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ESTIMATION OF GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN BREAD WHEAT (*Triticum aestivum* L.) GERMPLASM

Arpita Singh Tomar^{1*}, Gideon Synrem¹ and Sharad Pandey²

¹School of Agriculture, Forestry and Fisheries, Jigya University, Dehradun – 248197, Uttarakhand, India

²School of Agriculture, Uttaranchal University, Dehradun – 248007, Uttarakhand, India

*Corresponding author E-mail: arpitatomar.tomar@gmail.com

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ABSTRACT

A field experiment was conducted with Seventy-five germplasm of wheat (*Triticum aestivum* L.) along with five checks (HD 2851, HD 3086, RAJ 3765, DBW-187, PBW 343) grown in Augmented Complete Block Design having five blocks with 20 entries in each block (15 different wheat germplasm and 5 checks) during Rabi season 2022-2023 at the Crop Research Centre Field of School of Agriculture, Forestry and Fisheries, Jigya University Dehradun, India. The objective of the study was to assess the genetic variability and correlation in wheat through the study of fifteen quantitative characters viz Days to emergence, Days to 50% booting, Days to 50% Heading, Days to 50% flowering, Days to 50 % maturity, Grain filling days, Number of productive tillers per plant, Plant height, Peduncle length, Awn length, Spike length per plant, Spike weight per plant, Number of grains per spike, 1000 seeds weight and Seed yield per plant. The statistical analysis was performed by using the analysis of Augmented Randomized Complete block design R package version 0.1.7 of Aravind, J. Mukesh Shankar, S., Wankhede, D.P. and Kaur V. (2023) and using indostat 9.2 version. High genotypic coefficient of variation was noticed for the characters awn length (23.63 %), Spike weight (22.42 %) and Plant Height (23.32 %). The high heritability in percent coupled with high genetic advance as percentage of mean was recorded by Grain filling days (98.29, 27.36), Number of productive tillers (83.53, 33.98), Plant Height (99.50, 47.99), Peduncle length (91.61, 35.7), Awn length (96.78, 47.97), Spike length (90.66, 28.75), Spike weight (92.09, 44.39), Number of grains per spike (77.38, 35.54), 1000 seed weight (89.74, 26.71) and Seed yield per plant. (93.86, 31.92). The characters 1000 seed weight (0.92), Number of grains per spike (0.55), Spike weight (0.37), peduncle length (0.37), plant height (0.38) and number of productive tillers (0.26), showed high significant positive correlation with seed yield per plant. The path analysis estimates reveal the characters 1000 seed weight (0.92), spike weight (0.11), peduncle length (0.05), plant height (0.05), grain filling number of days (0.08), number of 50 % heading (0.22), number of 50 % booting (0.02) and number of days to emergence (0.05) showed positive direct effects on seed yield per plant.

Keywords : Wheat, *Triticum aestivum* L., Genotypic correlation, Path analysis, quantitative characters.

Introduction

Annual cereal crop wheat (*Triticum aestivum* L.) is part of the Gramineae (Poaceae) family. Six sets of chromosomes allow self-pollination. It contains AABBDD genome and 42 chromosomes ($2n = 6x$). It is one of the most widely produced crops and feeds many people. Wheat is vital because it keeps food and nutrition safe and can grow in temperate to subtropical

settings. The development of hexaploid wheat is fascinating (Meena, 2021). Tetraploid wheat (*Triticum turgidum*, AABB) and diploid goat grass (*Aegilops tauschii*, DD) naturally crossed. Allopolyploidization developed a genetically stable hexaploid species with higher genetic variety, adaptability and environmental tolerance. One wheat variety has three genomes, thus it changes a much. This crop is essential for plant geneticists and breeders worldwide (Singh, 2023). Due

to its genetic richness, hexaploid wheat can thrive in many regions and withstand many biotic and abiotic challenges. Wheat genetic variety is the amount of variation that may be passed forward. This helps improve genetics over time. A large genetic basis ensures yield, quality, stress tolerance and adaptation alleles. Genetic diversity is crucial in wheat breeding. This is because genetically homogeneous plants are more susceptible to disease, pests and weather damage (Thapa, 2019). Germplasm collections like landraces, wild cousins and advanced breeding lines provide useful genes for productivity and resilience. Without significant genetic variety, breeding progress slows and genetic advancements are difficult.

