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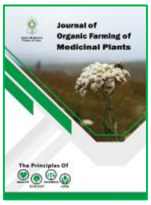

Original Article

Evaluation of phenotypic variation in some black cumin (Nigella sativa L.) landraces using the genotype by trait biplot model

Mahdi Mohebodini[a], Naser Sabaghnia[b], Mohsen Janmohammadi[b]

[a] *Department of Horticultural Science, Faculty of Agricultural Science and Natural Resources, University of Mohaghegh Ardabili, 7218759612, Ardabil, Iran.*
[b] *Department of Plant Production and Genetics, Faculty of Agriculture, University of Maragheh, 5518779842, Maragheh, Iran.*

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Corressponding Author:
Naser Sabaghnia
sabaghnia@yahoo.com

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ABSTRACT

Genetic improvement of black cumin (*Nigella sativa* L.), particularly with regard to yield performance, is needed for enhancing its productivity in semi-arid environments. This study aimed to assess the morphological diversity among 27 black cumin genotypes collected from various regions of Iran and to explore their genetic potential using the genotype × trait biplot model for trait associations. A total of 14 morphological traits were measured, including plant height (PH), length of internodes (LI), length of flowering stem (LFS), number of internodes of the main stem (IMS), chlorophyll content (CC), follicle width (FW), follicle length (FL), number of seeds per follicle (NSF), seed length (SL), seed width (SW), number of follicles per plant (NFP), capsule weight (CW), thousand seed weight (TSW) and seed yield (SY). Based on biplot analysis, 62 and 18% of total variation was explained by the first and second components, respectively. Genotypes G24 and G25 emerged as the most promising for high yield and favorable trait associations, being closest to the ideal genotype position. Traits such as FL, CW, LFS, and NSF were identified as the most discriminative traits for selecting high-yielding genotypes. Conversely, traits like TSW showed little correlation with SY and did not significantly influence yield performance in this study. The results also highlighted the importance of considering genotype × trait interactions in breeding programs, as these interactions significantly affect the selection of superior genotypes. The biplot analysis helped identify the best genotypes based on multiple traits, facilitating a more informed selection process for breeding purposes. Genotypes G24 (Mashhad-II) and G25 (Marivan) were recommended for further testing in multi-environmental trials to assess their adaptability and yield stability.

1. Introduction

As a member of Ranunculaceae, black cumin (*Nigella sativa* L.) is originating from West Asia and thrives in arid climates. This species is found across various regions within its native range and is cultivated in some areas. Growing to approximately 60 cm in height, the plant features thread-like, gray-green leaves. Its fruit is a capsule that houses numerous small, black and aromatic seeds (Moradzadeh et al., 2021). These seeds are dark gray to black in color and are rich in oil, proteins, alkaloids, quinones, saponins, and volatile compounds. The pharmacological and biological properties of black cumin, particularly thymoquinone, one of its active constituents, include antioxidant, anti-inflammatory, anti-ischemic, analgesic, anti-epileptic, and antitussive effects. Black cumin has demonstrated various medicinal benefits, such as reducing ischemia-reperfusion injury, anticancer potential of its extracts, and significant antimicrobial activity (Almatroudi et al., 2020). In light of the side effects associated with synthetic and industrial drugs, there has been a growing preference for plant-based medicinal alternatives since the late twentieth century. This trend reflects a global surge in the use of medicinal plants for treating diverse ailments. Consequently, medicinal plants hold substantial economic significance, and their trade has evolved into a thriving international industry. Natural populations hold significant value due to their long-term survival and ability to adapt effectively to the climatic conditions of their native regions. When these populations exhibit favorable traits, they serve as an essential genetic resource for developing improved cultivars (Swarup et al., 2021). However, environmental stresses pose major challenges to many crops, often altering the levels of medicinal compounds they produce. The interaction between environmental conditions and genotype plays a critical role in shaping trait relationships. As a result, the collection, preservation, maintenance, and evaluation of these diverse genetic resources are crucial for advancing breeding programs (Parker et al., 2022). One of the most accessible and cost-effective approaches to studying diversity among plant samples is the analysis of morphological traits. Assessing morphological diversity is aiding effective management of plant germplasm and offers deep perspective for researchers involved in plant breeding efforts.

