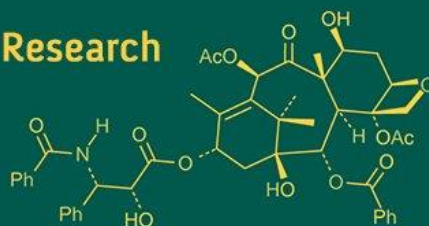


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Genetic parameters and their role in selection for yield traits in coriander (*Coriandrum sativum* L.)

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Abstract

Coriander (*Coriandrum sativum* L.) is a widely used seed spice with important roles in cooking, medicine, and industry. However, its production is often limited due to insufficient genetic improvement and the effects of changing environmental conditions. Genetic parameters such as variability, heritability, and genetic advance are fundamental for understanding trait inheritance and improving selection efficiency in crop breeding programmes. This review brings together and explains recent research on coriander, focusing on how plants differ from each other, how traits are passed from one generation to the next, how different traits are related, and how diverse different types of coriander are. It mainly highlights findings from studies carried out in the past ten years. Substantial genetic variability has been reported for important yield-contributing traits, including plant height, number of umbels per plant, seeds per umbel, and seed yield, indicating significant scope for genetic improvement. When certain traits show both high heritability and strong improvement over generations, it means these traits are mainly controlled by genes that can be reliably passed on, making selection more effective. Studies also show that the number of umbels per plant, the number of seeds in each umbel, and seed weight are the most important factors affecting overall seed yield. Furthermore, genetic divergence studies have highlighted the importance of selecting diverse parents to enhance hybridization efficiency. Despite these advancements, limited integration of multi-environment data and modern genomic tools remains a major constraint. The review emphasizes the need to combine classical genetic approaches with advanced breeding techniques to accelerate genetic gain and develop high-yielding, stable coriander varieties.

Keywords: Coriander, genetic variability, heritability, genetic advance, correlation, path analysis, genetic divergence, yield traits, plant breeding

1. Introduction

Genetic parameters, particularly variability, heritability, and genetic advance, constitute the cornerstone for understanding the inheritance of quantitative traits and play a decisive role in determining the efficiency of selection in crop improvement programmes (Singh *et al.*, 2019; Sharma *et al.*, 2020; Moharana *et al.*, 2023; Ali *et al.*, 2024) ^[5]. These parameters enable plant breeders to quantify, how different the plants are from one another within a group of plants and to estimate how they will improve when you select the best ones under varying environmental conditions (Yadav *et al.*, 2022; Verma *et al.*, 2020; Choudhary *et al.*, 2021) ^[9]. In self-pollinated crops such as coriander (*Coriandrum sativum* L.), rapid attainment of homozygosity enhances the effectiveness of selection, provided sufficient additive genetic variance exists within the population (Meena *et al.*, 2017; Patel *et al.*, 2019; Rai *et al.*, 2024) ^[4].

The success of any crop improvement programme largely depends on the availability and effective utilization of genetic variability, which provides the basic foundation for selection and genetic improvement in coriander (Moharana *et al.*, 2023; Basol *et al.*, 2024; Rai *et al.*, 2024). The partitioning of phenotypic variance into genotypic and environmental components provides a scientific basis for finding superior genotypes and formulating effective breeding strategies (Verma *et al.*, 2020; Yadav *et al.*, 2022; Basol *et al.*, 2024) ^[9]. Phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) are widely used to assess the magnitude of variability, where higher values indicate greater scope for improvement genetically through the process of selection (Singh *et al.*, 2019; Patel *et al.*, 2019; Rai *et al.*, 2024) ^[4, 5]. In coriander, substantial variability has been reported for important yield-attributing traits such as height of the plant, umbels number per plant, seeds number per umbel, and seed yield per plant, indicating the presence of exploitable genetic diversity within available germplasm (Meena *et al.*, 2017; Yadav *et al.*, 2022; Moharana *et al.*, 2023; Ali *et al.*, 2024) ^[9].

Genetic variability provides the basic foundation for crop improvement because selection becomes effective only when sufficient heritable variation is present within the population. Estimation of genetic parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance helps breeders identify superior genotypes and predict the efficiency of selection for economically important traits.

