Acta fytotechn zootechn, 29, 2026(2): 158–167
http://www.acta.fapz.uniag.sk

**Original Paper**

# Genetic Diversity and Trait Relationships in some *Camelina* Genotypes under Semi-Arid Conditions

Naser Sabaghnia*[1], Asghar Ebadi[2], Mohsen Janmohammadi[1], Mehdi Mohebodini[3]

[1]*University of Maragheh, Faculty of Agriculture, Department of Plant Production and Genetics, Maragheh, Iran*
[2]*Moghan College of Agriculture and Natural Resources, University of Mohaghegh Ardabili, Ardabil, Iran*
[3] *University of Mohaghegh Ardabili, Faculty of Agricultural Science and Natural Resources, Department of Horticultural Science, Iran*

Article Details: Received: 2026-02-07 | Accepted: 2026-03-02 | Available online: 2026-06-30

https://doi.org/10.15414/afz.2026.29.02.158-167

This research evaluated twelve camelina genotypes, including eleven accessions and one variety (Soheil), over two consecutive growing seasons (2023–2024) at the semi-arid experimental farm of Parsabad, northwestern Iran. Field trials followed a randomized block arrangement with three replicates, and phenological traits (days to flowering and maturity), morphological characteristics (plant height, stem diameter, and height of first branch), and yield attributes (thousand-seed weight, pods per plant, seeds per pod, and yield performance) were quantified. Results demonstrated substantial phenotypic variability among genotypes, particularly for yield-related traits, indicating significant potential for selection and genetic improvement, while phenological traits exhibited low variability. Cluster analysis revealed four and three distinct genotype groups in the first and second years, respectively, with some genotypes consistently grouped across years, reflecting relatively low-variability. Trait-based dendrograms divided measured traits into two functional categories as phenology and plant height versus seed yield and related components. Although environmental effects influenced the magnitude of trait expression across years, genotypes with superior seed yield and thousand-seed weight were identified as promising candidates for breeding. The findings highlighted the potential of combining morpho-physiological evaluation with multivariate and clustering analyses to identify high-performing, genetically divergent camelina genotypes. Genotypes 1 from unknown source, 8 from Germany, and 12 as check cultivar from Iran, offered opportunities for breeding programs aimed at improving yield stability, and adaptability to semi-arid conditions. These insights provided a foundation for both future breeding efforts and the broader adoption of camelina as a multifunctional oilseed crop under challenging environments.

**Keywords:** *Camelina sativa*, morpho-physiological traits, cluster analysis, seed yield

## 1 Introduction

As an ancient Brassicaceae oilseeds crops, camelina (*Camelina sativa* (L.) Crantz), is identified as gold of pleasure or false flax. It has been cultivated since the Iron Age, particularly across Europe, which is regarded as its primary centers of origin (Brock et al., 2022). Cultivation of camelina sharply reduced significantly after the WW-II with the widespread adoption of higher-yielding and economically competitive oilseed crops from Brassicaceae like rapeseed (Kuzmanović et al., 2021). Morphologically, camelina is a small to medium-sized annual plant, typically reaching heights between 0.4 and 0.9 m, which develops branching stems bearing alternatively, lanceolate leaf positions, and produces racemose inflorescences composed of ting yellow flowers (Ghidoli et al., 2023). The fruit is a smooth, leathery silique containing golden-brown seeds, each 2–3 mm in length, so thousand-seed weight commonly ranges from 0.7 to 1.3 g (Angelini et al., 2020). Camelina is characterized by a short and flexible life cycle, requiring approximately three or four months to maturity in spring types (Weiss et al., 2024), and six to seven months in winter types (Royo-Esnal and Valencia-Gredilla, 2018), which makes it particularly suitable for low-input farming systems and

---

***Corresponding Author:** Naser Sabaghnia, Amir Kabir Highway, Professor Ghanadi Blvd., Golshahr, University of Maragheh, P.O. Box 55136-553, Maragheh, Iran
e-mail: sabaghnia@maragheh.ac.ir ORCID: https://orcid.org/0000-0001-9690-6525

resilient under changing climatic conditions. Camelina holds significant potential for biofuel and vegetable oil production in temperate regions due to its resistance to diseases such as alternaria black spot and pests. This makes it an ideal candidate for optimizing agronomic potential, enhancing unique oil qualities, and ensuring biosafety in agricultural production system (Vollmann and Eynck, 2015).

The camelina has proven valuable in crop rotation and intercropping schemes, especially in semi-arid and marginal environments. It is well adapted to cold climate and provide effective soil cover, thereby reducing erosion and enhancing soil organic carbon accumulation (Schillinger, 2019). In addition, camelina can contribute to weed suppression through both physical competition and biochemical interactions, supporting more sustainable weed management strategies. In recent years, increasing interest has focused on brassicaceous crops, like camelina, as covering species. Field experiments have shown that the inclusion of camelina in rotation with cereals can reduce the incidence of root diseases and enhance subsequent crop growth and yield when compared with rotations involving other cover species like rye (Wojciechowski et al., 2023). These results underline the multifunctional role of camelina in improving soil quality, particularly in degraded or low-carbon soils, while simultaneously contributing to erosion control and disease suppression (Marcheva et al., 2024). Beyond its agronomic role, camelina has attracted renewed attention due to its broad range of end uses. Camelina seeds contain up to 40% oil, characterized by a high proportion of unsaturated fatty acids, including approximately 35% $\alpha$-linolenic acid, about 20% linoleic acid, and 16% oleic acid (Kurasiak-Popowska et al., 2020). This composition makes camelina oil a promising raw material for food, feed, and bio-based industrial applications.

