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# MORPHOLOGICAL AND FATTY ACID DIVERSITY IN *CAMELINA SATIVA* MUTANT LINES FOR LOW-INPUT BIODIESEL PRODUCTION IN SUB-TROPICAL ENVIRONMENTS

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## ABSTRACT

*Camelina sativa* has emerged as a promising oilseed crop for biodiesel and ethanol production due to its high yield potential under minimal input conditions, making it suitable for marginal and rainfed lands. In this study, a three-year field evaluation of 50 mutant lines was conducted under sub-tropical low-input conditions to assess morphological variation and oil quality. Significant genetic variability was observed across key agronomic traits such as plant height (48–78 cm), capsule number (338–5627), and seed yield (6–14 g per plant), indicating ample scope for selection. Fatty acid profiling revealed considerable variation in oleic acid (0–26.5%) and palmitoleic acid (0–63.6%), with several lines rich in unsaturated fatty acids, essential for biodiesel quality and oxidative stability. Notably, mutant lines 6783, 4844, 5958, 5989, and 6725 exhibited superior yield performance, while lines such as 6862, 6882, 5296, and 6795 showed desirable oil profiles for biofuel. These findings underline the potential of selected mutant lines to serve as climate-resilient, low-input feedstock for sustainable biodiesel production. This work contributes toward the development of environment-friendly cropping systems and energy diversification strategies aligned with climate adaptation and SDG 7 (Affordable and Clean Energy) and SDG 13 (Climate Action) goals.

**Keywords**: *Camelina sativa*; Mutant germplasm; Fatty acid composition; Low-input agriculture; Biodiesel feedstock; Climate-resilient crops.

## INTRODUCTION

*Camelina sativa* L. Crantz, commonly known as "wild flax," "false flax," or "gold-of-pleasure," is a member of the *Brassicaceae* family valued for its adaptability and low-input requirements (van Belle *et al*., 2025; Abdullah *et al*., 2024; Ahmad *et al*., 2022; Clark, 2011). Native to temperate regions, Camelina demonstrates strong resilience under diverse environmental conditions, including arid climates and marginal soils (Abdullah *et al*., 2024; Iskandarov *et al*., 2014; Kirkhus *et al*., 2013; Vollmann *et al*., 2005; Francis & Campbell, 2003). Its seeds are nutritionally rich, containing 25-45% protein and 35-49% oil (Jiang *et al*.,2014; Gugel, 2006). The oil is abundant in unsaturated fatty acids, particularlylinolenic (32.6-38.2%), oleic (14.5-19.7%), linoleic (16.9-19.6%), and gadoleic acid (12.4-16.2%), making it a valuable source for both food and biofuel applications (Clavijo-Bernal *et al*., 2024; Ahmad *et al*., 2022; Jiang *et al*., 2014; Zubr, 2003).

Driven by rising energy demands and environmental concerns, it has gained global attention as a non-food oilseed feedstock for biodiesel (Cai et al., 2024; Ahmad et al., 2022; USDA, 2010; Altin et al., 2001). Compared to jatropha and soybean, camelina offers a higher net energy ratio (5.22 vs. 3.74), greater adaptability to marginal lands, and significantly lower input costs (Aslam *et al.*, 2020; Gugel, 2006; USDA, 2010). In addition to its industrial relevance, camelina

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oil also offers health-promoting benefits, further increasing its value in diversified agro-industrial systems (Ehrensing and Guy, 2008; Johnson et al., 2006). Its growing popularity across Austria, Germany, the UK, and the USA reflects its expanding role in sustainable agriculture (Aslam et al., 2020; Angelini et al., 2020; Zanetti et al., 2017; McVay, 2008).

The primary barrier to widespread biofuel crop adoption in regions like Pakistan lies in balancing fuel production with food security and land use efficiency (Gugel, 2006; Vollmann et al., 1996). With its low nutrient demands and ability to thrive on marginal or rainfed lands (van Belle et al., 2025; Cai et al., 2024; and Clavijo-Bernal et al., 2024), it presents a viable solution. Comparative studies showed that it outperforms canola and soybean in oil quality under low fertilizer and irrigation regimes (Pavlista & Baltensperger, 2007). Its allelopathic response and wide adaptability across soil types and climatic zones further support its utility in rehabilitating degraded or underused agricultural landscapes (Ghidoli, 2024; Bernardo *et al.*, 2003; Lovett & Duffield, 1981).

By enhancing sustainable biofuel production and rehabilitating marginal lands (Clavijo-Bernal *et al*.,2024; Ghidoli *et al.*, 2023), camelina-based systems directly contribute to multiple United Nations Sustainable Development Goals (SDGs), including SDG 2 (Zero Hunger), SDG 7 (Affordable and Clean Energy), and SDG 13 (Climate Action). Its integration into Pakistan's agricultural landscape offers a climate-smart pathway to energy diversification and food system resilience (United Nations, 2015).

The Cholistan desert and other barani (rainfed) regions of Pakistan represent vast, underutilized territories suitable for climate-resilient oilseed crops. In this context, the evaluation of a large, genetically diverse population of *Camelina sativa* $M_5$ mutant lines, originating from the University of California, Davis, was undertaken. The present study aimed to assess the performance of these lines under low-input sub-tropical field conditions, focusing on morphological traits and fatty acid profiles. The goal was to identify high-yielding, oil-rich genotypes suited for biodiesel production, thereby reducing fuel import dependency while supporting eco-friendly agriculture.

