



Genetic Studies on Yield and Associate Characters in Wheat (*Triticum aestivum* L. em Thell)

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ABSTRACT: The present investigation was conducted on field experiment to estimate the analysis of variance for yield and yield contributing traits in wheat (*Triticum aestivum* L. em Thell) during rabi 2013-14 at agriculture research farm of B.R.D.P.G. College, Deoria (U.P.). The experimental materials of wheat germplasms were considered of 72 germplasm lines collected from wheat section, Department of Genetics and Plant Breeding, I. A.Sc., B.H.U, Varanasi (U.P.), India. The results of analysis of variance for augmented design of experiment involving 72 wheat germplasms in 9 blocks and 3 checks was done for each of the 14 characters, i.e. peduncle length, days to 50% flowering, plant height, number of effective tillers per plant, spikelets per spike, flag leaf area, length of spike, days to maturity, number of grains per spike, biological yield, harvest index, test weight and grain yield per plant. Blocks variations were highly significant except flag leaf area and test weight.

Key Words: Wheat (*Triticum aestivum* L.em Thell), Yield, Germplasm, Heritability, Genetic advance.

I. INTRODUCTION

Wheat is the world's largest famous energy rich 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 [1,2]. The ultimate goal of most of the breeding programmes is to increase the production per unit area in per unit time. Genetic improvement for quantitative traits depends upon the nature and amount of variability present in the genetic stock and the extent to which the desirable traits are heritable. Our mentioned genotype identified as statistically equal to best genotype for economic yield. The genotype showing very high mean performance for various characters may be utilized as donor for improving those characters in a component breeding approach. For effective selection of superior genotype in the germplasm lines, knowledge on genetically parameters such as variability, heritability and genetic advance is very much essential [3-8]. Keeping in this in view, the present investigation was undertaken to assess the genetic variability, heritability and genetic advance for yield and yield attributing traits in germplasm lines of rabi wheat.

II. MATERIALS AND METHODS

The experimental materials of wheat germplasm were considered of 72 germplasm lines collected from wheat section, Department of Genetics and Plant Breeding I. A. Sc. B.H.U. Varanasi, Uttar Pradesh. The field experiment under present investigation was conducted

during rabi 2013-14 at agriculture research farm of B.R.D.G.P.G. College Campus, Deoria (U.P.), India. The site of experiment is located at 26.5 degree north latitude, 83.79 degree east longitude and 68 meter (223 feet) above the sea level. The climate of district Deoria is semi-arid with hot summer and cold winter. The experiment with 72 genotype with 3 checks variety of wheat in augmented block design. A test genotype was present only one block while the three checks were replicated in all the 9 blocks. Each plot considered of two rows 2.5 meters length with spacing of 5 cm. within the rows and 25 cm. between the rows. The data on days to 50% flowering, flag leaf area, days to maturity, spike length, no. of effective tillers per plant, no. of spikelet's per spike, biological yield per plant, harvest index, grain yield per plant, grain yield per spike, peduncle length, 100-grain weight, plant height and no. of grains per spike were recorded and characters were analyzed to estimate genetic variability parameters. Genetic variability was measured and subjected to statistical analysis as suggested by Soni *et al* [9]. Heritability (Board Sense), genetic advance (GA) and genetic advance as a percent over mean (GAM) were worked by following the method suggested by Verma [10] and Wright [11].

III. RESULTS AND DISCUSSION

The Results of analysis of variance for augmented design of experiment involving 72 wheat germplasm in 9 blocks and 3 checks was done for each of the 14 characters.

The general mean for peduncle length was 36.02cm. The lowest and highest mean performance showed by Amad (31.41) and PBW65*2 (44.48), respectively. The top non-significant group for peduncle length comprised of fourteen entries. Out of which, top ten statistically at per genotypes were Amad (31.41), Meghdoot (31.78), spark (31.84), Trap (32.01), HUW-234 (32.55), HD-2329 (32.69), HD-2733 (32.86), MUS (32.70), NKT (32.89), Waxwing (32.94). None of the entry was found to be better than the best check, when compared by using the value of least significances between adjusted mean of genotype and check mean.

The days of 50% flowering ranged from 77.75 (Wbll1*2) to 90.91 (Attila*2) days with a general mean of 84.76 days. The non-significant group for days to 50% flowering comprised of 33 entries. Out of which, top ten flowered non-significantly earlier than the general mean, were Wbll1*2 (77.75), NKT (78.64), TRCH (78.89), HD-2967 (78.99), UP-2338 (78.99), Trap (79.08), Mesia (79.24), BORL-95 (79.55), PBW-502 (79.83) and HD-2733 (79.99). The top non-significant group for late 50% flowering was constituted only by the genotype, Attila*2 (90.91) which took significantly greater days for attaining 50% flowering than remaining entries. In an attempt to screen out better genotypes than the best check HD-2643 using adjusted mean of genotype and check. None of entries could surpass the best check.

