	44.00 (3)	15.13 (3)	900.12 (4)	55	1
III	55.11 (5)	93.23 (5)	80.54 (7)	29.42 (5)	151.30 (8)	8.91 (7)	18.07 (8)	38.65 (2)	42.22 (6)	15.12 (4)	891.96 (5)	62	3
IV	55.44 (7)	93.79 (6)	79.33 (4)	28.77 (4)	157.35 (6)	9.16 (4)	18.81 (3)	40.10 (1)	40.67 (10)	14.97 (7)	858.27 (9)	61	2
V	55.58 (8)	95.19 (8)	82.41 (9)	29.71 (6)	157.80 (5)	9.35 (3)	18.23 (7)	37.68 (4)	42.47 (5)	15.02 (6)	889.40 (6)	67	5
VI	55.42 (6)	94.62 (7)	80.20 (6)	29.86 (7)	161.66 (3)	9.16 (4)	18.56 (5)	36.69 (6)	42.01 (7)	15.31 (2)	854.94 (11)	64	4
VII	56.17 (9)	97.46 (9)	81.70 (8)	30.04 (9)	157.14 (7)	9.09 (5)	17.97 (9)	36.97 (5)	42.83 (4)	14.65 (9)	945.21 (3)	77	8
VIII	69.00 (12)	107.00 (12)	70.33 (2)	28.00 (3)	158.40 (4)	7.60 (10)	18.83 (2)	38.50 (3)	48.33 (2)	13.15 (11)	995.00 (1)	62	3
IX	57.00 (10)	105.00 (10)	88.00 (12)	24.50 (1)	166.35 (1)	11.59 (1)	18.50 (6)	25.85 (11)	34.76 (12)	16.85 (1)	870.00 (8)	73	7
X	52.00 (2)	82.00 (2)	79.96 (5)	39.62 (12)	117.50 (12)	8.49 (9)	20.17 (1)	31.83 (10)	41.35 (9)	14.20 (10)	855.00 (10)	82	9
XI	54.00 (3)	74.00 (1)	62.20 (1)	26.90 (2)	135.55 (11)	6.50 (11)	16.33 (12)	25.50 (12)	56.04 (1)	15.05 (5)	805.00 (12)	71	6
XII	50.00 (1)	83.00 (3)	85.00 (11)	31.67 (10)	140.00 (10)	8.75 (8)	17.50 (10)	36.50 (8)	38.82 (11)	14.40 (9)	960.00 (2)	83	10

Note – The values in the parenthesis indicates the ranks given

Table 14. Intra (diagonal) and inter cluster distances for 11 characters in wheat genotypes

	Grp1	Grp2	Grp3	Grp4	Grp5	Grp6	Grp7	Grp8	Grp9	Grp10	GRP11	Grp12
Grp1	6.494	750.96	577.43	744.43	748.04	751.47	740.57	1037.34	501.68	422.32	1189.08	606.45
Grp2		188.95	830.56	909.04	864.36	951.21	938.87	1181.43	796.32	652.54	1301.03	435.22
Grp3			157.64	853.92	815.37	776.01	786.08	1020.66	620.45	598.74	1255.92	719.22
Grp4				174.98	934.79	912.99	851.58	1154.81	695.48	723.42	505.42	843.82
Grp5					141.41	904.81	901.27	1125.86	693.77	360.57	1282.29	759.74
Grp6						205.49	937.01	349.52	772.56	728.42	1258.19	873.87
Grp7							169.57	1158.30	323.29	726.57	1226.21	827.98
Grp8								0.000	1030.51	997.42	1450.95	1120.04
Grp9									0.000	468.293	1112.92	659.49
Grp10										0.000	1139.82	526.43
GRP11											0.000	1238.56
Grp12												0.000

4.4.4 Intra and inter cluster distance

The intra and inter cluster distances are given in Table 14. Maximum differences among the genotypes within the same cluster was shown by cluster VI (205.49) followed by cluster II (188.95).

When diversity among clusters was studied, it showed a range of 323.29 to 1450.95. Cluster VIII and XI showed maximum inter cluster distance of 1450.95, followed by that between clusters II and XI (1301.03). The lowest inter cluster distance was noticed between clusters VII and IX (323.29), followed by that between clusters VI and VIII (349.52).

4.5 EXPERIMENT II: MORPHOLOGICAL AND MOLECULAR DIVERSITY

4.5.1 Morphological diversity

Difference was observed in proportion of contribution of each character to total diversity (Table 15). Grain yield per plot contributed highest (15.47%) towards diversity. This was followed by days to 50 per cent flowering (14.86%), spike length (11.86%) and peduncle length (10.66%), plant height and number of Spikelets per spike(10.21%) 1000 grain weight (6.01%), protein content (5.56%), days to maturity and number of tillers per meter length with the value of 4.20 per cent each.

A total of ten clusters were formed by grouping all the 37 genotypes in such a way that genotypes within each cluster had smaller D^2 value than those in other cluster. Cluster pattern revealed that cluster I, and III had more number of genotypes (6 genotypes each), followed by cluster II,V and VI (5 genotypes each), cluster IV was with 4 genotypes, VIII and X had 2 where as VII and IX were solitary clusters (Table 16).

4.5.2 Molecular diversity

Thirty seven wheat genotypes were subjected to RAPD assay to assess the molecular diversity. Ten random decamer primers revealed a high DNA polymorphism among genotypes (Table 17). Ten primers produced a total of 56 amplified products. Among these 54 were polymorphic with an average of 96.00 per cent polymorphism. All primers except OPA-07 gave highest (100%) polymorphism. The primer OPA-07 gave the lowest polymorphism (60%). The number of bands ranged from 3 (OPA-01) to 9 (OPA-15) with an average of 5.6 bands per primer.

The diversity coefficient ranged from 4.00 to 51.00. Among the genotypes Sonak and Sonalika showed lowest (4.11) diversity coefficient. While, WH-147 with DDK1001 and WH-147 with HS420 showed highest (70.21) diversity coefficient (Table 18). All the genotypes showed diversity among themselves indicating considerable amount of variation in the material used for study.

The dendrogram constructed from the pooled data (Fig. 2) revealed nine distinct clusters, in which five were solitary. Two main clusters were separated at 27 per cent diversity.

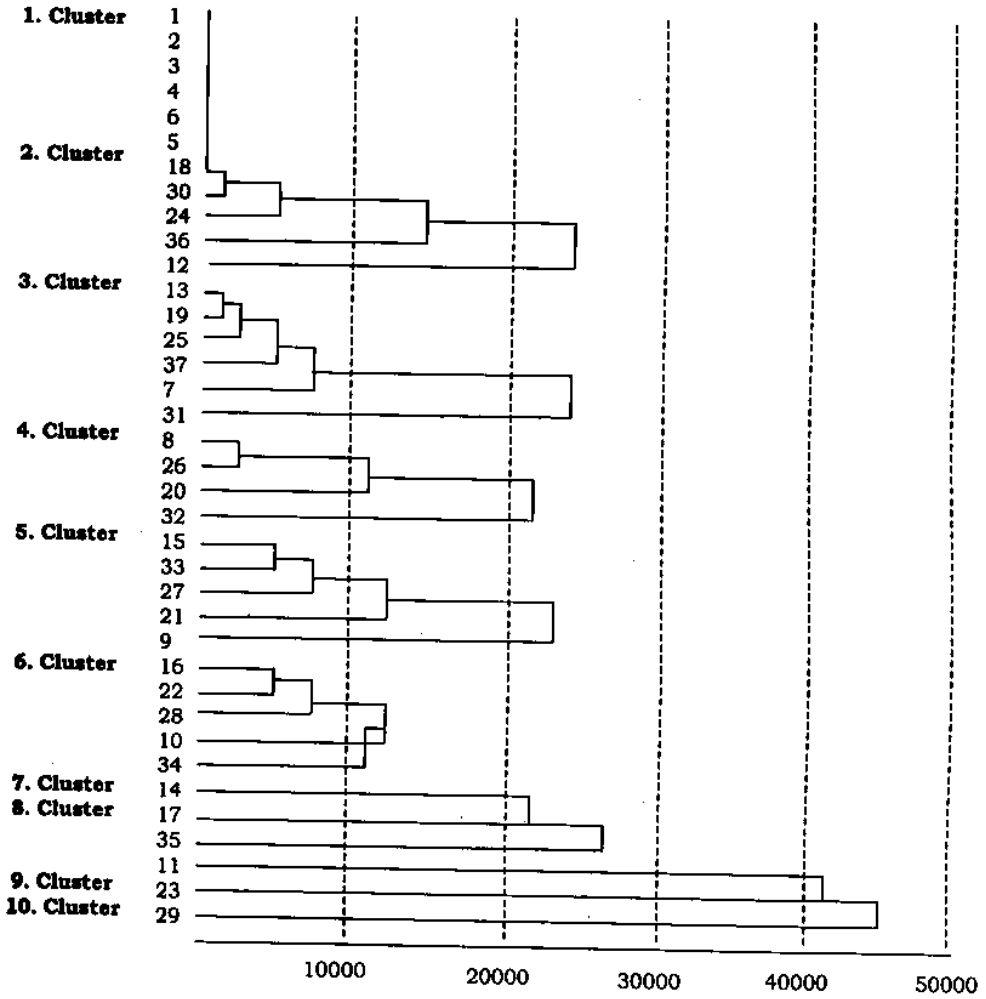


Fig. 1 : Dendrogram obtained from D^2 analysis of wheat genotypes

Fig 1. Dendrogram obtained from D^2 analysis of wheat genotypes

Table 15. Per cent contribution of different traits towards total diversity

Sl. No.	Source	Times ranked first	% contribution
1	Days to 50 per cent flowering	99	14.86
2	Days to maturity	28	4.20
3	Plant height	68	10.21
4	Peduncle length	71	10.66
5	Tillers per meter length	28	4.20
6	Spike length	79	11.86
7	Spikelets per spike	68	10.21
8	Grains per spike	45	6.76
9	1000 grain weight	40	6.01
10	Protein content	37	5.56
11	Yield per plot	103	15.47

