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Studies on genetic variability and traits associations in Wheat (*Triticum aestivum* L.) genotypes: A review

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Abstract

Wheat (*Triticum aestivum*) is India’s most important winter cereal crop, typically cultivated from November to mid-April. The varieties grown are predominantly spring-type bread wheat (*T. aestivum*). Genetic diversity is crucial in plant breeding, enabling the exploitation of heterosis and the development of high-performing recombinants. Selecting appropriate parents is vital for any breeding program, making it essential to understand the genetic diversity and relationships within the germplasm. A narrowed genetic base increases vulnerability to diseases and climatic stresses. Therefore, detailed insights into the extent and pattern of genetic diversity in wheat from major growing regions are key to identifying suitable parents for breeding superior cultivars. Utilizing diverse genotypes from existing germplasm is fundamental for the genetic improvement of wheat.

Keywords: *Triticum aestivum*, genetic variability, germplasm, varietal performance

Introduction

Wheat (*Triticum aestivum*) is India's most significant winter cereal crop, typically sown from November to mid-April. The varieties grown are mainly spring-type bread wheat (*T. aestivum*). Due to agro-ecological differences, wheat cultivation in India is divided into six zones. The Indo-Gangetic Plains, including the North Western (NWPZ) and North Eastern Plains Zones (NEPZ), represent the primary wheat-producing areas, followed by the Central (CZ), Peninsular (PZ), Northern Hill, and Southern Hill Zones. While the Northern Hill Zone still relies on traditional varieties maturing by May/June, the Southern Hill Zone accounts for only a small area under cultivation in tropical cold, humid climates.

Globally, wheat is grown across 215.48 million hectares, with a production of 670.87 million tons and an average yield of 31.17 q/ha. India’s wheat productivity has shown steady growth, reaching 3216 kg/ha as per Agricultural Statistics (2017-18). In 2017-18, India produced 97.11 million tonnes from 30.42 million hectares. Uttar Pradesh (UP) led production with 30.06 million tonnes, although its average yield (26.91 q/ha) was lower than Punjab (45.31 q/ha) and Haryana (40.66 q/ha). Together, UP, Madhya Pradesh, and Punjab contributed over 65% of India’s wheat output. National production peaked at a record 99.70 million tonnes in 2017-18, nearing the target of 100 MT. However, productivity still lags behind the potential.

With rising demand—expected to reach 100 million tonnes by 2030—and challenges from climate change, there is a pressing need to develop high-yielding, stress-tolerant wheat varieties. This requires leveraging the existing genetic diversity within the germplasm. Wheat is not only a dietary staple consumed as chapattis, puris, and dalia but also widely used in bakery products like bread, cookies, noodles, and pastries.

India’s food production success owes much to the introduction of high-yielding varieties, irrigation, fertilizers, and better agronomic practices. Yet, with a growing population and projected grain demand of 280 million tonnes (including 109 MT wheat) by 2020, enhancing wheat productivity remains crucial. Around 91% of national wheat output comes from six northern states, with Uttar Pradesh leading in area and production but falling behind Punjab and Haryana in yield.

Genetic diversity remains key to crop improvement. It enables the exploitation of heterosis and development of superior recombinants. Understanding genetic relationships in germplasm helps identify suitable parents for breeding. Loss of variability increases vulnerability to biotic and abiotic stresses. Therefore, careful selection and utilization of diverse genotypes is essential for sustainable wheat improvement.

Germplasm Evaluation and Genetic Variability

Genetic variability is the foundation of plant breeding, enabling the selection of superior genotypes for crop improvement (Simmonds, 1962). The total phenotypic variation observed in any trait is due to both genetic and environmental components, with the genotypic portion being heritable and critical for effective selection. Greater variability allows for more robust breeding strategies aimed at yield enhancement and stress tolerance.

Recent studies have documented substantial variability among wheat genotypes for key agronomic traits. Yogender found high genotypic and phenotypic coefficients of variation (GCV and PCV) for traits like number of grains per spike, tillers per meter, grain yield, harvest index, and 1000-grain weight, highlighting their importance in selection. Akanksha *et al.* (2017) observed significant genetic differences among genotypes, with moderate GCV and PCV for grain yield, biological yield, ear weight, and peduncle length. High heritability coupled with moderate genetic advance in traits like biological yield suggested additive gene effects and potential for effective selection.