Heritability is major key genetic parameter that measures the total proportion of phenotypic variation attributable to genetic factors and provides insight into the transmissibility of traits across generations (Sharma *et al.*, 2020; Verma *et al.*, 2020; Choudhary *et al.*, 2021). High heritability means that the visible traits of the plant are mostly controlled by its genes, so selecting plants based on what you can observe is likely to give good results. On the other hand, low heritability suggests that the environment has a stronger effect on how the trait appears, making selection less reliable (Singh *et al.*, 2019; Yadav *et al.*, 2022; Rai *et al.*, 2024) ^[5, 9]. However, heritability alone is insufficient to predict any kind of response to selection, as it does not consider the magnitude of genetic variation or selection intensity (Moharana *et al.*, 2023; Ali *et al.*, 2024). Because of this, genetic advance an estimate of how much improvement can be achieved through selection is studied along with heritability to identify traits mainly controlled by genes that respond well to selection (Patel *et al.*, 2019; Sharma *et al.*, 2020; Meena & Sharma, 2025) ^[4]. When both heritability and genetic advance are high, it usually means these traits are strongly influenced by such genes, making selection more effective and reliable (Meena *et al.*, 2017; Moharana *et al.*, 2023; Rai *et al.*, 2024).

Yield is one of the complex trait controlled by many genes and also affected by environmental conditions, so selecting plants based only on yield is often less efficient and not always reliable (Singh *et al.*, 2019; Sharma *et al.*, 2020; Yadav *et al.*, 2022) ^[5]. Consequently, indirect selection based on contribution of yield traits exhibiting high heritability and genetic advance is widely adopted in plant breeding programmes (Verma *et al.*, 2020; Choudhary *et al.*, 2021; Ali *et al.*, 2024). In coriander, traits like the number of umbels per plant, seeds per umbel, number of primary branches, and seed weight are strongly and positively related to seed yield (Moharana *et al.*, 2023; Rai *et al.*, 2024).

Correlation and path coefficient analyses both serve as important statistical tools for understanding the interrelationships among traits and for partitioning the direct and indirect effects of yield components (Verma *et al.*, 2020; Yadav *et al.*, 2022; Rai *et al.*, 2024) ^[9]. While correlation analysis indicates the degree and direction of association between traits, path analysis provides a more precise estimation of cause-and-effect relationships by separating direct and indirect contributions (Singh *et al.*, 2019; Sharma *et al.*, 2020; Choudhary *et al.*, 2021) ^[5]. These analytical approaches facilitate the identification of key yield-contributing traits that can be effectively utilized as selection indices in coriander breeding programmes (Patel *et al.*, 2019; Moharana *et al.*, 2023; Ali *et al.*, 2024) ^[4].

The nature of gene action governing yield and its component traits significantly influences the choice of breeding strategy (Sharma *et al.*, 2020; Moharana *et al.*, 2023; Rai *et al.*, 2024). Traits controlled predominantly by additive gene action respond well to simple selection

methods, whereas traits governed by non-additive gene action require alternative approaches such as hybridization and heterosis breeding (Singh *et al.*, 2019; Verma *et al.*, 2020; Meena & Sharma, 2025) ^[5]. In coriander, several studies have reported high heritability along with high genetic advance for key yield traits, indicating the predominance of additive gene effects and the effectiveness of direct selection (Meena *et al.*, 2017; Yadav *et al.*, 2022; Moharana *et al.*, 2023) ^[9].

Coriander (*Coriandrum sativum* L.) is an important seed spice from the Apiaceae family, widely grown for both its seeds and fresh leaves, which are used in cooking as well as in medicinal and industrial applications (Singh *et al.*, 2021; Mishra *et al.*, 2019; Varshney *et al.*, 2021) ^[3, 6, 7]. India is the leading producer, consumer, and exporter of coriander, playing a major role in the global spice market (Meena *et al.*, 2017; Sharma *et al.*, 2020; Basol *et al.*, 2024). The crop is also valued for its essential oil, mainly composed of linalool, which is widely used in medicines, cosmetics, and food products due to its antioxidant, antimicrobial, and health-promoting properties (Singh *et al.*, 2021; Yadav *et al.*, 2022; Ali *et al.*, 2024) ^[6, 9].