## MATERIALS AND METHODS

The field trials were conducted over three consecutive years at the research farm of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan (31°25′00″ N, 73°04′59″ E; elevation: 186 m). The region features an arid to semi-arid climate with high evapotranspiration, low annual rainfall (~13.4 mm), and significant temperature variation ranging from 21-28.6°C in winter and 30-45°C in summer (Weather Atlas, 2024). Average annual humidity was recorded at 35.17%. This data was sourced from the Agricultural Meteorology Cell, Department of Agronomy, UAF (https://www.weatheratlas.com/en/pakistan/faisalabad-climate#temperature).

A total of 3,000 $M_5$ mutant lines of *Camelina sativa*, obtained from the University of California, Davis, were initially screened. Based on three-year performance, 50 high-yielding and stable lines were selected for detailed morphological and biochemical assessment (Table 1).

**Table 1. *Camelina sativa* mutant lines ($M_5$) used in research.**

| | | | | |
|---|---|---|---|---|
| 6793 | 6767 | 6487 | 6633 | 4755 |
| 6889 | 6894 | 5627 | 6558 | 4844 |
| 6780 | 6797 | 6654 | 6350 | 5436 |
| 6795 | 6725 | 6475 | 3879 | 4640 |
| 6882 | 6846 | 6360 | 4601 | 4061 |
| 5296 | 6766 | 6825 | 5137 | 4100 |
| 6789 | 5651 | 6813 | 5151 | 3620 |
| 6860 | 5989 | 6783 | 5293 | 4712 |
| 6760 | 6392 | 3771 | 5127 | 5958 |
| 6747 | 6832 | 4841 | 4828 | 6570 |

The experiment followed a randomized complete block design (RCBD) with two replications. Each plot consisted of a single 2-meter row, spaced 30 cm between rows and 10 cm between plants. Sowing was performed manually using a dibbler, placing three seeds per hole at 1–2 cm depth and thinning to one seedling per hill at the 2-3 leaf stage. No synthetic fertilizers or irrigation were applied to simulate low-

input conditions, while standard agronomic and plant protection measures were maintained.

At physiological maturity (85-100 days), five representative plants per plot were randomly selected for data collection. Morphological traits recorded included plant height, number of capsules, number of inflorescences, primary and secondary branches, leaf area, and 1,000-seed weight. Biochemical traits, including total protein and oil content, were estimated using the Kjeldahl (1883) and Soxhlet (1879) methods, following the procedures of the AOAC (2000). Fatty acid profiling was performed using a Gas Chromatograph Analyzer (Perkin Elmer 3920), assessing palmitic, stearic, oleic, and linoleic acids.

The data were analyzed using R software, SPSS 12 (SPSS, Chicago, IL), Microsoft Excel (QI Macros), and MVSP 3.1 (Kovach Computing Services, Anglesey, Wales). Analysis of variance (ANOVA) was performed following Steel *et al*. (1997), and Tukey's HSD test was used for mean separation (Tukey, 1949). Principal Component Analysis (PCA) (Jeffers, 1967) and cluster analysis (Euclidean distance, UPGMA) were applied to assess multivariate diversity. Genotypic correlations were estimated as per Kwon & Torrie (1964) and tested for significance using Lothorp *et al.* (1985).

## RESULTS AND DISCUSSION

### Morphological Variability among Mutant Lines

Analysis of variance across nine quantitative traits revealed significant genetic variation among the 50 selected *Camelina sativa* mutant lines (Table 2). Notable variability was observed in traits such as plant height, capsule number, inflorescence count, number of primary and secondary branches, oil content, and seed yield (Ebrahimi *et al*., 2025). In contrast, relatively low variation was observed for leaf area and 1,000-seed weight. This observed diversity highlights the genetic richness of the mutant population, offering substantial potential for selection and trait improvement.

**Table 2.** ***Descriptive statistics of morphological traits among 50 Camelina sativa mutant lines under low-input field conditions.***

| *Variable* | *Mean* | *SE Mean* | *SD* | *Variance* | *C.V* | *Minimum* | *Maximum* | *Range* |
|---|---|---|---|---|---|---|---|---|
| *Plant height* | 65.37 | 1.05 | 7.43 | 55.24 | 11.37 | 48.00 | 78.00 | 30.00 |
| *Inflorescence No* | 54.98 | 3.96 | 27.99 | 783.39 | 50.91 | 18.50 | 179.50 | 161.00 |
| *Capsule no.* | 1305 | 120 | 849 | 720261 | 65.04 | 338 | 5627 | 5290 |
| *Primary Branches* | 12.470 | 0.615 | 4.348 | 18.902 | 34.86 | 4.000 | 26.000 | 22.000 |
| *Secondary branches* | 29.71 | 1.91 | 13.50 | 182.34 | 45.45 | 8.50 | 66.00 | 57.50 |
| *Leaf area* | 2.368 | 0.148 | 1.043 | 1.088 | 44.05 | 0.727 | 5.896 | 5.170 |
| *1000 seed weight* | 0.9133 | 0.0163 | 0.1155 | 0.0133 | 12.64 | 0.7160 | 1.2520 | 0.5360 |
| *Oil contents* | 37.295 | 0.211 | 1.494 | 2.233 | 4.01 | 34.190 | 41.630 | 7.440 |
| *Seed yield* | 9.900 | 0.287 | 2.028 | 4.112 | 20.48 | 6.000 | 14.000 | 8.000 |

As emphasized by, Katar *et al*. (2012); Sharma *et al*. (2003); Poehlman & Sleper (1995), the presence of high phenotypic variability underpins the success of genetic gain in any crop improvement program (Ghidoli *et al.*, 2023).