Basavaraja reported high GCV, PCV, heritability, and genetic advance for traits such as productive tillers per plant, grain yield, spike length, spikelets per spike, and resistance to leaf rust, indicating strong selection potential. Rudra found wide variability in most traits except plant height, with traits like grain yield and sedimentation value exhibiting high heritability and genetic advance.

Kumar recorded significant variation across all studied traits. High GCV and genetic advance were reported for grain yield, harvest index, grains per spike, biological yield, and plant height. Verma *et al.* (2013) [26] also observed wide variability among 108 genotypes, with maximum variation in plant height and grain yield. Dhananjay *et al.* (2012) [29] noted moderate PCV and GCV for biological yield, harvest index, and grain yield, and high heritability for several yield-related traits, suggesting their utility in selection programs.

Tripathi identified high variability in harvest index, biological yield, productive tillers, test weight, and grain yield, indicating good scope for genetic improvement. Dharmendra and Singh reported high GCV, PCV, heritability, and genetic advance for grains per spike, plant height, and grain yield in 20 wheat genotypes, suggesting these traits as suitable for selection.

Singh evaluated exotic germplasm and found strong positive associations of grain yield with biological yield, tiller number, ear length, and plant height, emphasizing the usefulness of these traits in breeding. Kumar and Khosla also reported high GCV, heritability, and genetic advance for biological yield, grain yield, and grains per spike.

Lal recorded considerable variability for traits such as plant height, tillers per plant, grain yield, spike length, grains per spike, and 1000-grain weight. These findings confirm the presence of substantial genetic diversity in Indian wheat germplasm, which can be harnessed for developing high-yielding, stress-resilient varieties.

Heritability and Genetic Advance

Genetic variability forms the foundation for any crop improvement programme, as the efficiency of selection is largely determined by the extent and nature of this variability in the available genetic material. Traits with high heritability and genetic advance are especially crucial for guiding effective selection strategies in breeding.

Rathwa *et al.* (2018) [9] evaluated genetic variability in durum wheat under different sowing conditions for heat tolerance. They observed that phenotypic coefficients of variation (PCV) were only slightly higher than genotypic coefficients of variation (GCV), suggesting minimal environmental influence. High heritability coupled with high genetic advance was recorded for traits like grains per main spike, harvest index, and biological yield, particularly under D_0 condition. This implied predominance of additive gene action, favoring effective selection.

Neeru *et al.* (2017) [14] analyzed 60 wheat genotypes under timely and late sowing. Significant variability was found for all traits across both conditions. Traits such as grain yield per meter and effective tillers per meter exhibited moderate PCV and GCV with high heritability and genetic advance. Grain yield correlated positively with effective tillers, canopy temperature, and anthesis-related traits. Path analysis highlighted effective tillers per meter as a major contributor to yield under both sowing timings.

Arya *et al.* (2017) [18] assessed 49 wheat genotypes and found significant genetic variation in traits like grain yield, plant height, spike characteristics, and gluten content. Grain yield per plant had the highest PCV and GCV values, along with high heritability and genetic advance, indicating strong potential for selection.

Yadwad reported that GCV and PCV values were high for most traits except days to 50% flowering, spike length, and spikelets per spike. Traits like productive tillers, plant height, grain yield per plant, and 1000-grain weight showed high heritability and genetic advance, suggesting their suitability for selection.

Mehta observed significant differences among durum wheat genotypes for all studied traits. High GCV and PCV values were noted for grain yield per plant, spike length, and 1000-grain weight. High heritability coupled with high genetic advance for grain yield per plant indicated that this trait could be improved effectively through selection.

Wani reported significant variability across 50 wheat lines for yield and physiological traits. High PCV and GCV were found for seed vigor index and yield-related traits. Most traits positively correlated with grain yield at both phenotypic and genotypic levels. Traits showing high heritability and genetic advance, especially those with strong correlations to yield, were recommended for use in breeding programs.

Correlation Coefficient

Phenotypic correlation refers to the relationship between two traits based on observable character values. Such correlations, whether at phenotypic or genotypic levels, help breeders identify traits that can serve as reliable indicators for selecting complex traits like yield.

