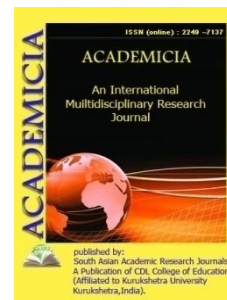


**ACADEMICA**  
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**Research Journal**  
 (Double Blind Refereed & Peer Reviewed Journal)



**DOI: 10.5958/2249-7137.2021.02239.4**

## CAMELINA AS A VIABLE ORGANIC CHEMICAL CROP

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### ABSTRACT

*Camelina is an underused Brassicaceae oilseed plant with significant agronomic potential in temperate areas for biofuel and vegetable oil production. Camelina is resistant to alternaria black spot and other diseases and pests, unlike other Brassicaceae. The camelina genome was sequenced and found to have an undifferentiated allohexaploid genome with a high number of genes and a low proportion of repetitive DNA. Because camelina and the genetic model plant Arabidopsis have a tight connection, this review will look at the possibility of converting fundamental Arabidopsis findings into a camelina oilseed crop for food and non-food uses. Recently, camelina has effectively expressed Arabidopsis genes for drought tolerance, enhanced photosynthesis, and overall productivity. Furthermore, gene constructs affecting lipid metabolism pathways have been engineered into camelina for the production of long-chain polyunsaturated fatty acids, hydroxy fatty acids, or high-oleic oils in specific camelina strains, which is of great interest in human food, industrial, or biofuel applications. These findings support camelina's promise as a biotechnology platform in biorefinery applications, indicating that further breeding and genetic research is needed to combine agronomic potential, distinctive oil quality characteristics, and biosafety in an agricultural production system.*

**KEYWORDS:** *Biofuel, Brassicaceae, Camelina, Genetic, Linolenic Acid.*

### 1. INTRODUCTION

Camelina is a Brassicaceae family oilseed crop that grows well in temperate climates. Camelina is an East European/West Asian plant that has been used since the late Neolithic Era in South-East Europe, when it was domesticated. Cultivation of camelina was verified from West Asia through the European peninsula and northward to Scandinavia during the Iron Age. Camelina

agriculture has been reduced throughout time as a result of competition from a variety of other crops.

Camelina has reawakened interest in the 1980s as a result of increasing demand for both food and biofuel oils, and pilot-scale production facilities have been built in both Europe and North America. Camelina has also been described as a low-input oilseed crop that has exceptional resilience to common and widespread Brassicaceae diseases and pests. As a result, camelina-derived biofuels have been regarded as sustainable jet fuel or diesel replacements, decreasing greenhouse gas emissions by 75–80% when compared to petroleum-based products based on life cycle evaluation[1].

Camelina may be economically viable in on-farm biofuel generation under certain market conditions. Apart from biofuel and other non-food applications, camelina oil has a new potential as a vegetable oil for food applications: Camelina oil is a unique source of alpha-linolenic acid, an important omega-3 fatty acid with many health advantages. Because the amounts of linolenic acid in soybean and canola oils have been decreased to minimize the health concerns associated with the production of trans fatty acids during processing and to improve shelf life, camelina oil may be used instead to supplement linolenic acid in healthy diets.

Camelina is a self-pollinating crop with modest outcrossing rates in rows 20 to 60 cm apart, ranging from 0.01 to 0.28 percent. Seehuber studied the genetic diversity in agronomic and seed quality characteristics of camelina germplasm accessions in the 1980s and launched the first camelina breeding programme, which focused on the creation of base populations for future yield enhancement. Breeding operations were then conducted in a number of European nations, as well as the United States and Canada. Meanwhile, genetic engineering techniques have been effective in altering the fatty acid content of camelina oil in order to produce certain fatty acids of interest, such as fish oil-like long chain omega-3 fatty acids. Camelina is closely related to the genetic model plant *Arabidopsis thaliana* (L.) Heynh., implying that genetic and genomic techniques established in *Arabidopsis* may be used to Camelina. As a result, camelina seems to have the potential to serve as a biotechnology platform for a variety of food, health, biofuel, and non-food oilseed uses. As a consequence, the goal of this study is to summarize plant breeding and biotechnology findings in order to highlight potentials and future research requirements for expanding camelina's use as a sustainable oilseed crop[2].