Enhancing seed yield in black cumin has been a key objective for plant breeders. However, this trait is heavily influenced by environmental factors, resulting in low heritability. Consequently, direct selection for yield often yields unpredictable outcomes. Breeders rarely focus on a single trait, emphasizing the importance of analyzing the relationships between yield and other traits. Traditional statistical methods may fall short in capturing these complex associations, prompting the adoption of advanced tools for modeling crop yields. Yan and Frégeau-Reid (2018) introduced a site regression method that utilizes biplots as graphical tools to analyze genotype-by-trait interactions. A biplot visually represents the effects of genotypes and traits simultaneously and is applicable to various types of two-dimensional data. It is created by plotting the first two principal components derived from the singular value decomposition of tester-centered data. Studies have demonstrated the utility of this method; for example, Ebrahimi et al. (2023) applied the genotype × trait biplot model in safflower research, while Sabaghnia et al. (2023) used it to investigate sunflower traits. Shariq et al. (2015) conducted a comprehensive evaluation of black cumin accessions collected from 10 regions in India, revealing significant diversity in seed traits such as size and weight. Their study highlighted that the largest seeds were found in accessions from Punjab, whereas the heaviest seeds were identified in samples from Kerala. This variation reflects the genetic richness across regions, offering valuable prospects for selective breeding programs. Similarly, Gholizade et al. (2019) analyzed 32 black cumin genotypes and reported substantial differences in the traits studied. A cluster analysis based on morphological data grouped these genotypes into two distinct clusters, providing insights into patterns of genetic similarity and diversity. Their multiple regression analysis identified biomass, seed length, and maturity period as key factors influencing economic performance. Golkar and Nourbakhsh (2019) also investigated genetic diversity in 30 black cumin genotypes, observing considerable variability in morphological traits, including yield components and overall yield. These studies emphasize the importance of evaluating genetic variation, especially in black cumin genotypes from diverse geographic regions, such as Iran, for effective conservation and utilization of plant materials. Despite the established medicinal and economic value of black cumin, there remains a significant gap in research on its genetic diversity. Addressing this gap, the primary focus of this study was to analyze morphological variation among selected Iranian black cumin genotypes. To identify the most desirable traits and genotypes, the genotype × trait biplot model was utilized. This model was implemented using the GGEbiplot application, a powerful analytical tool designed to graphically represent the complex interaction structures between genotypes (entries) and the traits (testers) being measured. The biplot provides a visual representation of the relationships among traits, as well as the performance and differentiation of genotypes in terms of those traits. Through this method, researchers can easily interpret key patterns in the data, such as which genotypes excel in particular traits, which traits are closely related, and how genotypes and traits interact under the given experimental conditions. This graphical approach is especially useful for summarizing large datasets, offering intuitive insights into the underlying relationships that might be less apparent through traditional tabular data presentations. The study aimed to assess black cumin landraces across multiple traits and to explore trait associations using the genotype × trait biplot model. The findings are expected to inform future breeding strategies and guide the development of high-yielding cultivars.

2. Materials and Methods

2.1 Trial and traits

A diverse collection of 27 black cumin genotypes was gathered from various geographical regions of Iran (Table 1), ensuring a broad genetic base for the study. To evaluate the performance of these genotypes, the experiment was meticulously designed and executed in a controlled greenhouse environment in Ardabil. A randomized complete block design with four replicates was employed. The seeds from each genotype were sown in pots with a diameter of 25 cm, filled with a uniform growing medium to standardize the environmental conditions. Initially, 10 seeds were planted in each pot to account for possible variability in germination rates and early-stage plant vigor. As the plants developed and reached an established growth stage, thinning was performed to reduce the number of plants per pot to five. This ensured that each plant had adequate space and resources for optimal growth, thereby promoting uniformity across treatments and minimizing competition among plants within a pot. Throughout the experimental period, meticulous care was taken to ensure favorable growing conditions. Manual irrigation was performed every two days, providing consistent moisture

Table 1. Name and altitude of 27 black cumin (*Nigella sativa* L.) landraces.