Principal Component Analysis (PCA) further explained the multidimensional diversity among mutant lines. The first two components (PC1 and PC2) accounted for 94.20% of total variation, with inflorescence number, capsule number, and plant height contributing most strongly (Table 3).

**Table 3.** ***Principal components and their eigenvalues explaining phenotypic variation among morphological traits in mutant genotypes.***

| | *PC1* | *PC2* |
|---|---|---|
| ***Eigen values*** | 1174.788 | 64.929 |
| ***Proportion*** | 89.267 | 4.934 |
| ***Cumulative*** | 89.267 | 94.201 |
| ***PCA variable loadings*** | | |
| | **Axis 1** | **Axis 2** |
| ***Plant height*** | 0.085 | **0.409** |
| ***Inflorescence number*** | **0.821** | **-0.385** |
| ***Capsule number*** | **0.453** | 0.012 |
| ***Primary branches*** | 0.064 | 0.095 |
| ***Secondary branches*** | 0.330 | **0.821** |
| ***Leaf area*** | -0.005 | -0.008 |
| ***1000 seed weight*** | 0.000 | 0.002 |
| ***Oil content*** | 0.000 | -0.021 |

| | | |
|---|---|---|
| ***Seed yield*** | -0.007 | 0.035 |

Although PC1 and PC2 explained most of the variance, traits such as oil content, 1,000-seed weight, and leaf area were also found to influence the variability captured by the first three principal components. These traits can serve as effective descriptors for future selection of high-performing lines under low-input environments.

Correlation analysis among morphological traits (Table 4) revealed several significant associations. Plant height was positively correlated with capsule number, inflorescence count, and number of secondary branches. Similarly, the number of inflorescences showed strong positive associations with capsule number and branching traits. Although seed yield was not significantly correlated with most morphological traits, these indirect associations suggest that improving component traits could still lead to better yield performance in a cumulative breeding approach. Oil content showed weak and mostly non-significant correlations, in line with earlier reports. Both Gauraha & Rao (2011) and Tadesse et al. (2009) noted similarly weak associations with yield traits, suggesting that oil content largely behaves independently of major yield determinants.

**Table 4. Pearson correlation coefficients among key morphological traits in *Camelina sativa* mutant lines.**

| | **Plant height (cm)** | **Inflorescence no.** | **Capsule no.** | **No. of primary branches** | **No. of secondary branches** | **Leaf area** | **1000-seed weight (g)** | **Oil contents %** |
|---|---|---|---|---|---|---|---|---|
| **Inflorescence no.** | 0.313* | | | | | | | |
| **Capsule no.** | 0.362** | 0.922** | | | | | | |
| **No. of primary branches** | 0.048 | 0.480** | 0.442** | | | | | |
| **No. of secondary branches** | 0.335* | 0.773** | 0.748** | 0.547** | | | | |
| **Leaf area ($cm^2$)** | 0.023 | -0.191 | -0.115 | -0.124 | -0.204 | | | |
| **1000 seed weight (g)** | 0.048 | -0.100 | -0.162 | 0.064 | 0.014 | -0.061 | | |
| **Oil contents %** | -0.146 | 0.012 | -0.059 | -0.094 | -0.007 | -0.150 | -0.142 | |
| **Seed yield (g)** | 0.064 | -0.128 | -0.026 | -0.219 | -0.029 | 0.021 | -0.127 | 0.072 |

**Fatty Acid Composition and Oil Quality**

Fatty acid profiling revealed wide variation among the 50 *Camelina sativa sativa* genotypes for all major oil components (Table 5). Particularly high coefficients of variation were observed for palmitoleic acid (up to 91.9%) and caproic acid (54.3%), while stearic acid showed relatively low variability.

These findings are consistent with earlier studies emphasizing the impact of genotype and environment on fatty acid profiles in oilseed crops (Ebrahimi *et al*.,2025; Berti *et al*., 2011; Bachlava *et al*., 2008; Pilgeram *et al*., 2007; Sharma *et al*., 2003).Multivariate analysis of fatty acid traits identified four principal components (PC1–PC4) explaining a cumulative 87.95% of total variation (Table 6). Palmitic and palmitoleic acids dominated PC1, while PC2 and PC3 included nonanoic and caproic acids.

