ISSN PRINT 2319 1775 Online 2320 7876

 UGC CARE Listed (Group -I) Journal Volume 11, Iss 06, 2022

Genetic Variability AND Trait Association Studies FOR Grain Yield AND Its Component Traits IN Wheat (*Triticum AESTIVUM* L.)

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Abstract

The study was conducted at research farm of FASAI, Rama University, Mandhana, Kanpur-209217 during Rabi 2021-22. It focused on the inheritance of grain yield and its components in 90 varieties of bread wheat, 45 indigenous and 45 exotics. The experiment used an Augmented Block Design and revealed a high degree of variability in all characters in both indigenous and exotic wheat lines. High to moderate estimates of broad sense heritability were recorded for various factors, including tillers per plant, days to maturity, spikelets per spike, harvest index, test weight, days to 50% flowering, grains per spike, and peduncle length. High estimates of genetic advance were also recorded for harvest index, days to maturity, tillers per plant, and plant height.

Kew Words: Bread Wheat, Grain yield, Heritability, GCV, PCV, Harvest Index

Introduction:

The normal bread Wheat (Triticum aestivum L.) is the main read wheat crop in India and stands just second biggest maker of wheat on the world after china. It is the biggest staple food yield of around two billion individuals (36% of the total populace) and a significant product on the world grain trade. Around the world, wheat gives almost 55% of the carbs and 20% of the food calories ate universally (Breiman and Graur, 1995). Sakamura revealed the chromosome number sets (genomes) for each normally perceived type. He isolated wheat into three gatherings viz. diploids (2n=14), tetraploids (2n=28) and hexaploids (2n=42) chromosomes. Major developed types of wheat include: Triticum aestivum, which is a hexaploid animal categories and is generally developed on the planet; Triticum durum, the just tetraploid type of wheat broadly utilized today, and the second most generally developed wheat; Triticum monococcum, a diploid animal types with wild and developed variations;

ISSN PRINT 2319 1775 Online 2320 7876

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Triticum dicoccum, a tetraploid animal category. These earliest developed structures were diploid (genome AA) (einkorn) and tetraploid (genome AABB) (emmer) wheats and their hereditary connections show that they began from the south-eastern piece of Turkey (Heun et al., 1997; Nesbitt, 1998; Dubcovsky and Dvorak, 2007).

Material and Method:

The experiment was directed to assess 90 (45 native and 45 Outlandish) germplasm lines with four checks (Specifically WR-544, HD-3086, HD-2967 and Hello 1544) in Expanded Block Plan at Principal of FASAI, Rama College, Mandhana, Kanpur-209217 during Rabi 2021-22. The exploratory field was separated into 6 blocks and 19 plots in each block (15 test genotypes alongside 4 checks) were obliged. Each plot comprises two lines of 2.5 m with dispersing of 5 cm inside the columns

Statistical analysis

The descriptive statistics including mean, range, coefficient of variability, Heritability and Genetic Advance were calculated using SPSS, Python and R language.

Estimation of coefficient of variability

The genotypic coefficient of fluctuation (GCV), phenotypic coefficient of changeability (PCV) was processed based on equation proposed by the Burton and de Vane (1953). spike length, number of spikelet per spike, number of grain per spike, test weight/1000-grain weight, grain yield per plant, organic yield per plant and gather file from each plot (With the exception of days to half blossoming and days to development where information was recorded on plot premise.) separately. Prescribed social practices were applied to raise a decent typical yield. The phenotypic and genotypic coefficients of variety which measure the size of phenotypic and genotypic

Heritability

Heritability in broad sense h^2 (b) was calculated as a ratio of genotypic variance to phenotypic variance (Robinson and Comstock 1949).

Result and Discussion:

Heritability, coefficient of changeability and hereditary development in percent of mean were assessed for every one of the 12 characters and are introduced in Table 1. High gauges of wide sense heritability (> 80%) were recorded for turners per plant (97.12%) trailed by days to development (94.81%), spikelets per spike (92.87%), reap file (92.11%), test weight (91.22%), days to half blooming (90.56%), grains per spikes (86.35%) and for the peduncle length (82.23%). The moderate appraisals of heritability (60-80%) were noticed for natural yield per plant (73.51%), grain yield per plant (71.30%) and plant level (66.63%). while the

ISSN PRINT 2319 1775 Online 2320 7876

 UGC CARE Listed (Group -I) Journal Volume 11, Iss 06, 2022

low gauges of expansive sense heritability (< 60%) were shown by spike length (56.37%). Present viewing as adjusted to those of Ali et al., (2008), Chaudhary et al., (2015), Deoraj et al., (2016) and Shashikala et al., (2012). The high gauges of hereditary development in percent of mean (>20%) were recorded for reap list (48.26%), days to development (40.972%), turners per plant (36.68%) and plant level (22.63%). Number of grains per spike (19.92%), days to half blooming (19.54%), grain yield per plant (14.87) and natural yield per plant (14.79%) showed moderate gauge for hereditary development (10-20%) in percent of mean. While the test weight (9.54%), spike length (5.48%) and plant level (4.98%), showed low gauge of (< 10%) hereditary development in percent of mean. These discoveries are affirmed with Deoraj et al., (2016) and Kabir et al., (2015) The phenotypic and genotypic coefficient of variety for every one of the 12 characters has been given in Table 1. By and large, the greatness of phenotypic coefficient of variety was higher than genotypic coefficient of variety for every one of the characters. The characters which showed higher appraisals (> 20%) of PCV and GCV were, collect record and days to development. The characters which displayed moderate assessments 10 - 20% of PCV and GCV were turners per plant, plant level, grains each spike days to half blooming and grain yield per plant. The leftover characters viz., organic yield per plant, spikelets per spike, peduncle length, and test weight showed low gauges (< 10%) of PCV and GCV. Present finding are in affirmation with Degewione et al., (2013), Maurya et al., (2014) and Yadav et al., (2014).

In conclusion, studies on variability, heritability and genetic advance showed that tillers per plant followed by days to maturity, spikelets per spike, harvest index, test weight, days to 50% flowering, grains per spikes and for the peduncle length are having considerable importance to breeder for selection. Because of this additive variability, selection for these characters would be highly sensitive, and a superior genotype could be produced as the environment had the least impact on the speech of these characters.

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 UGC CARE Listed (Group -I) Journal Volume 11, Iss 06, 2022

Table 1. Estimation of heritability, genetic advance and coefficient of variability in wheat

Characters	Heritability broad sense (%)	GCV (%)	PCV (%)	Genetic Advance	GA as % means
DAYS TO 50% FLOWERING	90.563	9.971	10.478	11.161	19.548
No. SPIKELETS/SPIKE	92.874	6.170	6.402	8.904	12.249
No. GRAINS/SPIKE	86.352	10.408	11.200	4.231	19.924
PLANT HIEGHT (CM)	66.636	13.461	16.490	2.354	22.636
SPIKE LENGTH (CM)	56.375	8.843	16.571	1.852	5.482
PEDUNCLE LENGTH (CM)	82.231	2.599	2.790	5.944	4.988
TILLERS /PLANT	97.121	18.071	18.337	20.097	36.687
DAYS TO MATURITY	94.813	20.426	20.978	12.943	40.972
BIOLOGICAL YIELD/PLANT (g)	73.510	8.379	9.773	6.539	14.799
HARVEST INDEX (%)	92.110	24.410	25.434	6.768	48.260
TEST WEIGHT (g)	91.220	4.680	8.320	1.230	9.540
GRAIN YIELD/PLANT (g)	71.301	8.550	10.126	3.213	14.872