The development of improved camelina varieties must take into account key agronomic traits, including seed yield and its components, earliness, and other target traits. Genetic improvement of camelina is complicated by its allohexaploid genome ($2n = 40$) and relatively narrow genetic base (Mandáková et al., 2019). Using conventional breeding strategy, Ghidoli et al. (2024), developed a distinct camelina line that combines desirable traits like early maturity, larger seeds, and high oil content, and released as a promising new variety (C1244) for agricultural use. Also, advances in genomic resources and the integration of marker-assisted selection approaches are expected to substantially enhance the efficiency of camelina breeding programs. Wiwart et al. (2019), demonstrated that morphology of camelina seed can be distinguished based on quantitative shape, whereas key features such as seed area, was correlated with seed weight, and showed stronger discriminatory power than color descriptors. Fallah et al. (2023), indicated significant differences among camelina genotypes for most morphologic traits, and showed that yield had positive correlations with pods per plant and biomass, suggesting that improvement in these traits would contribute to enhanced yield potential. Camelina holds high potential as an oilseed crop for industrial and health applications, but realizing this potential requires further breeding for improved agronomic traits and seed quality (Vollmann et al., 2007). In the present investigation, some camelina genotypes were evaluated via morphologic traits to identify genetically divergent accessions using cluster analysis.

## 2 Material and Methods

### *2.1 Trials and Traits*

Twelve camelina genotypes were included in this investigation, comprising eleven accessions, and one developed variety as Soheil (Table 1). Field trials were conducted at the experimental farm of Parsabad (39° 38′ N; 47° 54′ E; 33 m above sea level), Faculty of Agriculture and Natural Resources (Moghan Campus), University of Mohaghegh Ardabili, northwestern Iran. It experiences a warm semi-arid climate, characterized by warm to hot summers and cool winters. The climatic data throughout growing seasons indicated that average temperatures ranged from 20 °C during the growing season, with extremes between 5 °C in winter and 35 °C in summer. Relative humidity ranged from 45% to 75% during the growing season. Soil characteristics of the experimental field were as loamy sand type with neurtrally pH = 7.5, low organic matter content, and acceptable electrical conductivity.Nitrogen content was 0.15%, phosphorus content was 12.5 mg/kg, and potassium content was 120 mg/kg. Annual precipitation is moderate, generally under 500 mm, mostly falling during the cooler months, while summers are typically dry. Field trials were carried out across two seasons (2023 and 2024), followed a randomized block arrangement with three replicates per accession. Each plot covered approximately 2 $m^2$ (1.0 × 2 m). Planting was performed on tilled soil manually, and rows were spaced 0.25 m apart, and seeds were sown at a density of 160 plant per unit area. Phenological observations were recorded throughout the growing season as the number of days from sowing to flowering (DF), which was determined when approximately 50% of the plants within a plot displayed at least one open flower. At physiological maturity, the number of days from sowing to maturity (DM), was recorded and all units were harvested with hand by ground cutting. Also, stem diameter (SD), pods per plant (PP), plant height (PH), height of first branch (HFB), and seeds per pod (SP), were measured from ten random samples of each plot. Harvested plant material was air-dried in a dry environment to complete seed maturation. Seeds were subsequently recovered by manually opening the pods and cleaned, to record thousand seed weight (TSW), as g and seed yield (SY), as g per area.

**Table 1** Accession number of the studied camelina genotypes and names of donor countries

| # | Accession number | Donor Country |
|---|---|---|
| 1 | CAM 113 | unknown |
| 2 | CAM 76 | USSR |
| 3 | CAM 152 | Germany |
| 4 | CAM 254 | Germany |
| 5 | CAM 238 | USSR |
| 6 | CAM 189 | unknown |
| 7 | CAM 274 | Bulgaria |
| 8 | CAM 146 | Germany |
| 9 | CAM 136 | Poland |
| 10 | CAM 127 | unknown |
| 11 | CAM 154 | Germany |
| 12 | – | Iran |

### *2.2 Statistical Analysis*

To ensure the accuracy of the data sets, the distribution of each trait was evaluated via the Kolmogorov-Smirnov procedure. Description indices like average, coefficient of variation (CV), and etc. were computed for traits to summarize the central tendency and variability of the data. For the classification of camelina genotypes and associated traits, agglomerative hierarchical cluster analysis was applied. In this approach, standardized squared Euclidean distances were calculated to quantify the similarity between genotypes as well as traits, and clustering was performed using Ward's method, which iteratively merges clusters to minimize the variance within each group. The resulting dendrograms provided a visual representation of the relationships, allowing for the identification of groups of genotypes with similar performance across multiple traits, as well as identification of similar traits. These dendrograms were generated via the in S-Plus 8.0.4 (TIBCO Inc., USA). To statistically confirm the number of meaningful clusters identified by the dendrograms, multivariate analysis of variance was conducted on the original dataset. This analysis evaluated the significance of multiple multivariate test statistics, including Trace of Pillai, Lambda index of Wilks, T-squared statistic of Hotellins, and Maximum Root amount of Roy, using the Multivariate statement in SPSS 27.0 (SPSS Inc., USA). The outcomes of these tests provided objective criteria for defining cluster boundaries, ensuring that the identified groups were not only visually distinct but also statistically robust.

## 3 Results and Discussion

### *3.1 Descriptive Statistics*

Descriptive statistics for camelina genotypes across the two growing seasons are presented in Table 2. In

**Table 2** Descriptive statistics of camelina traits across both years

| | DF | DM | SD | PP | PH | HFB | SP | TSW | SY |
|---|---|---|---|---|---|---|---|---|---|
| Year-1 | | | | | | | | | |
| Mean | 60.06 | 91.14 | 4.48 | 163.24 | 17.99 | 71.50 | 39.12 | 1.00 | 66.55 |
| SE of Mean | 0.49 | 0.49 | 0.16 | 11.42 | 0.76 | 1.29 | 0.50 | 0.05 | 2.96 |
| Variance | 2.91 | 2.91 | 0.30 | 1564.81 | 7.00 | 20.06 | 3.02 | 0.02 | 105.30 |
| Skewness | -0.71 | -1.70 | -0.44 | -0.83 | -0.16 | 0.07 | -0.16 | 1.56 | 0.10 |
| Kurtosis | 0.96 | 4.00 | -0.79 | 0.42 | -0.06 | 0.62 | 0.03 | 5.43 | -0.29 |
| CV | 2.84 | 1.87 | 12.29 | 24.23 | 14.71 | 6.26 | 4.44 | 15.73 | 15.42 |
| Year-2 | | | | | | | | | |
| Mean | 58.50 | 89.83 | 4.27 | 143.81 | 16.08 | 70.13 | 36.73 | 0.95 | 65.64 |
| SE of Mean | 1.22 | 0.87 | 0.15 | 13.47 | 1.26 | 1.30 | 0.55 | 0.05 | 5.07 |
| Variance | 17.79 | 9.00 | 0.28 | 2176.43 | 19.06 | 20.27 | 3.64 | 0.02 | 308.75 |
| Skewness | -0.10 | 0.15 | -0.15 | 0.39 | -1.15 | 0.07 | -0.61 | 1.44 | -0.29 |
| Kurtosis | 0.73 | -0.53 | -0.46 | -1.24 | 1.15 | -0.37 | 1.20 | 3.88 | 0.80 |
| CV | 7.21 | 3.34 | 12.40 | 32.44 | 27.15 | 6.42 | 5.20 | 16.57 | 26.77 |

