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Genetic diversity evaluation of some agronomic traits in dill accessions using biplot model

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Summary: As a widely cultivated vegetable crop, dill (*Anethum graveolens* L.) is produced for both food and medicinal purposes. This research investigates the genetic diversity of 30 dill accessions from diverse regions of Iran. The evaluated traits included: seed number per umbel (SNU), number of umbellets per umbel (NUU), number of umbels per plant (NUP), node number before flowering (NNF), inflorescence fresh weight (IFW), plant fresh weight (PFW), inflorescence dry weight (IDW), plant dry weight (PDW), and seed yield (SY). The accession-by-trait biplot explained 83% (52% and 31% for the first and second principal components, respectively) of the total variation, indicating a complex pattern of interactions between accessions and traits in dill. Plant fresh and dry weight, and SY were related to seed of umbel, and umbellet of umbel, so these yield components can be used for improving both seed yield and biomass. Results revealed significant variation in traits across the accessions, with accessions 22 (Urmia) and 11 (Sarab) showing consistently high performance for both PDW and SY. Also, a graphical biplot analysis highlighted key trait associations, including strong positive relationships between IFW, IDW, and NUP. Accessions 22 and 11 were identified as the most reliable candidates for future breeding programs aimed at improving dill biomass and seed yield. Accession 24, followed by accessions 3, 22, and 30, were identified as the ideal accessions, suggesting their superior ability for discriminating across traits. PDW following to SNU and SY indicated the more potential for both representative and discrimination capabilities, positioned at the ideal trait location.

Keywords: accession-by-trait interaction, *Anethum graveolens* L., ideal accession, dill, yield

Introduction

Dill (*Anethum graveolens* L.), a green leafy vegetable and valuable medicinal plant, is an important source of nutrients, including essential minerals and vitamins. It is a widely distributed outcrossing species from the Apiaceae family, native to Central Asia. Weedy forms are also found in the

Mediterranean and other parts of Asia (Yaldiz et al., 2018). The plant is characterized by segmented leaves, sheathed petioles, and yellow flowers arranged in umbels with multiple peduncles. Each umbel contains numerous smaller umbels bearing oval, flat seeds with lateral wings (Singh et al., 2020). It is widely recognized for its aromatic properties and is commonly used to flavor a variety of foods, including salads, soups, seafood, and sauces. It also exhibits antioxidant and antimicrobial properties against several pathogens. The essential oil composition of dill varies depending on environmental conditions and agricultural practices, particularly regarding the ratio of carvone to α -phellandrene (Milenković et al., 2024). Both the shoots and seeds of dill contain fatty acids, essential oils, proteins, carbohydrates, vitamin A, niacin, and minerals such as Ca, K, Mg, and P (Biesiada et al., 2019). In contrast, the seed oil has a different composition, dominated by carvone, followed by dihydrocarvone and limonene (Ozliman et al., 2021).

Assessing genetic diversity in plant germplasm is a fundamental step in the identification, conservation, and utilization of genetic resources, and it plays a crucial role in plant breeding programs. Without sufficient genetic variation, breeders face significant limitations in developing new and improved cultivars. Understanding the extent of genetic diversity and the inheritance patterns of key traits in genotypes is essential for the effective selection of parents in breeding efforts (Swarup et al., 2021). Over recent decades, several studies have investigated quantitative traits in dill genotypes, successfully identifying a range of traits contributing to genetic diversity (Solouki et al., 2012; Ninou et al., 2017). Various types of markers are employed to assess genetic diversity across different crops. Among these, morphological traits are some of the earliest and most accessible indicators, widely used in genotype classification due to their simplicity, low cost, and minimal need for advanced technologies such as molecular or biochemical markers. Morphological diversity arises from genetic variation and is influenced by interactions between genetic and environmental factors. It serves as a valuable proxy for evaluating genetic diversity. Given diverse environmental conditions of Iran, the outcrossing nature of dill, and its long cultivation history in the region, considerable genetic variation is expected among Iranian dill genotypes as a result of adaptive processes (Sabaghnia et al., 2024b). Furthermore, concerns about genetic erosion and declining genetic diversity highlight the urgent need to identify, characterize, and conserve native landraces to support future breeding initiatives.