Table 16. Clustering pattern of 37 wheat genotypes

Cluster number	Number of genotypes	Genotypes
I	6	BIJAGA YELLOW, DDK 1001, DDK1009, DWR 162, DWR1006, HD 1982
II	5	MACS 2694, SONAK, PBN 142, WH 147, HW 517
III	6	HW 1085, MACS 2846, PBW 373, RIDLEY, CPAN 1676, SONALIKA
IV	4	HD 2135, RAJ 911, MLKS 11, SONARA 64
V	5	J-1-7, UP 301, RAJ 1555, N59, HP 1633
VI	5	K 68, NI5439, SAFED LERMA, HS 420, VL 401
VII	1	HYB 65
VIII	2	K852, VL829
IX	1	HUW 12
X	2	PBN 51, SHARABATI SONARA

Table 17. Analysis of RAPD banding patterns for wheat genotypes

Primers	Total number of bands	Polymorphic bands	Per cent polymorphism (%)
OPA 10	5	5	100
OPA 15	9	9	100
OPP 07	5	3	60
OPP 09	6	6	100
OPP 01	3	3	100
OPP 03	6	6	100
OPA 13	8	8	100
OPA 14	5	5	100
OPA 11	5	5	100
OPA 12	4	4	100
Total	56	54	96
Average	5.6	5.4	-

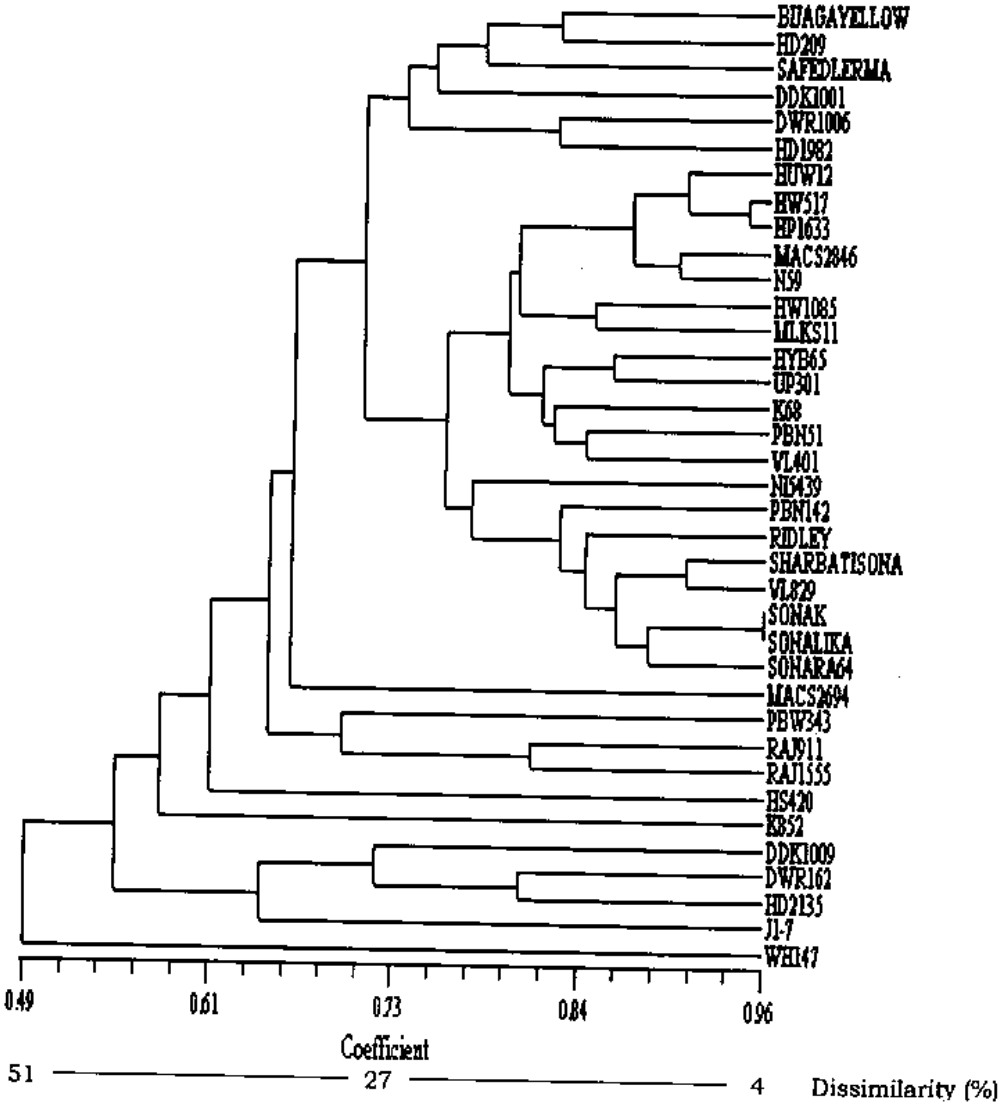
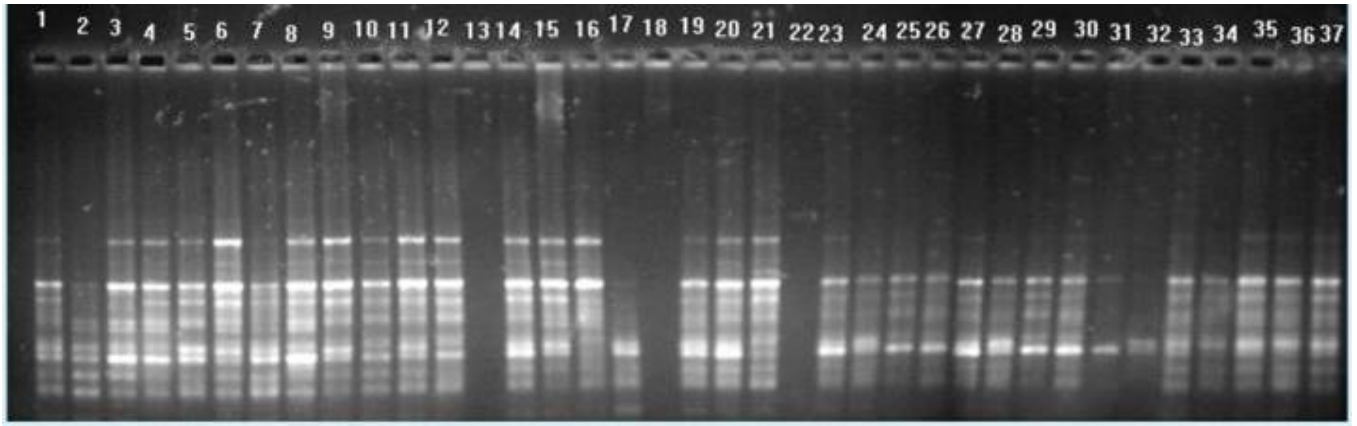
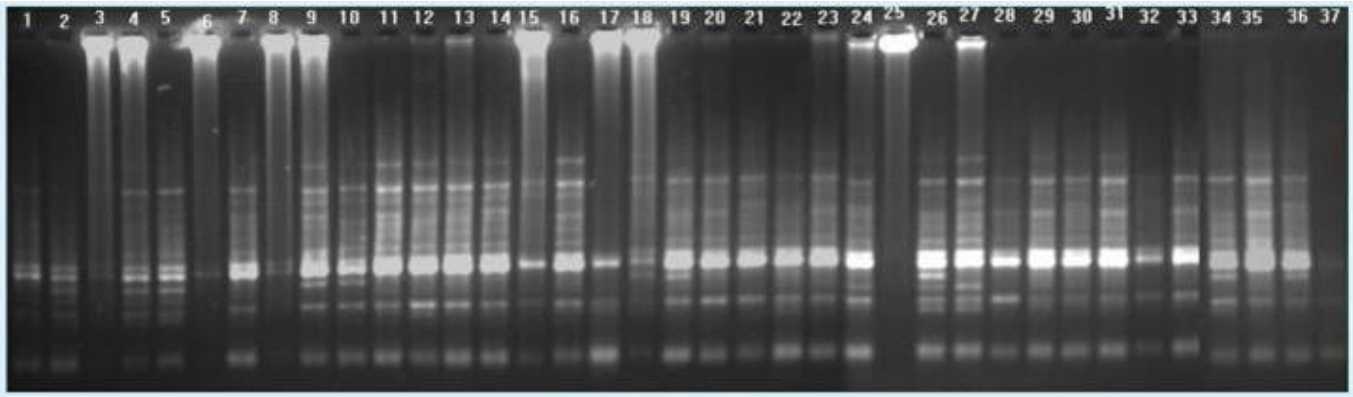


Fig. 2 : Dendrogram obtained from pooled data of RAPD profile of wheat genotypes

Fig 2. Dendrogram obtained from pooled data of RAPD profile of wheat genotypes



a) Primer : OPA-13



b) Primer : OPA-15

Plate 1. RAPD profile of 37 wheat genotypes

Table 18. Genetic distances between all possible pairs of wheat genotypes calculated as dissimilarities