Economically significant features' genetic variation determines wheat improvement programs' effectiveness. Selectivity depends on genetic diversity, which breeders can evaluate to anticipate its efficacy. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are typical measures of genetic and phenotypic variance (Geneti, 2022). GCV and PCV that are similar indicate that the environment doesn't affect attributes. Phenotypic selection would work. If these statistics are extremely different, the environment has a huge impact, therefore be careful when choosing solutions. Heritability estimates, especially in a wide context, show how much genetic variation affects phenotype. Heritability alone does not explain selection response. You should look at heritability and genetic progress to assess breeding (Anubhav, 2020). Genetic progress shows how much selection intensity improves a characteristic. This illustrates how selection improves genetics. High heritability and genetic progress typically indicate gene addition is the most prevalent gene activity. So selection would work fine. Based on phenotype, these features are straightforward to pick and enhance fast over generations. However, high heritability and little genetic progress may indicate that gene effects, like as dominance and epistasis, are not additive, making selection less effective (Ahmad, 2018). Thus, heritability and genetic advancement can anticipate genetic improvement and create appropriate wheat improvement breeding strategies. Wheat yield relies on numerous factors, including how many tillers each plant has, how long the spike is, how many grains are on each spike, how much biomass is created and how much a thousand grains weigh. To increase yields, you must understand how and how strongly these attributes are related. Correlation analysis reveals the amount and direction of the genotypic and phenotypic yield-trait association.

Genotypic correlations show inherent genetic relationships, whereas phenotypic correlations show genetic and environmental impacts. Yield and its parts are positively correlated. Selection can develop these qualities simultaneously. Correlation doesn't tell us if a characteristic affects yield directly or through other traits (Rajput, 2019).

Path coefficient analysis extends correlation analysis to avoid this issue. Path analysis divides correlation coefficients into direct and indirect effects. That makes it easy to identify how characteristics link. This study identifies features that affect grain yield the most and should be prioritized in selection programs. Strong favourable direct impacts and yield linkages are the strongest plant selection features. However, traits that are closely related to yield but don't directly affect it may indirectly affect it. Be cautious while interpreting these features. Path analysis has helped wheat breeders improve selection indices by emphasizing on features that increase yield genetically. To start an effective wheat breeding program, use statistical methods to analyze genetic variability (Bita, 2013). GCV, PCV, heritability, genetic progress, correlation, path coefficients. These measures indicate how characteristics are inherited, interact and respond to selection. Breeders can improve selection tactics to maximize genetic gain and reduce environmental noise by integrating variability analysis and association research. This strategy is crucial when the climate is changing because breeding goals must balance plant stability, stress resistance and yield. In areas with rising temperatures and heat waves, heat stress makes wheat production difficult. This is one of several non-living items that harm wheat productivity. Heat stress can harm wheat's growth, development and yield when it flowers or fills grains. Wheat yields decline 6% each 1°C temperature rise (Naghavi, 2014). It indicates how severe the issue is. Photosynthesis, respiration and assimilate partitioning are disrupted by higher temperatures. Grain size and food quantity decrease. Wheat failure increases when heat stress and other factors, including drought, occur together. Wheat plants have altered structure and function to cope with heat stress (Singh, 2022). Maintaining cell safety and metabolic function under high temperatures requires molecular-level heat shock protein (HSP) production. These molecular chaperones assist misshaped proteins fold and refold. This prevents permanent cell damage. Genetic changes in wheat germplasm improve heat tolerance. This lets you breed heat-tolerant plants. To choose genotypes that thrive in hot temperatures, you must examine genetic characteristics, correlations and path coefficients under normal and stress conditions. For long-term genetic gain in a changing environment,

high-yielding wheat backgrounds need heat tolerance genetic diversity. Selecting for yield in ideal conditions may not ensure stress-resistant performance (Khan, 2012). In heat stress situations, correlation and route analysis can identify features like early maturity, biomass partitioning and grain filling time that improve yield stability. Breeders may enhance wheat improvement projects by using variability analysis and advanced selection strategies to create high-yielding, climate-resistant cultivars (Ramesh, 2016).