Gholizadeh et al. (2021) evaluated the genetic variation of several dill ecotypes according to some morphologic traits and found significant associations among most traits. Through factor analysis, they identified vegetative traits, biomass and leaf size, leaf dry weight, and the number of lateral branches as the primary factors contributing to variability, collectively explaining 78% of the total variation. Additionally, cluster analysis grouped 30 ecotypes into four distinct clusters, revealing considerable differences in shoot yield performance. These findings indicate that Iranian dill ecotypes from various regions exhibit high morphological diversity, with several ecotypes demonstrating valuable traits. Similarly, Kadoglidou et al. (2023) assessed 22 accessions and cultivars from Greek germplasm using morphological traits. Their study showed clear morphological distinctions between landraces and cultivars, with landraces exhibiting greater plant height, number of umbels, foliage density, and leaf size. Moreover, some landraces contained higher levels of chlorogenic acid, α -phellandrene, and polyphenols compared to cultivars, suggesting their potential value for both yield and quality traits in next genetic improvement programs. The current study aims to evaluate the genetic diversity among selected Iranian dill accessions based on morphological traits, to identify superior genotypes with desirable commercial characteristics, and to incorporate them into breeding programs.

Material and Methods

Plant Materials: Seeds from 30 different dill accessions were collected from various regions of Iran, representing diverse geographical and climatic conditions. These accessions have been traditionally cultivated by local farmers over an extended period. The geographical details and names of the accessions are provided in Table 1.

Field Area: The trial was performed at the research farm in Ardabil (38°15'06"N 48°17'51"E), Iran. The soil was characterized as a silty clay loam. The average annual rainfall was 300 mm, and the mean annual temperature was 8.5 °C.

Experimental Design: The accessions were sown in April using a randomized block scheme via three replicates, whereas each plot size was measured as 80 × 60 cm with four rows and 5 cm spacing between rows.

Trial Management: Standard agronomic practices, including irrigation and weed control, were applied throughout the growing season. Seed germination occurred within 15–20 days. At the 50% flowering stage in July, morphological traits were measured on seven randomly selected plants per plot.

Traits: The following traits were recorded: seed number per umbel (SNU); number of umbellets per umbel (NUU); number of umbels per plant (NUP); and number of nodes before flowering (NNF). Additionally, inflorescence fresh weight (IFW); plant fresh weight (PFW); inflorescence dry weight (IDW); and plant dry weight (PDW) were measured using a digital scale with a precision of 0.01 g. To determine dry weights, gathered samples were within paper bags located in an oven at 70 °C for 24 hours. Seed yield (SY) per plant was assessed at the maturity stage using seven randomly selected plants from each plot.

Table 1. The name and coordinates of studied dill (*Anethum graveolens* L.) accessions

#	Name	Latitude	Longitude	#	Name	Latitude	Longitude
1	Jokar	48°41'N	34°25'E	16	Kerman	57°40'N	30°17'E
2	Andimeshk	48°21'N	32°27'E	17	Jolfa	45°37'N	38°56'E
3	Malayer	48°49'N	34°17'E	18	Mashhad	59°32'N	36°19'E
4	Meshkin-A	47°40'N	38°23'E	19	Esfahan	51°40'N	32°40'E
5	Tabriz	47°40'N	38°23'E	20	Gorgan	54°25'N	36°50'E
6	Jahrom	53°33'N	28°30'E	21	Kashmar	58°27'N	35°14'E
7	Eslam shahr	51°13'N	35°32'E	22	Urmia	45°40'N	37°33'E
8	Hamedan-A	48°30'N	34°47'E	23	Shiraz	52°32'N	29°35'E
9	Hendostan	36°36'N	43°13'E	24	Astara	48°52'N	38°25'E
10	Ahvaz	48°43'N	31°20'E	25	SomehSara	49°18'N	37°18'E
11	Sarab	47°32'N	37°56'E	26	Dezful	48°24'N	32°23'E
12	Varamin	51°38'N	35°19'E	27	Gazvin	50°00'N	36°16'E
13	Meshkin-B	46°18'N	38°4'E	28	Bushehr	50°50'N	28°57'E
14	Tehran	51°22'N	35°42'E	29	Rezvanshahr	51°50'N	32°42'E
15	Damghan	54°20'N	36°9'E	30	Hamedan-B	48°30'N	34°47'E