**Table 5. Descriptive statistics for major fatty acid components across 50 *Camelina sativa* genotypes.**

| *Fatty acids* | *Mean* | *Variance* | *St. dev.* | *CV* | *MIN* | *MAX* | *Range* |
|---|---|---|---|---|---|---|---|
| ***Oliec acid C18:1*** | 0.62 | 15.94 | 3.99 | 15.70 | 0 | 26.5 | 26.5 |
| ***Linoliec acid C18:2*** | 2.64 | 64.67 | 8.04 | 32.92 | 0 | 51.2 | 51.2 |
| ***Palmitic acid C16:0*** | 11.61 | 470.02 | 21.67 | 53.55 | 0 | 83.9 | 83.9 |
| ***Carproic acid C6:0*** | 7.76 | 204.12 | 14.28 | 54.33 | 0 | 75.1 | 75.1 |
| ***Nonanoic acid C9:0*** | 9.42 | 235.86 | 15.35 | 61.36 | 0 | 43.4 | 43.4 |
| ***Palmitoleic acid C16 :1*** | 20.79 | 511.99 | 22.62 | 91.90 | 0 | 63.6 | 63.6 |
| ***Caprilic acid C8:0*** | 3.27 | 92.73 | 9.62 | 33.98 | 0 | 50.5 | 50.5 |
| ***Capric acid C10:0*** | 1.24 | 5.44 | 2.33 | 53.29 | 0 | 9.4 | 9.4 |
| ***Stearic acid C18:0*** | 0.29 | 1.22 | 1.105 | 26.30 | 0 | 6.3 | 6.3 |
| ***Elaidic acid C18:1*** | 1.97 | 27.10 | 5.20 | 37.88 | 0 | 30.5 | 30.5 |
| ***Lauric acid C12*** | 0.54 | 6.28 | 2.50 | 21.57 | 0 | 12 | 12 |

**Table 6. Eigenvalues, variance explained, and major contributing fatty acids for the first four principal components among mutant genotypes.**

| *Eigenvalues* | **PC1** | **PC2** | **PC3** | **PC4** |
|---|---|---|---|---|
| ***Eigenvalues*** | 491.489 | 361.755 | 207.19 | 155.08 |
| ***Percentage*** | 35.564 | 26.176 | 14.992 | 11.221 |
| ***Cum. Percentage*** | 35.564 | 61.74 | 76.732 | 87.953 |
| ***PCA variable loadings*** | | | | |
| | **Axis 1** | **Axis 2** | **Axis 3** | **Axis 4** |
| ***Oleic Acid*** | 0.007 | 0.005 | -0.045 | -0.008 |
| ***Linoleic Acid*** | -0.037 | 0.084 | -0.07 | -0.038 |
| ***Palmitic Acid*** | **0.763** | **0.582** | **0.258** | **-0.099** |
| ***Carproic Acid*** | **0.113** | **-0.25** | **0.525** | **0.795** |
| ***Nonanoic Acid*** | 0.056 | **-0.45** | **0.651** | -0.578 |
| ***Palmitoleic Acid*** | **-0.629** | **0.61** | **0.471** | **-0.027** |
| ***Caprilic Acid*** | -0.003 | **-0.111** | 0.037 | -0.134 |
| ***Capric Acid*** | -0.003 | -0.032 | 0.047 | -0.04 |
| ***Stearic Acid*** | 0.015 | 0.005 | 0.017 | -0.012 |
| ***Elaidic Acid*** | -0.07 | 0.055 | -0.021 | -0.003 |
| ***Lauric Acid*** | -0.013 | 0.007 | 0.025 | 0.038 |
| ***Proteint (%)*** | -0.013 | -0.007 | 0.006 | 0.013 |
| ***Oil content (%)*** | -0.005 | -0.002 | -0.024 | 0.035 |

*Note: Bold values are greater than the arithmetic means of highest and lowest absolute values of eigen vectors within the column*

These traits serve as effective indicators of compositional diversity and can be targeted for trait-specific selection in biodiesel-oriented breeding programs (Gabriel, 1981). Correlation analysis (Fig. 1; Supplementary Table 1) revealed significant associations among key fatty acids and oil content. A strong positive correlation was observed among capric acid, caprylic acid, and nonanoic acid, suggesting possible co-regulation or shared biosynthetic pathways for these medium-chain fatty acids. In contrast, oleic acid showed a negative correlation with both stearic acid and overall oil content, which may affect the oxidative stability and quality of the derived biodiesel. These insights are essential for selecting genotypes with desirable fatty acid compositions, particularly those with elevated oleic acid and reduced linolenic acid, to enhance biodiesel performance under high-temperature conditions.