SE – standard error; CV – coefficient of variation; traits were DF, days to flowering; DM – days to maturity; SD – stem diameter; PP – pods per plant; PH – plant height; HFB – height of first branch; SP – seeds per pod; TSW – thousand seed weight; SY – seed yield general, mean values in the first year were slightly lower than those in the second year for most traits, reflecting the influence of seasonal environmental conditions. The coefficient of variation (CV) values for phenological traits, such as DF and DM, were low in both years, indicating minimal variability. In contrast, traits related to yield, such as PP, TSW, and PH, showed moderate to high CV values, especially in the second year (Table 2). From a breeding perspective, the high variability observed for PP and SY indicates significant potential for selection and genetic improvement in camelina. On the other hand, the low CV values for DF and DM suggest limited phenotypic plasticity, making these traits reliable targets for crop adaptation. Therefore, breeding efforts should prioritize highly variable yield components, particularly PP, while maintaining stable phenological traits to ensure consistent performance across diverse environments. A two-year field study of camelina revealed that environmental factors were the primary source of variation in yield-related traits, with genotype-by-environment interactions also affecting performance (Kuzmanović et al., 2021). The study found significant differences in yield components among genotypes and environments, further supporting the notion that traits such as plant height, seed number, and seed yield vary with season and environmental conditions, which is valuable for breeding selection. Consequently, genotypes with both high performance and low variability are promising candidates for future breeding programs aimed at improving yield adaptability (Varshney et al., 2021). Identifying genotypes with relatively stable trait expression is crucial for breeding efforts focused on ensuring reliable performance across different environments.

### *3.2 Clustering of Genotypes*

The dendrogram shown in Figure 1 was developed to reveal the clustering pattern among camelina genotypes. The determination of optimal cutoff points for both years was supported by significant multivariate test statistics, including the Trace of Pillai, the Lambda index of Wilks, the T-squared statistic of Hotelling, and the Maximum Root statistic of Roy (Table 3). Based on these thresholds, the genotypes were classified into four groups in the first year and three groups in the second year. Mean trait values for the identified groups across both years are summarized in Table 4, providing a clear differentiation of cluster characteristics. In the first year, Group-I consisted of three genotypes (1, 8, and 12, the check cultivar) and was characterized by superior yield performance, high TSW, as well as high DF and SD. Group-II, which also included three genotypes (2, 7, and 11), demonstrated high yield potential and longer phenological traits, such as DF and DM (Table 4). Similarly, Group-III, comprising

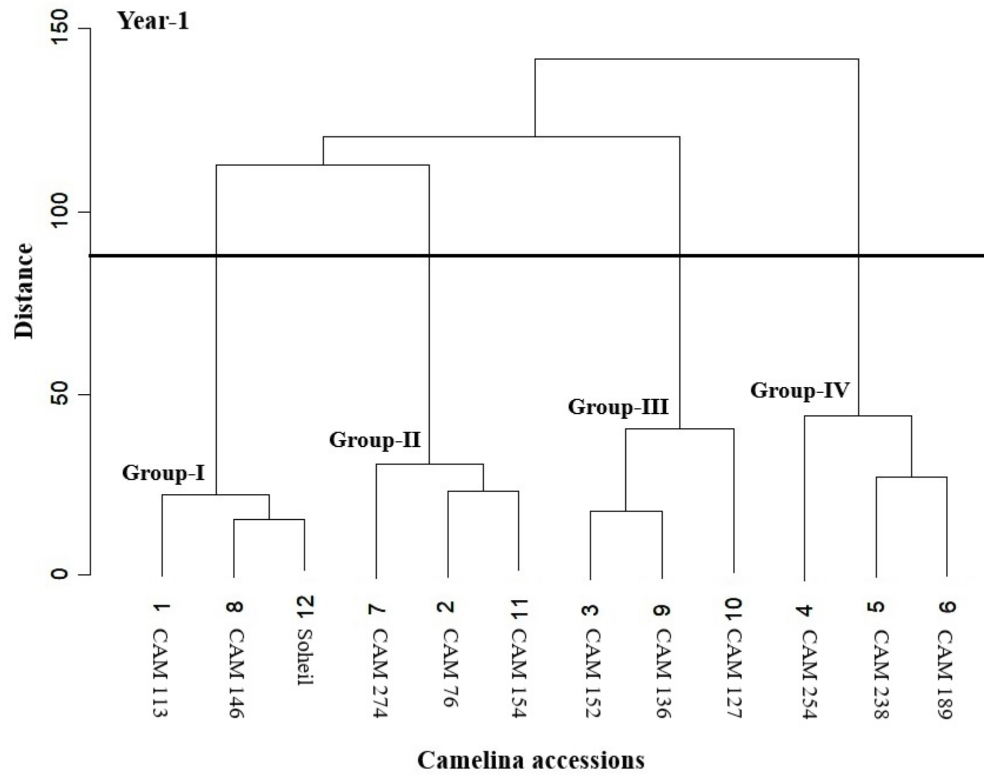

**Figure 1** Dendrogram of cluster analysis of twelve camelina genotypes in the first year

**Table 3** The results of multivariate analysis of variance for confirming the cutoff point in clustering of camelina genotypes across two years