### *1.1 Camelina Oil:*

#### *1.1.1 Camelina Grain Yield:*

A new crop's ability to compete in terms of agronomic performance with existing oil crops is a critical element in its economic viability. Camelina oil and biofuel production would have a lower environmental effect if seed yields were higher. Camelina has been identified as one of the most promising new crops for oil production in temperate areas, owing to its broad adaptability, cheap input requirements, short crop cycle, and other benefits. Despite its recent breeding history, camelina trials have shown acceptable yield performance and other positive agronomic characteristics when compared to other new crops, which may be attributed to camelina's lengthy history of adaptability.

Low yields may suggest a poor crop establishment due to drought stress, non-optimal sowing timing, or other unfavorable environmental effects, while grain yields of over 3000 kg/ha have

been obtained using genebank accessions, newly created cultivars, and breeding lines in favorable conditions. There have been significant genetic variations in yield stability across genotypes over a greater number of trials, suggesting that breeding for particular environment adaption or wider stability may enhance yield performance[3].

Camelina oil content has also shown significant fluctuation, ranging from 30 to 49 percent, similar to grain yield. Significant genetic variation as well as genotype by environment interaction have been reported in specific studies for both grain yield and oil content, suggesting that selection for better yield or oil content might be effective. Significantly favorable relationships between grain yield and oil content have been found for various oilseeds. Researchers found negative correlations between the two characteristics across a group of camelina genotypes in certain settings, highlighting the need of tracking the grain yield/oil content connection of individual populations when breeding for oil production[4].

### *1.1.2 Camelina Oil Fatty Acid Composition:*

A few main fatty acids, such as palmitic, oleic, or linoleic acid, predominate in most established oil crops. Medium-chain fatty acids, such as capric or lauric acid, are produced in a few new oilseeds, such as cuphea, while hydroxy fatty acids, such as lesquerolic acid, are discovered in lesquerella. Erucic acid is also produced in most Brassicaceae oilseeds, such as non-canola-quality rapeseed cultivars or crambe. When compared to conventional vegetable oils, such uncommon fatty acids have distinct physicochemical characteristics and a broader spectrum of oleochemical reactions for a variety of uses. Camelina seed oil is unusual in two ways: (i) the main fatty acid is polyunsaturated alpha-linolenic acid; and (ii) the concentration of erucic acid is low for a Brassicaceae species, while eicosenoic acid is produced as a long-chain fatty acid. Linolenic acid levels range from 30 to 43 percent, depending on genotype, agronomic treatment, and environmental factors. After earlier planting, at a greater N-fertilizer rate, and in seeds with a bigger 1000-seed weight, a winter-sown cultivar had higher linolenic acid content than a spring-sown cultivar. As with other oilseeds, the amount of linolenic acid seems to be lower in warmer regions like Spain than in colder climes like northern Germany. Linseed oil is the only vegetable oil that has a greater linolenic acid content than camelina oil. In most instances, camelina oil has less than 3% erucic acid, while eicosenoic acid levels vary from 11 to 19 percent, and saturated fatty acids are frequently found in quantities less than 10%. In mutant populations, there is a little more diversity in fatty acid composition[5].

Specific mutant genotypes could be used in crosses within selection programmes to change the concentration of individual fatty acids, similar to other oil crops: linolenic acid content could be increased for technical applications, but it should be reduced for camelina biodiesel applications due to a number of drawbacks associated with the chemical properties of linolenic acid methyl est. Furthermore, the amount of erucic acid in food may be decreased for food safety concerns, since greater erucic acid consumption has been linked to heart lipidosis in animal studies. Via conclusion, camelina oil's unique fatty acid composition suggests that it has significant fatty acid desaturase and elongase potential, both of which may be increased in genetic engineering methods to produce customised fatty acid profiles. Camelina also contains a seed protein, which seems to be a useful by-product but will not be discussed in this study.

Camelina can thus be grown as a winter or spring-sown crop in semi-arid, temperate, or even short-season environments such as Canada and the northern United States, as well as Central and

Northern Europe and Asia, for biofuel and food oil production, based on the agronomic and oil quality characteristics described above. Camelina has a similar response to nitrogen fertilizers as other oil crops, and its current yield level makes it competitive with other oil crops and for on-farm biofuel generation[6].

