Exploitation of Genetic Variability in Wheat (*Triticum aestivum* L.) Germplasms under Late Sown Condition

Patel Nikita[*], J. Raval Lata, Virendra Singh Shekhawat and Ramesh Kumar

Department of Genetics and Plant Breeding, College of Agriculture, University of Agriculture, Junagadh – 362 001, India

*Corresponding author

A B S T R A C T

Genetic variability parameters were carried out for grain yield and its attributes with a set of 48 genotypes of bread wheat (*Triticum aestivum* L.) at Wheat Research Station, Junagadh Agricultural University, Junagadh during *Rabi* 2016-17 in randomized block design with three replications under late sown condition. The characters studied were days to 50 % heading, days to anthesis, days to maturity, grain filling period, number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, grain yield per plant, biological yield per plant, harvest index, flag leaf area and chlorophyll content. The analysis of variance revealed that mean square due to genotypes was significant for all the traits in late sown condition. A wide range of variation was observed for important yield components. High phenotypic and genotypic coefficient of variations and high heritability coupled with high to moderate genetic advance as per cent of mean was observed for 1000-grain weight and biological yield per plant under late sown condition.

Introduction

Wheat is a crop of global significance grown in diversified environments. It is an important cereal crop of cool climate and plays an important role in food and nutritional security of world. It provides food for 40% of the global population and contributes 20% of the food calories (Bhutto *et al.,* 2016). The total production of wheat in the world is around 735.5 million tonnes with productivity of 3.27 tonnes per hectare (Anon., 2017). The main wheat growing countries are European Union, China, India, USA, Russian Federation, Canada, Australia, Pakistan, Turkey, Ukraine, Iran, (Anon., 2015a). It is the world's most widely cultivated food crop, followed by rice and maize (Gulbitti-Onarici *et al.,* 2009) and one of the oldest and most important among the cereal crops (Harlan, 1992), producing the

highest global grain production of any crop (Lamoureux *et al.,* 2005). The area and production of wheat in India was recorded 30.72 million ha and 97.44 million tonnes with an average productivity of 3172 kg ha^{-1} during year 2016-17 (Anon., 2017). In Gujarat, area and production of wheat was recorded as 9.96 lakh ha and 29.38 lakh metric tonnes, respectively with an average productivity of 2950 kg ha^{-1} during year 2016-17 (Anon., 2017).

Wheat grain contains starch (60-68%), protein (6-21%), fat (1.5-2.0%), cellulose (2.0-2.5%), minerals (1.8%) and vitamins (Das, 2008). The uniqueness of wheat in contrast to other cereals is that wheat contains gluten protein, which enables leavened dough to rise by forming minute gas cells and this property enables bakers to produce light breads (Das, 2008). Wheat is one of the most important crop used mainly for human consumption and support nearly 35% of the world population (Mohammadi-joo *et al.,* 2015) and providing 20 per cent of the total food calories (Anon., 2014).

One of the most important objectives of any breeding program is to produce high-yielding and better-quality lines. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be isolated for further breeding programme to achieve the target. Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic variability, the change in mean value among successive generations (Shukla *et al.,* 2006).

The basic rational in any crop improvement programme is to increase the yield potential of the crop. Grain yield is a complex and polygenic trait, and in order to study it properly, different factor affecting the grain yield must be considered and evaluated with regard to their contribution to grain yield. For a particular crop, information on extent of variability parameters may be helpful to improve the yield by selecting the yield component traits because yield is a complex trait, whose manifestation depends on the component traits. Generally, the estimates of heritability (h^2) of traits are environment specific (Shimelis and Rhandzu, 2010). Thus, selection of yield and yield related traits based on heritability and genetic variability as percent of mean is of great importance to the breeder for making criteria for improvement in yield and yield related traits.

Materials and Methods

The present investigation was carried out quality Wheat (*Triticum aestivum* L.)" at Wheat Research Station, Junagadh Agricultural University, Junagadh, Gujarat during *rabi* 2016-17. The experimental material consisting of 48 genotypes presented in Table 1. In this experiment, genotypes were evaluated in randomized block design with three replications during *rabi* 2016-17 in randomized block design with three replications under late sown conditions. Observations for all traits (days to 50 % heading, days to anthesis, days to maturity, grain filling period, number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, grain yield per plant, biological yield per plant, harvest index, flag leaf area, chlorophyll content and canopy temperature depression) were recorded on five randomly selected competitive plants of each entry in each replication except for days to 50 % heading,

days to anthesis, days to maturity, grain filling period where observations were recorded on plot basis.

Statistical analysis

Statistical analysis was done on the mean values of five randomly selected plants or plot basis in each row.

The statistical software (INDOSTAT) was used to work out ANOVA, genetic parameters and the statistical methods adopted were as follows.

