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Genetic diversity and character association study for yield and its contributing traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops grown globally and plays a crucial role in food security and nutrition. An on-going increase in wheat productivity is essential to supply the food requirement of an expanding population in future climatic conditions. The yield of wheat is a polygenetic quantitative trait, which varies with many genetic and environmental factors and their interaction. Thus, wheat breeders must be aware of the genetic variation and linkage between yield contributing traits to develop high yielding wheat cultivars. The genetic variability is the raw material of selection and crop improvement and the correlation and path coefficient analysis are used by breeders to identify genetically correlated traits desirable for improving yield. Significant genetic differences have been found in several studies among bread wheat genotypes in several important agronomic characters including plant height, number of productive tillers, spike length, grains per spike, test weight, biological yield and harvest index. Many of these characters have been found to have high heritability and high genetic advance and hence are believed to be under additive gene action and direct selection will be effective. A positive and significant correlation was found between grain yield and productive tillers, biological yield, grains per spike, and harvest index in correlation studies. Path coefficient analysis also showed that these characters had a strong positive direct effect on grain yield and serve as a good selection criterion in breeding programmes. The use of modern molecular breeding tools, such as marker-assisted selection and quantitative trait loci (QTLs), has helped to speed up wheat improvement programs. Genetic diversity, variability parameters, association of characters, path analysis and molecular approaches are important for improving the yield and yield related traits of bread wheat and are highlighted in this review.

Keywords: Bread wheat, genetic variability, correlation, path analysis, heritability, genetic advance

1. Introduction

Wheat is one of the oldest and most widely grown cereal crops and the staple food for almost one-third of the world's population. In terms of cultivated wheat species, bread wheat (*Triticum aestivum* L.) is cultivated over the largest area, with its superior baking quality, high productivity, and adaptability. Wheat is an important crop in human nutrition and food security due to its rich nutritional and nutraceutical composition including carbohydrates, proteins, vitamins and minerals (Phougat *et al.*, 2017) [33]. India is the second largest producer of wheat next to China. Wheat production plays an important role in the agricultural economy and plays a strong livelihood support role for millions of farmers. But, due to growing population, climate change, soil degradation, and the prevalence of biotic and abiotic stresses have been tremendous challenges for wheat production. So, production of high yield and stress resistant, adaptable wheat varieties have become a prime goal of plant breeders (Roy *et al.*, 2021) [36]. Wheat yield is influenced by many genes and environmental factors and is a polygenetic trait. It is influenced by a number of component characters like number of tillers, length of the spikes, number of grains per spike, test weight, harvest index and biological yield. Selection for grain yield is sometimes difficult since it is lowly heritable and strongly influenced by environment. Thus information on the correlation between the various yield contributing traits is necessary for successful selection. The basis of any crop improvement program is genetic diversity (Nagar *et al.*, 2018; Phougat *et al.*, 2017) [28, 33]. There is variation between different plant genotypes which

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allows breeders to choose plants bearing desirable traits. Important statistical tools used to explain the nature and magnitude of relationships between the traits are correlation and path coefficient analyses. These analyses can be used to identify characters that will directly or indirectly affect grain yield and thus to help formulate efficient breeding strategies (Kumar *et al.*, 2021) ^[20]. More recently, molecular breeding techniques have contributed to increasing the accuracy and effectiveness of wheat improvement programmes. A number of molecular markers and quantitative trait loci for yield and stress tolerance traits have been successfully applied in marker-assisted breeding. So, combining traditional and molecular methods can greatly speed up the process of improving wheat production (Dutamo *et al.*, 2015) ^[11]. Thus, the present review work gives the information on the genetic diversity and character association for yield and its contributing traits in bread wheat.