Despite its economic importance, coriander productivity remains relatively low due to limited genetic improvement, narrow genetic base, and strong environmental influence on yield expression (Patel *et al.*, 2019; Sharma *et al.*, 2020; Moharana *et al.*, 2023) ^[4]. The absence of stable, high-yielding genotypes adapted to diverse agro-climatic conditions further constrains its yield potential (Moharana *et al.*, 2023; Rai *et al.*, 2024). Therefore, the assessment of genetic variability and the application of efficient selection strategies based on genetic parameters are essential for enhancing yield and stability in coriander (Verma *et al.*, 2020; Sharma *et al.*, 2020; Rai *et al.*, 2024).

The availability of diverse germplasm resources plays a crucial role in broadening the genetic base and facilitating effective selection and hybridization (Moharana *et al.*, 2023; Yadav *et al.*, 2022; Basol *et al.*, 2024) ^[9]. In coriander, considerable genetic variability has been documented for yield and its contributing traits, indicating the presence of ample scope for genetic improvement (Meena *et al.*, 2017; Patel *et al.*, 2019; Choudhary *et al.*, 2021) ^[4]. The effective exploitation of this variability through selection based on genetic parameters can significantly enhance breeding efficiency and genetic gain (Singh *et al.*, 2019; Verma *et al.*, 2020; Ali *et al.*, 2024) ^[5].

Recent advances in plant breeding have integrated conventional quantitative genetic approaches with genomic-assisted breeding methods to improve selection efficiency and accelerate genetic gain. Technologies such as marker-assisted selection and genomic selection are increasingly used in crop improvement programmes for precise identification of superior genotypes and prediction of complex quantitative traits (Crossa *et al.*, 2017; Varshney *et al.*, 2021; Xu *et al.*, 2017) ^[1, 7, 8]. However, the practical application of these molecular breeding tools in coriander is still limited, and most coriander improvement programmes continue to rely primarily on phenotypic selection based on genetic parameters (Moharana *et al.*, 2023; Basol *et al.*, 2024).

Despite considerable research on genetic variability and trait association in coriander, there remains a gap in integrating genetic parameters with modern breeding strategies across diverse environments. Furthermore, the limited utilization of

genomic tools highlights the need for a more comprehensive and integrated approach to coriander improvement. Therefore, the present review aims to provide a comprehensive understanding of genetic parameters and their role in selection for yield traits in coriander, with special emphasis on integrating classical quantitative genetics with recent advances in plant breeding to enhance selection efficiency and develop high-yielding, stable cultivars (Moharana *et al.*, 2023; Rai *et al.*, 2024; Basol *et al.*, 2024).

2. Methodology of Review

Literature included in the present review was collected from scientific databases such as Google Scholar, Scopus, Web of Science, ScienceDirect, and ResearchGate. Research articles published mainly between 2015 and 2025 related to genetic variability, heritability, genetic advance, correlation analysis, path coefficient analysis, genetic divergence, and breeding approaches in coriander (*Coriandrum sativum* L.) were critically reviewed. Relevant keywords including “coriander genetic variability”, “heritability in coriander”, “yield traits in coriander”, “path coefficient analysis”, “genetic divergence”, and “molecular breeding in coriander” were used during literature searches. Priority was given to peer-reviewed research articles, review papers, and recent advancements in plant breeding and quantitative genetics.

4. Literature Review

In *Coriandrum sativum* L., substantial variability has been reported for yield and its contributing traits across diverse environments, indicating the presence of exploitable genetic diversity (Moharana *et al.*, 2023; Basol *et al.*, 2024; Bohra *et al.*, 2021). Coriander is a one-season (annual) medicinal and aromatic seed spice from the Apiaceae family. It is widely grown across Asia, Europe, and Africa and is economically important because it is used in cooking, medicines, and essential oil production (Basol *et al.*, 2024; Singh *et al.*, 2021)^[6].