Genotypic coefficient of variance (GCV)

The magnitude of genetic variance existing in a character was estimated as per the formula suggested by Burton (1952).

$$GCV\ (\%) = \frac{\sqrt{V_g}}{\bar{x}} \times 100$$

Phenotypic coefficient of variance (PCV)

The magnitude of phenotypic variance existing in a character was estimated as per the formula given by Burton (1952).

$$PCV\ (\%) = \frac{\sqrt{V_p}}{\bar{x}} \times 100$$

Heritability Broad sense (H)

It is the proportion of genotypic variance to the phenotypic variance. It was estimated by the formula as suggested by Burton and Devane (1953) and Jonson *et al.,* (1955).

$$H\ (\%) = \frac{V_g\,(\sigma^2 g)}{V_p\,(\sigma^2 p)} \times 100$$

Expected genetic advance (G.A.)

It is the percentage of expected genetic advance over the mean. The expected genetic advance at 5% selection intensity was calculated by the formula given by Lush (1945) and Johnson *et al.,* (1955).

$$GA = \frac{V_g}{V_p} \times \sqrt{V_p} \times K$$

Where, GA = Genetic advance, K = selection differential (constant) 2.06 at 5% selection intensity (Allard, 1960), Vg = Genotypic variance and Vp = Phenotypic variance

Results and Discussion

The information on genetic variability for different yield and yield contributing characters of economic importance is a pre requisite for a breeder to work with crop improvement. The analysis of variance revealed that mean square due to genotypes was significant for all the traits (Table 2). Among the studied traits, highest variability was observed for grain yield per plant followed by ear height and numbers of seeds per row which lower variability were recorded for Ear length and protein content (Table 3). In general, the study revealed sufficient variability for all the yield and yield contributing traits and quality traits and thus helped in selection of specific genotype for different characters.

Genotypic and phenotypic coefficient of variation

High genotypic coefficient of variation was observed for a character that was harvest index followed by biological yield per plant. The estimated GCV values were moderate in case of grain yield per plant, number of productive tillers per plant, 1000-grain weight, chlorophyll content and number of grains per spike, number of spikelets per spike, grain filling period, flag leaf area, spike length. Plant height, days to anthesis, days to 50% heading, days to maturity had lower GCV

value. However, the high phenotypic coefficient of variation was observed for harvest index followed by grain yield per plant, biological yield per plant, number of productive tillers per plant and 1000-grain weight. The estimated values were moderate in case of number of grains per spike, chlorophyll content, number of spikelets per spike, flag leaf area and grain filling period. The estimated values were low in case of spike length, plant height, days to anthesis and days to 50% heading and days to maturity. The estimates of genotypic and phenotypic coefficient of variability indicated that the values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the traits studied, indicating less effect of environment on the expression of characters studied. For these characters indicate that, the traits are more influenced by genetic factors with minimum influence of environment and also suggest that, the selection based on these characters would facilitate successful isolation of desirable genotypes. Malav, 2015 and Rathwa, 2017 were earlier reported similar type of observations for yield and yield contributing traits.

Table.1 Details of genotypes used in experiment

Sr. No.	Sr. No.	Source	Sr. No.	Genotype	Source
1.	MACS-6660	Maharashtra	25.	HD 3159	New Delhi
2.	HD-3184	New Delhi	26.	UAS 361	Karnataka
3.	WH 1184	Haryana	27.	K 1314	Uttar Pradesh
4.	UAS-375	Karnataka	28.	DBW 148	Haryana
5.	HI-1563	Madhya Pradesh	29.	PBW 719	Punjab
6.	DBW-71	Haryana	30.	HD 3164	New Delhi
7.	HD-3059	New Delhi	31.	DBW 148	Haryana
8.	DBW-107	Haryana	32.	PBW 707	Punjab
9.	DBW-90	Haryana	33.	HD 3165	New Delhi
10.	HD-2932	Haryana	34.	PBW 716	Punjab
11.	DBW-175	Haryana	35.	HI 1604	Madhya Pradesh
12.	HI-1612	Madhya Pradesh	36.	CG 1015	Chhattisgarh
13.	UP-2903	Uttarakhand	37.	DBW 147	Haryana
14.	AKAW 4842	Maharashtra	38.	DBW 107	Haryana
15.	DBW-172	Haryana	39.	HUW 688	Uttar Pradesh
16.	NIAW-2495	Maharashtra	40.	UAS 360	Karnataka
17.	WH1181	Haryana	41.	GW 463	Gujarat
18.	WH 1124	Haryana	42.	K 1312	Uttar Pradesh
19.	PBW-725	Punjab	43.	WH 1179	Haryana
20.	DBW-173	Haryana	44.	PBW 709	Punjab
21.	GW-477	Gujarat	45.	PBW 718	Punjab
22.	NW-6046	Uttar Pradesh	46.	DBW 150	Haryana
23.	PBW-737	Punjab	47.	UP 2883	Uttarakhand
24.	IC 138852	-	48.	K 1313	Uttar Pradesh