2. Importance of Genetic Diversity in Wheat Improvement

Genetic diversity is the variation between individuals or genotype in a species. In the case of bread wheat, genetic diversity is an important factor in crop improvement since it serves as the source for selection and hybridisation. Satisfactory genetic variability in economically important traits, grain yield, plant height, tiller number, spike length, grains per spike, test weight and resistance to different biotic and abiotic stresses, are critical for successful plant breeding programs (Walli *et al.*, 2022) ^[45]. Wheat genotypes with high genetic variability have higher chances to produce superior plants with useful agronomic traits, which can be used in breeding programs to create high yielding and stress tolerant grain. Wheat breeding is carried out deliberately with genetically diverse parents to obtain hybrids which have a greater genetic variability and greater recombination in the segregating generations (Mir *et al.*, 2012) ^[25]. The crosses of genetically divergent parents yield more heterosis, larger segregation, and better transgressive segregants than the crosses of closely related parents do. The hybrid combinations are more likely to achieve the desired gene pairing which can enhance yield potential, adaptability and stress resistance. Thus, it is important to evaluate genetic diversity of available germplasm prior to effective selection for wheat improvement programs (Dutamo *et al.*, 2015) ^[11]. There have been several reports of high genetic diversity in bread wheat genotypes with respect to yield and its component traits. There is significant genotype to genotype variation, which suggests there are good opportunities for selecting and genetically improving. Highly diverse genotypes are important resources to breeders since they provide useful alleles that could be used to increase productivity and adaptability in varying environments (Nielsen *et al.*, 2014) ^[30]. Furthermore, the use of genetically diverse germplasm provides a wider genetic base of cultivated wheat, which helps to lower genetic susceptibility and increase wheat's resistance to emerging stresses such as drought, heat, salinity and diseases. Morphological, statistical and molecular methods are commonly used to assess the genetic diversity of wheat. Morphological characterization uses plant observable traits like plant height, spike length, days to flowering, and grain traits (Singh *et al.*, 2018) ^[38]. The size of the variability of the population is estimated by the statistical parameters phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). There are several multivariate approaches, such as cluster analysis, principal component analysis (PCA) and Mahalanobis D² statistics, that are widely used for genotype classification into various groups according to the genetic divergence. Of these techniques, Mahalanobis D² analysis is

regarded as one of the most reliable methods for measuring genetic divergence since it takes into account several characters (Kalimullah *et al.*, 2012) ^[19]. Genotypes grouped into different clusters are regarded as genetically diverse and are preferred for hybridization to obtain superior recombinants. Molecular marker analysis is an important technique in recent years for genetic diversity studies in wheat. The molecular markers (SSRs, SNPs, RAPDs and AFLPs) give more exact information about the genetic relationship between the genotypes at the DNA level and are less affected by environmental factors. The techniques have been very useful for the efficient characterization of germplasm and choice of parents for modern wheat breeding programmes (Arya *et al.*, 2017) ^[6]. In summary, assessment and use of genetic diversity are crucial for wheat sustainable improvement. An effective use of the various genetic resources will enable the creation of wheat more productive, more resistant to climate change and more nutritious that can meet future needs (Wani *et al.*, 2018) ^[46].

3. Genetic Variability Studies

Genetic variability in a crop is one of the most essential conditions in any programme of improvement as it is the foundation on which to base selection and breeding. Bread wheat has the potential for adequate variability among different genotypes for yield and yield components, making it possible to select the superior lines and produce better cultivars. The success of selection is much dependent on the kind and degree of variation available in the breeding material (Fikre *et al.*, 2015) ^[12]. Hence, genetic property estimation including phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance is important to understand the nature of the inheritance of various agronomic traits to formulate optimum breeding strategy (Zewdu *et al.*, 2024) ^[48]. Different points are discussed below:

3.1 Phenotypic and Genotypic Coefficient of Variation

The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) are important statistical parameters that are used to estimate how much variability exists in a population. While PCV reflects the overall variation in a trait due to all environmental and genetic effects, GCV reflects the portion of variation that is primarily due to genetic effects. These parameters are useful for breeders to identify the amount of variation that can be selected for, and the effect of the environment on the expression of the trait (Hassani *et al.*, 2022). It is observed that in majority of the studies, the values of PCV obtained for various traits are observed to be greater than the corresponding values of GCV which in turn suggests the role of environmental factors in the expression of the phenotype. If the difference between PCV and GCV values are small, then it indicates that environmental effects are small and the trait is more under genetic control (Abdurezake *et al.*, 2024) ^[1]. These are supposed to be more dependable for selection as their phenotype corresponds to their genetic potential. High values of GCV and PCV have been reported by several researchers on certain yield contributing characters like grain yield per plant, number of productive tillers, biological yield, harvest index and spike length of bread wheat. High variability for these traits suggests potential for selection to improve their genes (Gudeta *et al.*, 2025) ^[16]. Generally, traits such as those that vary from high to low are the most amenable to selection because there are more differences between the different genotypes. Some traits, like plant height, grains per spike and test weight, have been moderately variable, suggesting moderate genetic variability for

these characters. However, some characteristics such as days to flowering and days to maturity tend to have low values of GCV and PCV, indicating low genetic variability and relatively high environmental stability (Geneti *et al.*, 2022) ^[15]. This is because there is limited genetic variation which means that such traits are less dependent on selection. In general, the evaluation of PCV and GCV can be used to provide valuable knowledge into the nature and extent of variation present in the wheat germplasm and enable breeders to select the desirable traits (Chauhan *et al.*, 2022) ^[18].

3.2 Heritability

Heritability is an important genetic parameter which quantifies the fraction of the total variation in a trait that is due to genetic variation. It represents the heritability of the characteristic and provides the information that allows the breeder to appreciate the effectiveness of selection based on the phenotypic criterion. If a trait has a high heritability, that means that most of the variation is genetic and not environmental, making selection for the trait more effective. High heritability has been reported for such traits as test weight, plant height, spike length, grains per spike, and grain yield per plant in wheat breeding programs (Zewdu *et al.*, 2024) ^[48]. These are less dependent on the environment and mainly determined by genetic or hereditary factors. Thus, under phenotypic selection, much improvement is possible in future generations for such traits. Moderate heritability has been found for biological yield and harvest index, which suggest that they are influenced by both genetics and environmental factors. Heritability can be used as an aid in deciding about the efficiency of selection but is not completely sufficient in determining the expected genetic gain (Ahmad and Gupta, 2023) ^[12]. A trait can be highly heritable and yet have little improvement if there is little genetic variation. The study of heritability is therefore done in conjunction with a genetic advancement to gain insight into the inheritance pattern and potential for selection of various traits. They tend to be highly heritable, and follow additive gene action, allowing them to be easily enhanced by straightforward selection (Mullualem *et al.*, 2025) ^[27].

3.3 Genetic Advance

Genetic advance is the amount of improvement one can expect to get in a trait by selection over one or more generations. It can be typically quoted as a percentage of the population mean and gives an indication of how much progress can be achieved with selection. Genetic advance relies on a number of factors such as genetic variability, heritability and selection intensity. Heritability and genetic advance have been used together, and the combination of these two is more reliable than heritability alone in predicting the effectiveness of selection (Zewdu *et al.*, 2024) ^[48]. High heritability and high genetic advance imply that additive gene action is predominant, thus making it possible to improve the trait by direct selection. These are characters which are normally determined by additive genes, and have a greater response to selection in a breeding program. High heritability and high genetic advance have been observed for bread wheat characters like productive tillers per plant, grain yield per plant, spike length, biological yield and test weight (Zerga, 2022) ^[37]. These are thus regarded as desirable selection characteristics since they are highly amenable to improvement by breeding. Genetic advance for these characters is high, suggesting that outstanding genotypes can be produced by selection based on their appearance. On the other hand, high heritable traits with low genetic advance are generally under non-additive gene

action (dominance, epistasis) and may need other breeding techniques like hybridization and recurrent selection to achieve improvement (Patil *et al.*, 2024) ^[32]. The study of genetic advance is therefore useful to the wheat breeder to select the most appropriate breeding strategy and traits to use in creating high yielding varieties. Overall, the estimation of genetic advance offers valuable information on the degree of genetic progress that can be expected, and play an important role in the success of wheat improvement programs (Lamara *et al.*, 2022) ^[23].