The global cultivation area and production of coriander have steadily increased due to rising demand for its seeds and leaves, firmly establishing it as a commercially valuable crop (Basol *et al.*, 2024; Singh *et al.*, 2021)^[6].

The present review synthesizes recent information on genetic variability, heritability, correlation, and divergence into a unified framework for selection. By emphasizing consistently important traits across studies and integrating recent advancements, this review provides a more comprehensive and application-oriented approach to coriander improvement, offering new insights for future breeding programmes (Ali *et al.*, 2024; Rai *et al.*, 2024; Kumar *et al.*, 2021).

In general, higher estimates of genotypic and phenotypic coefficients of variation for yield-related traits indicate wider genetic diversity among coriander genotypes. Traits showing high variability provide greater opportunities for effective selection and genetic improvement. However, differences in variability estimates across studies also indicate the influence of environmental conditions and genotype × environment interactions on trait expression.

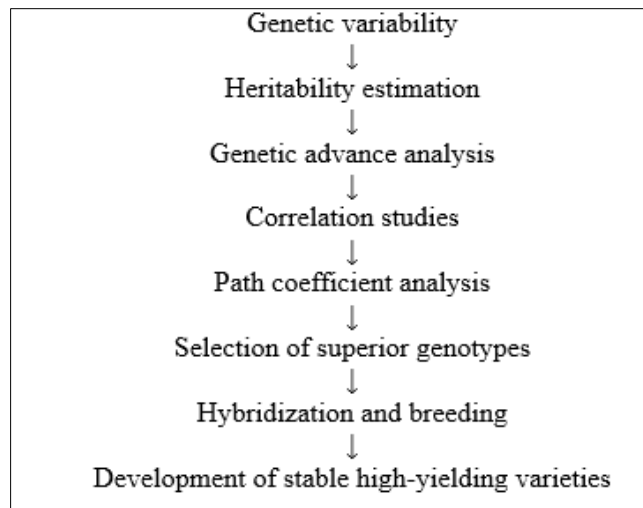


Fig 1: Role of Genetic Parameters in Coriander Improvement

4.1 Genetic Variability in Coriander

Genetic variability forms the cornerstone of crop improvement programmes, as it determines the scope of selection and the magnitude of genetic gain achievable in a population (Basol *et al.*, 2024; Crossa *et al.*, 2017; Kumar *et al.*, 2021; Heffner *et al.*, 2019)^[1, 2].

Studies conducted over the last decade have shown high genotypic and phenotypic coefficients of variation (GCV and PCV) for traits such as number of umbels per plant, seed yield per plant, biomass, and essential oil content, suggesting strong potential for selection (Rai *et al.*, 2024; Choudhary *et al.*, 2021; Ali *et al.*, 2024; Kumar & Malhotra, 2020; Meena *et al.*, 2018).

Phenotypic variability often exceeds genotypic variability for most traits, indicating a notable environmental influence, yet the consistent expression of variation across locations highlights the presence of heritable genetic differences (Rai *et al.*, 2024; Basol *et al.*, 2024). Genetic stability of key traits across environments has also been validated through multi-location trials, confirming that observed variation is largely genetic rather than purely environmental (Rai *et al.*, 2024; Choudhary *et al.*, 2021; Basol *et al.*, 2024).

Table 1: Important studies on genetic variability in coriander

Author	Year	Major Findings	Important Traits
Moharana <i>et al.</i>	2023	High GCV and PCV observed	Umbels per plant, seed yield
Rai <i>et al.</i>	2024	High heritability and genetic advance	Umbel diameter, seed yield
Basol <i>et al.</i>	2024	Significant genetic diversity detected	Yield and oil traits
Choudhary <i>et al.</i>	2021	Positive trait association with yield	Umbels per plant
Patel <i>et al.</i> ^[4]	2019	Additive gene action reported	Seed yield and test weight

4.2 Heritability and genetic advance

Heritability and genetic advance are important measures that help predict how well traits will respond to selection and how much they are controlled by genes in coriander. High heritability for traits such as plant height, number of umbels per plant, seeds per umbel, and seed weight suggests that these traits are mainly controlled by additive genetic effects, making them reliable for direct selection (Rai *et al.*, 2024;

Choudhary *et al.*, 2021; Moharana *et al.*, 2023; Ali *et al.*, 2024; Kumar *et al.*, 2021).. The association of high heritability with moderate to high genetic advance further supports the effectiveness of direct selection for these traits (Rai *et al.*, 2024; Ali *et al.*, 2024; Bohra *et al.*, 2021). Evaluating heritability under different environmental conditions has also been emphasized to ensure the stability and reliability of selection, especially for traits with high genotype × environment sensitivity (Basol *et al.*, 2024; Meena *et al.*, 2018).