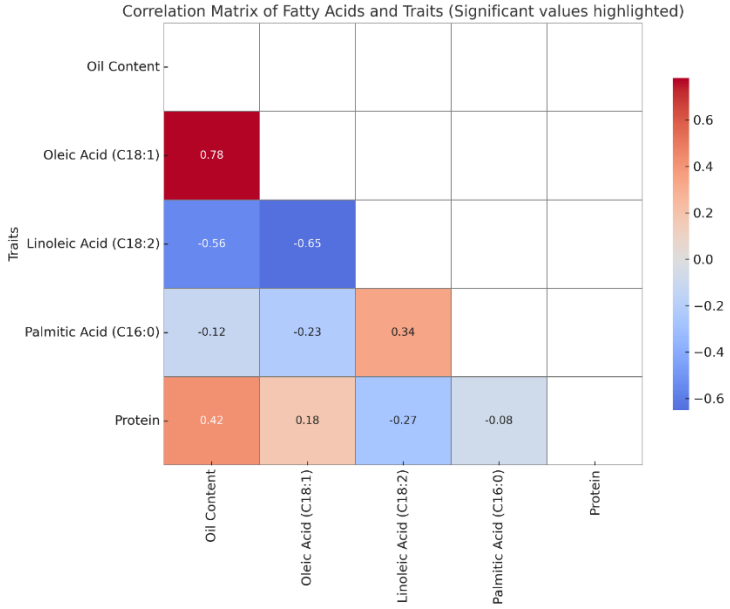


**Fig1.** Heatmap showing Pearson correlation coefficients among oil content, protein, and individual fatty acids in *Camelina sativa* . Positive correlations are shown in shades of red and negative correlations in blue. Strong correlations (|r| > 0.5) are highlighted in bold. The heatmap reveals strong positive associations among capric acid (C10:0), caprylic acid (C8:0), and nonanoic acid (C9:0), suggesting potential co-regulation or shared biosynthetic pathways. In contrast, oleic acid (C18:1) showed negative correlations with both oil content and stearic acid (C18:0), which may have implications for biodiesel quality and oxidative stability.

**Genotype Clustering and Multivariate Visualization**

Biplot analysis (Fig. 2) provided a clear visual distinction among genotypes based on their fatty acid contributions (Yan & Kang, 2011). Vectors representing palmitic, stearic, caproic, and nonanoic acids showed meaningful divergence, highlighting their utility in differentiating accessions (Muduli & Patnaik, 1994). Genotypes grouped in the direction of long vectors are presumed to have stronger expression of those traits.

Hierarchical cluster analysis categorized the 50 lines into three distinct morphological and oil composition clusters (Figs. 3-5). Cluster 3 had the highest number of genotypes and showed better alignment with high-yielding and oil-rich lines. The integrated cluster (Fig. 5) showed some shifts in fatty acid trait relationships (e.g., capric acid and elaidic acid) between the individual and combined analyses, further supporting the influence of genotype-by-environment interactions.

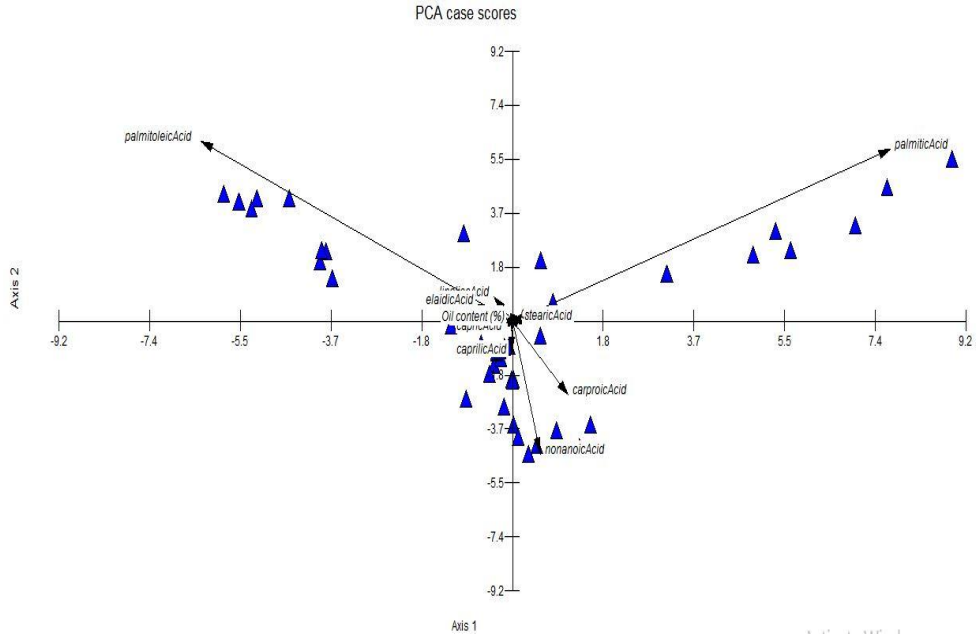


**Fig 2.**Principal Component Analysis (PCA) biplot of 50 *Camelina sativa* genotypes based on fatty acid composition and oil content. The plot displays the distribution of genotypes (blue triangles) across two principal components (Axis 1 and Axis 2). Vectors represent the contribution and direction of key traits,including caproic, caprylic, nonanoic, palmitic, palmitoleic, stearic, oleic, linoleic, linolenic, and elaidic acids, as well as total oil content,highlighting correlations among traits and their influence on genotype clustering.