Sl. No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.00																		
2	22.39	0.00																	
3	44.83	48.94	0.00																
4	23.29	29.03	28.30	0.00															
5	20.55	32.26	47.17	26.47	0.00														
6	26.47	29.82	41.67	26.98	17.46	0.00													
7	17.33	21.88	49.09	25.71	20.00	35.38	0.00												
8	38.71	45.10	28.57	19.30	36.84	30.77	38.98	0.00											
9	34.33	42.86	57.45	32.26	29.03	33.33	43.75	45.10	0.00										
10	23.81	34.25	53.13	24.05	26.58	29.73	25.93	38.24	31.51	0.00									
11	23.26	36.00	51.52	25.93	28.40	31.58	22.89	37.14	33.33	6.52	0.00								
12	30.00	39.13	56.67	33.33	25.33	22.86	32.47	43.75	30.43	11.63	11.36	0.00							
13	24.39	35.21	61.29	37.66	35.06	36.11	26.58	51.52	38.03	15.91	11.11	19.05	0.00						
14	22.35	37.84	50.77	25.00	27.50	30.67	24.39	36.23	32.43	12.09	5.38	17.24	12.36	0.00					
15	40.98	40.00	46.34	32.14	42.86	37.25	41.38	28.89	40.00	43.28	42.03	36.51	50.77	44.12	0.00				
16	28.00	46.88	63.64	40.00	28.57	32.31	36.11	49.15	28.13	20.99	15.66	16.88	18.99	14.63	44.83	0.00			
17	39.68	30.77	53.49	41.38	44.83	39.62	33.33	48.94	65.38	42.03	43.66	44.62	37.31	37.14	47.83	50.00	0.00		
18	41.94	41.18	61.90	36.84	29.82	38.46	42.37	47.83	41.18	38.24	37.14	37.50	36.36	36.23	37.78	25.42	44.68	0.00	
19	21.95	29.58	54.84	27.27	27.27	30.56	24.05	42.42	38.03	13.64	11.11	21.43	18.60	7.87	41.54	16.46	34.33	33.33	0.00
20	29.58	36.67	52.94	36.36	30.30	24.59	35.29	38.18	40.00	22.08	24.05	15.07	30.67	25.64	29.63	20.59	42.86	30.91	22.67
21	23.08	34.33	58.62	31.51	28.77	29.41	22.67	41.94	46.27	16.67	13.95	17.50	17.07	12.94	44.26	20.00	30.16	35.48	9.76
22	30.56	31.15	61.54	40.30	34.33	38.71	27.54	46.43	50.82	28.21	22.50	29.73	18.42	18.99	49.09	27.54	29.82	28.57	18.42
23	28.95	44.62	67.86	40.85	29.58	33.33	31.51	50.00	44.62	19.51	19.05	20.51	20.00	18.07	49.15	17.81	40.98	36.67	17.50
24	24.32	36.51	62.96	42.03	27.54	34.38	32.39	55.17	39.68	30.00	34.15	28.95	25.64	28.40	47.37	26.76	35.59	31.03	25.64
25	36.51	46.15	48.84	37.93	37.93	47.17	30.00	44.68	61.54	44.93	38.03	47.69	40.30	40.00	43.48	40.00	45.83	40.43	37.31
26	32.43	36.51	59.26	33.33	33.33	50.00	21.13	51.72	49.21	37.50	31.71	39.47	28.21	30.86	47.37	32.39	38.98	34.48	25.64
27	35.29	43.86	54.17	36.51	30.16	44.83	29.23	46.15	43.86	40.54	34.21	40.00	33.33	36.00	49.02	29.23	50.94	26.92	38.89
28	23.29	29.03	58.49	38.24	26.47	33.33	22.86	54.39	45.16	29.11	23.46	28.00	19.48	25.00	50.00	28.57	37.93	33.33	24.68
29	19.44	31.15	65.38	40.30	22.39	29.03	24.64	53.57	37.70	25.64	27.50	21.62	28.95	31.65	41.82	24.64	43.86	39.29	28.95
30	21.13	40.00	60.78	36.36	30.30	37.70	26.47	49.09	40.00	27.27	26.58	28.77	22.67	25.64	40.74	26.47	42.86	30.91	28.00
31	17.33	34.38	60.00	37.14	20.00	29.23	22.22	52.54	34.38	23.46	22.89	19.48	21.52	26.83	41.38	19.44	46.67	32.20	26.58

32	26.47	33.33	58.33	39.68	33.33	31.03	32.31	50.00	36.84	27.03	26.32	25.71	25.00	28.00	41.18	23.08	43.40	26.92	27.78
33	15.79	35.38	57.14	32.39	23.94	33.33	20.55	46.67	35.38	21.95	19.05	23.08	20.00	22.89	38.98	20.55	47.54	33.33	25.00
34	30.67	37.50	63.64	40.00	31.43	29.23	38.89	55.93	34.38	20.99	22.89	19.48	13.92	24.39	44.83	16.67	43.33	25.42	21.52
35	31.51	48.39	62.26	41.18	32.35	36.51	40.00	50.88	35.48	26.58	23.46	20.00	22.08	25.00	42.86	17.14	51.72	29.82	27.27
36	26.03	35.48	62.26	35.29	29.41	36.51	31.43	50.88	38.71	24.05	25.93	28.00	19.48	30.00	42.86	31.43	44.83	29.82	29.87
37	62.07	70.21	63.16	66.04	66.04	58.33	67.27	66.67	70.21	46.88	48.48	43.33	38.71	47.69	56.10	38.18	48.84	42.86	48.39

Contd…

Sl. No.	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
1																		
2																		
3																		
4																		
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16																		
17																		
18																		
19																		
20	0.00																	
21	23.94	0.00																
22	35.38	13.89	0.00															
23	24.64	15.79	20.00	0.00														
24	28.36	24.32	20.59	16.67	0.00													
25	46.43	33.33	33.33	31.15	38.98	0.00												

26	46.27	24.32	26.47	30.56	28.57	25.42	0.00											
27	40.98	38.24	35.48	39.39	37.50	35.85	18.75	0.00										
28	36.36	20.55	16.42	15.49	18.84	24.14	24.64	30.16	0.00									
29	26.15	25.00	36.36	22.86	23.53	43.86	38.24	41.94	28.36	0.00								
30	28.13	23.94	23.08	18.84	13.43	32.14	31.34	31.15	15.15	23.08	0.00							
31	23.53	22.67	24.64	17.81	15.49	33.33	29.58	29.23	14.29	13.04	11.76	0.00						
32	24.59	26.47	19.35	21.21	15.63	35.85	37.50	37.93	17.46	25.81	11.48	10.77	0.00					
33	24.64	23.68	25.71	18.92	19.44	31.15	30.56	27.27	15.49	17.14	7.25	4.11	12.12	0.00				
34	23.53	22.67	24.64	17.81	18.31	43.33	32.39	38.46	22.86	27.54	23.53	19.44	20.00	23.29	0.00			
35	24.24	28.77	31.34	15.49	21.74	41.38	33.33	30.16	23.53	31.34	21.21	22.86	26.98	23.94	14.29	0.00		
36	30.30	28.77	28.36	21.13	18.84	37.93	33.33	30.16	14.71	28.36	9.09	17.14	20.63	12.68	17.14	17.65	0.00	
37	37.25	44.83	42.31	39.29	40.74	48.84	55.56	54.17	50.94	57.69	45.10	49.09	41.67	50.00	30.91	39.62	43.40	0.00

V. DISCUSSION

The ultimate goal of plant breeding programmes is to improve the plant traits for agronomic and economic superiority.

The knowledge of nature and extent of genetic variation and diversity available in the germplasm or breeding material helps the breeder for planning sound breeding programmes. Hence, the present investigation was undertaken to evaluate 169 wheat genotypes cultivated in different agro ecological areas. Results of the present investigation are discussed in the light of available literature and explanation wherever possible is provided for the trends revealed by these observations under following heads.

5.1 Genetic variability, heritability and genetic advance

5.2 Character association and path analysis

5.3 Genetic diversity

5.4 Morphological and molecular diversity

5.5 Comparative study of mean and range of expression of variation among the different wheat species

5.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

In the present investigation, 169 diverse genotypes of wheat were studied to assess their genetic potential. All the genotypes exhibited significant differences for all the traits. Many early workers including Pawar *et al.* (1988), Hanchinal and Maled (1995), Sharma *et al.* (1995), Kamat (1996) and Kamboj *et al.* (2000) reported high variability for different traits in wheat. Thus, it is implied that there was reasonably sufficient variability in the material used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

The assessment of heritable and non-heritable components in the total variability observed is indispensable in adapting suitable breeding procedure. The heritable portion of the over all observed variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance.

In the present study the phenotypic and genotypic coefficient of variation was found to be moderate for days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter, spike length, number of spike lets per spike, number of grains per spike and 1000 grain weight. For all these traits except 1000 grain weight for which genotypic coefficient of variation was found to be low. Similar observations were also reported by Pathak and Nema (1985), Pawar *et al.* (1988), Jagashoran (1995) and Muhammed and Hussain (2004) for plant height. Dixit (1990) reported moderate GCV for days to 50 per cent flowering, Bahadur *et al.* (1994) and Jagashoran (1995) reported moderate PCV and GCV for number of grains per spike. Reports of Singh *et al.* (1996) and Sharma *et al.* (1998) support our results for 1000 grain weight for GCV and PCV, respectively.

There were no reports of moderate GCV and PCV for the traits such as number of spike lets per spike, spike length and peduncle length. However, Pawar *et al.* (1989) reported low PCV and GCV for number of spike lets per spike and spike length. Whereas, Dixit and Patil (1983) reported high PCV and Sharma *et al.* (1998) reported low PCV and GCV for peduncle length.

The result for number of productive tillers was in accordance with Mahesh *et al.* (2001) for moderate GCV.

Results obtained from present investigation has revealed moderate GCV and PCV indicating still there is possibility of improvement of genotypes through these characters.

The protein content exhibited low GCV and PCV values, similar results were obtained by Nayeem *et al.* (2002) in durum genotypes. Sharma *et al.* (1998) and Bergale *et al.* (2001) reported high PCV and GCV for grain yield per plot by using 300 genotypes of bread wheat and durum wheat and 50 bread wheat cultivars, respectively which supported the present results, indicating selecting genotypes through these characters will be effective.