Statistical analysis: The normality of the dataset was assessed using Q-Q plots. To analyze the accession-by-trait interaction matrix, a graphical biplot approach was employed, applying symmetric

scaling to obtain adjusted values for both accessions and traits, following the method described by Yan et al. (2023).

$$\frac{\alpha_{ij} - \beta_j}{\delta_j} = \sum_{n=1}^2 \lambda_n \Omega_{in} \Psi_{jn} + \xi_{ij}$$

where α_{ij} is the accession i for trait j , β_j is the value of trait j , δ_j is the square root of variability for trait j , λ_n is the eigenvalue of component n , Ω_{in} is value for accession i on component n , Ψ_{jn} is value for trait j on component n , and ξ_{ij} is the model residual. In the biplot analysis, Scaling = 1 was used to standardize the adjusted data across traits, ensuring comparability among variables. Centering = 2 was applied to center the accessions by the mean of each trait. To evaluate ideal traits, Singular Value Decomposition (SVD) = 2 was applied, which projects the singular values onto the eigenvectors of the traits. Similarly, SVD = 1 was used to project the singular values onto the eigenvectors of the accessions, allowing the identification of ideal accessions. All figures generated in this research were produced via GGEbiplot application (Yan, 2001).

Results

Biplot Fitting: The accession-by-trait biplot explained 83% of the total variation (Figure 1), indicating a complex pattern of interactions between accessions and traits in dill. Despite this complexity, the fitted model effectively captured the general structure of the interactions. Analysis of variance (results not shown) was conducted to determine the suitability of each trait for multivariate analysis. The significant magnitude of accession-by-trait interactions supported the use of the biplot approach for exploring the current dataset (Sabaghnia et al., 2024b).

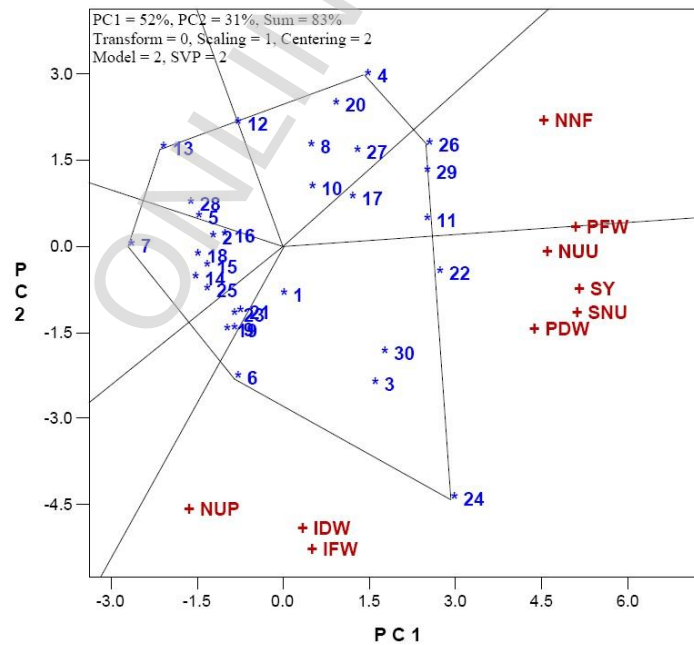


Figure 1. The hexagon shape of biplot model for traits of 30 dill (*Anethum graveolens* L.) accessions

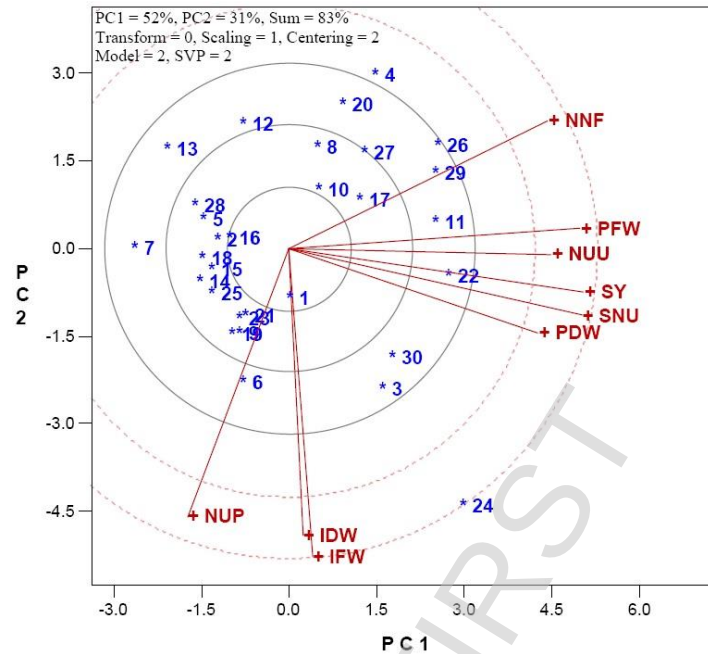


Figure 2. The vectors mood of biplot model for traits of 30 dill (*Anethum graveolens* L.) accessions