| | Value | *F*-test | Hypothesis df | Error df | Sig. |
|---|---|---|---|---|---|
| Year-1 | | | | | |
| Pillai's trace | 6.73 | 3.33 | 24 | 9 | 0.005 |
| Wilks' lambda | 0.16 | 5.39 | 24 | 3.5 | 0.003 |
| Hotelling's trace | 155.63 | 58.36 | 8 | 3 | 0.004 |
| Roy's largest root | 141.48 | 53.05 | 8 | 3 | 0.004 |
| Year-2 | | | | | |
| Pillai's trace | 15.36 | 11.62 | 18 | 4 | 0.044 |
| Wilks' lambda | 0.24 | 18.34 | 18 | 2 | 0.038 |
| Hotelling's trace | 115.82 | 25.74 | 9 | 2 | 0.040 |
| Roy's largest root | 105.29 | 23.40 | 9 | 2 | 0.042 |

genotypes 3, 9, and 10, exhibited comparatively higher values for DM, SD, PP, HFB, and SP, though with low yield performance. Group-IV, made up of genotypes 4, 5, and 6, was characterized by low yield performance and low values for most traits, except for SD and PH (Table 4). Interestingly, these groupings did not reflect the geographical origins of the genotypes, suggesting that phenotypic similarity was independent of region. This observation aligns with the findings of Mastroberardino et al. (2025), who reported that morphological trait-based clustering of camelina genotypes did not produce distinct geographic groupings.

In the second year, the genotypes were classified into three distinct groups based on their performance (Figure 2). Group-A consisted of three camelina genotypes (1, 8, and 12, the check cultivar), which exhibited the lowest values for most traits, except for high SD and TSW (Table 4). Group-B comprised five genotypes (4, 5, 6, 7, and 11), which also showed low yield potential and yield components but were characterized by longer phenological periods and taller plants. Group-C included four genotypes (2, 3, 9, and 10), which demonstrated high or moderate values for all measured traits (Table 4). Across the two years, some genotypes maintained consistent grouping, while others shifted, reflecting the influence of environmental conditions on trait expression. Genotypes 1, 8, and 12 clustered together in both years. These genotypes had high yield and TSW in the first year, but their yield decreased in the second year, despite maintaining high SD and TSW. Other genotypes showed more variable performance. Those with longer phenological periods and taller plants in the second year (4, 5, 6, 7, and 11) often ranked lower for yield, highlighting the impact of year-to-year conditions on camelina traits and the importance of multi-year evaluations for selection. From a breeding perspective, local adaptation results from the accumulation of favorable gene combinations through selection acting on existing genetic variability, ultimately leading to phenotypic uniformity (Smulders et al., 2025). Therefore, phenotypic divergence among

**Table 4** Mean values of camelina traits for the identified clusters in both years

| Triats | Year-1 | | | | Year-2 | | |
|---|---|---|---|---|---|---|---|
| | I | II | III | IV | A | B | C |
| DF | 60.67 | 60.67 | 58.78 | 60.11 | 56.33 | 59.93 | 58.33 |
| DM | 90.00 | 91.33 | 91.78 | 91.45 | 88.00 | 91.33 | 89.33 |
| SD | 4.74 | 4.46 | 4.88 | 3.85 | 4.64 | 3.91 | 4.45 |
| PP | 171.86 | 170.53 | 204.37 | 106.21 | 144.14 | 99.06 | 199.50 |
| PH | 17.11 | 15.92 | 18.65 | 20.27 | 13.70 | 16.48 | 17.37 |
| HFB | 72.45 | 70.73 | 76.17 | 66.64 | 70.83 | 66.71 | 73.89 |
| SP | 39.21 | 38.65 | 40.45 | 38.16 | 36.98 | 35.54 | 38.02 |
| TSW | 1.13 | 0.96 | 0.97 | 0.93 | 1.08 | 0.87 | 0.96 |
| SY | 71.41 | 74.58 | 62.68 | 57.54 | 56.57 | 60.18 | 79.26 |

Traits were DF – days to flowering; DM – days to maturity; SD – stem diameter; PP – pods per plant; PH – plant height; HFB – height of first branch; SP – seeds per pod; TSW – thousand seed weight; SY – seed yield