It is interesting to note that the differences between GCV and PCV values were minimum implying least influence of environment and additive gene effects indicating genotypes can be improved and selected for these characters.

The coefficient of variation indicated only the extent of variability present in these characters and does not indicate the heritable portion. This could be ascertained from heritability estimates which in broad sense include both additive and non-additive gene effects and in narrow sense include the proportion of heritable variation which is due to additive component (Lush, 1949). The knowledge of heritability is helpful in assessing merits and demerits of a particular trait as it enables the plant breeder to decide the course of selection procedures to be followed under a given situation.

In the present study, heritability values for all the characters *viz.,* number of days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter length, spike length, number of spikelets per spike, number of grains per spike, 1000 grain weight, protein content and grain yield per plot was found to be high.

High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by environment. In confirmation with results of earlier workers *viz.,* Singh and Rai (1987) and Bijendrapal and Garg (1992) also noticed higher heritability value for plant height, days to 50 per cent flowering, number of productive tillers per meter length, grain yield, test weight and number of grains per spike. Thakur *et al.* (1999) also reported high heritability values for plant height, tillers per meter and spike length. Kamboj *et al.* (2000) reported high heritability values for number of grains per spike, 1000 grain weight and grain yield per plot.

Heritability estimates are useful in deciding the characters to be considered while making selection, but selection based on this factor alone may limit the progress, as it is prone for changes with environment, material etc (Johanson *et al.,* 1955 and Athwal and Gain Singh 1966). In other words, estimates of heritability have a role to play in determining the effectiveness of selection of a character, provided they are considered in conjugation with the predicted genetic advance as suggested by Panse (1942) and Johnson *et al.* (1955).

In the present study for most of the characters *viz.,* number of days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter length, spike length, number of spikelets per spike, number of grains per spike and grain yield per plot, had shown high heritability and genetic advance as per cent mean, however, the same character exhibited moderate GCV and PCV hence direct selection of genotypes can be done through these characters for further improvement of genotypes. The results are in accordance with reports of earlier work done by Thakur *et al.* (1999) for plant height, number of productive tillers per meter and spike length. In confirmation with these results Mandal *et al.* (1991) and Mahamood and Shahad (1991) also reported high genetic advance for plant height and number of spikelets per spike with respect to days to maturity high genetic advance was reported by Jag Shoran (1995) and Dhanda and Sethi (1996). In the present study moderate genetic advance as per cent mean was recorded for 1000 grain weight and protein content where as Mahamood and Shahad (1991) and Shah (1998) reported high genetic advance for 1000 grain weight. However, Jitendra Kumar and Lutra (1995) reported low genetic advance for number of days to 50 per cent flowering and number of grains per spike. Nirmala and Jhan (1998) also reported low genetic advance for number of grains per spike.

In these characters where high heritability was associated with high genetic advance, the variation was mostly due to additive gene effects.

In the present study high heritability coupled with moderate genetic advances was observed for 1000 grain weight and protein content suggesting further improvement of

genotypes for these characters for further selection and subsequent use in breeding programme.

5.2 CHARACTER ASSOCIATION

5.2.1 Association analysis

Grain yield is the end product of interactions of many factors known as contributing components hence it is complex trait. Understanding of the interaction of characters among themselves and with the environment has been of great use in the plant breeding, correlation between different characters of plant could arise because of linkage, pleiotrophy or developmentally influenced functional relationships. Correlation studies provide an information on the nature and extent of association between any two pairs of metric characters. From this it could be possible to bring about genetic upgradation in one character by selection of the other pair.

In general, the genotypic correlation coefficient values were higher than the phenotypic values. This indicated that strong intrinsic associations were some what masked at phenotypic level due to environmental effects.

Grain yield per plot exhibited significant association in positive direction with days to 50 per cent flowering only at genotypic level and at phenotypic level no such association was noticed indicating influence of environment on association. This result was in confirmation with the report of Khan *et al.* (1999) and Nayem *et al.* (2002), respectively. Wherein, they observed positive and significant association of grain yield with days to 50 per cent flowering, in which, they used F_1 crosses and parents of wheat for experimentation.

None of the traits other than days to 50 per cent flowering exhibited significant association with grain yield per plot except the traits such as plant height, peduncle length, protein content exhibited negative significant association with grain yield per plot.

Days to maturity was recorded the non significant association with grain yield. Similar report, have come from Nirmala and Jha (1996) in segregating population in contrast, Jadhav (1994) noticed positive and significant correlation of days to maturity with grain yield.

The plant height and peduncle length had shown significant negative association with grain yield. These results were in confirmation with the Mahammad Shahid *et al.* (2002) who reported strong negative association for plant height, Naik (2000) and Gautam and Sethi (2002) has reported significant negative and negative association respectively for peduncle length. Further, plant height exhibited positive significant association with peduncle length, 1000 grain weight, protein content and positive association with grains per spike indicating selection of genotypes through these characters could be effective.

This suggested that dwarf varieties are preferred as they could withstand lodging and hence these could be used to the advantage in direct selection for grain yield.

5.2.2 Path coefficient analysis

The correlation coefficient indicated the relationship existing between pair of characters. But, a dependent character is an interaction of product of many mutually associated component characters and change in any one component will disturb whole network of cause and effect system. The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relationship between the variables which is unique in partitioning the association into direct and indirect effects through other dependent variables. The path coefficient analysis also measure the relative importance of causal factors involved. This is simply standardized regression analysis, wherein total correlation value is subdivided into causal scheme. Li (1956) emphasized the importance of path diagram which facilitates the understanding of the nature of cause and effect system. The path analysis suggested by Dewey and Lee (1959) helps to resolve these correlations further and throws more light on the way in which component traits contribute towards specifically identifying important component traits.

Among the various traits studied days to 50 per cent flowering had high positive direct effect followed by productive tillers per meter length and 1000 grain weight at both genotypic and phenotypic levels on grain yield. Out of these traits among the traits had shown significant association except days to 50 per cent flowering which had significant association only at genotypic level.

The results of high direct positive effect of days to 50 per cent flowering on grain yield at both genotypic and phenotypic levels supported by work of Chaturvedi and Gupta (1995) and Halloli (1997). So direct selection of genotypes for grain yield through days to 50 per cent flowering could be effective.

However, the productive tillers per meter length had high positive direct effect on grain yield, but failed to show any association with grain yield, the high direct effect was present to nullify undesirable indirect effects produced by them via different traits.

Days to maturity exhibited negative direct effect on grain yield per plot. Therefore results suggested that due to its high negative direct effect but non-significant association with grain yield, this trait can not be used as criterion of selection.

Plant height and peduncle length had shown negative direct effects on grain yield per plot Hence, dwarf varieties are preferred, as they could withstand lodging, this association could be used advantageous for development of dwarf varieties.

5.3 GENETIC DIVERSITY

Quantification of genetic diversity existing with in and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Murthy and Arunachalam, 1966; Bhatt, 1970; Hussaini, 1973).

Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships.

5.3.1 Contribution of character towards divergence

Among the 11 characters studied, the most important character contributing to the divergence was days to 50 per cent flowering (15.19%). This was followed by number of spikelets per spike, yield per plot, productive tillers per meter length, plant height, 1000 grain weight number of grains per spike, protein content, peduncle length, days to maturity and spike length. These observations are in accordance with Walia and Garg (1996) for grain yield and number of tillers per unit length, Bergale *et al.* (2001) for plant height and Nimbalkar *et al.* (2002) for number of grains per spike, 1000 grain weight and number of productive tillers. In this study all the 11 characters studied contributed towards divergence.

5.3.2 Genetic diversity in different groups

Based on D^2 values 169 genotypes were grouped into 12 clusters, 28 genotypes were present in cluster III, while cluster II, IV, V, VI, VII had 26 genotypes in each cluster. Cluster I had 6 genotypes and remaining clusters (VIII, IX, X, XI and XII) were solitary clusters. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. The intra cluster distance varies from 6.494 in cluster I to maximum distance of 205.49 in cluster VI. This revealed the presence of divergent genotypes with in different clusters. The inter cluster D^2 values also ranged widely with minimum value of 323.29 between cluster VII and cluster IX and maximum value of 1450.95 between cluster VIII and cluster XI indicating high diversity among the genotypes. Cluster VIII and cluster XI with solitary genotypes were the most divergent groups with a maximum inter cluster distance (1450.95). It is desirable to select accessions from clusters showing high inter cluster distance (cluster VIII and cluster XI) and also with high grain yield as parents in recombination breeding programmes for obtaining desirable segregants.

It was observed that genotypes representing diversified geographic regions of their adoption were grouped together. Maximum number of genotypes (28) were grouped in the same cluster III followed by II, IV, V, VI and VIII which had 26 genotypes in each cluster, even though their area of adoption is different, this was due to unidirectional selection practiced by plant breeders of different states (Singh and Bains, 1968). Similar results were observed by Walia and Garg (1996), Bergale *et al.* (2001), Dotlacil *et al.* (2000), in which they reported non-parallelism between geographic and genetic diversity.

It was evident from the results that the genotypes of different ploidy levels *viz.,* tetraploid (*T. durum, T. dicoccum*) and hexaploid (*T. aestivum*) also grouped in a same cluster (I, II, III, IV, V, VI and VII). This indicated that diversity is not only concerned with geographic origin or ploidy levels of genotypes but also with other characters.

In conformity with this result earlier Sharma *et al.* (1998) also reported that the genotypes of heterogenous origin/place of release and of different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. But, Murthy and Arunachalam (1966) were of the opinion that the wide adaptability would be possible due to factors like heterogeneity, genetic architecture of populations, past selection history, developmental traits and degrees of general combining ability. It appeared that varieties having same geographical origin differed and possessed wide divergence factors, since rapid ecotype differentiation was taking place even in the absence of reproductive isolation (Bennet, 1970).