Hexagon Shape: The polygon (Figure 1) was formed by six vertex accessions; 4, 6, 7, 13, 24, and 26, which facilitated the comparison of accessions and the identification of those with superior performance in specific trait sectors. These vertex accessions represent potential heterotic parents for future breeding programs or candidates for cultivar release. The polygon was divided into six sectors by perpendicular lines, aiding the visual assessment of accession performance. Accession 26 exhibited superior performance for node number before flowering (NNF), while accession 24, along with accessions 3 and 30, showed the best performance for most of the remaining traits. In contrast, accessions 4, 6, 7, and 13, despite being vertices, did not show high values for any specific trait, as indicated by their sector positions in the biplot. Although, the biplot does not capture all trait variability and may not precisely represent trait means, it provides a useful overview of the dataset structure and trait–accession relationships. The accessions showed notable variation for most traits, confirming the presence of substantial genetic diversity, much of which is maintained by local farmers through traditional cultivation practices. These long-standing efforts to select and preserve landraces have contributed to the expansion of genetic variability in dill (Ninou et al., 2017). This biodiversity is a valuable resource for breeding programs aiming to develop new cultivars that are well-adapted to diverse environmental conditions and future agricultural demands. The wide range of geographical conditions, diverse bioclimatic zones, and the long history of dill cultivation in Iran have collectively contributed to the development of diverse morphological traits in local landraces.

Vector of Traits: To visually explore the main patterns among traits, trait vectors originating from the biplot center were generated to aid in interpreting associations, assuming that the model explained a sufficient portion of the total variation. Relationships between traits were assessed using cosine values, where an angle of 0° (cosine = +1), shows a positive association, 180° (cosine = -1), shows a negative association, and 90° (cosine = 0) indicates no association. The strength or significance of a trait's contribution is represented by the length of its vector (Figure 2). Clear positive

associations were observed among inflorescence fresh weight (IFW), number of umbels per plant (NUP), and inflorescence dry weight (IDW), as revealed by the acute angles. Similarly, positive relationships were identified among plant fresh weight (PFW), seed number per umbel (SNU), plant dry weight (PDW), number of umbellets per umbel (NUU), and seed yield (SY), also reflected by acute angles (Figure 2). In contrast, the near-perpendicular orientation of IFW, IDW, and NUP in relation to PFW, PDW, SNU, NUU, and SY suggested weak or negligible associations among these trait groups. Moreover, the obtuse angle between node number before flowering (NNF) and NUP indicated a relatively negative relationship between these two traits. Current results are consistent with past reports, like Rathore (2020), who observed positive correlations among the umbels of plant and its umbellets, as well as seeds of umbel, and seed yield performance in dill. Similar trait associations have also been reported by Holubowicz & Morozowska (2011), who found positive relationships between seed yield and yield components. While many of the observed relationships can be supported by correlation analysis, exact correspondence between visual and numerical correlations should not be expected. The biplot model reflects associations based on the dominant patterns in the dataset, while numerical values explain pairwise interrelationships. Additionally, discrepancies between the two approaches can arise because the biplot accounts for 83% of the total variance, rather than the full dataset variability.