Material and Methods

The experimental material consisting 80 diverse wheat cultivars, grown in an Augmented Block Design including five checks during 2023-24 at the Research Farm, Department of Genetics and Plant Breeding, Jigyasa University, Dehradun. The observations were recorded on various quantitative characters viz. Days to emergence, Days 50 % booting, Days 50 % heading, Days to 50 % flowering, Days to 50 % maturity, Grain filling days, Number of productive tillers, Plant Height, Peduncle length, Awn length, Spike length, Spike

weight, Number of grains per spike, 1000 seed weight, Seed yield per plant. Five randomly selected competitive plants in each plot were screened to be recorded for all the characters under study except of days to 50 per cent flowering and days to maturity which were recorded on plot basis. The mean performance of individual genotypes was embayed for statistical analysis. Analysis of variance to test the significance for each character was carried out as per methodology given by Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton and Vane (1953) and genetic advance given by Johnson *et al.* (1955). The correlation was computed using the methodology described by Al-jibouri *et al.* (1958). The statistical technique provided by Wright (1921, 1960) and developed by Dewey and Lu (1959) was used to evaluate the direct and indirect contribution of numerous factors to grain yield determined by path coefficient analysis.

Table 1 : Table of the details of the experiment in Augmented Block Design of 80 wheat germplasm with 5 check varieties for the study of 14 quantitative characters of wheat.

Design used	Augmented Block Design
Total No. of genotypes	80
No. of checks	05
Name of checks	DBW 187, PBW 343, HD 3086, HD 2851, RAJ 3765
Date of Sowing	16 December 2023 (LATE SOWN)
Location	Crop Research center, Jigyasa University
Gross Area	1702.4 m ²
Length	121 .6m
Breadth	14m
Spacing	Row to row was 23cm Plant to plant Was 10 cm
Recommended NPK Urea, DAP, MOP	120:60:40 Urea 1.196 kg (applied in 3 split doses) during sowing, first irrigation, before flowering respectively. DAP- 2.698 kg during sowing. MOP- 1.333 kg during sowing.

Results and Discussion

Genetic variability

The Table 2 and Fig 1, 2 and 3 presents estimates of genetic variability parameters for seed yield and its contributing traits in bread wheat (*Triticum aestivum* L.), including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), heritability (broad sense), genetic advance (GA) and genetic advance as percent of mean (GAM). Overall, PCV values were slightly higher than GCV for all traits, indicating that although environmental factors influenced trait expression, the magnitude of difference was generally small, suggesting a strong genetic

control. High GCV and PCV were recorded for plant height, awn length, spike weight, number of productive tillers, number of grains per spike, peduncle length and seed yield per plant, reflecting the presence of substantial genetic variability among the genotypes for these traits and offering good scope for selection. Heritability estimates were high for most traits, ranging from 77.38% (number of grains per spike) to 99.50% (plant height). High heritability coupled with high genetic advance as percent of mean (GAM) was observed for plant height, awn length, spike weight, number of productive tillers, peduncle length, number of grains per spike and seed yield per plant. This combination indicates the predominance of additive gene action, suggesting that improvement through

simple phenotypic selection would be effective for these traits. Moderate to high heritability with moderate GAM was observed for grain filling days and 1000-seed weight, indicating that both genetic and environmental factors play a role, but selection would still be rewarding. In contrast, phenological traits such as days to 50% booting, heading, flowering and maturity showed high heritability but low genetic advance and GAM, suggesting the influence of non-additive gene action and a limited response to direct selection. In summary, the variability analysis indicates that traits like plant height, number of productive tillers, spike weight, number of grains per spike, 1000-seed weight and seed yield per plant are promising targets for selection in bread wheat improvement programs due to their high genetic variability and expected genetic gain.