5.3.3 Analysis of cluster means

All the genotypes were spread over 12 clusters and means were scored across the clusters for all the 11 characters.

The lowest cluster mean was given the first rank and next cluster possessing next best means were given 2^{nd}, 3^{rd} and so on up to 12^{th} rank for all the traits except for days to 50 per cent flowering, days to maturity, plant height and peduncle length where lowest mean was given first rank.

Based on the overall score across 11 traits, the clusters were ranked. The lowest scoring cluster was given first rank and next cluster possessing the score above the previous ones were given 2^{nd}, 3^{rd} and so on up to 12. Accordingly, cluster II with 26 genotypes ranked first with overall score of 55 across all the 11 characters. This was followed by cluster V, III and VIII indicating presence of most promising genotypes in them and can be extensively used for further breeding programmes to generate new breeding material.

Some elite genotypes for different traits from different groups are represented in table 19. These superior genotypes can be used in future breeding programmes for improvement of the concerned traits.

The mean value of each of the 11 characters showed that the different clusters were superior in respect different characters.

5.3.4 Molecular diversity

Genetic variation is a pre-requisite for any crop improvement programme to be successful. DNA based molecular markers acted as versatile tools to study variability and diversity in different plant species. Though a range of plant characters are currently available for distinguishing between closely related individuals, their sensitivity to environment and less genome coverage hinders their usage. DNA based molecular markers clearly allow the comparison of genetic material of two individual plants avoiding any environmental influence on gene expression.

Presently, many kinds of 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 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

Table 19 : List of elite genotypes identified for important characters

Characters	Elite genotypes
Days to 50 per cent flowering	DDK 1001#, DDK1009#, VL829*, WH 147*, RIDLEY*
Days to maturity	DBW14*, MOTIA*, PBW 396*, SHARBATISONARA*, SKAML 1*
Plant height	DBW14*, HD1982*, HD2009*, KRL-19*, PBN51*
Peduncle length	PBN51*, PBW343*, PBW373*, PBW502*, WH711*
Number of productive tillers/m	DDK1009#, DL153-2*, UP1109*, JNK-4W-184+, K-9006*
Spike length	K-852*, K9006*, K-9644*, HD-2824*, AJANTA*
Number of spikelets /spike	DDK-1001#, DDK-1009#, HS-375*, WH-533*, WH-711*
Number of grains/spike	HUW-318*, J-1-7*, HUW-468*, NIDW-15+, RAJ-821*
1000 grain weight	HW-741*, MACS-2846+, N-59+, NIDW-15+, K-9465*,
Protein content	K-9107*, NI-917*, VIJAY+, NP-836*, K-53*
Grain yield per plot	MACS-2496*, DWR-195*, HP-1731*, HDR-77*, HD-2009*

** - T. aestivum* *+ - T. durum* *# - T. dicoccum*

banding pattern of the amplification products occurs because of variation in the length of DNA sequences flanked by the primers.

The present study utilized 37 wheat genotypes for RAPD analysis with 11 random decamer primers. The primers produced high degree of polymorphism with an average of 96.00 per cent. All the primers except OPA-07 gave highest polymorphism (100%). On an average 5.6 bands per primer were amplified. The diversity ranged from 4 to 51.00 per cent indicating diverse nature of the genotypes used. Maximum diversity was observed between WH-147 with DDK1001 and HS420 (70.21). Similarly, Barcaccia *et al.* (2002) reported the genetic diversity as high as 48 per cent among the local cultivars of Italian emmer wheat.

In this study, it might be because of the highly divergent lines examined. More appropriately, the chosen primers were able to recognize the genetic differences among genotypes. High level of polymorphism based on RAPD has been reported among the genotypes of wheat (Zhang *et al*., 1996; Rajbir Yadav *et al*., 2002 and Mandoulakani *et al*., 2003).

The dendrogram constructed from the pooled data revealed nine distinct clusters in which five were solitary. The two main clusters were separated at 27.00 per cent diversity. The clustering pattern not followed any definite character base, geographic area of adoption or ploidy level. The set of primers used were not able to group the genotypes into phenotypically intended categories.

Table 20. Comparative study of mean and range of expression of variation of different wheat species

Characters	*T. aestivum*		*T. durum*		*T. dicocum*	
	Mean	**Range**	**Mean**	**Range**	**Mean**	**Range**
Days to 50% flowering	55.17	41.0-69.5	58.07	43.0-69.0	66.00	61-69
Days to maturity	94.04	67.0-116.0	99.14	78.0-116.0	108.00	105-110.5
Plant height(cm)	81.09	55.0-113.0	80.67	66.8-104.8	66.42	59.38-76.5
Peduncle length (cm)	29.43	19.17-40.5	31.37	26.3-38.0	31.26	27.33-33.7
Number of productive tillers/mt	157.92	96.0-213.35	150.84	111.1-204.5	179.78	149.2-210.0
Spike length(cm)	9.39	6.35-12.60	7.40	6.09-10.11	8.83	6.66-10.55
Number of spikelets / spike	18.37	12.66-26.33	17.77	14.0-20.67	22.55	16.0-26.33
Number of grains / spike	37.74	23.83-61.0	36.31	24.5-58.0	37.55	35.0-38.83
1000 grain weight (g)	41.83	30.99-56.04	46.92	40.81-52.75	41.92	37.2-47.41
Protein content	15.10	12.50-17.75	14.78	12.25-17.25	14.75	13.19-15.4
Grain yield per plot	891.18	360-1635	860.80	520-1170	1115.0	1075-113

5.4 COMPARISON BETWEEN MORPHOLOGICAL AND MOLECULAR DIVERSITY

It is clear from the D^2 analysis as well as from molecular profiling of genotypes using RAPD markers that, there was sufficient diversity among the genotypes used for study. But, the grouping of genotypes based on morphological diversity *i.e.* D^2 analysis and DNA fingerprinting was not concurrent.

The genotypes which exhibited low diversity at phenotypic level, exhibited higher diversity at molecular level. For instance, the genotypes DDK1001, DDK1009, DWR162, DWR1006 and HD1982 were grouped together in cluster-I, indicating morphological similarity among themselves. Whereas the same genotypes were present in different clusters at molecular level. The 21 genotypes which were distributed in different clusters at morphological level were grouped into the same clusters at molecular level indicating higher degree of genetic similarity at molecular level.

However, the solitary clusters farmed by the genotypes MACS2694, J1-7, HS420, K852 and WH-147 at molecular level were also present at different clusters at morphological level

The difference between morphological and molecular diversity may be due to the screening or use of limited number of RAPD markers. The grouping of genotypes or diversity is independent of geographical location and ploidy level or even phenotypic markers.

Accessions with the most distinct DNA profiles are likely to contain the greatest number of novel alleles. The present study indicates that RAPD markers are suitable to assess genetic diversity. They can be used to identify diverse sources in crop germplasm collections or to select groups of genotypes with desired characters and contrasting phenotypes, if large numbers are employed. Particularly, genetic distance estimates might help in identifying suitable germplasm for introgression into breeding stocks.

5.5 COMPARATIVE STUDY OF MEAN AND RANGE OF EXPRESSION OF VARIATION BETWEEN DIFFERENT WHEAT SPECIES

The comparison of mean and range of variability between 143 *aestivum*, 22 *durum* and three *dicoccum* species indicate that the mean was high for most of the characters in *T.aestivum* and *T. dicoccum* species. Where as low mean values were observed for *T. durum* species. Similarly the range was high for *T. aestivum* species and low for *T. dicoccum* species. *T. durum* species were with moderate range, so it is clear from comparative study that, *T. aestivum* species have high potentiality worth considering in improvement of wheat (Table.20)

FUTURE LINE OF WORK

1. The study of character association and path analysis suggest that days to 50 per cent flowering, plant height, peduncle length and number of tillers per meter length can be used as an important selection criterion in future breeding programme
2. The genotype identified for higher grain yield HP-1731 can be tested further to confirm its superiority in large scale trials
3. The present study consists of diversified wheat genotypes, so there is need to test the quality parameters like starch, gluten and backing quality which help to improve the nutritional content and quality of wheat in future
4. There is need to use more number of RAPD markers to get more reliable results

VI. SUMMARY

Wheat is the most important cereal crop of the world and ranks first among world food crops. In India, wheat is the second most important cereal crop after rice. Estimation of genetic variability and genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate recombinants.

EXPERIMENT I: ASSESSMENT OF GENETIC DIVERSITY IN WHEAT

The present investigation was carried out to evaluate a set of wheat genotypes for variability in morphological characters, extent of genetic variability, character association, path analysis, genetic divergence. The material for the study comprised of 169 wheat genotypes in which one check *viz*., DWR-162 and Kalyansona was included. These were evaluated in simple lattice design with two replications during *rabi* 2004, at Wheat Improvement Project, Main Agricultural Research Station, Dharwad. The experimental results are summarised below.

1. Analysis of variance revealed highly significant differences among the accessions for all the parameters.

2. Environmental influence was very meagre on expression of these characters as it was evident by narrow gap between genotypic and phenotypic coefficients of variation.

3. The genotypes exhibited high variability for the characters like days to 50 per cent flowering, plant height, peduncle length, number of productive tillers per meter, spike length, number of spikelets per spike, number of grains per spike, 1000 grain weight and grain yield per plot except protein content.

4. The characters *viz*., days to 50 per cent flowering, plant height, peduncle length, number of productive tillers per meter, spike length, number of spikelets per spike, number of grains per spike, grain yield per plot and protein content exhibited high heritability coupled with a high genetic advance indicating that simple selection scheme would be sufficient for these traits to bring genetic improvement in desired direction.

5. Grain yield had positive and highly significant association with days to 50 per cent flowering at genotypic level, at both genotypic and phenotypic level plant height, peduncle length and protein content exhibited significantly negative association with grain yield per plot.