4. Character Association Studies

Association studies of character are of significance in plant breeding since they enable the relationship between various agronomic characters and their contribution to grain yield to be determined. In bread wheat, yield is a quantitative character and is affected by several component characters and environmental factors. Hence, yield selection is sometimes more challenging and less successful. Reliable estimation of the degree of association between two or more traits is achieved by correlation analysis and assists breeders in understanding the repercussions of one trait on another (Reddy *et al.*, 2021) ^[35]. The sign of the correlation coefficient depends on the nature of the relationship between the traits and its magnitude depends on how strong the relationship is between the traits; it can be negative or non-negative and significant or non-significant. A positive correlation means that when one trait gets better, the other trait will get better, and a negative correlation means that when one trait gets better the other trait will get worse (Kumar *et al.*, 2025) ^[22]. In bread wheat, there are several reports of significant positive correlations with yield contributing traits like number of productive tillers, biological yield, harvest index, spike length, grains per spike and test weight. These positive correlations suggest that an improvement in these characters would be able to improve the yield of grain. Of these, the biological yield and harvest index are regarded as the most significant factor in production of grain since they affect the rate and efficient partitioning of assimilates to yield (Makwana *et al.*, 2025) ^[24]. The positive correlation between productive tillers and grain yield indicates that the genotypes with higher number of fertile tillers are more productive. Likewise, the contribution of spike length and grain per spike are direct to grain formation whereas test weight is more on the grain size and quality which influences yield potential. Correlation studies can also be used to detect the undesirable relationships between traits (Chumamo, 2025) ^[10]. However, some characters have been found to be negatively associated with each other in some instances. However, sometimes plant height has been found to be negatively correlated with grain yield under high input situations. This may be because shorter or semi-dwarf wheat varieties are less prone to lodging and their nutrient utilization and partitioning of photosynthate to grain production more efficient. The Green Revolution was greatly influenced by such results, which led to development of high yielding semi-dwarf wheat varieties (Singh *et al.*, 2025) ^[39]. Knowing what and how much relationships between the various traits is extremely useful to plant breeders as it makes it possible to improve more than one character by indirect selection. Inbreeding programs, traits with high positive correlation to grain yield are good selection criteria. Therefore, character association studies provide valuable information for identifying important yield contributing traits and formulating effective breeding strategies aimed at developing high yielding and superior wheat cultivars (Soomro *et al.*, 2025) ^[40].

5. Path Coefficient Analysis

Path coefficient analysis is one of the useful statistical methods employed in the plant breeding program to assess direct and indirect contribution of various traits to grain yield. While correlation analysis is useful to understand the relationship between traits, it fails to clearly explain the relationship between a given trait and the yield in terms of direct or indirect effect of the given trait on yield due to its association with other characters (Gudeta *et al.*, 2025) ^[16]. Hence, a method known as path coefficient analysis was developed that broke down the correlation coefficients into direct effects from the traits and indirect effects based on the traits correlated with each other. To study the direct and indirect effects of the traits in relation to the grain yield, therefore, a method called path coefficient analysis was developed which breaks down the correlation coefficients into direct and indirect effects of the traits (Rajput *et al.*, 2025) ^[34]. Grain yield of bread wheat is a composite character of a number of interrelated characters. Path analysis can be used to determine the most important yield contributing traits that bear a strong direct correlation with grain yield; these traits can then be considered as reliable selection criteria for use in breeding programmes. In wheat, a number of studies have indicated that biological yield, harvest index, productive tillers/plant, grains/spike, and test weight have strong positive direct impacts on grain yield (Tolwani *et al.*, 2025) ^[43]. Of these characters, biological yield, in most cases, has the greatest direct effect, resulting in a significant contribution to the overall productivity. Harvest index is also an important factor since it indicates the effectiveness of plant utilization of the total biomass for economic product. Traits with both positive correlation and positive direct effects are desirable and have a high probability of yielding a high yield gain when improving them in breeding programs (Chauhan *et al.*, 2025) ^[9]. For instance, the number of productive tillers per plant increases the number of spikes per plant, and grains per spike and test weight increase grain production and final yield. So selection for such traits can be used to increase wheat yield. It also emphasizes the importance of indirect effects between traits using path analysis. A trait sometimes will not have a direct effect on yield but may have an indirect effect through association with another important trait. For example, the length of the spikes can be indirectly positive to grain yield by increasing the number of grains per spike and tiller numbers can be indirectly positive via biological yield (Alemu *et al.*, 2025) ^[3]. Indirect contributions of this sort are valuable in helping the breeder to understand the intricacies of interrelationships among the various traits and to prevent erroneous conclusions from a correlation analysis. In general, path coefficient analysis is a good method to understand the cause and effect relationship between yield and its component traits. It allows breeders to determine the best criteria for selection and to develop an efficient breeding strategy for the development of high yielding wheat varieties. Hence, it is necessary to take both direct and indirect effects into account when choosing more desirable genotypes in wheat-breeding programmes (Gaur *et al.*, 2025) ^[14].