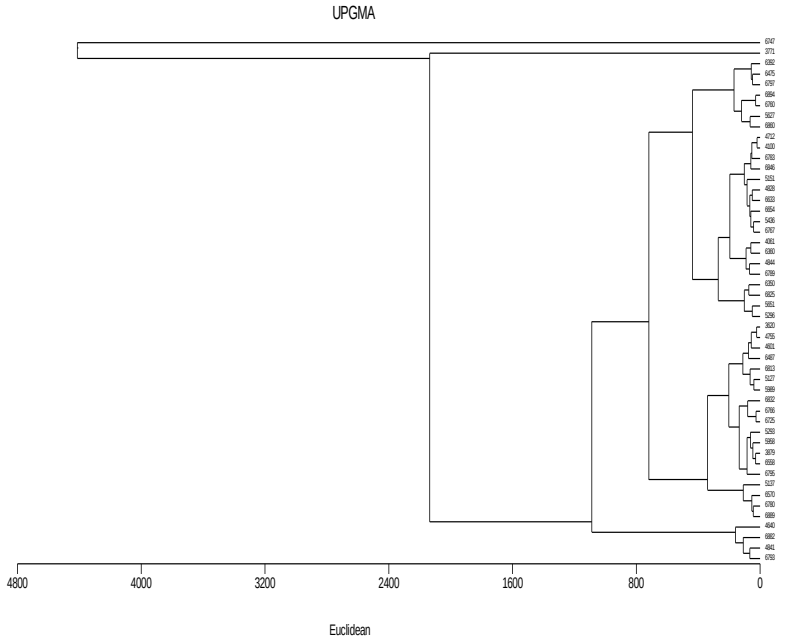


**Fig 3.** UPGMA dendrogram representing genetic relationships among *Camelina sativa* mutant genotypes based on nine morphological and agronomic traits. Clustering was performed using Euclidean distance and morphological traits. The resulting clusters highlight phenotypic divergence and can aid in the identification of promising genotypes for breeding and selection programs.

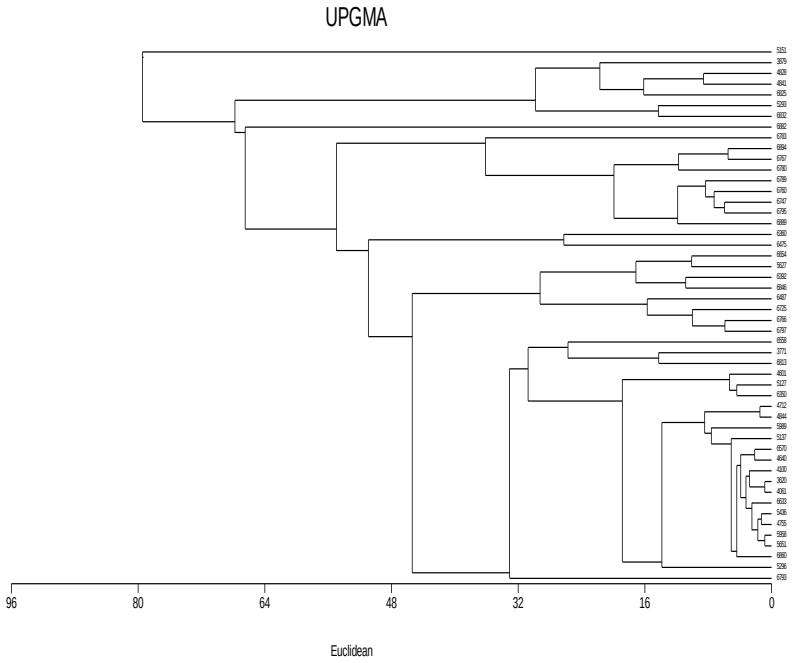


**Fig 4.** UPGMA dendrogram illustrating genetic clustering of *Camelina sativa* genotypes based on seed oil fatty acid composition. Cluster analysis was performed using the Euclidean distance and UPGMA method, incorporating the relative proportions of key fatty acids. The resulting clusters reveal genotypic variability in oil profile, useful for targeted breeding and industrial applications.

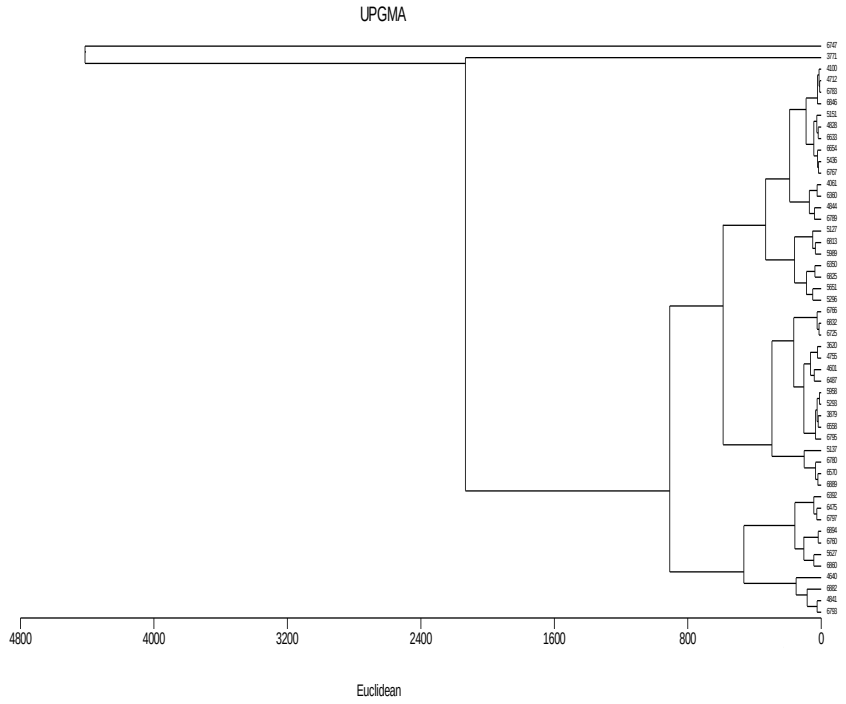


**Fig5.** UPGMA-based hierarchical clustering of *Camelina sativa* mutant lines using combined morphological and fatty acid composition traits. The dendrogram illustrates the genetic divergence among 50 mutant lines based on Euclidean distances, grouping them into distinct clusters that reflect underlying phenotypic and biochemical variability. This clustering provides insight into the relationships among genotypes and potential candidates for selection in breeding programs.