High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and greater effectiveness of phenotypic selection. Such traits can be improved efficiently through simple selection methods. However, traits showing high heritability but low genetic advance may be influenced by non-additive gene effects and environmental factors, limiting the effectiveness of direct selection.

Table 2: Heritability and genetic advance of important traits

Trait	Heritability Level	Genetic Advance	Gene Action	Breeding Importance
Plant height	High	Moderate	Additive	Useful for direct selection
Umbels per plant	High	High	Additive	Major yield trait
Seeds per umbel	High	High	Additive	Important yield contributor
Test weight	Moderate to high	Moderate	Partial additive	Useful indirect selection trait
Seed yield per plant	Moderate	Moderate	Complex inheritance	Requires multi-trait selection

4.3 Correlation and path analysis

Yield is a complex trait affected by many related factors, so methods like correlation and path coefficient analysis are important for understanding how different traits are connected and how they influence yield (Choudhary *et al.*, 2021; Moharana *et al.*, 2023; Kumar & Malhotra, 2020).Positive and significant correlations have been observed between seed yield and traits such as umbels per plant, seeds per umbel, 1000 seed weight, and biological yield, identifying them as promising indirect selection criteria (Rai *et al.*, 2024; Choudhary *et al.*, 2021; Ali *et al.*, 2024). Path coefficient analysis in coriander further revealed

that umbels per plant and biological yield exert strong direct effects on seed yield, highlighting them as primary selection indices for yield improvement (Bohra *et al.*, 2021; Meena *et al.*, 2018).

Although correlation analysis helps identify the association among traits, it does not clearly distinguish direct and indirect contributions toward yield. Therefore, path coefficient analysis becomes essential for determining the actual contribution of individual traits. Traits showing strong positive direct effects on yield can serve as reliable selection criteria in coriander improvement programmes.

Table 3: More seeds per umbel improve yield through enhanced reproductive efficiency significantly

Trait	Correlation with Yield	Direct Effect	Importance in Selection
Umbels per plant	Positive	High	Major yield component
Seeds per umbel	Positive	Moderate to high	Useful indirect trait
Biological yield	Positive	High	Important for productivity
Test weight	Positive	Moderate	Contributes to seed yield

4.4 Genetic Divergence and Multivariate Analysis

Genetic divergence analysis is vital for identifying genetically diverse parents for hybridization programmes. Multivariate techniques such as Mahalanobis D² statistics, cluster analysis, and PCA have been used to assess genetic diversity among coriander genotypes (Basol *et al.*, 2024; Crossa *et al.*, 2017) ^[1]. These studies demonstrate significant divergence among genotypes, with traits like plant height, seed yield, and essential oil content contributing most to total variability (Rai *et al.*, 2024; Basol *et al.*, 2024; Solis *et al.*, 2018). Identifying divergent parents enhances heterosis and improves the efficiency of breeding programmes (Ali *et al.*, 2024; Choudhary *et al.*, 2021).

Advanced statistical methods like principal component analysis (PCA), cluster analysis, and heat map analysis are used to group different types of coriander based on their similarities and differences (Basol *et al.*, 2024; Crossa *et al.*, 2017; Heffner *et al.*, 2019) ^[1, 2].

The identification of genetically diverse parents is important for broadening the genetic base and improving heterosis in breeding programmes. Multivariate techniques such as principal component analysis and cluster analysis help classify genotypes into distinct groups based on multiple

traits, thereby assisting breeders in selecting suitable parents for hybridization.