Code	Name	Altitude	Code	Name	Altitude	Code	Name	Altitude
G1	Ardabil-I	1377	G10	Piranshahr	1460	G19	Lorestan	2300
G2	Ardabil-II	1377	G11	Torbat	1333	G20	Kashan	945
G3	Amlash	15	G12	Takestan	1265	G21	Kashmar	1215
G4	Ahwaz	12	G13	Semirom	2400	G22	Kordestan	1500
G5	Arak	1700	G14	Sarbisheh	1820	G23	Mashhad-I	1050
G6	Isfahan-I	1570	G15	Shiraz	1514	G24	Mashhad-II	1050
G7	Isfahan-II	1570	G16	Qazvin	1316	G25	Marivan	1320
G8	Brojen	2200	G17	Karaj	1300	G26	Miandoab	1314
G9	Birjand	1491	G18	Lordegan	1700	G27	Neyshabur	1193

to support healthy plant growth while avoiding water stress. Additionally, weeds were regularly and carefully removed by hand to prevent resource competition and maintain the integrity of the experimental setup. These agronomic practices were performed with precision to ensure that the observed differences among genotypes were due to inherent genetic variations rather than environmental inconsistencies. At the critical 50% flowering stage, an extensive array of morphological traits was measured to comprehensively assess the performance of each genotype. These traits included plant height (PH), length of internodes (LI), length of flowering stem (LFS), number of internodes of the main stem (IMS), chlorophyll content (CC), follicle width (FW), follicle length (FL), number of seeds per follicle (NSF), seed length (SL), seed width (SW), number of follicles per plant (NFP), capsule weight (CW), thousand seed weight (TSW) and seed yield (SY). The comprehensive analysis of these traits not only facilitated the evaluation of individual genotypes but also laid the groundwork for future breeding strategies.

2.2 Data analysis

To ensure the reliability and validity of the subsequent analyses, the dataset was rigorously tested for normality via Anderson–Darling test and the uniformity of error variances via Bartlett's test. Both tests verified the normal distribution shape and uniformity of residuals for all traits. These preliminary checks are critical for confirming that the data meet the assumptions required for robust statistical modeling and accurate interpretation of results. In the context of the genotype × trait biplot model, the following calculation is used:

$$\frac{Y_{ij}-\overline{Y_j}}{SD_j}=\sum_{n=1}^{2}\Phi_n\Psi_{in}\Omega_{jn}+R_{ij}$$

where Y_{ij} is the mean performance of genotype i for trait j, $\overline{Y_j}$ is the mean of genotypes in trait j, SD_j is the standard deviation, Φ_n is the eigenvalue associated with the principal component n, Ψ_{in} and Ω_{jn} are values for genotype i and trait j on the principal component n, R_{ij} is the error amount of the fitted equation related to genotype i for trait j. To achieve symmetrical scaled amounts between genotypes and traits, the eigenvalues are adjusted through vector absorption. This correction ensures a balanced representation of genotypes and testers by applying the z-score transformations. The interaction biplots are then constructed using these symmetrically scaled values. In the biplot, each genotype and trait are represented by a distinct symbol, enabling a clear and interpretable graphical display of the relationships. The symmetric scaling approach ensures that the graphical interpretation of the data is both balanced and accurate, providing valuable insights into the complex interactions between genotypes and traits.

3. Results

3.1 Biplot model

The first two principal components (PCs) extracted from the analysis accounted for 80% of the total variation observed among the black cumin genotypes (Fig. 1) so that the first principal component explained 62% of the variance, while the second PC contributed 18%. This substantial proportion of the variability captured by the biplot highlights the critical role of both non-crossover and crossover interactions within the entry-by-tester dataset. The presence of these interaction types signifies shifts in the ranking of black cumin genotypes across different traits. These studies collectively emphasize the challenges of relying solely on indirect selection processes without properly accounting for the effects of entry-by-tester interactions. Failure to consider these interactions could lead to misleading conclusions about genotype performance across varying traits. Given the importance of these interactions in the current study of black cumin genotypes, the use of biplot analysis proves particularly advantageous. As recommended by Yan (2024), biplot representation serves as an effective tool for exploring the complex relationships between genotypes and traits. By leveraging this approach, researchers can visually interpret the interactions, identify superior genotypes, and pinpoint traits that significantly influence the overall performance.