### *1.2 Camelina Disease:*

Camelina, being a member of the Brassicaceae family, is susceptible to the same pests and diseases that threaten other cruciferous crops. Surprisingly, two fungal diseases that are critical to the global production of Brassica crops are entirely absent from the illness data. While no source of resistance has been identified within the Brassica genus, camelina resistance to *Alternaria* spp. has been reported by a number of writers. *Alternaria* spp. containment in *C. sativa* and *A. thaliana* has been linked to the synthesis of two indole phytoalexins, camalexin and methoxy-camalexin. Camalexin has structural similarities with the synthetic systemic fungicide thiabendazole, however it is not found in any other farmed crucifer species. Although camalexin has direct antimicrobial action against *Alternaria* spp. in vitro, it is possible that it also contributes to *Alternaria* resistance indirectly by inhibiting the synthesis of the *Alternaria* toxin destruxin B. It was also shown that *C. sativa* can detoxify destruxin B[7].

The economic significance of black spot disease for Brassica crop production throughout the globe, along with *C. sativa*'s full resilience, has made it an ideal option for intraspecific hybridizations with other Brassicas. However, significant cross-incompatibility and ploidy variations between *C. sativa* and farmed Brassica species make *Alternaria* resistance transfer problematic. Insufficient rhizogenesis and sterility of the hybrids hindered attempts to transfer camelina-derived *Alternaria* resistance to *B. carinata* and *B. oleracea* via protoplast fusions.

Furthermore, resistance transfer based on camalexin elicitation may not be as simple as one would think: detoxification of the phytoalexin brassinin in *L. maculans* cultures rose significantly in the presence of camalexin. This indicates that, while improving *Alternaria* resistance, adding the camalexin route into plants that produce brassinin, such as *B. napus*, may also increase sensitivity to *L. maculans*. Finally, the implications of expressing a phytoalexin in a new plant species must be thoroughly studied.

The most common disease of Brassica crops is *Leptosphaeria maculans*, which causes blackleg or stem canker. Despite the fact that camelina is essentially resistant to this disease, making it an appealing source of resistance for improving vulnerable Brassica crops, relatively little study has been done to explain the processes behind camelina's blackleg resistance. Phytoalexin production may be one of the key reasons once again.

Camelina shows diversity in resistance to damping-off and root-rot, sclerotinia stem rot (and downy mildew) in addition to full resistance to black spot and black leg disease, suggesting that the creation of resistant cultivars is possible. Camelina, on the other hand, is vulnerable to diseases such as clubroot, white rust, and aster yellows, which may represent a danger to increased camelina output unless resistant cultivars or appropriate management techniques can be developed.

Flea beetles are a major pest of canola and mustard crops in the northern Great Plains of the United States and Canada. Flea beetles may be seen on camelina plants in the wild, but they do not eat on them. Feeding on camelina does not begin until the beetles have been trapped to the

plants for many days. However, once feeding began, it tended to continue, suggesting that *C. sativa* resistance to *Phyllotreta* may be due to a lack of feeding signals rather than the presence of feeding deterrents. Insects' assessment of the chemical makeup of the plant's surface and volatile chemicals determines whether or not they would accept it as a host plant[8].

Glucosinolates are a class of compounds present in and on the surfaces of cruciferous plants that may function as insect pest repellents or attractants, and have been demonstrated to have a role in the identification of host plants by insects like the flea beetle. Because *C. sativa* has a low amount of glucosinolates, it may not provide enough chemosensory cues to stimulate eating. Second, none of the farmed Brassica species have three glucosinolates that *C. sativa* has. As a result, in addition to quantitative variation in glucosinolate concentration, qualitative variation in glucosinolate content may also play a role in host selection.

Only a few studies indicate camelina's resistance to other insect pests, and the camelina/flea beetle system is the best-studied relationship between this plant species and insects. Diamondback moth and mustard sawfly have been found to be deterred by *C. sativa*. Female cabbage root flies also did not lay eggs on *C. sativa* plants. The cabbage seedpod weevil seems to be resistant to *Camelina* as well. Although the second study's test findings were ambiguous owing to poor plant growth, they were backed up by the discovery of a significant decrease in *Ceutorhynchuspallidactylus* leaf area consumption in *Camelina alyssum* compared to *B. napus*. Camelina's unique features of insect pest resistance may aid in the modulation of feeding cues in crops such as *B. napus*, reducing the effect of insect pests on Brassica crops.

### *1.3 Genetic Resources and Applications in Genomics:*

Several collecting institutes preserve camelinagenebank accessions, although the number of accessions accessible in most collections is relatively low, reflecting camelina's minor significance as a field crop in the past. As of June 2014, EURISCO, the European database of plant germplasm collections, has a total of 793 accessions of *C. sativa*. The majority of camelina accessions are kept in Germany, Poland, the Czech Republic, Bulgaria, and Austria, according to the EURISCO catalogue, although many accessions seem to be duplicated in national inventories. According to taxonomic searches as of June 2014, the Plant Gene Resources of Canada database has 137 *C. sativa* accessions, while the USDA National Plant Germplasm System holds 44 accessions[9].