Phenotypical Correlation Matrix

The phenotypical correlation matrix results is shown in Table 3 revealed the nature and magnitude of associations among yield and yield-contributing traits in bread wheat, reflecting the combined influence of genetic and environmental factors. Seed yield per plant showed a strong and positive correlation with 1000-seed weight (0.9258), number of grains per spike (0.5595), spike weight (0.3731), plant height (0.3833) and peduncle length (0.3793), indicating that these traits are closely associated with higher productivity. In contrast, seed yield per plant exhibited negative correlations with most phenological traits such as days to emergence, days to 50% booting, heading, flowering and maturity, suggesting that early growth and maturity favor better yield performance. Positive inter-correlations among plant height, peduncle length, spike weight and number of grains per spike further highlight the coordinated contribution of these traits toward yield improvement, although correlation alone does not clarify whether these effects are direct or indirect. Same observation was recorded by Ahmad (2018), Leilah (2005), Jaisi (2021).

Path Matrix of Seed Yield per Plant

Path coefficient analysis results is shown in Table 4 and it provided a clearer understanding of the direct and indirect contributions of different traits to seed yield per plant. Among all traits, 1000-seed weight exerted the highest positive direct effect (0.9260), followed by number of grains per spike (0.5166), plant height (0.3171), peduncle length (0.3075) and spike weight (0.3058), confirming their primary role in yield determination. Several traits influenced seed yield indirectly through these major components, particularly via 1000-seed weight and number of grains

per spike. Phenological traits showed negligible or negative direct effects, indicating limited usefulness as direct selection criteria for yield improvement. The high coefficient of determination ($R^2 = 0.8896$) demonstrated that the majority of variation in seed yield per plant was explained by the studied traits, while the low residual effect (0.3323) suggested minimal influence of unaccounted factors, validating the reliability of the path model for selection in wheat breeding programs. The same observation recorded by Fellahi, (2018), Verma (2023), Okuyama (2024)

Phenotypical Path Diagram for Seed Yield per Plant

The phenotypical path diagram shown in Figure 4 illustrates the direct and indirect relationships among different yield and yield-contributing traits and their influence on seed yield per plant in bread wheat (*Triticum aestivum* L.). In the diagram, single-headed arrows represent direct effects, while curved double-headed arrows depict phenotypical correlations among the independent traits. The magnitude and direction of each effect are indicated by the numerical values associated with the arrows, providing a comprehensive view of how individual traits contribute to seed yield. Among all characters, 1000-seed weight exhibited the highest positive direct effect on seed yield per plant, indicating that grain weight is the most influential component determining yield. This strong direct contribution explains its high positive correlation with seed yield observed in the correlation analysis. Number of grains per spike also showed a substantial positive direct effect, emphasizing the importance of sink size in yield formation. Traits such as plant height, peduncle length and spike weight exerted moderate but positive direct effects on seed yield, suggesting that robust plant architecture and better spike development enhance yield potential both directly and indirectly. Several traits contributed to seed yield mainly through indirect effects. For instance, plant height and peduncle length influenced yield indirectly via their strong positive associations with spike weight, number of grains per spike and 1000-seed weight. Conversely, phenological traits such as days to emergence, days to 50% booting, heading, flowering and maturity showed either negligible or negative direct effects on seed yield and their indirect effects through other traits were also generally unfavorable. This indicates that delayed phenological development may reduce yield efficiency under the studied conditions. The residual effect (0.332) depicted in the diagram indicates that most of the variation in seed yield per plant was adequately explained by the traits included in the analysis. Overall, the phenotypical path diagram clearly

demonstrates that selection focused on 1000-seed weight, number of grains per spike, spike weight, plant height and peduncle length would be most effective for

improving seed yield in bread wheat germplasm. Such result were also recorded by Singh (2021), Singh (1959).