Singh *et al.* (2019) [8] conducted correlation and path coefficient analysis on 44 wheat genotypes and observed that grain yield per plant had a highly significant and positive correlation with biological yield and number of productive tillers per plant. Harvest index also showed a positive association with grain yield.

Ayer found that biological yield and harvest index had strong positive correlations with grain yield and exerted high direct effects, suggesting their importance for direct selection in yield improvement.

Shara *et al.* (2016) [20] reported significant negative association between grain yield and 1000-grain weight, while grain weight per spike had a strong positive correlation with spike length. A significant negative correlation was also observed between number of grains per spike and 1000-grain weight.

Bhutto *et al.* (2016) [21] noted that tillers per plant and grains per spike were strongly and positively associated, indicating these as key selection traits for yield improvement. Plant height showed positive correlations with spikelets per spike and grain number.

Dutamo evaluated 64 bread wheat genotypes and observed that grain yield was positively correlated with grain filling duration, spike characteristics, 1000-grain weight, biomass yield, and harvest index at both genotypic and phenotypic levels.

Parnaliya also reported stronger genotypic than phenotypic correlations. Grain yield was significantly associated with biological yield, productive tillers, grain filling period, and grains per main spike at both levels.

Rahman reported that grain yield per plant was positively associated with days to maturity. Yahaya observed positive correlations of grain yield with spike length, spikelets per spike, spike weight, and plant height.

Baloch indicated that yield was positively associated with tillers per plant, spike traits, seed index, and harvest index. Rajpoot found significant positive correlations between yield and number of tillers, seed per ear, and test weight.

Iftikhar observed that flag leaf area, spikelets per spike, grains per spike, and 1000-grain weight were significantly correlated with grain yield at both genotypic and phenotypic levels, while tillers per plant had a negative association.

Singh and Tiwari found that number of tillers and grains per spike were positively correlated with grain yield, whereas plant height and spike length showed negative associations.

Maqbool and Singh both reported positive associations of plant height and tiller number with yield. Ajmal found that grains per spike and 1000-grain weight were strongly linked to grain yield, though tillers had negative relationships with some yield traits.

Atta and Ali reported strong positive correlations of grain yield with productive tillers, spikelets, and spike length, emphasizing these as reliable selection traits.

Path Coefficient Analysis

While correlation analysis indicates the degree of association between traits, path coefficient analysis partitions these relationships into direct and indirect effects, offering more precise insights into which traits directly influence grain yield.

Ayer found that biological yield and harvest index had the highest direct positive effects on grain yield, suggesting their suitability as primary selection criteria. Similarly, Shara *et al.* (2016) [20] noted that 1000-grain weight had the most positive direct effect, while grain weight per spike had the highest negative direct effect on yield. Grain weight per spike and number of grains per spike contributed indirectly to yield via 1000-grain weight.

Dabi *et al.* (2016) [22] reported harvest index as the key trait with a strong positive direct effect, while plant height and number of spikelets per spike had smaller effects.

Parnaliya concluded that biological yield, harvest index, and grain weight per main spike showed high direct contributions to grain yield, with most traits contributing indirectly via biological yield.

Dutamo emphasized harvest index and biomass yield as key yield determinants with notable direct and indirect effects, although they recommended further multi-location trials for conclusive results.

Rahman observed that days to booting and days to maturity exerted positive direct effects on grain yield, highlighting them as promising traits for genotype selection. Kumar *et al.* (2014) reported high direct effects of harvest index and biological yield, with supporting positive correlations from traits like tillers per meter row and number of grains per spike.

Rajpoot indicated that ear length and test weight made the largest direct contributions to yield. Similarly, Degewione *et al.* (2013) [25] found days to heading, grain filling period, number of tillers, and grains per spike as major contributors to yield via direct effects.

Identified 1000-seed weight and plant height as traits with the strongest direct impact on grain yield, recommending their use in selection programs.

Tsegaye *et al.* (2012) [30] highlighted biological yield (0.679) and harvest index (0.48) as traits with substantial direct effects, reinforcing their value in improving durum wheat yield.

Noted that plant height, spike length, grains per spike, and 1000-grain weight had positive direct effects on yield, while traits like tillers per plant and flag leaf area showed negative direct effects. This suggests prioritizing spike-related traits for selection.