The populations mean for plant height was 194.34 and plant height varied from 77.95 (Mesia) in case of 104.45 (Kalyansona). The non-significant group for plant height comprised of thirty five entries. Ten entries, Mesia (77.95), K-307 (78.18), LOK-1 (91.06), Amsel (91.68), Becar (91.68), Hoites (92.24) and PBW-343 (92.25). Showed significantly shorter stature than the general mean. But UP-2338, RAJ-2534, HAR-311, KBIRD, HUW-234, Halana, CBW-38 and Kukuna showed the shortest plant stature than the best check (HD-2643).

The number of tillers per plant had general mean of 8.237 with a range of 4.75 (Tukuru) to 12.77 (TRCH). The non-significant group for higher number of tillers per plant was constituted by Tukuru alone because it was statistically superior to other entries for this trait. Some other promising lines for higher tillers per plant through statistically inferior to the best entry were thirty four. Out of which, ten most promising lines were TRCH (12.77), Kachu (10.86), PASTOR (10.35), Francolin # 1 (10.33), Attila*2 (10.21), Spark (10.20) and Vardan (10.11). None of the genotype exhibited higher number of tillers per plant than the best check PBW-154 (8.204).

The number of spikelet's per spike had a general mean of 19.62 with a range of K-307 (14.58) to HUW-234 (24.13). Ten entries, namely, (24.13) HUW-234, (23.82) KBIRD, (23.29) Trap, (23.26) Mesia, (23.18) BAV-92*2, (22.95) PBW65*2, (22.92) HD-2733, (22.84) UP-262, (22.46) CNO-79 and (22.28) CROC-1

exhibited significantly higher number of spikelet's per spike has general mean. Only two genotypes, namely MUS and Wbll1*2 were possessed higher number of spikelet's per spike than the best check HD-2643.

The general mean for flag leaf area was 30.88 cm². The genotype, BORL-95 had lowest flag leaf area (21.22), while the highest flag leaf area (45.29) was recorded for PASTOR. The top non-significant group for greater flag leaf area comprised of thirty two genotypes. Out of thirty two, top ten genotypes in order of merit were, PASTOR (45.29), PVN (43.51), HD-3043 (43.16), UP-262 (41.04), BAV-92*2 (40.44), Raj-2534 (35.19), K-307 (38.46), Becard (35.92) and Amad (35.61).

The general mean of spike length varied from (9.73cm) BORL-95 to (15.51) PVN. Out of thirty five, top ten genotype in order of merit were BORL-95 (15.51), Tukuru (14.19), Vouda (14.19), HD_2985 (14.17), Amsel (14.06), UP-2425 (14.00), Amad (13.99), LOK-1 (13.83), HAR-311 (13.67), Sonalika (13.57) for spike length. None of the entry was able to constitute the non-significant group for the trait, where as a good number of thirty genotypes exhibited greater spike length than the best check (PBW-373) 12.79, when comparison was made by using the value of adjusted mean of genotype and check mean.

The days to maturity ranged from (99.46) Amsel to (114.91) PBW-343 day with a general mean of 107.02 days. The non-significantly earlier than the general mean, Amsel (99.46), Wbll1*2 (99.58), CROC-1 (100.08), Kukuna (100.08), Pfau (100.42), UP-2824 (100.92), PBW-220 (101.46), PIFED (101.46), Spark (101.91) and Francolin#1 (101.91). In an attempt to sort out better genotype than the best check. None of the entries were found to be better.

The general mean of grains per spike varied from 26.04 (Frncin) to 57.89 (HUW-234). The non-significant group for grain per spike comprised of thirty two entries. The top ten entries HUW-234 (57.89), PBW65*2 (56.89), Raj-1482 (53.83), K-7903 (53.01), KAVZ*2 (52.81), Francolin#1 (51.14), UP-2425 (49.01), Sonalika (48.76), Ganga Kaveri (48.70) and Meghdoot (47.70). only four genotypes, namely HD-2723, ROLFO-7, Amsel and NW-1076 were possessed higher number of grain per spike than the best check PBW-154.