Table.2 Analysis of variance for fifteen traits under late sowing condition

SN	Source	Replication [1]	Genotypes [2]	Error [3]
1	Days to 50% heading	25.08*	12.04**	6.46
2	Days to anthesis	21.34	15.29**	8.51
3	Days to maturity	14.25**	9.98**	0.87
4	Grain filling period	50.17**	21.70**	9.18
5	No. of productive tillers per plant	5.81**	3.91**	0.45
6	Plant height (cm)	94.16**	57.37**	15.14
7	Spike length (cm)	1.36*	1.12**	0.35
8	No. of spikelets per spike	0.71**	10.94**	2.77
9	No. of grains per spike	50.67	70.13**	16.8
10	1000-grain weight (g)	70.3	254.87**	29.69
11	Grain yield per plant (g)	1285.32**	62.70**	19.54
12	Biological yield per plant (g)	976.09*	3292.55**	310.82
13	Harvest index (%)	470.82**	41.73**	11.62
14	Flag leaf area (cm^2)	0.05**	0.01**	0
15	Chlorophyll content (CCI)	20.93	67.99**	14.62

*, ** Significant at 5 % and 1 % level of significance respectively.

Table.3 Estimates of genetic variability for 15 characters in wheat under late sowing condition

SN	Character	Mean	Range	GCV	PCV	h^2 (%)	Genetic advance	Genetic advance as per cent of mean (%)
1	Days to 50% heading	51.00 to 60.00	55.50	5.20	2.46	22.33	1.33	2.39
2	Days to anthesis	54.00 to 64.00	58.32	5.63	2.58	20.98	1.41	2.43
3	Days to maturity	91.00 to 99.00	93.26	2.12	1.87	77.65	3.16	3.39
4	Grain filling period	28.33 to 41.00	34.94	10.46	5.85	31.26	2.35	6.74
5	No. of productive tillers per plant	3.66 to 9.00	5.54	22.85	19.38	71.89	1.88	33.84
6	Plant height (cm)	62.30 to 84.80	75.62	7.15	4.96	48.18	5.36	7.09
7	Spike length (cm)	8.35 to 11.40	9.92	7.91	5.12	41.84	0.68	6.82
8	No. of spikelets per spike	13.00 to 22.00	16.78	13.97	9.83	49.56	2.39	14.25
9	No. of grains per spike	22.66 to 47.00	34.65	16.97	12.17	51.41	6.23	17.97
10	1000-grain weight (g)	26.08 to 66.88	45.90	22.29	18.87	71.65	15.10	32.90
11	Grain yield per plant (g)	9.26 to 34.70	19.26	30.24	19.67	42.39	5.09	26.40
12	Biological yield per plant (g)	103.33 to 243.33	156.38	23.10	20.16	76.18	56.68	36.24
13	Harvest index (%)	5.71 to 20.10	12.85	36.21	24.64	46.33	4.44	34.56
14	Flag leaf area (cm^2)	0.86 to 1.35	1.06	10.83	5.49	25.69	0.06	5.73
15	Chlorophyll content (CCI)	17.06 to 37.00	29.17	19.52	14.46	54.88	6.43	22.06

Heritability (h^2) in broad sense (%) and genetic advance as per cent over Mean

GVC alone is not sufficient for the determination of amount of heritable variation. Burton (1952) suggested that, GCV together with the heritability estimates would give the best picture of the extent of advance to be expected by selection. The heritability estimates ranged from 20.98 per cent (for anthesis days) to 77.65 per cent (for maturity days). The estimates of genetic advance as per cent over mean were found to vary from 2.39 per cent (for days to 50% heading) to 36.52 per cent (for Biological yield per plant). Under late sown condition, high magnitude of heritability have been reported for days to maturity followed by number of productive tillers per plant, 1000-grain weight, biological yield per plant. It was observed moderate for chlorophyll content, number of grains per spike, number of spikelets per spike, plant height, harvest index, grain yield per plant and spike length. Grain filling period, flag leaf area, days to 50% heading and days to anthesis had low estimates of heritability.

High estimates of heritability coupled with high to moderate genetic advance as per cent of mean was observed for biological yield per plant, number of productive tillers per plant, 1000-grain weight in late sown condition. This situation indicates that the genetic variances for this trait are probably owing to their high additive gene effects (Johnson *et al.,* 1955) and thus there is better scope for improvement of these traits through direct selection.

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