Found biological yield and days to maturity as direct contributors to yield, while traits like tillers per plant and 1000-grain weight contributed indirectly. Khokhar *et al.* (2010) also reported high direct positive effects, except for spike length, which had a negative direct effect.

Confirmed that productive tillers per plant and grains per spike had the strongest direct influence on grain yield and should be prioritized in selection. Cluster analysis in Ali *et al.*, 2008, study further categorized 70 genotypes into four distinct groups for selection.

Genetic Divergence

Genetic divergence analysis is essential in understanding the degree of genetic variability among genotypes and helps in identifying divergent parents for hybridization. This approach, based on Mahalanobis D^2 statistics (Mahalanobis, 1936; Rao, 1952), helps assess genetic relationships that may not correspond to geographic origins.

Shyam evaluated 22 wheat genotypes for 14 traits and grouped them into three clusters. The greatest inter-cluster divergence was observed between clusters I and III, indicating their suitability for hybridization to obtain wider variability and desirable recombinants.

Pandey *et al.* (2017) [13] assessed 84 genotypes and found maximum divergence between clusters VI and XII. Traits like peduncle length, grain yield, biological yield, and 1000-grain weight contributed most to the genetic divergence, with cluster X and VI showing high cluster means for key agronomic traits.

Kamble *et al.* (2017) [15] grouped genotypes into six clusters and reported the highest inter-cluster distance between clusters V and VI. Cluster III exhibited superior cluster means for grain yield and yield-contributing traits. Major contributors to diversity included plant height, protein content, and 1000-grain weight.

Arya *et al.* (2017) [18] observed wide genetic diversity between clusters VII and VIII. Grain yield per plant contributed most (31.46%) to total divergence, suggesting that crosses involving genotypes from these clusters could maximize heterosis and produce superior recombinants.

Rahman reported that days to anthesis, days to maturity, and grain yield per plant were key contributors to divergence among clusters. Maximum genetic distance was found between clusters

II and III.

Ali observed highest variability for traits like days to flowering, plant height, panicle length, and grain yield. Cluster V displayed the largest inter-cluster distance and highest trait values, indicating it could serve as a promising parent group.

Kumar studied 30 wheat lines and found highest genetic distance between clusters VII and III. Cluster VIII exhibited the greatest intra-cluster variability, suggesting high divergence within.

Dhakar grouped 25 genotypes into 7 clusters, with random distribution of genotypes from different origins. Genotypes from the same region often occurred in different clusters, suggesting that geographic origin did not always align with genetic diversity.

Toria used dendrogram clustering to group landraces into five major clusters. The results showed clear genetic variability and utility in cluster-based parent selection for breeding programs.

Soni analyzed 160 exotic and indigenous lines and grouped them into 7 clusters. No clear relationship was found between geographic origin and genetic divergence, and clusters I and VII were most distant.

Singh evaluated 305 genotypes using Euclidean cluster analysis and grouped them into 7 clusters. Members of cluster VII showed high grain yield and tiller numbers. Significant diversity was found between clusters III and VII, making them suitable candidates for crossing.

Conclusion

The evaluation of germplasm and genetic variability is indispensable for successful crop improvement programs, as it provides the fundamental basis for selection and breeding of superior genotypes. The reviewed literature highlights substantial genetic diversity in wheat for a range of yield-contributing and agronomic traits across diverse environments and genotypes. High genotypic and phenotypic coefficients of variation, coupled with significant heritability and genetic advance for key traits such as grain yield, biological yield, spike characteristics, and plant height, suggest that these attributes are governed predominantly by additive gene action and can be improved effectively through selection.

The strong correlations observed between yield and traits like biological yield, harvest index, and productive tillers underscore their utility as indirect selection indices. Moreover, path coefficient analyses reveal that biological yield and harvest index often exert the most direct positive effects on grain yield, offering clear targets for selection. Genetic divergence studies further support the existence of wide variability among genotypes, with several clusters identified as potential sources of heterotic crosses. These findings not only facilitate the identification of diverse parents for hybridization but also contribute to broadening the genetic base of cultivated wheat.

In conclusion, the integration of variability assessment, heritability estimates, correlation studies, and divergence analysis provides a comprehensive framework for identifying and utilizing elite wheat genotypes. This holistic approach paves the way for the development of high-yielding, resilient varieties capable of meeting future food security demands under changing climatic conditions.

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