The researchers examined the phenotypic variety of agronomic and seed quality characteristics in a group of camelinagenebank accessions, highlighting significant variance and high heritability for time to flowering, plant height, and 1000-seed weight, with less variation for fatty acid concentrations. Researchers divided 130 accessions into four groups based on seed size, seed oil, and protein content; they found 15 polymorphic RAPD markers for a sample of genotypes, however there was no correlation between genetic and phenotypic estimates of variety. From a camelina genomic DNA library, researchers created SSR markers. While the majority of their SSR primer pairs amplified multiple fragments, they were able to select a number of useful polymorphism primers for grouping 40 genebank accessions into different groups.

Scholars utilized sequence analysis of the ITS region as a marker system to distinguish between *Camelina* species and identify interspecific hybrids. Researchers used AFLP markers to create a genetic linkage map and found QTL areas for seed production, 1000-seed weight, plant height,



oil content, and individual fatty acid concentrations in a bi-parental population, showing the viability of marker-assisted selection.

However, future camelina breeding may benefit significantly from high-density genetic maps and genomic information obtained from modern genome and transcriptome sequencing methods, thanks to recent advances in sequencing and analytics. Transcriptome analysis of developing camelina seeds, for example, revealed several genes involved in seed storage protein and lipid biosynthesis metabolism; this information could be used in gene suppression or transgene expression approaches to improve camelina seed quality by targeting specific protein or lipid properties.

#### *1.4 Camelina Breeding Methods:*

Camelina flowers are tiny and seldom visited by insects. As previously stated, camelina outcrossing rates are extremely low, comparable to soybean outcrossing rates, and outcrossing occurs only over short distances. Honey bees, wild bees, and other insects visited the flowers, but seed set parameters did not vary substantially between open pollination and self-pollination. As a result, camelina may be classified as a mostly autogamous species.

Pure line breeding seems to be the technique of choice for cultivar creation based on camelina flowering biology. Segregating generations may be managed via pedigree or bulk breeding methods after artificial hybridization. The single-seed descent method has been used in camelina breeding and mapping experiments for rapid generation advancement to homozygosity; because spring-types of camelina do not require vernalization, three to four generations of a segregating population could be grown per year in a greenhouse, similar to rapid cycling brassicas.

In camelina, mutation induction techniques have been employed in addition to hybridization to create new genetic diversity. Seed treatment with EMS or seed irradiation with gamma rays from a <sup>60</sup>Co source have both been successful in changing the fatty acid content. Camelina was also effectively treated with EMS seed to decrease its susceptibility to acetolactate synthase inhibitor herbicides, giving resistance to imazethapyr, sulfosulfuron, and flucarbazone[10].

Another significant method for speeding breeding programmes is the generation of double haploids obtained from other cultures or isolated microspores. The best rate of embryogenesis was reported in the Camelina protocol for microspore embryogenesis, when small floral buds of <1 mm buds were used which looked like the late-uninucleate stage of the development of the microspore; some 70% of regenerating plants had spontaneous chromosome twinning with normal seed set but the efficiency of double-shaped production.

## **2. DISCUSSION**

Camelina is considered a platform for the generation of bio-industrial petroleum. In addition to an adequate yield and processing capacity, fully established methods for breeding and enhancement of traits are available in genetic engineering because of the high gene sequence of genes between Arabidopsis and camelina. Genetic transformation methods based on the transformation of the agrobacterium-mediated floral dip have been established and in recent years have produced a series of effective transformation reports. In camelina, the genes for changing the fatty acid content, increased seed and oil production or dryness resistance were expressed in addition to selection markers.

RNAi removal of fatty acid desaturase (FAD2) and elongase (FAE1) genes has led to lower linoleic, linolenic and eicosaenoic acid concentrations, whereas the amount of oleic acid accumulated at 66%; camelina strains with high oils are of considerable value for biofuel production and further technical uses, as biodiesel with low oxygenation is of high linolenic acid. Compared to spontaneous genetic or environmental changes in the content of fatty acids, suppression lines have a significant effect on the adaptation of oils. Other types of camelina made from desaturase fatty acid and elongase cassette genes have generated up to 31% eicosapentaenoic acid, or up to 14% docosahexaenoic acid, both of which have a distinct medical and nutritional significance and are now supplied mainly by marine fish oils.