Table 2 : Table of the Genetic parameters Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Environmental Coefficient of Variation, Broad sense heritability Genetic Advance and Genetic Advance as percent of Mean for 14 quantitative characters of wheat

Trait	GCV	PCV	ECV	Broad sense heritability	Genetic advance	GAM %
Days to 50% emergence	9.98	10.57	3.48	89.14	1.37	19.44
Days 50 % booting	3.11	3.18	0.64	95.93	6.12	6.29
Days 50 % heading	2.66	2.72	0.56	95.72	5.53	5.38
Days to 50 % flowering	2.84	2.87	0.47	97.31	6.54	5.77
Days to 50 % maturity	1.77	1.86	0.55	91.05	5.16	3.49
Grain filling days	13.38	13.49	1.77	98.29	8.97	27.36
Number of productive tillers	18.02	19.72	8.00	83.53	1.24	33.98
Plant Height	23.32	23.38	1.65	99.50	28.25	47.99
Peduncle length	18.11	18.92	5.48	91.61	3.07	35.76
Awn length	23.63	24.02	4.31	96.78	3.27	47.97
Spike length	14.64	15.37	4.70	90.66	2.27	28.75
Spike weight	22.42	23.36	6.57	92.09	4.17	44.39
Number of grains per spike	19.58	22.26	10.59	77.38	14.65	35.54
1000 seed weight	13.67	14.43	4.62	89.74	10.09	26.71
Seed yield per plant	15.97	16.49	4.09	93.86	2.10	31.92

Table 3 : Phenotypical Correlation matrix for 14 quantitative characters in wheat

	Days to emergence	Days 50% booting	Days 50% heading	Days to 50% flowering	Days to 50% maturity	Grain filling days	Number of productive Tillers	Plant Height	Peduncle length	Awn length	Spike length	Spike weight	Number of grains per spike	1000 seed weight
Days to emergence	1.0000	0.2702	0.2601	0.2613	0.0674	-0.0671	-0.0282	-0.0936	-0.0628	-0.1349	-0.1785	-0.1761	-0.1970	-0.0788
Days 50 % booting	0.2702	1.0000	0.9525	0.8901	0.0460	-0.1393	-0.3651	-0.3145	-0.3517	0.0904	-0.1020	-0.4403	-0.4351	-0.1484
Days 50 % heading	0.2601	0.9525	1.0000	0.9168	0.0253	-0.1929	-0.4197	-0.3293	-0.3582	0.0727	-0.0361	-0.3533	-0.3900	-0.1412
Days to 50 % flowering	0.2613	0.8901	0.9168	1.0000	0.0476	-0.1485	-0.2684	-0.3182	-0.3088	0.1721	-0.0334	-0.3584	-0.4037	-0.1603
Days to 50 % maturity	0.0674	0.0460	0.0253	0.0476	1.0000	0.5956	0.0004	-0.3649	-0.0761	-0.0046	-0.0419	-0.3070	-0.3066	-0.2960
Grain filling days	-0.0671	-0.1393	-0.1929	-0.1485	0.5956	1.0000	0.2273	-0.2819	-0.0745	0.0003	-0.1599	-0.2395	-0.1458	-0.2374
Number of productive tillers	-0.0282	-0.3651	-0.4197	-0.2684	0.0004	0.2273	1.0000	0.1944	0.2562	-0.0216	-0.0375	0.2498	0.4157	0.3293
Plant Height	-0.0936	-0.3145	-0.3293	-0.3182	-0.3649	-0.2819	0.1944	1.0000	0.7585	0.0594	0.0965	0.5447	0.6350	0.3425
Peduncle length	-0.0628	-0.3517	-0.3582	-0.3088	-0.0761	-0.0745	0.2562	0.7585	1.0000	0.0026	0.1115	0.4696	0.6067	0.3320
Awn length	-0.1349	0.0904	0.0727	0.1721	-0.0046	0.0003	-0.0216	0.0594	0.0026	1.0000	-0.0262	-0.1809	-0.1347	0.0781
Spike length	-0.1785	-0.1020	-0.0361	-0.0334	-0.0419	-0.1599	-0.0375	0.0965	0.1115	-0.0262	1.0000	0.3935	0.2803	0.0880
Spike weight	-0.1761	-0.4403	-0.3533	-0.3584	-0.3070	-0.2395	0.2498	0.5447	0.4696	-0.1809	0.3935	1.0000	0.7544	0.3303
Number of grains per spike	-0.1970	-0.4351	-0.3900	-0.4037	-0.3066	-0.1458	0.4157	0.6350	0.6067	-0.1347	0.2803	0.7544	1.0000	0.5579
1000 seed weight	-0.0788	-0.1484	-0.1412	-0.1603	-0.2960	-0.2374	0.3293	0.3425	0.3320	0.0781	0.0880	0.3303	0.5579	1.0000
Seed yield per plant	-0.0159	-0.1471	-0.1375	-0.1929	-0.2606	-0.1880	0.2961	0.3833	0.3793	-0.0179	0.0528	0.3731	0.5595	0.9258