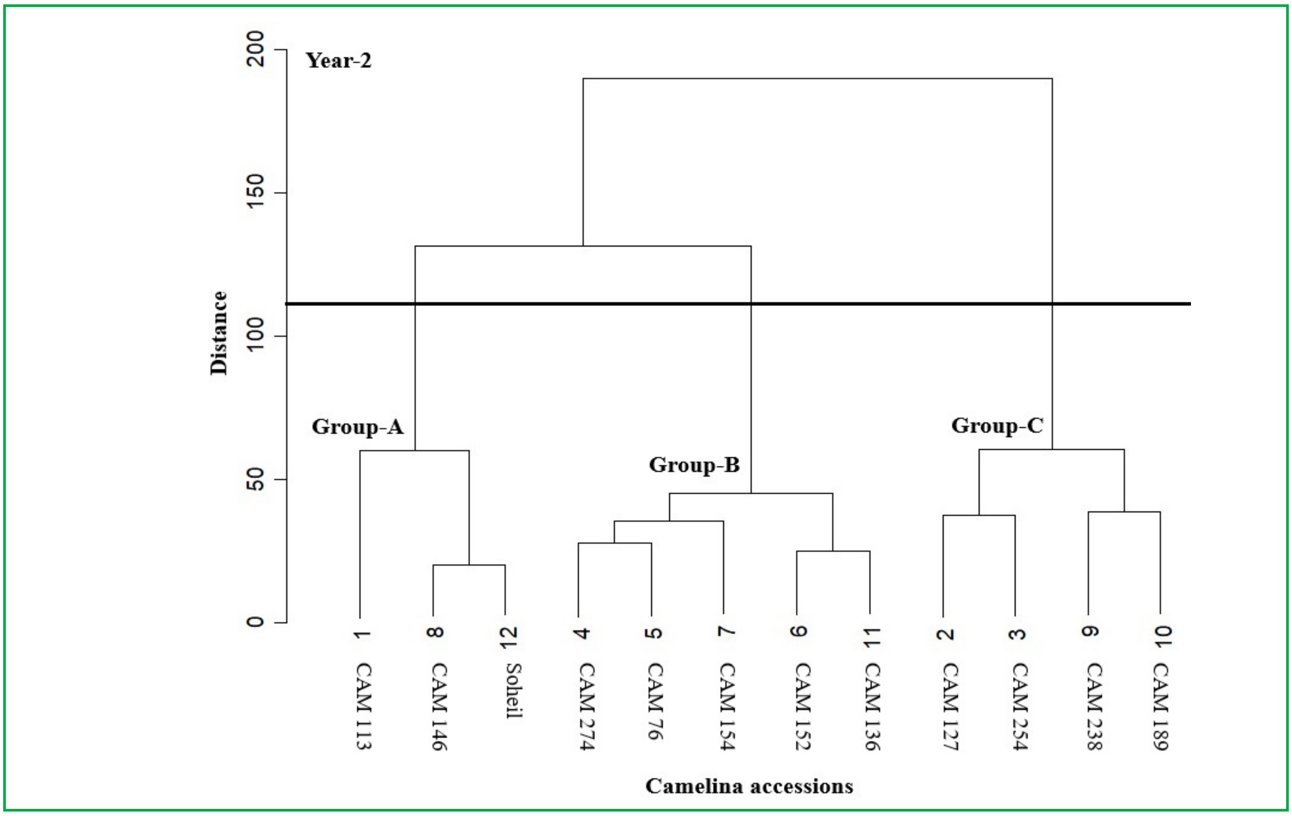

**Figure 2** Dendrogram of cluster analysis of twelve camelina genotypes in the second year

camelina genotypes may not necessarily reflect their genetic relatedness. Genotypes 1, 8, and 12 can be considered the best high-yielding genotypes across both years, as they consistently grouped together and showed superior or relatively stable performance for key yield components, such as yield and TSW.

### 3.3 *Clustering of traits*

Another dendrogram (Figure 3) was used to explore the relationships among camelina traits in the first year, with the cutoff point validated through multivariate analysis of variance. Significant results from the Trace of Pillai, Lambda index of Wilks, the T-squared statistic of Hotelling, and the Maximum Root statistic of Roy confirmed that the selected cutoff accurately represented the data structure (Table 5). As a result, the traits were classified into two main groups: Category-I, which included DF, DM, and PH, reflecting phenological characteristics and plant height, and Category-II, which encompassed SD, PP, HFB, SP, TSW, and SY, corresponding to seed yield and yield components (Figure 3). Yohannes et al. (2025) evaluated seed yield and related traits

**Table 5** The results of multivariate analysis of variance for confirming the cutoff point in clustering of measured traits camelina in both years

| | Value | *F*-test | Hypothesis df | Error df | Sig. |
|---|---|---|---|---|---|
| Year-1 | | | | | |
| Pillai's Trace | 37.81 | 13.91 | 7 | 1 | 0.002 |
| Wilks' Lambda | 36.83 | 10.48 | 7 | 1 | 0.002 |
| Hotelling's Trace | 109.83 | 268.17 | 7 | 1 | 0.002 |
| Roy's Largest Root | 109.83 | 268.17 | 7 | 1 | 0.002 |
| Year-2 | | | | | |
| Pillai's Trace | 36.54 | 21.14 | 7 | 1 | 0.004 |
| Wilks' Lambda | 33.39 | 10.03 | 7 | 1 | 0.004 |
| Hotelling's Trace | 99.08 | 241.91 | 7 | 1 | 0.004 |
| Roy's Largest Root | 99.08 | 241.91 | 7 | 1 | 0.004 |

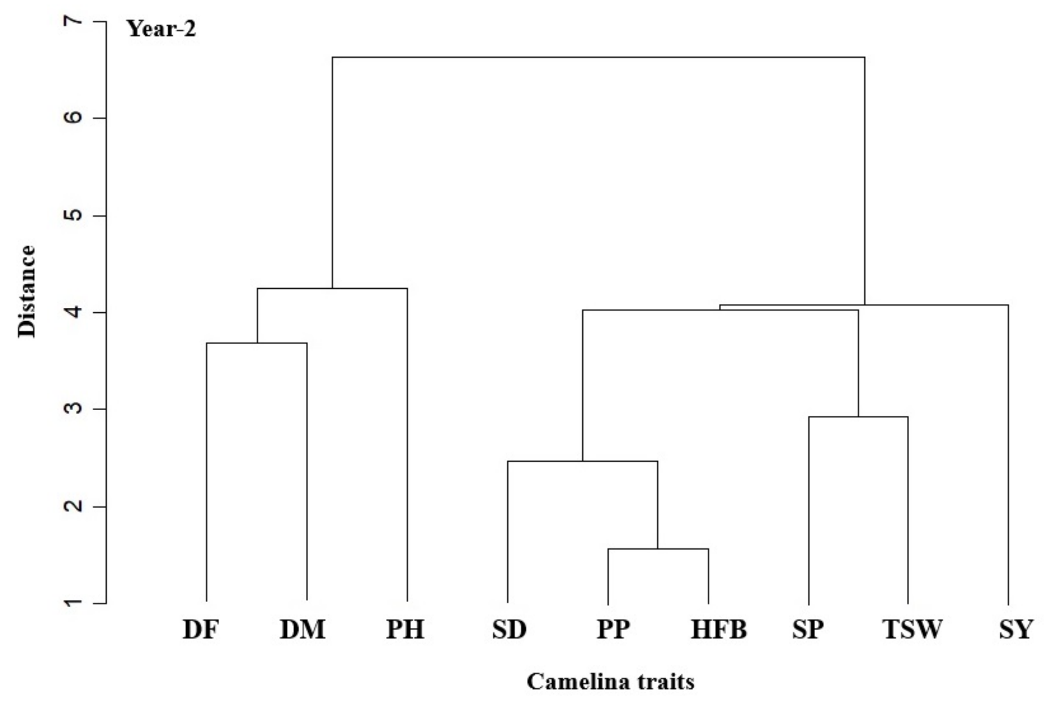

**Figure 3** Dendrogram of cluster analysis of traits of camelina in the first year
Traits were DF – days to flowering; DM – days to maturity; SD – stem diameter; PP – pods per plant; PH – plant height; HFB – height of first branch; SP – seeds per pod; TSW – thousand seed weight; SY – seed yield