The general mean for yield per spike 1.76 of which varied from 0.92 for NW-1014 to 2.92 for ROLFO-7. Thirty six entries each possessed significantly higher yield per spike than the general mean for this trait. The top ten significant group for higher yield per spike was comprised genotypes which were, ROLFO-7 (2.92), BAV-92 (2.80), KAVZ*2 (2.64), UP-2425 (2.53), HUW-234 (2.38), KBIRD (2.34), up-262 (2.32), Akuri (2.18) and Waxwing (2.17). In the attempt to screen out better genotypes than the best check PBW-373, only two genotypes, namely Kukuna and CROC-1 were found to be excellent genotypes for this trait.

Table 1: Analysis of variance of augmented design for fourteen characters of wheat germplasms.

S. No.	Characters	Source of variation		
		Blocks	Checks	Error
1	Peduncle length (cm)	4.778***	2.281**	0.302
2	Day to 50% flowering	22.635***	2.270	0.761
3	Plant height (cm)	23.220***	1.261	1.346
4	Number of effective tillers per plant	2.852***	0.315*	0.077
5	Spikelets per spike	6.832***	1.245*	0.288
6	Flag leaf area	25.752*	31.339*	8.589
7	Length of spike (cm)	1.383***	0.084	0.113
8	Days to maturity	19.317***	5.270**	0.728
9	Number of grains per spike (g)	36.858***	6.658*	1.541
10	Yield per spike (g)	0.412***	0.081**	0.012
11	Biological yield (g)	51.943***	8.506**	1.089
12	Harvest index (%)	6.815***	0.194	0.180
13	Test weight	10.216	30.776*	7.013
14	Grain yield per plant (g)	38.256***	4.399*	0.695

*Significant at 5% probability level, **Significant at 1% level of probability and ***Significant at 0.5% probability level, respectively.

The general mean for biological yield was 27.70g with a range of (16.09) CNO-79 to (43.73) TRCH. The number of entries exhibiting statistically higher mean performance for biological yield were thirty one. The top ten significant group for higher biological yield was constituted by TRCH (43.73), UP-2824(40.16), K-7903(37.71), Francolin#1(35.67), LOK-1(35.14) and PBW-343(32.88). Only eight genotypes, namely ankurkedar, Tukuru, PVN, Attila*2, Raj-1482, Vouda NW-1076, BAV-9, Amad were found suitable for higher biomass production than the best check HD-2643.

The grain yield per plant ranged from 4.73 (CNO-79) in case of 15.38 (TRCH) with a general mean of 9.32 (gm). Thirty three producing significantly higher grain yield per plant. The top ten significantly highly higher grain yield per plant was comprised genotypes which were, TRCH (15.38), Kachu (13.51), LOK-1 (12.49), HD-2967 (12.12), KAVZ*2 (12.10), Meghdoot (11.52), Ganga Kaveri (11.29), Francolin #1 (11.22), Amsel (11.16) and Becard (10.90), had significantly higher grain yield per plant than the general mean. In an attempt to screen out better genotypes than the best check HD-2643, only seventeen genotypes, namely HD-2985, K-65, Kalyansona, DBW-17, PBW-343, Raj-1482, Vouda, Halana, NW-1076, Kukuna, KINGBIRD#1, RROLFO-1, Wbll1*2, Spark, Vardan, Ankur Kedar and NW-1014 were found to be excellent genotypes for this trait.

The general mean for harvest index was 35.13% which varied from 28.28 (K-65) to 47.10 (Becard). Fourty seven entries, fourty seven entries each possessed significantly higher harvest index the general mean. Top ten significant group for higher harvest index was comprised genotype which were, Becard (47.10), HD-

2733 (42.15), BAV-92*2 (41.40), MUS (40.05), HD-2967 (39.63), HUW-234 (39.27) Tukuru (38.69), Kachu (38.67), Gaanga Kaveri (38.67) and PVN (38.04). Twelve genotypes were performed better than the best check PBW-373 namely Wbll1*2, Ankurkedar, LOK-1, HD-2985, Sonalika, Raj-1972, PASTOR, DBW-17, HD-2329, Halana, Hoites and ROLFO-7.

The general mean for test weight was 35.01(g) and the test weight varied from 26.45g in case of K-65 to 46.10g for HD-2967. Fourteen entries viz., HD-2967 (41.10), Tukuru (44.75), HD-2985 (42.20), LOK-1 (41.07), UP-2425 (40.67), HD-2723 (40.57), DABV (40.51), Anpurna (40.49), UP-2824 (40.37) and NKT (40.10). had top ten significantly higher test weight than the general mean. Only fifteen genotypes, namely Wbll1*2, KAVZ*2, K-7903, NW-1014, Sonalika, BAV-92*2, Kalyansona, Ganga Kaveri, PBW-220, Becard and ROLFO-7 could excel for higher test weight than the best check PBW-373.

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