Table 4 : PATH matrix of Seed yield per plant

	Days to emergence	Days 50% booting	Days 50% heading	Days to 50% flowering	Days to 50% maturity	Grain filling days	Number of productive tillers	Plant Height	Peduncle length	Awn length	Spike length	Spike weight	Number of grains per spike	1000 seed weight
Days to emergence	0.0542	0.0147	0.0141	0.0142	0.0037	-0.0036	-0.0015	-0.0051	-0.0034	-0.0073	-0.0097	-0.0096	-0.0107	-0.0043
Days 50 % booting	0.0055	0.0204	0.0194	0.0182	0.0009	-0.0028	-0.0074	-0.0064	-0.0072	0.0018	-0.0021	-0.0090	-0.0089	-0.0030
Days 50 % heading	0.0588	0.2153	0.2260	0.2072	0.0057	-0.0436	-0.0948	-0.0744	-0.0810	0.0164	-0.0082	-0.0798	-0.0881	-0.0319
Days to 50 % flowering	-0.0574	-0.1955	-0.2014	-0.2197	-0.0105	0.0326	0.0590	0.0699	0.0678	-0.0378	0.0073	0.0787	0.0887	0.0352
Days to 50 % maturity	0.0000	0.0000	0.0000	0.0000	-0.0003	-0.0002	0.0000	0.0001	0.0000	0.0000	0.0000	0.0001	0.0001	0.0001
Grain filling days	-0.0054	-0.0113	-0.0156	-0.0120	0.0481	0.0808	0.0184	-0.0228	-0.0060	0.0000	-0.0129	-0.0194	-0.0118	-0.0192
Number of productive tillers	0.0002	0.0028	0.0032	0.0020	0.0000	-0.0017	-0.0076	-0.0015	-0.0019	0.0002	0.0003	-0.0019	-0.0032	-0.0025
Plant Height	-0.0052	-0.0175	-0.0184	-0.0177	-0.0204	-0.0157	0.0108	0.0558	0.0423	0.0033	0.0054	0.0304	0.0354	0.0191
Peduncle length	-0.0037	-0.0208	-0.0211	-0.0182	-0.0045	-0.0044	0.0151	0.0448	0.0590	0.0002	0.0066	0.0277	0.0358	0.0196

Awn length	0.0078	-0.0052	-0.0042	-0.0100	0.0003	0.0000	0.0013	-0.0034	-0.0002	-0.0579	0.0015	0.0105	0.0078	-0.0045
Spike length	0.0071	0.0041	0.0014	0.0013	0.0017	0.0064	0.0015	-0.0039	-0.0045	0.0011	-0.0400	-0.0157	-0.0112	-0.0035
Spike weight	-0.0198	-0.0496	-0.0398	-0.0403	-0.0346	-0.0270	0.0281	0.0613	0.0529	-0.0204	0.0443	0.1126	0.0849	0.0372
Number of grains per spike	0.0150	0.0330	0.0296	0.0306	0.0233	0.0111	-0.0316	-0.0482	-0.0461	0.0102	-0.0213	-0.0573	-0.0759	-0.0423
1000 seed weight	-0.0730	-0.1374	-0.1307	-0.1484	-0.2741	-0.2199	0.3049	0.3171	0.3075	0.0723	0.0815	0.3058	0.5166	0.9260
Seed yield per plant	-0.0159	-0.1471	-0.1375	-0.1929	-0.2606	-0.1880	0.2961	0.3833	0.3793	-0.0179	0.0528	0.3731	0.5595	0.9258
Partial R ²	-0.0009	-0.0030	-0.0311	0.0424	0.0001	-0.0152	-0.0022	0.0214	0.0224	0.0010	-0.0021	0.0420	-0.0425	0.8573