6. Genetic Divergence Analysis

Genetic divergence analysis is important in plant breeding for estimating the genetic variability in different breeding genotypes. Evaluation of genetic divergence is a necessary step in bread wheat for the selection of genetically divergent parents capable of being used effectively in a wheat hybridization program. There is more genetic variation between parental lines, so there is a higher chance of creating better recombinants, as

well as more variance in segregating generations. This variation offers better chances to identify desirable genotypes with enhanced yield, adaptability and stress resistance (Mokhtar *et al.*, 2026) ^[26]. Thus, knowledge on genetic divergence is very important in the development of high yielding wheat varieties. Mahalanobis D² statistics is one of the widely accepted and reliable measures of genetic divergence. The method of multivariate analysis is used to consider several characters as a whole to estimate the divergence between genotype. Wheat genotypes are classified into clusters, based on genetic similarity or dissimilarity (Nelwadker *et al.*, 2026) ^[29]. Genotypes within the same cluster are taken as genetically similar and those in different clusters as genetically diverse. The clustering pattern is important to breeders for selecting parents for crossing programmes designed to produce maximum variation/hybrid vigour. The grain yield, productive tiller, biological yield, harvest index and spike length are some of the traits in bread wheat that have been found to account for a major portion of the total genetic divergence between the genotypes in several studies (Kumar *et al.*, 2026) ^[21]. These characteristics are regarded as significant because they have a direct impact on productivity and plant performance. The role of these characters in divergence shows that there is a significant amount of variation for economically important characters which can be utilized in breeding programs. Outcrossing is generally preferred between remote clusters as greater heterosis, transgressive segregants and genetic variability is more likely to be realized in the next generation (Gaddam *et al.*, 2026) ^[13]. These crosses improve the likelihood of producing the best combinations from two parent lines and yield the best recombinants with greater yield potential and adaptability. However, crosses between closely related genotypes can lead to a lack of variation and a limited ability to select (Sharma *et al.*, 2026) ^[37]. Overall, genetic divergence analysis can be helpful for understanding the genetic relationship between wheat genotypes and for choosing appropriate parents for wheat hybridization. Careful use of genetically diverse germplasm can greatly improve the effectiveness of wheat breeding programs and be a part of efforts to develop high-yielding, climate-resilient wheat cultivars (Pani *et al.*, 2026).

7. Molecular Approaches in Wheat Breeding

Breeding of conventional wheat is largely based on the phenotypic selection and field evaluation, which are time-consuming and labour intensive and are strongly affected by environmental factors. Bread wheat has a quantitative inheritance and the yield of the grain or many other agronomic traits are sensitive to environmental interactions; therefore, the use of conventional breeding practice is not always the most rapid and accurate way of achieving improvement (Tanaka *et al.*, 2026) ^[41]. The use of modern molecular techniques in recent years has greatly improved the efficiency, accuracy and timeliness of wheat breeding programs. Molecular techniques coupled with traditional breeding techniques have helped wheat breeders select desirable genotypes more precisely and fasten the development of better wheat varieties. One of the most important tools of current wheat breeding is molecular markers (Alqurashi *et al.*, 2026) ^[4]. These markers are specific DNA sequences that are linked to certain genes or regions of the genome and are not affected by the environment. Simple sequence repeats (SSR), single nucleotide polymorphisms (SNP), random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP) markers are commonly used in wheat. The markers are useful for