4.5 Modern Breeding Approaches in Coriander

Over the last decade, research in coriander has increasingly focused on integrating classical breeding methods with modern statistical and genomic tools to improve selection efficiency. Multi-environment trials have gained importance for identifying stable and high-yielding genotypes, while advanced analytical methods have improved the accuracy of genetic parameter estimation (Basol *et al.*, 2024; Heffner *et al.*, 2019) ^[2]. However, the adoption of genomic tools and marker-assisted selection in coriander breeding is still in its early stages, representing a critical gap between available technologies and their practical application (Crossa *et al.*, 2017; Varshney *et al.*, 2021; Xu *et al.*, 2017) ^[1, 7, 8].

The integration of molecular breeding tools with conventional selection approaches can significantly improve breeding efficiency in coriander. Marker-assisted selection enables early identification of superior genotypes, while genomic selection improves prediction accuracy for complex quantitative traits. Despite their potential, these advanced breeding technologies remain underutilized in coriander improvement programmes.

Table 4: Enables rapid, accurate identification of superior genotypes using molecular markers efficiently

Breeding Tool	Application in Coriander	Advantages	Current Limitation
Marker-assisted selection (MAS)	Selection of superior genotypes	Faster and precise selection	Limited marker availability
Genomic selection (GS)	Prediction of complex traits	Improves selection accuracy	Limited genomic database
PCA and Cluster Analysis	Genetic diversity assessment	Identification of diverse parents	Requires multi-location data
Multi-environment trials	Stability analysis	Identification of stable cultivars	Time and resource intensive

4.6 Genotype × Environment Interaction

Genotype × environment interaction plays an important role in the expression of quantitative traits in coriander. The performance of genotypes often varies under different environmental conditions due to climatic and soil differences. Therefore, multi-location and multi-season testing are essential for identifying stable and adaptable genotypes suitable for wider cultivation. Stability analysis helps breeders select genotypes with consistent performance across environments and improves the reliability of selection programmes.

5. Research Gaps and Future Prospects

Despite considerable progress in understanding genetic variability and selection parameters in coriander, several important research gaps still remain. Most studies have been conducted under limited environmental conditions and are based mainly on morphological and quantitative traits. Multi-environment evaluation of genotypes is still insufficient, which restricts the identification of stable and widely adapted cultivars.

In addition, the use of molecular markers, genomic selection, and marker-assisted breeding in coriander remains very limited compared to other spice and horticultural crops. The absence of high-density genetic maps and limited genomic resources further constrain the application of advanced breeding technologies. Future research should therefore focus on integrating conventional quantitative genetic approaches with modern genomic and molecular techniques to improve selection accuracy and accelerate genetic gain.

Special emphasis should also be given to breeding for climate resilience, drought tolerance, disease resistance, essential oil quality, and adaptability under changing environmental conditions. The integration of high-throughput phenotyping, genomic prediction, and artificial intelligence-based breeding approaches may further enhance coriander improvement programmes in the future.

6. Discussion

This review shows that genetic factors like variability, heritability, and genetic advance are very important for deciding how to select better coriander (*Coriandrum sativum* L.) plants. Many studies have found good variation in traits such as number of umbels per plant, seeds per umbel, and seed weight, which means there is useful genetic diversity available that breeders can use to improve the crop (Moharana *et al.*, 2023; Basol *et al.*, 2024; Rai *et al.*, 2024).

Multi-environment studies further confirm that this variability is largely genetic rather than environmental, reinforcing the reliability of these traits in breeding programmes (Basol *et al.*, 2024; Crossa *et al.*, 2017) ^[1].

Variability estimates differed among studies due to differences in environmental conditions, germplasm sources, and experimental designs, indicating the importance of genotype × environment interactions in coriander improvement programmes.

High heritability along with moderate to high genetic improvement for yield-related traits suggests that these traits are mainly controlled by genes that can be reliably passed on, making selection based on visible characteristics very effective (Rai *et al.*, 2024; Ali *et al.*, 2024; Choudhary *et al.*, 2021; Singh *et al.*, 2019) ^[5]. However, the performance of these traits can change depending on the environment, so testing plants in different locations is important to identify varieties that perform consistently well under varying conditions (Basol *et al.*, 2024; Verma & Singh, 2023; Bohra *et al.*, 2021) ^[6].