R SQUARE = 0.8896 RESIDUAL EFFECT = 0.3323

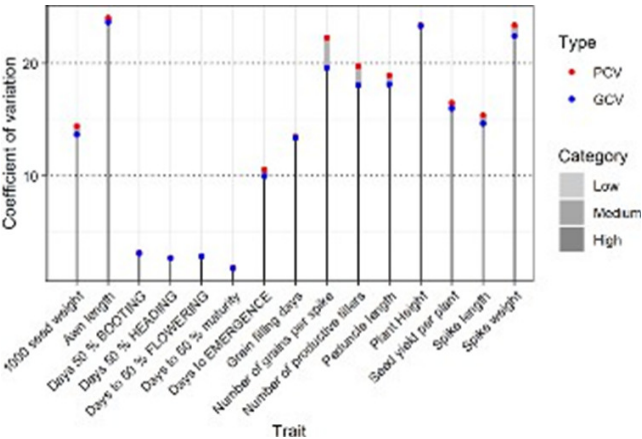


Fig. 1 : Graphical representation of GCV and PCV for 14 quantitative characters of wheat

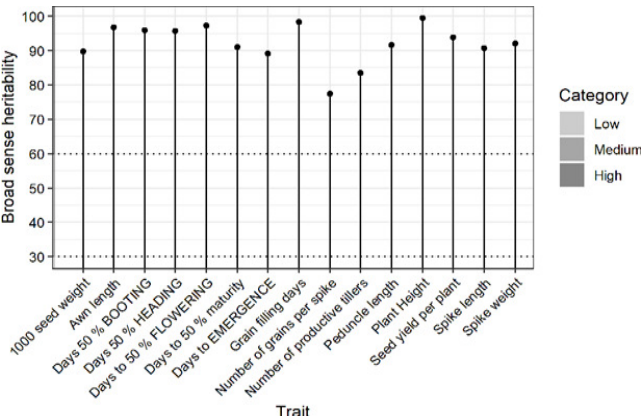


Fig. 2 : Graphical representation of Broad sense heritability for 14 quantitative characters of wheat

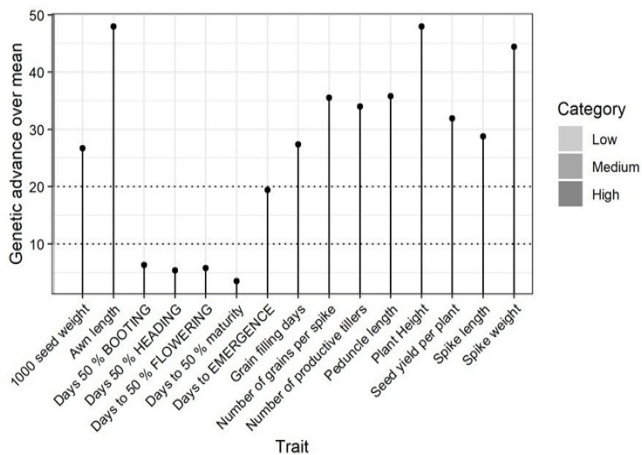


Fig. 3 : Graphical representation of Categorical Genetic advance over Mean for 14 quantitative characters of wheat