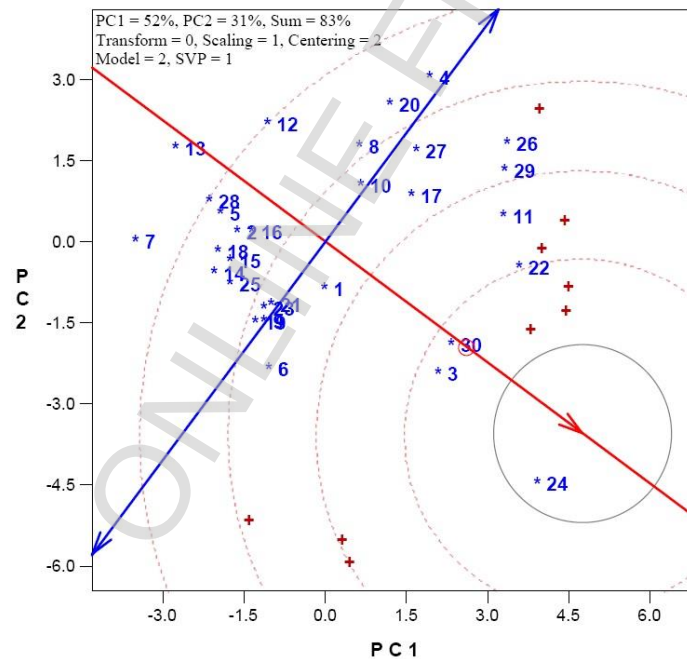


Figure 3. The ideal accession of biplot model for traits of 30 dill (*Anethum graveolens* L.) accessions

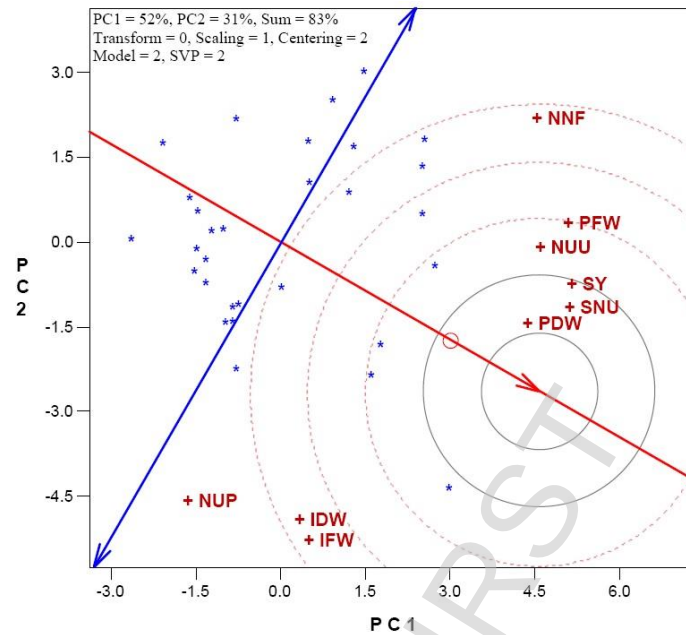


Figure 4. The ideal trait of biplot model for traits of 30 dill (*Anethum graveolens* L.) accessions

Ideal Accession: In Figure 3, a virtual ideal accession is depicted at the center of the concentric circles, located along the vertical axis, representing the mean value of traits with the longest vector and a zero projection on the horizontal axis. This position indicates low variability and high stability. Accessions closest to this ideal point are considered the most desirable. Accordingly, accession 24, followed by accessions 3, 30, and 22, were positioned nearest to the virtual accession, suggesting their superior performance and stability across traits. In contrast, the most distant accessions; 7 and 13, followed by 12 and 28, were deemed the least desirable, indicating limited ability to distinguish variation among dill traits (Figure 3). Accessions 3 (Malayer, western Iran), 22 (Urmia, northwestern Iran), 24 (Astara, northern Iran), and 30 (Hamedan-B, western Iran) demonstrated strong discriminative potential and can be used in breeding programs targeting multiple trait improvements. Sabaghnia et al. (2016) applied a similar approach in spinach (*Spinacia oleracea* L.), where the ideal genotype was defined by high scores on the first principal component (trait means) and low scores on the second (variability). Their findings confirmed the method's effectiveness in evaluating genotype performance and identifying superior accessions in vegetable crops.