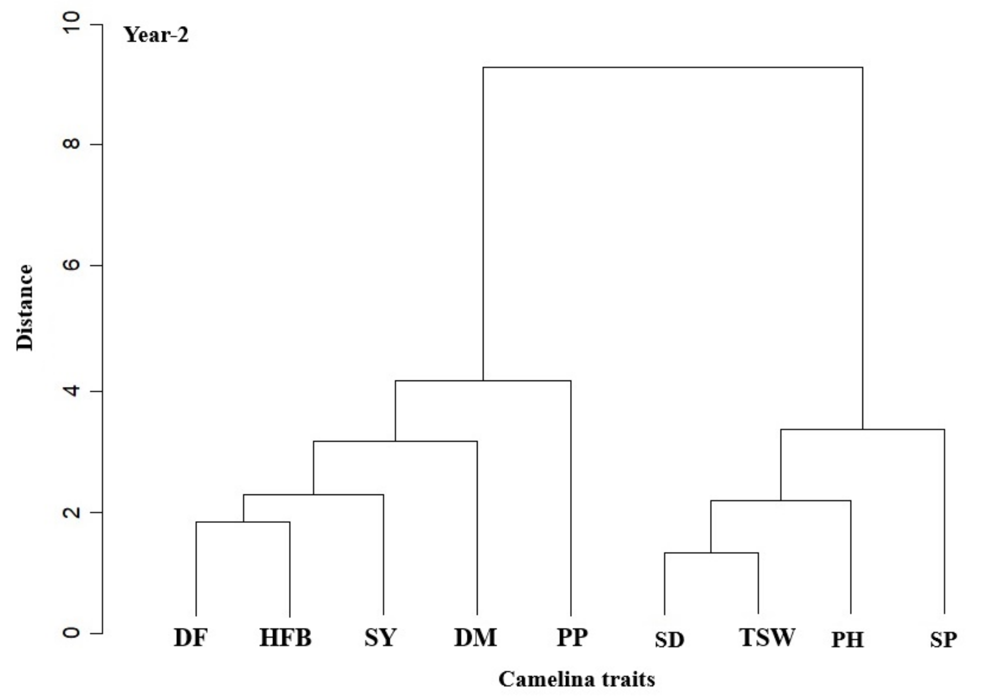

**Figure 4** Dendrogram of cluster analysis of traits of camelina in the second year
Traits were DF – days to flowering; DM – days to maturity; SD – stem diameter; PP – pods per plant; PH – plant height; HFB – height of first branch; SP – seeds per pod; TSW – thousand seed weight; SY – seed yield.

in camelina, such as the number of pods, seeds, and TSW, across different agroecological regions. They found significant variation in yield and yield components due to genotype-by-environment interactions and observed similar correlations between yield and component traits, helping to identify which components most influence yield. In the second year (Figure 4), the evaluated traits were divided into two major groups based on their functional significance. Category-A included DF, DM, PP, HFB, and SY, capturing phenological development, seed yield, and pods per plant. Category-B consisted of SD, PH, SP, and TSW, representing two yield components and plant architecture (Figure 4). These traits were more related to the physical structure of the plant and individual seed characteristics, such as stem thickness, plant height, seed size, and seeds per pod, which reflected plant architecture and components contributing to yield, but not yield directly. Although, both years grouped traits into categories based on phenology/yield versus architecture/components, the specific composition of each group shifted slightly, highlighting the dynamic contributions of traits like pods per plant and plant height to performance across years.

### *3.4 Discussion*

Camelina has gained attention as a promising oilseed crop for sustainable agriculture due to its short life cycle, adaptability to marginal environments, and diverse applications. This study assessed multiple camelina genotypes over two growing seasons, providing important insights into breeding strategies, agronomic management, and the broader potential of camelina in semi-arid cropping systems. The observed phenotypic differences and the potential for improving yield stability, adaptability, and utility under such conditions have significant practical implications. Vollmann et al. (2007) highlighted the critical role of environmental conditions in shaping agronomic performance of camelina, noting that genotype-by-environment interactions, while present for several traits, were often secondary to the primary influence of environmental factors. This suggests that adaptability of camelina across environments can be leveraged to select for stable, high-performing genotypes. Breeding efforts should focus on identifying genotypes with optimal combinations of seed size, plant architecture, and phenology, as these traits are strongly linked to yield potential and resilience (Alberghini et al., 2025). This research identifies pods per plant, thousand seed weight, and early flowering as key agronomic traits associated with superior yield performance. Conventional selection for these traits can expedite breeding cycles and improve trait predictability. However, as Vollmann et al. (2015), and Blume et al. (2023), also emphasized, relatively narrow genetic base of camelina which limits the range of available genotypes, underscoring the importance of broadening genetic diversity through the introduction of traits from wild relatives or other Brassicaceae species, which is crucial to enhance genetic variation and support future breeding programs.

Phenological traits, such as days to flowering and days to maturity, play a pivotal role in crop adaptation to specific environments. Gesch et al. (2022) suggested that short-season genotypes offer the advantage of fitting into tight crop rotations, especially in areas with limited growing periods, thus enabling camelina to be incorporated into double-cropping systems. In contrast, longer-season genotypes may produce higher biomass but risk exposure to late-season drought or heat stress (Smith and Lu, 2024). This study supports the notion that selecting genotypes with appropriate flowering and maturity windows for local climates is essential for optimizing yield and minimizing environmental stress. As noted by Ahmad et al. (2023), even small shifts in flowering time can significantly influence yield, disease pressure, and harvest efficiency. In practical terms, optimizing plant architecture through selection for traits like plant height, stem diameter, and robust stems is essential for improving agronomic performance of camelina. This can enhance light interception, reduce lodging, and improve mechanical harvesting efficiency. Genotypes with moderate plant height and sturdy stems are less prone to lodging under high biomass conditions, facilitating easier harvest (Bakhshandeh et al., 2023). Vollmann et al. (2007) also found that seed size and uniformity are critical for post-harvest handling and oil extraction efficiency, which further underlines the importance of these traits for the economic viability of camelina cultivation.