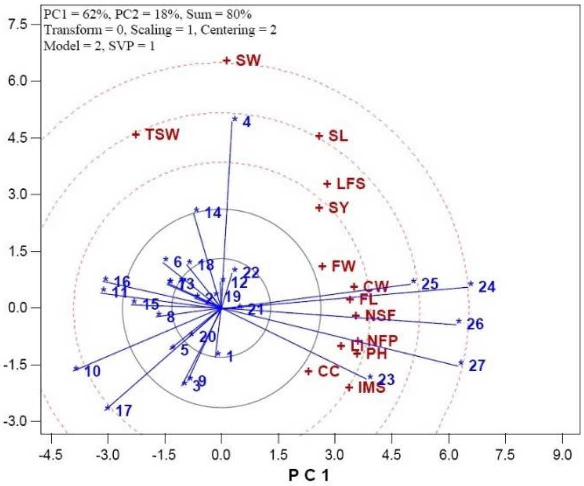

Fig. 1. The vector option of biplot model for association of 27 black cumin genotypes.

This methodology not only facilitates a deeper understanding of the genetic and phenotypic relationships but also enhances the efficiency of the breeding and selection processes.

3.2 Relations of genotypes

The biplot model successfully captured a significant amount of variability within the dataset, allowing for the analysis of genotype associations based on the cosine of their vectors. In this context, the cosine values indicate the degree of correlation between genotypes: cos0∘=+1 (positive relationship), cos90∘=0 (no relationship), and cos180∘=−1 (negative relationship). The biplot revealed considerable variability, represented by long vectors in the graphical output (Fig. 2). Key observations from the first-year analysis include: (i) Positive correlations among genotypes G23, G24, G25, G26, and G27, as indicated by vectors that are close to each other in direction. (ii) Positive correlations between genotypes G10 and G17, which were similarly aligned in the biplot. (iii) Positive correlations between genotypes G11 and G16, reflecting their similarity in traits.

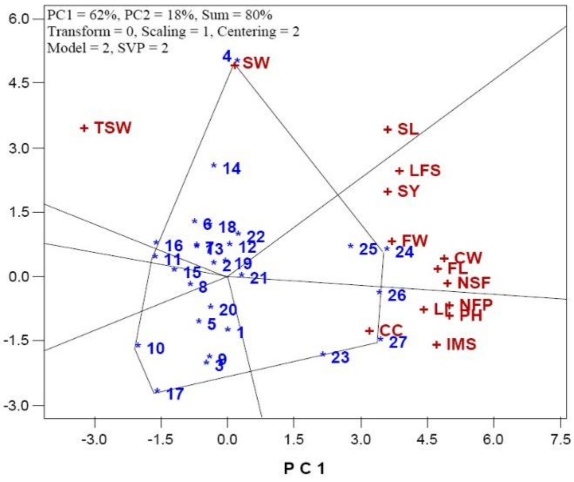

Fig. 2. The polygon option of biplot model for fourteen traits of 27 black cumin genotypes.

In contrast, near-zero correlations were observed in several instances, signifying a lack of strong association; a near-zero correlation was detected between the group of genotypes (G23, G24, G25, G26, and G27) and G4, as well as between G11 and G16 and G4, with vectors of these genotypes appearing nearly perpendicular to each other. Also, strong negative correlations were identified between the group of genotypes (G23, G24, G25, G26, and G27) and both G10 and G17, as well as between G11 and G16. These relationships were represented by obtuse angles in the biplot, suggesting antagonistic interactions among the genotypes in these groups (Fig. 2). This highlights the biplot's effectiveness in illustrating complex genotype relationships in a concise manner. It is also important to note the distinction between the biplot method and traditional correlation analysis. While the biplot illustrates the associations between traits in relation to the entire dataset structure, correlation coefficients specifically measure the direct interrelationships between traits. As such, the correlation coefficients and the biplot results may not always perfectly align, as the biplot captures a broader, multi-trait interaction that may not always be reflected in pairwise trait correlations.