identification and characterization of genetic variation between genotypes and finding genes linked to economically important traits (Mokhtar *et al.*, 2026) ^[26]. Other applications of molecular markers include germplasm characterization, genetic mapping, diversity analysis and parent selection in breeding programs. The discovery of quantitative trait loci (QTLs) has contributed to the development of molecular breeding in wheat. The QTLs are regions of the genome that are linked to the inheritance of quantitative traits like grain yield, resistance to drought and heat stress, spike architecture, and disease resistance (Tripathi *et al.*, 2026) ^[44]. There are multiple QTLs identified in the bread wheat genetic map which regulate these valuable agronomic traits. Identification of QTLs provides the background for understanding the genetic basis of complex traits which in turn provides an opportunity to transfer desirable genes to elite cultivars. One of the major uses of molecular markers in plant breeding is marker-assisted selection (MAS) (Bhadana *et al.*, 2026) ^[7]. With MAS, breeders can identify desired genotypes by using specific DNA markers associated with desired traits, before the plants are actually planted in the field. This is especially beneficial for traits that cannot be assessed easily in the field or that are very sensitive to environmental conditions, or only observed at later growth stages. Marker-assisted selection provides faster breeding programs, more efficient selections and can shorten time for improved varieties to develop (Jeon *et al.*, 2026) ^[18]. Besides marker-assisted breeding, new genomic tools like genome editing technologies and genomic selection are gaining ground as effective wheat improvement tools of the future. Genomic selection, based on genome-wide marker information, is used to provide improved selection accuracy for complex traits, such as grain yield and stress tolerance. The precise modification of target genes such as those of important agronomic characters is possible using genome editing technologies like CRISPR/Cas9 (Alshamrani *et al.*, 2026) ^[5]. These new technologies have tremendous potential to develop high yielding, climate smart and disease resistant wheat varieties to support food security in the future. In general, molecular technologies have changed the face of wheat breeding and are likely to be key components of sustainable wheat improvement programmes (Teku *et al.*, 2026) ^[42].

8. Future Prospects

Breeding programs for future wheat should aim at the effective use of the existing wheat genetic diversity to create high yielding and climate resilient wheat varieties. As abiotic stresses such as drought, heat and salinity along with biotic stresses like diseases and insect pests are becoming more of a challenge, there is a growing need to have more tolerance to these stresses. Improvement of nutrient use efficiency is also crucial for sustainable wheat production under limited resource conditions and should also be the objective of breeding. Combining traditional plant breeding with molecular techniques, including marker-assisted selection, genomic selection and genome editing will improve the accuracy and effectiveness of crop improvement efforts. Moreover, by using innovative genomic techniques, high throughput phenotyping and biotechnology, the identification and development of better wheat genotypes will be accelerated for increased productivity, adaptability and nutritional quality.

9. Conclusion

Genetic diversity and character association studies play a significant role in bread wheat improvement programs. There is a large genotypic variation between wheat cultivars in terms of

yield and yield components. In the event of selecting for grain yield, traits with a high positive association effect and direct effect on grain yield, e.g., productive tillers, biological yield, grains per spike, harvest index and test weight, should be emphasized. The high heritability and high genetic advance of many yield related traits suggests the importance of an additive mode of gene action and points to the efficiency of direct selection. Path coefficient analysis is also useful in determining the most contributing traits to yield. The combination of traditional breeding with molecular approaches like Marker Assisted Selection and QTL analysis presents high potential to speed up the breeding of wheat cultivars with high yields and stress tolerance. Thus, the proper use of genetic diversity and selection indices can have a major impact on sustainable wheat production and world food security.

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