The genotype-by-environment interactions observed in camelina underscore the necessity of multi-year and multi-location trials, as environmental factors such as precipitation and temperature heavily influence seed yield and its components (Clemente et al., 2025). For semi-arid regions, water availability during flowering and pod-filling stages is crucial. Therefore, breeding should prioritize genotypes that exhibit high yield and environmental plasticity, enabling them to perform well under variable conditions (Neupane et al., 2020). Additionally, practical cultivation strategies, such as supplemental irrigation during critical periods or optimizing planting dates to avoid heat stress during flowering, can further stabilize yield across seasons. One of the notable advantages of camelina is its potential role in sustainable cropping systems. Its short growth cycle and adaptability make it a valuable break crop in cereal-based rotations, offering benefits such as soil cover, organic matter input, and weed suppression. These qualities can help improve soil health while maintaining economic viability, especially in regions that face challenges in managing crop residues (Olba-Zięty et al., 2025). However, integrating camelina into crop rotations requires careful planning, considering planting dates, termination methods, and nutrient management to ensure the following crops are not negatively impacted.

Despite its potential, camelina faces practical challenges, such as small seed size, which can complicate sowing and require precise equipment for uniform emergence and target plant density. Additionally, susceptibility to fungal pathogens like Alternaria and Sclerotinia can reduce seed quality and yield if not managed effectively (Zamani-Noor, 2021). Vollmann et al. (2007), and Yin et al. (2025) emphasized that the introduction of resistant varieties, along with crop rotation practices that help reduce pathogen loads, is essential for mitigating these risks. Moreover, the integration of multi-trait evaluation in breeding programs allows for the selection of genotypes with stable performance across environments. Key traits such as pod number and seed weight should be prioritized, alongside maintaining favorable plant architecture and phenological characteristics that facilitate mechanized harvesting and adaptability to diverse environments (Kınay et al., 2019).

To fully realize camelina's potential, future research should focus on expanding its genetic base through introgression from wild relatives, as well as exploring the molecular basis of key agronomic traits. Climate-resilient traits and disease resistance should be prioritized to ensure stable production in the face of changing climatic conditions. Agronomic research should also refine management practices, including optimal sowing densities, fertilization regimes, and water management, to maximize yield and oil quality. With its short growth cycle, camelina can provide farmers with flexibility in crop rotations, cover cropping, and erosion control, while industrial stakeholders can benefit from its high-quality oil. The integration of conventional and genomic breeding approaches, supported by sound agronomic practices, positions camelina as a promising crop for both food and non-food applications in diverse agricultural systems.

## 4 Conclusions

Camelina genotypes displayed considerable variation in yield-related traits, plant architecture, and seed characteristics, while phenological traits remained relatively stable and low in variability across both years. Traits with higher variability, such as pods per plant and seed yield, offer significant potential for genetic improvement through selective breeding. Cluster analysis identified four distinct clusters in the first year and three in the second year, reflecting the differences in genotype performance and trait combinations. Notably, three genotypes; 1 (from an unknown source), 8 (from Germany), and 12 (the check cultivar from Iran), grouped together and exhibited consistently high yield and stable thousand-seed weight. These genotypes stand out as strong candidates for breeding programs, demonstrating the potential for stable performance and adaptation in semi-arid environment.

### Conflict of Interest

The authors have no affiliation with any organization that has a direct or indirect financial interest in the subject matter discussed in the manuscript.

### Author Contributions

M.J. and A.E. created the original concept proposal. N.S. developed the theory and performed the computations. A.E. verified the analytical methods. M.J. Design and implementation of an experimental plan on the field. N.S. and M.M. collected agronomic data. N.S. and A.E. conducted the statistical analysis and graph preparation. All authors discussed the results and contributed to the final manuscript.

## References

Ahmad, M. et al. (2023). Changing Climate Scenario: Perspectives of *Camelina sativa* as Low-Input Biofuel and Oilseed Crop. In Ahmed, M. (eds) *Global Agricultural Production: Resilience to Climate Change*. Springer, Cham. https://doi.org/10.1007/978-3-031-14973-3_7

Alberghini, B. et al. (2025). Assessing different physiological, seed yield and quality responses of camelina lines to drought. *Industrial Crops and Products*, 234, 121528. https://doi.org/10.1016/j.indcrop.2025.121528

Angelini, L. G. et al. (2020). Performance and potentiality of camelina (*Camelina sativa* L. Crantz) genotypes in response to sowing date under Mediterranean environment. *Agronomy*, 10(12), 1929. https://doi.org/10.3390/agronomy10121929

Bakhshandeh, E. et al.(2023). Quantifying plant biomass and seed production in camelina (*Camelina sativa* (L.) Crantz) across a large range of plant densities: Modelling approaches. *Annals of Applied Biology*, 183(1), 23–32. https://doi.org/10.1111/aab.12830

Blume, R. Y. et al. (2023). Overcoming genetic paucity of *Camelina sativa*: possibilities for interspecific hybridization conditioned by the genus evolution pathway. *Frontiers in Plant Science*, 14, 1259431. https://doi.org/10.3389/fpls.2023.1259431

Brock, J. R., Ritchey, M. M., & Olsen, K. M. (2022). Molecular and archaeological evidence on the geographical origin of domestication for *Camelina sativa*. *American Journal of Botany*, 109(7), 1177–1190. https://doi.org/10.1002/ajb2.16027

Clemente, C. et al. (2025). Effect of environmental conditions on seed yield and metabolomic profile of camelina (*Camelina* *sativa* (L.) Crantz) through on farm multilocation trials. *Journal of Agriculture and Food Research*, 21, 101814. https://doi.org/10.1016/j.jafr.2025.101814