6. Path coefficient analysis revealed that days to 50 per cent flowering, productive tillers per meter, number of spikelets per spike, number of grains per spike and 1000 grains weight exhibited direct positive effect on grain yield. Hence, it would be rewarding to lay stress on these characters in selection programme for increasing yield.

7. Using Mahalanobis D^2 statistics method, 169 genotypes were grouped into 12 divergent clusters, cluster III had the maximum number of 28 genotypes followed by cluster II, IV, VI and VII with 26 genotypes, cluster I had 6 genotypes the remaining clusters were solitary with single genotypes. Intra cluster distance was highest (205.49) in cluster VI followed by cluster II (188.95). Inter cluster D^2 values ranged from 323.29 between clusters VII and IX to 1450.95 between clusters VIII and XI, indicating wide genetic variability. It is desirable to select accessions from clusters having high inter cluster distance and also with high grain yield as parents in the recombination breeding programmes.

8. The cluster means were calculated for each characters and ranks were given based on scores obtained for all the 11 characters. Of the clusters, cluster II with 26 genotypes ranked first and appears to be the most potential group. Similarly, other clusters IV and VIII were next in ranking order and can be utilized for future breeding programme.

9. The study also revealed that no relationship is existing between genetic diversity and geographical diversity. It was also found that highest contribution towards the genetic diversity of wheat genotypes was contributed by grain yield per plot followed by days to

50 per cent flowering, spike length, peduncle length, plant height, number of spikelets per spike, number of grains per spike, 1000 grain weight, protein content number of tillers per meter length and days to maturity.

EXPERIMENT II: MORPHOLOGICAL AND MOLECULAR DIVERSITY

Using Mahalanobis D^2 statistics method, 37 genotypes of wheat were grouped into 10 different clusters. Among these 2 solitary clusters were observed. The study revealed that the clustering pattern was independent of ploidy level and geographical location. It was also found that higher contribution towards the genetic diversity was contributed by grain yield per plot followed by days to 50 per cent flowering, spike length, peduncle length and plant height.

Genetic diversity at molecular level was estimated by using RAPD markers. RAPD profiles for all the 37 genotypes were generated with 10 random decamer primers. The level of polymorphism generated (96.00%) among the genotypes was very high. On an average 5.6 bands per primer were produced. Maximum diversity was noticed between WH147 with DDK1001 and WH147 with HS420 (70.11). The dendrogram constructed from the pooled data revealed two distinct clusters. The grouping was not based on any character such as geographical area of adoption or ploidy level.

A comparison was made between genetic diversity at morphological level and molecular level. This study revealed that the genotypes, which exhibited low diversity at morphological level exhibited higher diversity at molecular level. This study also revealed that the grouping of genotypes based on morphological diversity and DNA fingerprinting was not concurrent.

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Appendix I : Mean performance of 169 wheat genotypes

Sl. No.	Genotypes	Species	Days to 50% flowering	Days to maturity	Plant height (cm)	Peduncle length (cm(	No. Of productive tillers/m	Spike length (cm)	No. of spikelents per spilke	No. Of grains per spike	1000 grain weight (g)	Protein content	Grainf yield per plot (g)
1	AJANTA	*T.aestivum*	58	99	60.75	23.42	167.45	12.26	16.67	32.5	42.29	15.25	875
2	AKW 1071 (PURNA)	*T.aestivum*	63.5	109	68.38	35.38	130.4	10.15	16.5	38.5	42.88	16.2	925
3	BIJAGA YELLOW	*T. durum*	63	107.5	90.79	37.5	132.1	9.16	17.83	30	46.19	15.8	885
4	BW 11 (PURBALI	*T.aestivum*	57	104.5	64.5	25.88	147.5	9.91	19.33	39	45.51	14.25	990
5	C 306	*T.aestivum*	65	110	84.88	38	162.5	10.3	16.83	41.5	40.18	13.65	870
6	CHHOTI LERMA	*T.aestivum*	58	101.5	72	35.5	123.35	9.4	17	33	33.68	14.4	735
7	CPAN 1676 (ROHINI)	*T.aestivum*	60	102	77.38	38	96	9.07	19.83	34.5	35.45	14.75	700
8	CPAN 1796	*T.aestivum*	59	99	78.38	40.5	160.85	8.51	18	37	37.69	13.65	515
9	DBW 14	*T.aestivum*	53	87	60.88	30.38	189.3	8.85	18.33	38.5	43.58	14.25	660
10	DDK 1001	*T. dicoccom*	69	108.5	59.38	33.79	180.1	9.28	25.33	38.83	41.12	13.9	1135
11	DDK 1009 (GANGA)	*T. dicoccom*	68	110.5	63.38	32.67	210	10.55	26.33	35	37.22	15.45	1075
12	DL 153-2 (KUNDAN)	*T.aestivum*	55	99.5	67.29	34.92	208.9	10.43	16	36	54.28	15.8	825
13	DL 784-3 (VAISHALI)	*T.aestivum*	53	87	56.92	31.17	141.75	7.84	12.66	30	41.15	14.5	900
14	DL 803-3 (KANCHAN)	*T.aestivum*	51.5	98.5	70.25	29.96	148.1	9.49	20	39.5	41.14	14.3	1175
15	DT 46	*Triticae*	52	82	79.96	39.62	117.5	8.49	20.17	31.83	41.35	14.2	855
16	DWR 16 (KEERTHI)	*T.aestivum*	60	107.5	68.12	23.5	106.7	10.1	19.67	36	40.15	15.1	1065
17	DWR 39 (PRAGATI)	*T.aestivum*	58	107.5	74.46	28	106.1	10.3	18	43.33	40.18	14.25	965
18	DWR 137 (KIRAN)	*T. durum*	54	98	70.62	28	131.55	7.89	15.84	24.5	45.82	16.1	845
19	DWR 162	*T.aestivum*	58	100	70.00	26	127.50	7.85	18.00	34.00	42.01	14.75	1095
20	DWR 185	*T. durum*	59	100	74.00	28	112.00	6.55	16.00	36.00	40.09	12.25	1000
21	DWR 195 (ANURADHA)	*T.aestivum*	59	100	76.67	23	137	10.41	21.33	34.5	44.00	14.75	1635
22	DWR 1006	*T. durum*	64	107	80.71	34.54	100	7.28	20.67	26	40.00	13.00	812.5
23	GW 273	*T.aestivum*	57	98.5	73.5	33.9	139.3	9.5	18.83	35	40.74	13.95	840
24	GW 322	*T.aestivum*	56	98	80.29	27.33	128.5	9.53	18	36	40.35	12.5	895
25	GW 405	*T.aestivum*	54	78.5	86.68	30.95	122.65	8.5	14	32.5	45.57	13.6	925
26	GW 496 (GUJARAT WHEAT)	*T.aestivum*	54	78.5	83.08	34.35	147.5	8.72	16.5	27.5	43.69	13.15	997.5
27	GW 503	*T.aestivum*	55	79	76.64	30.3	176.2	8.15	13.66	37.5	42.9	13.5	1075
28	GW 1139	*T.aestivum*	59	100.5	82.45	30.86	120.45	10.11	16.5	25.83	46.55	14.5	560

Contd…

Sl. No.	Genotypes	Species	Days to 50% flowering	Days to maturity	Plant height (cm)	Peduncle length (cm(	No. Of productive tillers/m	Spike length (cm)	No. of spikelents per spilke	No. Of grains per spike	1000 grain weight (g)	Protein content	Grainf yield per plot (g)
29	HB 208	*T.aestivum*	54	74	62.2	26.9	135.55	6.5	16.33	25.5	56.04	15.05	805
30	HD 1982 (JANAK)	*T.aestivum*	54	82	59	24	172.5	7.68	14	34	39.42	14.25	1020
31	HD 2009 (ARJUN)	*T.aestivum*	58	102	56.33	21.33	155.85	9.16	20.17	34	39.07	13	1205
32	HD 2135 (NILGIRI)	*T.aestivum*	58	108	61.67	27.5	136	9.8	19.33	37	39.01	14.75	955
33	HD 2428	*T.aestivum*	53	97	61.5	23.83	163.9	9.47	18	33.17	47.55	12.75	810
34	HD 2501	*T.aestivum*	44	75	85.29	35.04	175	9	16	25.5	39.49	13.35	840
35	HD 2643 (GANGA)	*T.aestivum*	47	74.5	69.46	25.08	161.7	10.02	18	41	44.18	14.1	775
36	HD 2687 (SHRESHTH)	*T.aestivum*	58	95	79	28.46	155.9	6.91	20	30.5	39.1	15.25	1125
37	HD 2733	*T.aestivum*	67	110.5	75.83	26.79	165.85	9.07	21.17	31	47.47	15.6	1485
38	HD 2781 (ADITYA)	*T.aestivum*	59	115	79.96	30.71	132.35	9.24	18.33	27.17	49.73	14.85	1055.5
39	HD 2824	*T.aestivum*	60.5	113	75.25	22.29	124.9	12.6	20.33	35.5	46.88	13.35	1345
40	HD 2833	*T.aestivum*	41	76	70.57	27.6	171.25	10.43	18	25	42.08	15.05	750
41	HD 4672 (MALVA RATNA)	*T.durum*	61	115	80.24	27.63	148.5	6.78	19.67	35.33	45	14.15	775
42	HDR77	*T.aestivum*	60	116	80.75	32.49	201.3	10.3	17.67	25	49.46	14.3	1200
43	HI 977	*T.aestivum*	56	95	80	32.83	147.95	8.84	18	30	41.13	14.1	910
44	HI 1077 (MANGLA)	*T.aestivum*	55	95.5	83.83	27.67	127.05	9.99	19	35.67	45.68	14.55	825
45	HI 1500 (AMRITA)	*T.aestivum*	60	101.5	111.95	38.5	133.65	10.32	16	31.83	43.45	14.5	874.5
46	HI 8381 (MALVASHRI)	*T.durum*	69	107	70.33	28	158.4	7.6	18.83	38.5	48.33	13.15	995
47	HI 8498 (MALAV SHAKTI)	*T.durum*	59	95	76.33	32.67	140.7	6.09	18	35.67	51.09	12.65	950
48	HP 1633 (SONALI)	*T.aestivum*	49	82.5	106	32.5	161.15	9.59	18.33	39.5	49.5	13.75	1095
49	HP 1731 (RAJ LAKSHMI)	*T.aestivum*	54	81.5	74.17	33.33	195.8	9.5	16	48	37.74	14.6	1210
50	HP 1744 (RAJESHWARI)	*T.aestivum*	56	83	81.5	28.33	134.85	9.09	13.84	34.5	43.14	14.2	935
51	HP 1761 (JAGDISH)	*T.aestivum*	54	81.5	77.67	27.33	130.35	9.41	19.33	39.33	38.4	14	960
52	HS 375	*T.aestivum*	62	108.5	81.58	27.92	143.55	10.34	26.33	52	37.48	14.8	1100
53	HS 420 (9SHIVALIK)	*T.aestivum*	58	102	78.92	31.5	109.2	10.16	19.33	54	40.6	14.5	995
54	HS 1097-17 (GIRIJA)	*T.aestivum*	58	104	89	37.67	141.75	9.59	18.67	46.33	43.35	13.55	890
55	HS 1138-6-4 (SHAILAJA)	*T.aestivum*	59	99	83.71	29.58	140.35	9.91	15.84	33.33	44.32	13.3	1010
56	HUW 12 (MALVIYA 12)	*T.aestivum*	58	99	83.83	28.08	151.15	8.59	18.5	45	42.68	12.75	1162.5
57	HUW 55 (MALVIYA 55)	*T.aestivum*	59	97	88.5	32.33	162.25	8.34	18.33	45.17	38.99	14.75	1040
58	HUW 206 (MALVIYA 206)	*T.aestivum*	60	107	82.67	28.33	124	11.14	20	48.33	44.4	15.6	980