Camelina lines overexpressed the GTP-binding protein signalling AGG3 showed an increased efficiency in photosynthesis, associated with higher fruit, 1000-seed weight, seed yield and oil content than controls, showing that quantitative agribusiness can be developed through regulations on plant organ size. The increased resistance to the drought, which has been obtained via the overexpression of an arabidopsis gene for cuticular wax biosynthesis on camelina leaf surfaces, is an essential application with special importance for biofuel production at marginal soil.

The examples show the potential of camelina to translate fundamental genetic and biotechnological findings into various biorefinery applications for agricultural biofuel and other vegetable oils. In addition, because of the minimal danger of outcrossing, no crossing with common Brassicaceae species, and a limited potential for weeds compared to other Brassicaceae, genetically modified camelina also has a low level of biosecurity and is therefore ideal for platforming plants.

### 3. CONCLUSION

Although camelina has considerable agronomic potential and a unique composition of fatty acid, grain yield and oil content are important breeding objectives for making the crop more competitive to other widely known olive seeds. Due to the synthesis of phytoalexins, camelina is resistant to key Brassicaceae diseases and may also serve as a model for resistance to other significant species. Since the camelina genome is allohexaploid with many unquiet gene loci, genomic selection may speed up breeding progress with phenotypic selection, since it can deal with complicated epistatic effects more effectively. The sequence collinearity of Arabidopsis may be used in many genomic and transgenic methods such as lipid biosynthesis metabolic engineering. Further study is required to maximise the content of target fatty acids in transgenic camelina strains while avoiding unwanted metabolomic byproducts, seed protein engineering and problems of biosafety.

### REFERENCES

1. C. Boyle, L. Hansen, C. Hinnenkamp, and B. P. Ismail, "Emerging Camelina Protein: Extraction, Modification, and Structural/Functional Characterization," *JAACS, J. Am. Oil Chem. Soc.*, 2018, doi: 10.1002/aocs.12045.
2. L. H. Zhu *et al.*, "Dedicated Industrial Oilseed Crops as Metabolic Engineering Platforms for Sustainable Industrial Feedstock Production," *Sci. Rep.*, 2016, doi: 10.1038/srep22181.
3. G. Na, N. Aryal, A. Fatihi, J. Kang, and C. Lu, "Seed-specific suppression of ADP-glucose

- pyrophosphorylase in *Camelina sativa* increases seed size and weight 06 Biological Sciences 0607 Plant Biology,” *Biotechnol. Biofuels*, 2018, doi: 10.1186/s13068-018-1334-2.
4. M. Leclère, C. Loyce, and M. H. Jeuffroy, “Growing camelina as a second crop in France: A participatory design approach to produce actionable knowledge,” *Eur. J. Agron.*, 2018, doi: 10.1016/j.eja.2018.08.006.
  5. D. Moeller, H. L. Sieverding, and J. J. Stone, “Comparative Farm-Gate Life Cycle Assessment of Oilseed Feedstocks in the Northern Great Plains,” *Biophys. Econ. Resour. Qual.*, 2017, doi: 10.1007/s41247-017-0030-3.
  6. M. B. Betancor *et al.*, “Oil from transgenic *Camelina sativa* containing over 25 % n-3 long-chain PUFA as the major lipid source in feed for Atlantic salmon (*Salmo salar*),” *Br. J. Nutr.*, 2018, doi: 10.1017/S0007114518001125.
  7. A. L. Pilgeram *et al.*, “*Camelina sativa* , A Montana Omega-3 and Fuel Crop,” *Proc. sixth Natl. Symp. Creat. Mark. Econ. Dev. New Crop. New Uses.*, 2007.
  8. D. R. Shonnard, L. Williams, and T. N. Kalnes, “Camelina-derived jet fuel and diesel: Sustainable advanced biofuels,” *Environ. Prog. Sustain. Energy*, 2010, doi: 10.1002/ep.10461.
  9. B. Wittkop, R. J. Snowdon, and W. Friedt, “Status and perspectives of breeding for enhanced yield and quality of oilseed crops for Europe,” *Euphytica*, 2009, doi: 10.1007/s10681-009-9940-5.
  10. J. R. Petrie *et al.*, “Metabolic engineering *Camelina sativa* with fish oil-like levels of DHA,” *PLoS One*, 2014, doi: 10.1371/journal.pone.0085061.