Correlation and path coefficient analyses consistently reveal positive associations between seed yield and traits such as umbels per plant, seeds per umbel, and biological yield (Choudhary *et al.*, 2021; Moharana *et al.*, 2023; Kumar & Malhotra, 2020; El-Dhoyle & El-Morsy, 2022). Path analysis further identifies direct contributors to yield, providing breeders with reliable selection indices for improving productivity (Rai *et al.*, 2024; Choudhary *et al.*, 2021). The integration of these analyses with stability parameters allows for a comprehensive understanding of trait interrelationships under varying environmental conditions (Basol *et al.*, 2024; Crossa *et al.*, 2017) ^[1].

Although most studies identified umbels per plant as the primary yield determinant, certain reports highlighted biological yield and seed weight as stronger contributors under specific agro-climatic conditions.

Genetic divergence studies underscore the importance of selecting genetically distant parents to exploit heterosis and maximize breeding gains (Basol *et al.*, 2024; Kumar *et al.*, 2021). Multivariate methods like cluster analysis and principal component analysis are useful for grouping different coriander types based on their similarities and differences. This helps breeders choose suitable parent plants for crossing and developing improved varieties (Basol *et al.*, 2024; Rai *et al.*, 2024; Bohra *et al.*, 2021).

Although still used to a limited extent in coriander, modern tools such as molecular markers and genomic techniques can further improve the accuracy of studying genetic diversity and selecting better plants (Varshney *et al.*, 2021; Xu *et al.*, 2017; Heffner *et al.*, 2019) ^[2, 7, 8].

Recent advances emphasize the integration of classical quantitative genetics with modern genomics to accelerate genetic gain (Basol *et al.*, 2024; Crossa *et al.*, 2017; Varshney *et al.*, 2021) ^[1, 7]. While successful in other crops, such approaches are still emerging in coriander, highlighting the need to combine phenotypic selection, multivariate analysis, and genomic-assisted breeding for more efficient improvement (Moharana *et al.*, 2023; Basol *et al.*, 2024).

7. Conclusion

Genetic variability, heritability, and genetic advance are key factors that determine how effective selection will be in coriander breeding programs (Moharana *et al.*, 2023; Basol *et al.*, 2024; Rai *et al.*, 2024). The presence of good

variation in yield and related traits across different coriander types provides a strong base for improving the crop through direct selection and hybridization (Basol *et al.*, 2024; Moharana *et al.*, 2023; Ali *et al.*, 2024).

When traits such as umbels per plant, seeds per umbel, and test weight show high heritability along with moderate to high genetic advance, it means these characteristics are mainly controlled by genes that respond well to selection, making direct selection more effective (Rai *et al.*, 2024; Choudhary *et al.*, 2021; Singh *et al.*, 2019) ^[5].

In addition, correlation and path coefficient studies help identify which traits contribute most to yield. These relationships can be used as reliable indicators for indirect selection, thereby improving the overall efficiency of breeding programs (Choudhary *et al.*, 2021; Rai *et al.*, 2024; Kumar & Malhotra, 2020; El-Dhoyale & El-Morsy, 2022).

Genetic divergence and multivariate analyses have proven valuable in identifying diverse parental genotypes, which can maximize heterosis and improve breeding outcomes (Basol *et al.*, 2024; Moharana *et al.*, 2023). Despite advancements, gaps remain due to limited multi-environment evaluation and minimal integration of genomic tools. Future research should focus on combining classical genetic parameters with high-throughput molecular techniques to enhance precision, accelerate genetic gain, and develop high-yielding, stable, and quality coriander cultivars (Varshney *et al.*, 2021; Crossa *et al.*, 2017) ^[1, 7].

In summary, the integration of genetic parameters with modern breeding approaches provides a pathway to bridge theoretical concepts and field-level application, facilitating the development of coriander varieties that are both productive and adaptable to diverse agro-climatic conditions (Moharana *et al.*, 2023; Basol *et al.*, 2024; Singh *et al.*, 2021; Mishra *et al.*, 2019) ^[3, 6].

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