Contd…

Sl. No.	Genotypes	Species	Days to 50% flowering	Days to maturity	Plant height (cm)	Peduncle length (cm(	No. Of productive tillers/m	Spike length (cm)	No. of spikelents per spilke	No. Of grains per spike	1000 grain weight (g)	Protein content	Grainf yield per plot (g)
59	HUW 213	*T.aestivum*	47.5	74	68.67	27	131.55	7.59	17.33	38.83	39.93	13.4	962.5
60	HUW 234	*T.aestivum*	56	72	74.67	25	120.45	9.16	18.17	45.33	44.53	16	950
61	HUW 318 (MALVIYA WHEAT)	*T.aestivum*	59.5	103	77	27.25	103.65	9.59	18	55	38.9	16.15	950
62	HUW 468 (MALVIYA WHEAT)	*T.aestivum*	49	78	95.92	30.5	158.9	9.09	16	51.83	48.29	16.75	850
63	HUW 533	*T.aestivum*	64.5	113	81.75	28.83	135.85	8.16	18	36.17	43.33	15.15	700
64	HW 517	*T.aestivum*	49	69.5	76	27.92	172.2	7.59	18.67	41.17	43.29	15.9	1120
65	HW 657	*T.aestivum*	53	81	83.5	32.67	139.7	8.25	18.17	33.67	38.2	13.85	950
66	HW 741	*T.aestivum*	49	69.5	75.75	29.83	179.1	8.91	19.33	37.83	50.64	12.75	1075
67	HW 1085 (BHAWANI)	*T.aestivum*	54	97	75.92	22.5	136.4	8.5	19	54	40.86	14.7	1025
68	HW 2004 (AMAR)	*T.aestivum*	62	112	89.83	30.64	149.9	8.66	19	37.67	43.96	14.35	980
69	HW 2045	*T.aestivum*	53	85	79	29.33	133.65	9.09	17.83	46.33	43.06	13.15	930
70	HYB 65	*T.aestivum*	52	101	83.33	29.49	187.5	8.34	16.33	35.5	44.76	14.15	920
71	J-1-7	*T. aestivum*	54	95	80.67	23.33	193.2	9.91	21.83	54.5	37.53	15.35	612.5
72	JNK-4W-184 (JAIRAJ)	*T.durum*	58	93.5	93.17	30.42	204.5	6.53	19.33	38.67	44.52	15.15	1170
73	K 68	*T.aestivum*	54	114	93.33	29.92	182.6	9	22.5	37.67	43.56	15.45	890
74	K 852	*T.aestivum*	61	105	87.5	32.94	181.35	12.41	19.83	40.67	38.28	14.7	1145
75	K 7410 (K-POORVI)	*T.aestivum*	51	75	83.4	31.67	149.35	10.51	18.33	43.83	39.4	15.25	1035
76	K 8020 (TRIVENI)	*T.aestivum*	61	105	87.25	26.17	170.5	10.16	23	39.17	44.31	14.55	965
77	K 8027 (MAGHAR)	*T.aestivum*	68	114.5	90.57	30.53	199.1	9.59	18.67	38	42.74	14.65	1170
78	K 8804	*T.aestivum*	60	103	72.63	25.83	135.95	9.66	20	38.83	40.09	15.5	1045
79	K 8962 (INDRA)	*T.aestivum*	54	75	76.6	29.53	199	10.75	18	31.17	48.08	15.75	1035
80	K 9006 (UJIYAR)	*T.aestivum*	57	85	76.64	31.99	205	11.75	19.33	30	43.75	15.35	910
81	K 9107 (DEWA)	*T.aestivum*	57	107	85.57	32.17	171.6	11.4	20	36.17	46.93	16.9	810
82	K 9465 (GOMTI)	*T.aestivum*	53	77	103.08	33.5	172.45	9.5	14.5	23.83	49.25	16.6	775
83	K 9644	*T.aestivum*	57	105	92.5	30.5	188.1	12.25	21.33	42.33	42.15	15.35	940
84	KALYANSONA	*T.aestivum*	50	83	85	31.67	140	8.75	17.5	36.5	38.82	14.4	960
85	KHARCHIA 65	*T.aestivum*	51	101	100.17	26	175	9.25	18.5	32.33	37.66	14.5	865
86	KRL 1-4	*T.aestivum*	49	93	76.67	31	135	8.84	16.83	32.33	35.82	13.9	870

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Sl. No.	Genotypes	Species	Days to 50% flowering	Days to maturity	Plant height (cm)	Peduncle length (cm(	No. Of productive tillers/m	Spike length (cm)	No. of spikelents per spilke	No. Of grains per spike	1000 grain weight (g)	Protein content	Grainf yield per plot (g)
87	KRL-19	*T.aestivum*	49	93	56.2	26.42	194.7	9.75	18.5	39.67	32.32	14.8	930
88	KSML 3	*T.aestivum*	63	107	81	27.5	161.7	10.09	19.83	33.33	40.08	15.2	940
89	LERMA RAJO	*T.aestivum*	50	85	81.5	31	170	9.75	17	36.5	35.51	13.6	765
90	LOK 1	*T.aestivum*	55	97	91.5	36.33	173.25	10.45	20.5	34.33	45.34	15.5	820
91	MACS 1967	*T.durum*	47.5	93	97.17	34.5	168.85	6.25	16	38.83	48	15.3	1100
92	MACS 2496	*T.aestivum*	59	105	74.17	24.83	213.35	10.25	18.83	39	46.08	13.5	1225
93	MACS 2694	*T.durum*	63	106	82.83	34.17	167.2	6.5	20.5	34.83	49.96	13.65	940
94	MACS 2846	*T.durum*	58	98	77.67	32.67	165.55	6.5	16.5	42.67	50.54	14.25	940
95	MLKS 11	*T.aestivum*	51	95	74.17	27.5	201	9.75	20.17	37	37.59	14.9	1125
96	MOTIA (BANSI 168)	*T.aestivum*	42	67	94.37	35.83	171.6	6.35	15	34	43.53	16.5	812.5
97	N59	*T.durum*	57	85	98.83	38	174.35	9.03	18.5	48.17	51.62	14.5	550
98	NI 917	*T.aestivum*	63.5	114.5	79.33	31.5	124.85	7.36	17.67	40.83	30.99	17.75	675
99	NI 5439	*T.aestivum*	54	96.5	83.67	35.33	162.5	6.84	14	35.5	39.47	15.95	1175
100	NI 5643	*T.aestivum*	54	96	81.17	34.5	210	6.75	14.66	36.5	39.6	15.25	1075
101	NI 5749	*T.durum*	54	96	79.33	32.5	175.75	7.16	14	43.33	45.03	14.25	850
102	NIAW 34	*T.aestivum*	50	80.5	84	28.5	153.95	8.22	18	41.17	41.76	15.25	835
103	NIDW 15	*T.durum*	58	98	104.83	37.83	116.6	7.59	18.33	58	52.75	14.2	560
104	NIDW 295	*T.aestivum*	60	104	81.5	33.67	142.05	7.14	15.5	37.67	39.42	13.95	960
105	NP 884	*T.aestivum*	49	85	100.5	34.26	172.5	7.18	19.33	31	45.47	16.9	825
106	NW 1012	*T.aestivum*	55	95	81.3	30.17	163.6	7.97	20	39.83	38.12	16.05	725
107	NW 1014	*T.aestivum*	54	75	70.67	26.17	136.95	8.53	15	28	40.7	14.4	940
108	NW 2036	*T.aestivum*	49	69	70.33	25.17	142.6	7.75	16.83	37	39.66	16.15	975
109	PBN 51	*T.aestivum*	62	102	55	19.33	133.5	10.5	18	33.5	38.53	16.65	680
110	PBN 142 ((KAILASH)	*T.aestivum*	48	115	87.5	28.67	147.4	9.9	17.67	40	42.94	15.2	790
111	PBW 65	*T.aestivum*	48	75	90.67	33.17	149.6	9.74	19.17	43.83	40.36	15.35	855
112	PBW 343	*T.aestivum*	63	105	72.5	20.5	168.85	10.25	19.83	44.17	41.77	16.6	881
113	PBW 373	*T.aestivum*	62	104.5	75.33	19.67	177.65	10.84	18.67	45	40.97	16.85	1105
114	PBW 396	*T.aestivum*	43	67	72.67	33.57	210	8.66	18	35.17	39.63	15.2	850
115	PBW 443	*T.aestivum*	63.5	105	79.5	24.17	168.05	10.39	20.33	36.67	39.68	16.95	870
116	PBW 502	*T.aestivum*	60	104.5	79.2	20.33	146.85	11	23.33	37	43.92	16.45	955