Ideal Trait: Figure 4 illustrates the representational and discriminative capabilities of dill traits, with vector length serving as an indicator of discrimination capability. Longer vectors represent traits with a greater ability to discriminate among accessions. The representational ability of each trait is determined by the extent of its projection onto the mean trait coordinate, where shorter distances from the center indicate a higher degree of representativeness. Among the traits, seed yield, plant dry weight, and seed number per umbel, exhibited the strongest potential for both representational and discriminative capabilities, as they were positioned closest to the ideal trait location (Figure 4). SNU, PDW, and SY are less affected by environmental variations (Alan et al., 2022; Surve et al., 2024), making them crucial traits for inclusion in dill breeding programs. Moreover, by selecting accessions with high SNU, PDW, and SY, breeders can enhance the performance of dill crops, especially in the face of changing climatic conditions. These traits, being less sensitive to environmental fluctuations,

offer stability and reliability, which is particularly valuable in variable agricultural environments. Therefore, focusing on traits such as SNU is especially advantageous for genetic improvement projects aimed at breeding resilience and yield in response to climate change (Hołubowicz and Morozowska, 2011).

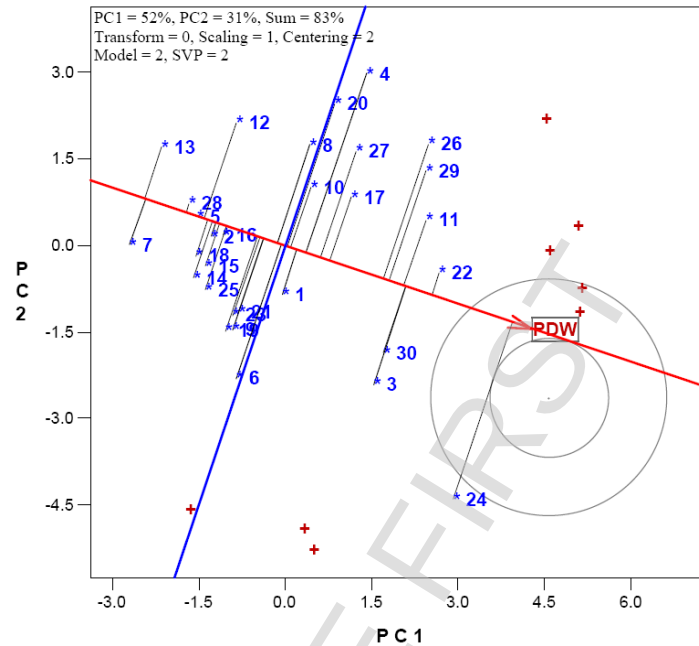


Figure 5. The examination of plant dry weight (PDW) in 30 dill (*Anethum graveolens* L.) accessions

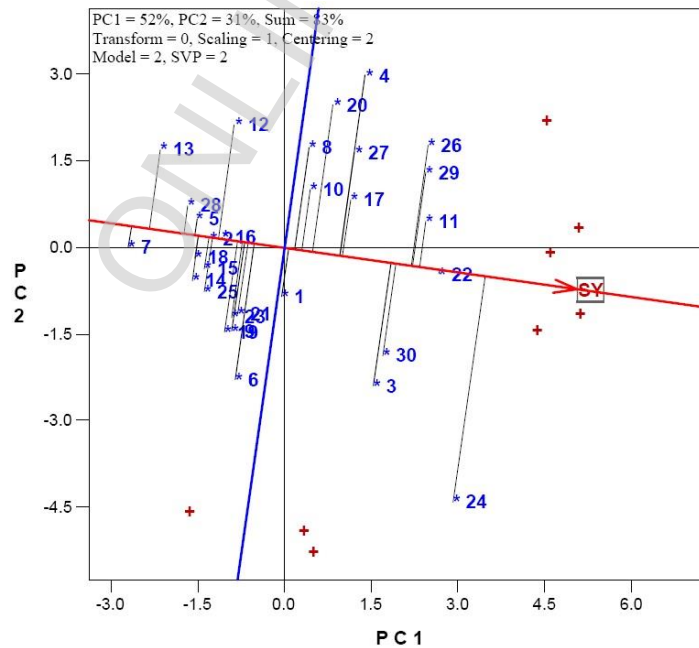


Figure 6. The examination of seed yield (SY) in 30 dill (*Anethum graveolens* L.) accessions