Fallah, F., Kahrizi, D., Rezaeizad, A., Zebarjadi, A., Zarei, L., & Doğan, H. Ü. L. Y. A. (2023). Assessment of genetic variability and genetic parameters of morphological and agro-physiological traits in *Camelina sativa* (L.). *Turkish Journal of Agriculture and Forestry*, 47(2), 242–251. https://doi.org/10.55730/1300-011X.3082

Gesch, R. W. et al. (2022). Double-cropping oilseed sunflower after winter camelina. *Industrial Crops and Products*, 181, 114811. https://doi.org/10.1016/j.indcrop.2022.114811

Ghidoli, M. et al. (2024). Genetic study of *Camelina sativa* oilseed crop and selection of a new variety by the bulk method. *Frontiers in Plant Science*, 15, 1385332. https://doi.org/10.3389/fpls.2024.1385332

Ghidoli, M. Et al. (2023). *Camelina sativa* (L.) Crantz as a promising cover crop species with allelopathic potential. *Agronomy*, 13(8), 2187. https://doi.org/10.3390/agronomy13082187

Kınay, A. et al. (2019). Yield and quality parameters of winter and summer-sown different camelina (*Camelina sativa* L.) genotypes. *Turkish Journal of Field Crops*, 24(2), 164–169. https://doi.org/10.17557/tjfc.631133

Kurasiak-Popowska, D., Graczyk, M., & Stuper-Szablewska, K. (2020). Winter camelina seeds as a raw material for the production of erucic acid-free oil. *Food Chemis*try, 330, 127265. https://doi.org/10.1016/j.foodchem.2020.127265

Kuzmanović, B. et al. (2021). Yield-related traits of 20 spring camelina genotypes grown in a multi-environment study in Serbia. *Agronomy*, 11(5), 858. https://doi.org/10.3390/agronomy11050858

Mandáková, T. et al. (2019). Origin and evolution of diploid and allopolyploid Camelina genomes were accompanied by chromosome shattering. *The Plant Cell*, 31(11), 2596–2612. https://doi.org/10.1105/tpc.19.00366

Marcheva, M. et al. (2024). Positive effect of Camelina intercropping with legumes on soil microbial diversity by applying NGS analysis and mobile fluorescence spectroscopy. *Applied Sciences*, 14(19), 9046. https://doi.org/10.3390/app14199046

Mastroberardino, R., Zanetti, F., & Monti, A. (2025). Exploring intraspecific variation in salinity tolerance at germination and seedling development stages in *Camelina sativa*. *Frontiers in Plant Science*, 16, 1713651. https://doi.org/10.3389/fpls.2025.1713651

Neupane, D. et al. (2020). Camelina production parameters response to different irrigation regimes. *Industrial Crops and Products*, 148, 112286. https://doi.org/10.1016/j.indcrop.2020.112286

Olba-Zięty, E. et al. (2025). Economic efficiency of production of camelina and spelt wheat in organic intercropping systems. *Industrial Crops and Products*, 237, 122190. https://doi.org/10.1016/j.indcrop.2025.122190

Royo-Esnal, A., & Valencia-Gredilla, F. (2018). Camelina as a rotation crop for weed control in organic farming in a semiarid Mediterranean climate. *Agriculture*, 8(10), 156. https://doi.org/10.3390/agriculture8100156

Schillinger, W. F. (2019). Camelina: Long-term cropping systems research in a dry Mediterranean climate. *Field Crops Research*, 235, 87–94. https://doi.org/10.1016/j.fcr.2019.02.023

Smith, B. E., & Lu, C. (2024). Heat stress during reproductive stages reduces camelina seed productivity and changes seed composition. *Heliyon*, 10(4). https://doi.org/10.1016/j.heliyon.2024.e26678

Smulders, M. J. et al. (2025). Resilience through diversity: The potential of modelling species and variety interactions to enhance resilience of production systems. *Plants, People, Planet*. https://doi.org/10.1002/ppp3.70095

Varshney, R. K. Et al. (2021). Breeding custom-designed crops for improved drought adaptation. *Advanced Genetics*, 2(3), e202100017. https://doi.org/10.1002/ggn2.202100017

Vollmann, J., & Eynck, C. (2015). Camelina as a sustainable oilseed crop: Contributions of plant breeding and genetic engineering. *Biotechnology Journal,* 10(4), 525–535. https://doi.org/10.1002/biot.201400200

Vollmann, J. et al. (2007). Agronomic evaluation of camelina genotypes selected for seed quality characteristics. *Industrial Crops and Products*, 26(3), 270–277. https://doi.org/10.1016/j.indcrop.2007.03.017

Weiss, R. M. et al. (2024). Bioclimatic analysis of potential worldwide production of spring-type camelina [*Camelina sativa* (L.) Crantz] seeded in the spring. *GCB Bioenergy*, 16(2), e13126. https://doi.org/10.1111/gcbb.13126

Wiwart, M. et al. (2019). Variation in the morphometric parameters of seeds of spring and winter genotypes of *Camelina sativa* (L.) Crantz. *Industrial Crops and Products*, 139, 111571. https://doi.org/10.1016/j.indcrop.2019.111571

Wojciechowski, A. et al. (2023). Effects of cover crops on maize establishment, root mycorrhizal colonization, plant growth and grain yield depend on their botanical family: A global meta-analysis. *Agriculture, Ecosystems & Environment,* 356, 108648. https://doi.org/10.1016/j.agee.2023.108648

Yin, C. et al. (2025). Crop Rotation Effects on the Population Density of Soybean Soilborne Pathogens Under a No-Till Cropping System. *Plant Disease*, 109(7), 1541–1550. https://doi.org/10.1094/PDIS-09-24-1953-RE

Yohannes, G. et al. (2025). Yield and nutritional traits of Camelina (*Camelina sativa* L.) in response to sowing dates and Agroecological variations in Northern Ethiopia. *Discover Applied Sciences*, 7, 1125. https://doi.org/10.1007/s42452-025-07593-y

Zamani-Noor, N. (2021). Baseline sensitivity and control efficacy of various group of fungicides against *Sclerotinia sclerotiorum* in oilseed rape cultivation. *Agronomy*, 11(9), 1758. https://doi.org/10.3390/agronomy11091758