3.3 Polygon view

Fig. 2 visually illustrates the performance of the black cumin genotypes, highlighting which genotypes excelled in specific traits. Several key traits, including CC, LI, NFP, PH, and IMS, were closely associated with genotype G27, which emerged as the leading genotype for these characteristics. In contrast, traits such as LFS, FW, FL, NSF, capsule weight (CW, and SY were grouped in a separate section, with genotype G24 identified as the most favorable genotype for these traits. Additionally, SW, SL, and TSW were found to align more closely with genotype G4 in the biplot (Fig. 2). Interestingly, genotypes G10, G16, and G17 did not show any significant preference for any of the traits measured in this study, indicating that these genotypes may not exhibit a particular strength in the target traits of black cumin. However, in this study, no significant correlation was observed between thousand seed weight and seed yield, indicating possible differences in the factors driving yield performance across different studies. The entry-by-tester biplot method provided valuable insights into the genotype responses, enabling a clear visualization of how different genotypes performed across various traits. This approach was instrumental in identifying the most promising genotypes for future breeding programs. In line with these findings, genotype G24 followed by G25 stand out as top candidates for commercial cultivar development. To ensure their adaptability and stability across different environments, further testing of these genotypes through multi-environmental trials is recommended before any official release.

3.4 Perfect genotype

The ability of a genotype to distinguish itself based on the measured traits and its potential to exhibit the ideal characteristics of black cumin genotypes can be effectively assessed by positioning the genotypes relative to an assumed "ideal" genotype (Fig. 3). Genotypes located near this ideal position are considered the most desirable, while those positioned farther away are less favorable. In this analysis (Fig. 3), genotypes G24 and G25, followed closely by G26 and G27, are identified as the most ideal, as they are closest to the ideal position. Conversely, genotypes G10 and G17, located on the opposite side and farthest from the ideal position, are the least desirable in terms of their ability to distinguish themselves and their overall potential based on the traits measured. The genotypes G24, G25, G26, and G27, which are closest to the perfect position, can be considered as ideotypes**,** which demonstrate high performance across a range of important traits. However, challenges arise when associations between these traits are not always significant or consistent.

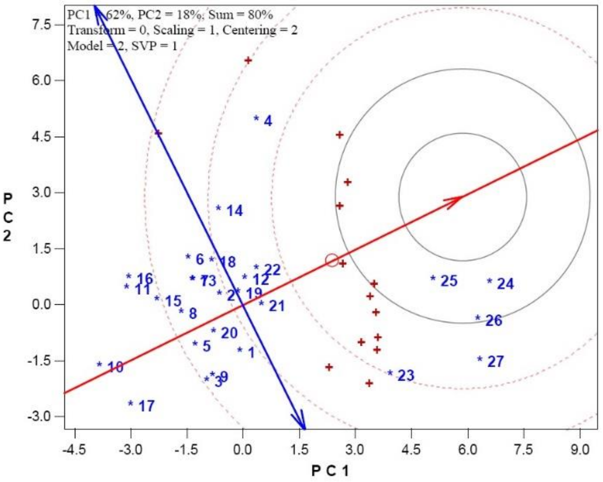

Fig. 3. The perfect genotype option of biplot model for 27 black cumin genotypes.

This issue becomes particularly problematic in black cumin breeding programs, where seed yield and quality characteristics, such as essential oil content and other yield components, play a central role in selection. In many cases, the relationships between seed yield and these quality traits are either weak or even negative, as reported by Attia et al. (2021). This lack of strong positive correlations between yield and quality traits complicates the selection process. Given these challenges, it becomes clear that strategies for genetic improvement in black cumin must incorporate sophisticated multivariate statistical tools, particularly those that offer graphical representations, to better inform ideotype selection. By leveraging these advanced analytical methods, breeders can more effectively determine the ideal genotypes and optimize breeding programs to enhance both yield and quality characteristics in black cumin.