Examining of PDW and Seed Yield: When examining plant dry weight (PDW) across the dill accessions, it was evident that accession 24, followed by accessions 22, 30, 3, and 11, exhibited high plant dry weight (Figure 5). Accessions 22 and 11, with the shortest distances from the vertical axis, showed relatively low variation in PDW, suggesting stable performance. Conversely, accessions 7 and 13 had the lowest PDW (Figure 5). Based on these findings, accessions 22 (Urmia, northwest Iran) and 11 (Sarab, northwest Iran) stand out as promising candidates for future breeding programs aimed at cultivar release to achieve high biomass. Both accessions, originating from the northwest of Iran, appear well-adapted to upland, cool climatic conditions and are expected to exhibit minimal genotype-by-environment interactions. Local landraces, such as these, are valuable sources for identifying adaptation mechanisms and tolerance to biotic and environmental stresses (Ali et al., 2025). While plant breeders typically focus on short-term goals and elite genotypes, which may not always have suitable adaptation traits, landraces provide a more reliable option due to their strong adaptability. Therefore, accession 24, followed by accessions 22, 11, 26, 29, 30, and 3, exhibited high seed yield (Figure 6). Like PDW, accession 22 (Urmia) and accession 11 (Sarab) showed minimal variation in seed yield. Thus, these accessions, which maintain both high plant dry weight and seed yield potential, are suitable candidates for cultivar development after multi-environmental trials testing.

Discussion

Dill is a highly valuable crop, both as a vegetable and a medicinal plant, and its cultivation has been widespread across the world. In current research, the genetic diversity in some agronomic traits of 30 dill accessions was examined. The findings indicated the basic variation in morphological and yield performances, which have important implications for breeding programs focused on developing new cultivars. Genetic diversity has a critical role in the success of breeding programs, because it provides the needed raw plant materials for improving target traits. The analysis of morphological traits, like plant dry weight, seed yield, and other related components, showed remarkable variations across accessions. This variation suggests that Iranian dill accessions as local landraces, had a valuable genetic diversity that can be used for future breeding programs. Accessions 22 (Urmia) and 11 (Sarab) from northwest Iran, in particular, demonstrated consistent high performance for traits such as PDW and SY.

Landraces, such as those from the northwest of Iran, have long been recognized as important sources of genetic diversity, particularly for traits related to adaptation to local environmental stresses. These landraces have been shaped over generations by natural selection and cultivation practices, resulting in their enhanced ability to cope with biotic and environmental stresses. Marone et al. (2021), highlighted the huge role of local landraces in providing tolerance to environmental extremes, such as drought, temperature stresses, and infections of disease and pests. This is particularly relevant for dill, as environmental factors significantly affect its growth and yield. Although, elite accessions generated in breeding programs may show high performance under ideal conditions, they often lack the necessary adaptation traits to thrive under variable field conditions. However, landraces are a valuable resource, as they offer a higher degree of adaptability. Furthermore, landraces typically exhibit lower susceptibility to environmental stresses, which is critical in the context of climate change (Broccanello et al. 2023). As the climate continues to change, the resilience of landraces will become increasingly important in maintaining crop yield performances.

The results demonstrated the importance of selecting accessions with stable performance for key traits, particularly those that are less influenced by environmental factors. Traits such as seed number per umbel, plant dry weight, and seed yield were found to have strong discriminative power across the accessions, indicating their potential utility in breeding programs. Also, accessions 22 and

11 stood out for their high PDW and SY, demonstrating that these traits can be reliably used as indicators of productivity potential in dill breeding. The ability to consistently identify high-yielding accessions is particularly valuable for the development of improved cultivars (Varshney et al. 2021). Both PDW and SY are crucial indicators of plant performance, as they directly related with biomass and reproductive attributes, respectively. The identification of accessions with high PDW is significant for improving the overall biomass of dill, which is important for both food and medicinal purposes. The findings align with previous studies on other crops, which have shown that traits such as plant dry weight and seed yield are less sensitive to environmental fluctuations, making them ideal targets for selection in breeding programs (Langridge & Reynolds, 2021; Sabaghnia et al., 2024a). In the case of dill, accessions with high SNU and PDW are less influenced by environmental conditions, providing breeders with a stable genetic foundation for the development of new cultivars.

Genotype-by-environment interactions are a key factor in determining the stability and performance of crop genotypes across different environments. The genotype-by-environment interactions occur when the performance of genotypes varies significantly across environmental conditions, which can complicate the selection of stable and high-performing cultivars. In this study, the analysis of genotype-by-environment interactions were conducted through the graphical biplot, which provided insight into the patterns of interaction between accessions and traits. The ability of these accessions to maintain consistent performance for PDW and SY under diverse environmental conditions suggests that they possess a strong adaptability to changes in climate and growing conditions. This adaptability is an important issue for next breeding programs, as it ensures that the selected genotypes will perform reliably in a range of environments. Accessions with low genotype-by-environment interactions are especially valuable in the context of climate change, as they are less susceptible to the unpredictable effects of changing weather patterns.