The heat map (Fig. 6) effectively visualized fatty acid concentrations across all lines, clustering similar profiles vertically. Lines such as 6862, 6882, 5296, 6795, 6789, and 6760 exhibited high concentrations of unsaturated fatty acids,specifically oleic and linoleic acids,making them promising candidates for biodiesel production.

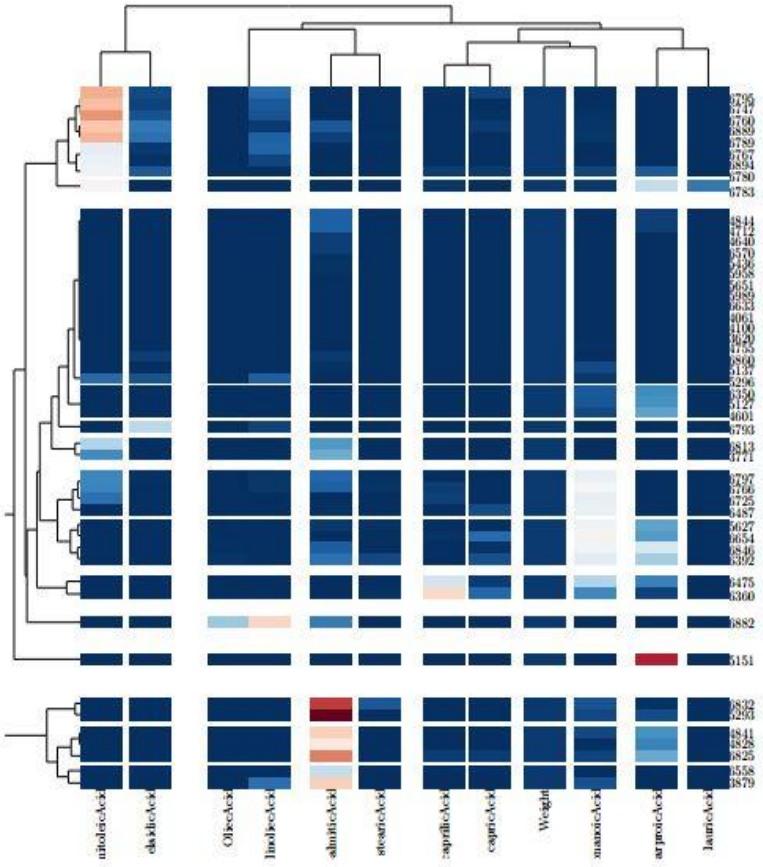


**Fig 6.** Hierarchical clustering heatmap depicting the variation in fatty acid composition and related traits across different *Camelina sativa* genotypes. The heatmap visualizes the relative abundance of key fatty acids (e.g., oleic, linoleic, linolenic, stearic, capric acids) and traits like seed weight and oil content. Color intensity reflects the magnitude of trait values, with red indicating higher and blue indicating lower values. Dendrograms show clustering based on similarity among genotypes (rows) and traits (columns), revealing potential trait correlations and genotype groupings useful for selection in oil quality improvement.

The observed genetic diversity among mutant lines of *Camelina sativa* offers a valuable opportunity to develop climate-resilient (Hunsaker *et al*., 2012), low-input oilseed cultivars (Ghidoli*et al.,* 2023;Gesch and Cermak, 2011; Bang, 2010) suited for industrial applications. The combined assessment of morphological traits and fatty acid profiles identified promising lines (e.g., 6862, 6783, 5296) for biodiesel optimization. This study establishes key germplasm and phenotypic benchmarks for integrating molecular tools such as GWAS and genomic selection. The findings align with sustainable agriculture goals and renewable energy demands. Ultimately, they advance the development of alternative crops for bio-based economies in underutilized agro-ecological zones.

## CONFLICT OF INTEREST

The authors declare no competing interests.