3.5 Perfect trait

The discriminative potential of a trait is determined by its standard deviation, where larger values indicate a higher capacity for distinguishing between genotypes. This potential is represented in an idealized position of the measured traits (Fig. 4), where the most effective traits are positioned close to this ideal, and the least effective ones are further away. Based on this analysis FL and CW were identified as the most discriminative traits, followed by LFS, FW, NSF, and SY. These traits exhibited a high level of variability, making them effective at distinguishing differences between black cumin genotypes. On the other hand, although the remaining traits, except for TSW, also had discriminative potential, they were more aligned with the average potential, suggesting that while they still discriminate genotypic differences, their impact is less pronounced (Fig. 4).

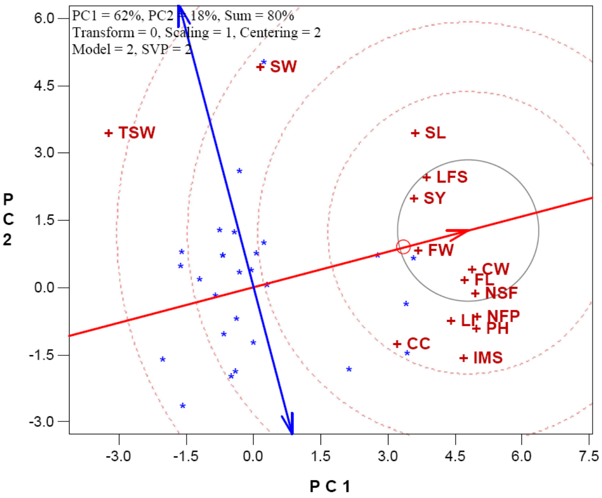

Fig. 4. The perfect trait option of biplot model for fourteen traits of black cumin.

Moreover, the "typical potential" of a trait, which reflects how well it captures the symbolic properties of the genotype, is measured by its angle relative to the axis of the average trait. Smaller angles indicate a greater typical potential, as these traits more effectively characterize the target genotype. In this context, the most desirable traits, FL, CW, LFS, FW, NSF, and SY, formed very small angles with the axis of the average trait, indicating they possessed higher typical potential. In contrast, traits such as SW, IMS, and CC exhibited larger angles, suggesting they have relatively lower typical potential (Fig. 4). The performance of medicinal plants, including their growth, yield, and essential oil content, is influenced by both their genetic structure and environmental factors, including climate conditions, soil properties, and farming practices.

3.6 Seed yield

For black cumin breeders, it is crucial to adopt a systematic approach to crop improvement, especially regarding yield components, and the applied biplot model uses as a powerful tool for this purpose (Fig. 5). As highlighted earlier, traits such as NSF, NFP, TSW, and SY were plotted to understand their relationships (Fig. 5).

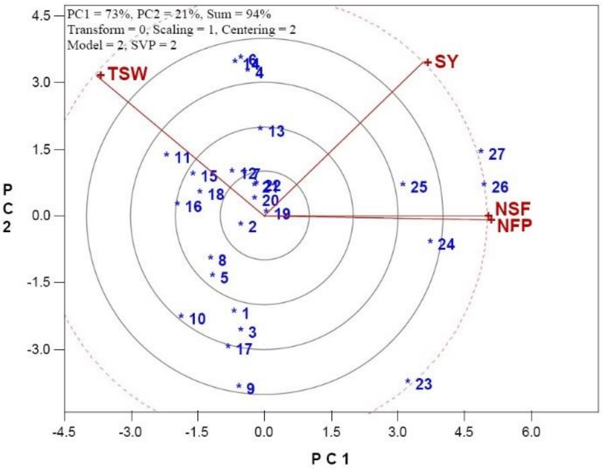

Fig. 5. The vector option of biplot model for association of yield components in black cumin.