The study highlighted the importance of understanding the interaction between genotypes and traits. The graphical biplot approach proved effective in illustrating the complex relationships between different traits and accessions, providing breeders with a powerful tool for identifying desirable genotypes (Mohebodini et al., 2024). By examining the biplot and the patterns of trait interactions, breeders can select accessions that not only perform well for key traits but also exhibit low genotype-by-environment interactions, making them ideal candidates for cultivar development. The findings of current research have significant implications for the improvement of dill cultivars through breeding programs. The identification of accessions with high PDW and SY, such as accessions 22 (Urmia) and 11 (Sarab), provides breeders with a solid foundation for developing new cultivars with improved biomass and seed yield. These accessions, with their stable performance across different environments, are valuable resources for future breeding efforts. The identification of local landraces with high adaptability to environmental stresses offers a unique opportunity to enhance the resilience of dill cultivars in the face of climate change (Ahmed et al., 2025). The use of landraces in breeding programs can help ensure that new cultivars are better suited to withstand environmental stresses, thereby maintaining productivity in the long term. Given the growing concerns about climate change and its potential impact on agriculture, the incorporation of landraces with strong adaptation traits is crucial for developing climate-resilient crops (Mondal et al., 2023).

The importance of selecting traits that are less influenced by environmental factors, such as SNU, PDW, and SY, was emphasize in this research. These traits provide breeders with reliable indicators of plant performance and can help ensure the stability of new cultivars across different growing conditions. By focusing on these traits, breeders can develop dill cultivars that not only perform well under ideal conditions but also maintain high productivity in the face of changing environmental conditions. These accessions, along with other local landraces, offer significant promise

for the development of climate-resilient dill varieties. The obtained results contribute to our understanding of the genetic diversity in dill and prepare a basis for next breeding efforts aimed at improving the performance and adaptability of this valuable crop.

Conclusion

The findings emphasize the value of landraces in breeding programs, as a sustainable genetic resource. Accessions 22 (Urmia) and 11 (Sarab) consistently performing well for important target traits like plant seed yield and dry weight of plant. Seed of umbel, plant dry weight, and seed yield were found to have strong discriminative power across the accessions. Fresh and dry weights of plants, seeds of umbel, umbellets of umbel, and seed yield were positively associated, so selecting of seeds and umbellets of umbel, can improve both seed yield and biomass of dill.

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Data availability statement: All the data are embedded in the manuscript. Raw data is available from corresponding author on reasonable request.

Ethical issues statement: No assistance from AI tools has been used for the writing of this manuscript.

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**Procena genetičkog diverziteta nekih agronomskih osobina
u genotipovima mirođije korišćenjem biplot modela**

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Sažetak: Kao široko gajena povrtarska kultura, mirođija (*Anethum graveolens* L.) se proizvodi za hranu i u medicinske svrhe. Ovo istraživanje analizira genetsku raznolikost 30 genotipova mirođije iz različitih oblasti Irana. Biplot varijacije genotip × osobina objasnio je 83% (52% i 31% za prvu i drugu glavnu komponentu, redom) ukupne varijacije, što ukazuje na složen obrazac interakcija između genotipa i osobina mirođije. Sveža i suva masa biljke, kao i prinos semena bili su povezani sa brojem semena po štitu i brojem sitnih cvasti po štitu, tako da se ove komponente prinosa mogu koristiti za poboljšanje i prinosa semena i biomase. Rezultati su otkrili značajne varijacije u osobinama među genotipovima, pri čemu genotipi 22 (Urmia) i 11 (Sarab) pokazuju konstantno visoke performanse i za suhu masu biljke i za prinos semena. Genotipovi 22 i 11 su identifikovani kao najpouzdaniji kandidati za buduće programe oplemenjivanja usmerene na poboljšanje biomase mirođije i prinosa semena, dok su genotipovi 24, 3, 22 i 30 identifikovani kao idealni.

Ključne reči: *Anethum graveolens* L., idealni genotip, interakcija genotip×osobina, mirođija, prinos