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**Supplementary Table 1:** ***Correlation coefficients among oil compositional traits Selected mutant genotypes of Camelina sativa***

| Fatty acids (%) | Oleic acid | linoleic acid | palmitic acid | carproic acid | nonanoic acid | palmitoleic acid | caprilic acid | capric acid | stearic acid | elaidic acid | lauric acid | Protein | Oil content |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **linoleic acid** | .929** | | | | | | | | | | | | |
| G-1 | 0.00 | | | | | | | | | | | | |
| G-2 | .979** | | | | | | | | | | | | |
| G-3 | -.212 | | | | | | | | | | | | |
| **palmitic acid** | .014 | -.005 | | | | | | | | | | | |
| G-1 | .216 | -0.099 | | | | | | | | | | | |
| G-2 | .742** | .693** | | | | | | | | | | | |
| G-3 | .216 | -.099 | | | | | | | | | | | |
| **carproic acid** | -.063 | -.162 | .015 | | | | | | | | | | |
| G-1 | .216 | -0.110 | 0.216 | | | | | | | | | | |
| G-2 | -.205 | -.309 | -.131 | | | | | | | | | | |
| G-3 | -.108 | -.110 | .216 | | | | | | | | | | |
| **nonanoic acid** | -.069 | -.151 | -.108 | .217 | | | | | | | | | |
| G-1 | -.108 | -0.102 | 0.036 | 0.352 | | | | | | | | | |
| G-2 | -.289 | -.411 | .058 | .398 | | | | | | | | | |
| G-3 | -.108 | -.102 | .036 | .352 | | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **palmitoleic acid** | -.083 | .143 | -.212 | -.161 | -.181 | | | | | | | | |
| G-1 | -.212 | -0.069 | 0.165 | -0.144 | -.134 | | | | | | | | |
| G-2 | -.353 | -.203 | -.369 | -.305 | -.690** | | | | | | | | |
| G-3 | .194 | -.069 | .165 | -.144 | -.134 | | | | | | | | |
| **caprilic acid** | -.034 | -.070 | -.102 | .009 | .194 | -.099 | | | | | | | |
| G-1 | -0.02 | -0.050 | -0.094 | 0.006 | .853** | -.066 | | | | | | | |
| G-2 | -.126 | -.184 | -.246 | .021 | .100 | -.341 | | | | | | | |
| G-3 | 0.01 | -.050 | -.094 | .006 | .853** | -.066 | | | | | | | |
| **capric acid** | -.045 | -.079 | -.107 | .124 | .461** | -.032 | .527** | | | | | | |
| G-1 | 0.3 | -0.050 | -0.094 | 0.006 | .853** | -.066 | 1.000** | | | | | | |
| G-2 | -0.207 | -.266 | -.357 | .069 | .314 | -.340 | .520* | | | | | | |
| G-3 | 0.02 | -.050 | -.094 | .006 | .853** | -.066 | 1.000** | | | | | | |
| **stearic acid** | -.019 | -.064 | .355* | .049 | .203 | -.092 | -.018 | .129 | | | | | |
| G-1 | 0.01 | -0.050 | -0.094 | 0.006 | .853** | -.066 | 1.000** | 1.000** | | | | | |
| G-2 | -.201 | -.220 | .214 | -.141 | .457* | -.164 | .076 | -.068 | | | | | |
| G-3 | 0.02 | -.050 | -.094 | .006 | .853** | -.066 | 1.000** | 1.000** | | | | | |
| **elaidic acid** | -.048 | .080 | -.155 | -.161 | -.173 | .317* | -.068 | -.037 | -.063 | | | | |
| G-1 | 0.00 | 0.997** | -0.099 | -0.112 | -.105 | -.071 | -.051 | -.051 | -.051 | | | | |
| G-2 | -.213 | -.125 | -.088 | -.335 | -.493* | .728** | -.215 | -.146 | -.041 | | | | |
| G-3 | 0.01 | .997** | -.099 | -.112 | -.105 | -.071 | -.051 | -.051 | -.051 | | | | |
| **lauric acid** | -.021 | -.045 | -.075 | .262 | -.068 | .238 | -.014 | -.056 | -.036 | -.049 | | | |
| G-1 | 0.00 | 0.3 | 0.03 | 0.002 | 0.038 | 0.028 | 0.23 | .023 | .003 | 0.032 | | | |
| G-2 | -.081 | -.120 | -.168 | .530* | -.182 | .174 | -.066 | -.142 | -.138 | -.152 | | | |
| G-3 | 0.02 | 0.23 | .023 | .003 | 0.032 | 0.3 | 0.03 | 0.002 | 0.3 | 0.03 | | | |
| **Protein** | -.161 | -.119 | -.154 | .075 | .011 | .093 | -.034 | -.051 | -.122 | -.159 | .144 | | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G-1 | 0.02 | -.169 | -0.115 | 0.102 | -.215 | .054 | -.239 | -.239 | -.239 | -.184 | 0.02 | | |
| G-2 | -.384 | -.364 | -.390 | .110 | .012 | .206 | -.054 | -.103 | -.303 | -.034 | .243 | | |
| G-3 | 0.03 | -.169 | -.115 | .102 | -.215 | .054 | -.239 | -.239 | -.239 | -.184 | 0.02 | | |
| **Oil content** | .035 | .006 | -.126 | .076 | -.293* | -.045 | .038 | -.088 | -.135 | .032 | .095 | .026 | |
| G-1 | -0.02 | 0.076 | -0.027 | 0.220 | .264 | .128 | -.019 | -.019 | -.019 | .052 | -0.02 | -.029 | |
| G-2 | .223 | .254 | -.053 | -.085 | -.399 | .190 | .231 | .003 | -.097 | .045 | .277 | .205 | |
| G-3 | -0.02 | .076 | -.027 | .220 | .264 | .128 | -.019 | -.019 | -.019 | .052 | -0.02 | -.029 | |