Despite the lack of a strong positive or negative correlation between TSW and SY, as indicated by the angle between them, it is evident that achieving high performance in both traits simultaneously is challenging. Furthermore, there exists a relatively weak positive correlation between seed yield and both seeds and follicles numbers. These traits can potentially be combined to enhance yield performance, but breeders should primarily focus on optimizing the number of seeds and follicles to improve overall yield, as suggested by Moradzadeh et al. (2021). The seed yield performance of genotypes, considered the final goal trait, is further explored in Fig. 6, where the horizontal axis represents seed yield and the direction of the arrow indicates the axis orientation. Based on this analysis, genotypes G24, followed by G25, G26, G4, G27, G23, and G14, are the most desirable ones in terms of seed yield performance. Conversely, genotypes G10 and G17 are the least favorable for this trait (Fig. 6). The distance of each genotype from the horizontal axis indicates the standard deviation of its seed yield performance. Smaller distances are more desirable for selection, as they suggest less variability in performance. Genotypes G24 (Mashhad-II from northeastern Iran) and G25 (Marivan from western Iran) exhibit low variability and are recommended for selection. For instance, while genotype G4 has a high seed yield, it is positioned farther from the horizontal axis, indicating greater variability and making it less favorable in terms of stability. Thus, G4 is considered less desirable in comparison to genotypes with smaller distances from the axis.

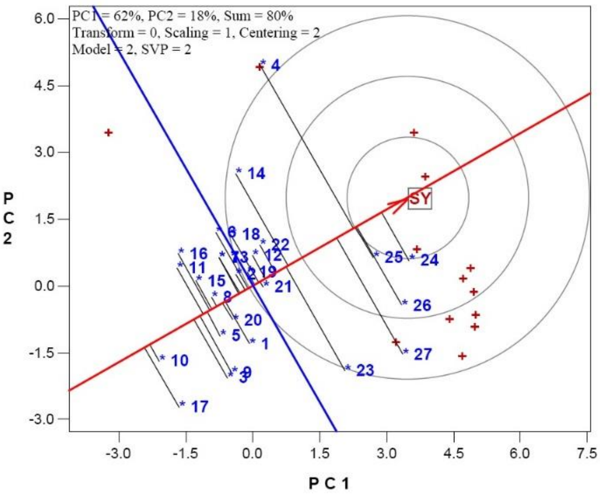

Fig. 6. The examination of seed yield (SY) of 27 black cumin genotypes.

4. Discussion

The genetic pool of the currently released black cumin cultivars is relatively limited, which presents a constraint for advancing genetic improvement programs. Therefore, evaluating black cumin genotypes is crucial to prevent the erosion of plant genetic resources and to effectively manage breeding efforts. The genotypes under study exhibited considerable variation, which aligns with previous studies that have highlighted significant diversity in black cumin (Ahmadi et al., 2024; Gebremedin et al., 2024). The genotype × trait biplot model used in this study effectively explained a substantial portion of the observed variation (over two-thirds) and confirmed the presence of both straightforward and complex interactions between the black cumin genotypes and the measured traits. Such variability aligns with findings from Mohebodini et al. (2024), who observed similar interaction dynamics in purslane (*Portulaca oleracea* L.), and Sabaghnia et al. (2024a), who reported comparable results in summer savory (*Satureja hortensis* L.). These varying interaction types led to different rankings of the genotypes for certain traits, making the selection of the best genotypes challenging, particularly in semi-arid environments. The complexity of genotype × trait interactions further complicate the process of indirect selection, as these interactions make it difficult to identify the most superior genotypes (Raffo & Jensen, 2023). Despite the complexity of these interactions, their consideration is crucial in genetic improvement programs, as they reduce genetic progress. Genotypes G24 and G25 performed better than the others across most traits, especially seed yield and related characteristics such as follicle and seed properties. The identified pattern of polygon suggests that yield performance may be more strongly influenced by the characteristics of the follicles and capsules. While Fikre et al. (2023) also reported a positive relationship between follicle and capsule traits and seed yield in black cumin, they also found that thousand seed weight played a similarly important role. However, key yield components in black cumin include the number of follicles, capsules, seeds, and thousand seed weight, yet the role of thousand seed weight in this study was not significant. This could be attributed to the fact that the current genotypes are local landraces with smaller seeds under natural growing conditions, meaning this trait had minimal impact on yield performance. The biplot model provided a clear and intuitive visual summary of genotype associations within the black cumin dataset, echoing similar findings from Mollafilabi and Moodi (2020), who reported positive correlations between seed yield performance and the number of seeds per follicle and number of follicles per plant in their study. Genotypes G24 and G25, showing strong performance, are promising candidates for commercial cultivar development. However, before release, these genotypes must undergo multi-environmental trials to assess their adaptability and yield stability, followed by statistical analysis to confirm their potential.