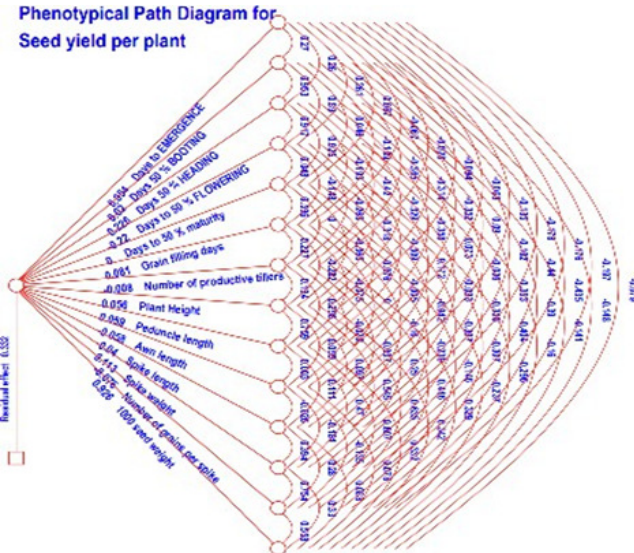


Fig. 4 : Graphical representation of Phenotypic path diagram for 14 quantitative characters of wheat

Conclusion

Selection-based genetic improvement is suggested by bread wheat (*Triticum aestivum* L.) seed production genotype heterogeneity and associated factors. Most features exhibited close genotypic- phenotypic coefficients of variation, indicating that heredity dominated and environmental influences had minimal effect. High heritability estimates and genetic progress as a percentage of the mean for plant height, productive tillers, peduncle length, awn length, spike weight, number of grains per spike, 1000-seed weight and seed output per plant suggested additive gene Direct phenotypic selection enhances them. Seed yield per plant increased with 1000-seed weight, spike weight, number of grains per spike, plant height and peduncle length. Most phenological characteristics negatively influence seed production, indicating an early development and maturity environment. Evaluation of how attributes influenced yield following correlation analysis required path coefficient analysis. Path studies showed that 1000 seed weight and grains per spike improved plant seed yield most. Plant height, peduncle length and spike weight followed. Features also aided indirect yield implications from other measures. The selected factors explained most seed

yield variability due to their high coefficient of determination and minimal residual influence. Reliable analytical models were shown.

Since phenology doesn't effect yield, direct selection criteria are useless. Genetic variability, correlation and route coefficient study revealed bread wheat yield factors. 1000-seed weight, grains per spike, spike weight, plant height and peduncle length boost seed yield genetics. Scientists produce stable, climate-adaptable, high-yielding wheat using genotype diversity. These findings can help scientists produce weather-independent wheat. Genetic heterogeneity in bread wheat (*Triticum aestivum* L.) seed production genotypes and related variables suggests selection-based genetic improvement. Close matches between genotypic and phenotypic coefficients of variation for most characteristics demonstrated that heredity dominated and environmental factors had little influence. High heritability estimates and genetic advancement as a percentage of the mean for plant height, productive tillers, peduncle length, awn length, spike weight, number of grains per spike, 1000-seed weight and seed production per plant indicated additive gene activity. This showed direct phenotypic selection improves them. The combination of 1000-seed weight, spike weight, number of grains per spike, plant height and peduncle length enhanced seed yield per plant. Most phenological parameters negatively affect seed production, demonstrating the present environment favours early development and maturity. Path coefficient analysis was needed to evaluate how characteristics affected yield after correlation analysis. Path research found that 1000 seed weight and grains per spike increased seed output per plant most. Plant height, peduncle length and spike weight followed. The features also helped indirect yield implications from other metrics. The chosen characteristics explained most seed yield variability due to their high coefficient of determination and low residual impact. Reliable analytical models were presented. Direct selection criteria aren't useful since phenological features don't affect yield. Genetic variability, correlation and route coefficient analysis made bread wheat yield variables clear. For seed yield genetic improvement, 1000-seed weight, grains per spike, spike weight, plant height and peduncle length work well. Genotype diversity allows scientists breed stable, climate-adaptable, high-yielding wheat. Scientists can breed weather-independent wheat using these results.

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