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Sl. No.	Genotypes	Species	Days to 50% flowering	Days to maturity	Plant height (cm)	Peduncle length (cm(	No. Of productive tillers/m	Spike length (cm)	No. of spikelents per spilke	No. Of grains per spike	1000 grain weight (g)	Protein content	Grainf yield per plot (g)
117	PDW 215	*T.durum*	61	103	66.83	26.83	147.95	7.09	18.5	33.33	48.42	16.45	860
118	PDW 233	*T.durum*	62	105	75.33	26.33	145.75	7.41	16.5	36.33	41.34	16.85	890
119	RAJ 821	*T.aestivum*	66.5	111	74.33	23.67	134.2	9.84	21.5	61	36.82	16.2	725
120	RAJ 911	*T.durum*	57	95	75.83	27.83	198.55	7.25	19	40.83	45.09	16	1100
121	RAJ 1482	*T.aestivum*	57	83	83.33	31.17	195.7	8.14	21.5	33.33	36.13	14.05	890
122	RAJ 1555	*T.durum*	55	99	85.83	35.5	148.5	7.25	18.5	27.67	47.63	15.05	1150
123	RAJ 3765	*T.aestivum*	54	81	82.5	29.17	167.5	9.5	16.67	35	39.1	13.8	1000
124	RAJ 4037	*T.durum*	55	85	69.5	27.47	186.45	8.43	15.34	31	40.81	14.5	825
125	SAFED LERMA	*T.aestivum*	43	68	83.9	32.17	179.9	8.5	16	37.83	39.56	14.5	965
126	SAGARIKA SHARBATI	*T.aestivum*	51	83	88.5	32.17	184.25	11.25	18	29	43.31	14.5	855
127	SONORA	*T.aestivum*	47	67	68.17	23.67	140	8.25	18.5	38.83	34.59	15.6	745
128	SKAML 1	*T.aestivum*	46	67	73.07	27.97	183.7	8.4	19	26.5	40.06	15.25	865
129	SONAK	*T.aestivum*	47	68	74.83	29.17	167.75	10.65	15.84	35.17	42.28	16.1	795
130	SONALIKA	*T.aestivum*	56	98.5	72.17	30.5	159.2	9.84	16	40.17	46.13	15.5	825
131	SONORA 64	*T.aestivum*	43	77	68.33	25.67	199.55	8.59	18	31.67	38.91	16.75	840
132	UP 301	*T.aestivum*	58	92.5	82.67	32.33	156.95	9.84	20	40.33	41.92	13.8	837.5
133	UP 368	*T.aestivum*	53	95	67.67	25.35	200.2	10.41	17.17	36	39.57	15.2	955
134	UP 1109	*T.aestivum*	51	95	87.83	30.67	212.5	9.5	19.17	44.33	39.8	14.65	940
135	UP 2003	*T.aestivum*	64	110.5	75.33	19.33	141.9	9.97	20.83	48.17	39.08	15.6	840
136	UP 2113	*T.aestivum*	60	113	91.67	30.33	171.35	11.26	21.33	43.67	40.83	15	835
137	UP 2121	*T.aestivum*	65.5	113	79.17	20.67	117.75	9.74	23.83	52.83	39.14	15	725
138	UP 2338	*T.aestivum*	51	97	79	28.17	169.7	9.84	19.33	39	49.11	14.65	855
139	UP 2382	*T.aestivum*	52	99	77.5	32.83	167.2	8.09	18	38.17	41.55	15.9	445
140	UTKALIKA	*T.aestivum*	49	68	84.83	26.44	186.45	7.59	16.17	46.17	39	16	860
141	VINATA (N 8223)	*T.aestivum*	51	85.5	101.5	34	172.45	9.25	19.33	42.67	45.43	14.25	615
142	VL 401	*T.aestivum*	42	67	75.33	29.83	168.3	9.57	16.5	40	38.13	16.1	570
143	VL 804	*T.aestivum*	53	83	83.67	30.83	135.85	9.75	18	46.17	38.33	15.55	990
144	VL 829	*T.aestivum*	65.5	115	87.71	27.17	119.9	11.6	23	44	43.51	16.1	760
145	VL 832	*T.aestivum*	46.5	83	84	31.5	139.4	10.91	18.67	48.33	38.56	15.5	945
146	WH 147	*T.aestivum*	69.5	111.5	91.67	31	187	10.25	20	39.33	46.69	13.75	770

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147	WH 533	*T.aestivum*	59	109.5	66.5	22.33	143.15	11.25	23.83	40.5	41.97	15.2	890
148	WH 542	*T.aestivum*	52	81	59.83	22.47	160.85	9.03	18.67	41.33	32.55	16.35	760
149	WH 896	*T.durum*	61	116.5	68.17	28.17	111.1	7.91	20	32	42.9	16.15	520
150	WH 711	*T.aestivum*	60	98	62.5	19.17	162.25	9.91	23.83	37.5	43.1	15.9	825
151	PBW 524	*T.aestivum*	54	79	70.63	29.15	133.5	9.36	20	40.17	42.14	15.3	1025
152	JAY	*T.dicoccum*	61	105	76.5	27.33	149.25	6.66	16	38.83	47.41	14.9	1135
153	K 53	*T.aestivum*	61	116	93.08	27.47	140.95	10.66	16	38.5	36.35	17.15	525
154	K 65	*T.aestivum*	55	103	101.17	32.75	137.9	10.75	18.67	31.67	44.03	15.7	475
155	MONDHYA 3-2	*T.aestivum*	58	96	95.33	24.97	186.55	10.05	17.33	44	35.6	16.2	530
156	NP 165	*T.aestivum*	53	95	113	33.33	187.4	8.39	18.67	38.17	42.28	16.25	743
157	NP 718	*T.aestivum*	55	99	95.17	29.17	139.3	8.34	18.67	40	37.5	16.85	510
158	NP 737	*T.aestivum*	57	105	88	24.5	166.35	11.59	18.5	25.85	34.76	16.85	475
159	NP 745	*T.aestivum*	53	95	103.33	36	193.2	8.16	18	36.83	38.92	16.75	640
160	NP 760	*T.aestivum*	43	80	104.5	38.25	202.3	8.5	14.34	40	41.92	16.6	785
161	NP 761	*T.aestivum*	44	67	95.67	35.99	155.2	7.66	16	31.67	39.35	16.8	460
162	NP 771	*T.aestivum*	51	75	104.5	34.5	157.3	9.84	18	29.5	38.79	15.85	640
163	NP 823	*T.aestivum*	56	99	102.67	31.17	149.25	9	15.66	39	49.62	15.3	835
164	NP 824	*T.aestivum*	51	96	97	30.83	163.35	10.4	14.34	29.33	47.65	15.05	875
165	NP 825	*T.aestivum*	53	115	106	34.83	183.25	9.84	14	26.67	47.72	16.25	360
166	NP 836	*T.aestivum*	49	84	90.75	34.5	154.75	8.66	19.33	36.17	40.73	17.7	680
167	NP 890	*T.aestivum*	49	79	100.83	33.5	142.6	9	18	29	47.32	16.5	765
168	RIDLEY	*T.aestivum*	66.5	116	94.5	26	132.55	9.16	19.67	38.33	46.01	16.85	960
169	VIJAY	*T.durum*	43	78	80.33	30.7	140.1	6.5	16	38.67	48.99	17.25	660

ANALYSIS OF GENETIC DIVERSITY IN WHEAT

SHASHIKALA S. K. 2006 Dr. R. R. HANCHINAL

ABSTRACT

A study was conducted during *rabi* 2004, at Wheat Improvement Project, University of Agricultural Sciences, Dharwad to investigate variability, correlation, path coefficient analysis and genetic diversity for quantitative and quality traits in wheat genotypes. The experiment was laid out in simple lattice design with two replications.

Two different experiment were conducted, first experiment included 169 wheat genotypes including checks *viz.,* DWR 162 and Kalyansona evaluated for 11 traits. The study revealed wide range of variability and high heritability for all the traits. The genetic advance as per cent mean suggesting still there is scope for further improvement of genotypes for these characters. Correlation studies revealed that grain yield per plot was positive and significantly associated with days to 50 per cent flowering and negatively significant with plant height, peduncle length and protein content. The maximum direct effect on grain yield was exhibited, by days to 50 per cent flowering followed by number of tillers per meter length.

D^2 analysis revealed that days to 50 per cent flowering and number of spikelets per spike contributed greatly towards divergence. Twelve different clusters were formed with maximum number of genotypes (28) in cluster (III).

In second experiment 37 wheat genotypes were used for genetic diversity analysis at morphological and molecular level. D^2 analysis including all the 11 traits revealed the grain yield per plot and days to 50 per cent flowering contributed greatly towards divergence. Genetic diversity at molecular level was estimated by using RAPD markers has revealed that grouping of genotypes based on morphological diversity *i.e.,* D^2 analysis and DNA fingerprinting was not Concurrent. Ten random decamer primers generated diverse RAPD profiles indicating high genetic diversity among the genotypes.