We found that genotypes G24 and G25 exhibited a high level of trait distinction and demonstrated notable symbolic potential as representative black cumin genotypes. These genotypes can be valuable for future studies aimed at exploring the relationships among various traits in black cumin. In the entry-by-tester biplot model, when the first principal component is significantly associated with the effects of the genotypes, the ideal position of the genotypes reflects their higher values, indicating the potential for high performance. Additionally, low absolute values in the second principal component suggest minimal variability in response at the ideal position. The effectiveness of the ideal position tool in identifying the most favorable genotypes based on multiple traits has been previously demonstrated by Sabaghnia et al. (2016) in spinach (*Spinacia oleracea* L.) and Kendal (2019) in durum wheat. However, the behavior of the first and second principal components, as observed in multi-environmental trials, may vary across different two-way datasets. To address this, Yan (2024) recommended an alternative model, used in this investigation, where the first principal component is replaced by predictions from a linear regression model applied to tester-centered data on genotype effects, thereby making the model more interpretable. The traits identified as the most discriminative, such as follicle length, capsule weight, length of flowering stem, follicle width, seeds of follicle, and yield performance, were identified to be the key factors for differentiating black cumin genotypes. These traits also demonstrated high symbolic potential for indicating the characteristics of the genotypes. Thus, evaluating black cumin genotypes based on these traits yields more reliable results and better captures the variations among the genotypes. The utility of the ideal position tool for identifying the most favorable traits has also been confirmed in previous studies, such as those by Yari et al. (2018) on rye (*Secale cereale* L.) and Sabaghnia et al. (2024b) on chickpea (*Cicer arietinum* L.). This application of the biplot model, based on regression adjustment of the primary biplot model, was used for our entry-by-tester dataset. Given the importance of seed yield, the performance of the genotypes was primarily evaluated in terms of this target trait. As a result, genotypes G24 and G25 were identified as the most favorable black cumin genotypes. While studies focusing on different genotypes within the same ecological conditions help explain genetic variation, studies using the same genetic material across varying climates reveal the influence of environmental factors (Leites et al., 2023). Additionally, while there is significant research on the variation between cultivated and natural populations of medicinal plants, distinguishing between genetic and environmental contributions to this variation remains challenging (Nurzyńska-Wierdak et al., 2023; Hasan et al., 2024); therefore, identifying the most suitable environmental conditions or traits for assessing genotype performance is critical for both farmers and consumers. According to the obtained results, it is recommended that future evaluations of black cumin genotypes prioritize the most discriminative and typical traits, such as FL, CW, LFS, FW, NSF, and SY, to enhance breeding programs and improve commercial outcomes.

5. Conclusion

Among the fourteen traits of black cumin assessed in this study, seed yield showed significant associations with traits such as length of flowering stem, follicle width, seed length, capsule weight, and follicle length. These traits can be utilized to select the most promising genotypes. Based on their ability to discriminate and represent the genotypes, seed yield, length of flowering stem, follicle width, capsule weight, number of seeds per follicle, and follicle length emerged as the most valuable traits. Evaluating multiple traits is essential for identifying the best genotypes, providing breeders with the necessary information to develop new cultivars with improved yield performance, especially under rainfed conditions in semi-arid environments. Among the genotypes, G24 and G25 were identified as the most favorable, making them strong candidates for cultivar release.

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