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Regulatory Pathways Controlling Fatty Acid Composition in *Brassica napus*

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Abstract The fatty acids contained in rapeseed have a direct impact on the nutritional value, industrial use and economic benefits of rapeseed. This review mainly discusses the synthesis mechanism of rapeseed fatty acids, the regulation mechanism of fatty acid composition, and the influence of genetic, biochemical and environmental factors on it. Among them, some enzymes are introduced, mainly some enzymes that play a key regulatory role, such as fatty acid desaturase (FADs). The article will also introduce several more important regulatory genes, such as BnaLEC1s and BnaRGAs. These enzymes and genes are relatively important regulatory entities in rapeseed plants, affecting the transcriptional regulation and hormone regulation network in rapeseed. At the same time, researchers have also used new technologies such as genome-wide association analysis (GWAS), transcriptome analysis and epigenetic methods to identify key genes and regulatory regions related to fatty acid traits. The article will also mention the effects of environmental conditions (such as temperature changes and abiotic stresses) on fatty acid composition. In order to reduce the impact of the environment on fatty acid composition, scientists have developed many breeding methods and biotechnology means, some of which, such as CRISPR/Cas9 gene editing, metabolic engineering and acetylation modification, have been applied. These tools can effectively increase the oleic acid content and reduce the linoleic acid ratio, thereby improving the overall oil quality. Combining multiple omics technologies with artificial intelligence is also a new way to optimize fatty acid metabolism. Subsequent research can make greater use of these tools to cultivate new rapeseed varieties with better oil quality and stronger stress resistance.

Keywords Fatty acid composition; *Brassica napus*; Gene regulation; Metabolic engineering; Genome-wide association study

1 Introduction

Rapeseed is also called cabbage rapeseed. The fatty acids contained in its oil will directly affect the quality of the oil and how much it can be sold for. For example, the amount of oil in the seeds and the ratio of oleic acid to linoleic acid are very important. These components are not only related to whether the oil is nutritious, but also determine whether it can be used to make industrial products (Yan et al., 2021). In fact, the fatty acids in rapeseed are not grown randomly. Their production is controlled by many genes and biochemical processes. Studies have found that some plant hormones, such as gibberellin (GA), affect the synthesis of fatty acids. It works through a signaling pathway called GA-BnaRGA-BnaLEC1. This pathway affects something called transcription factors, which directly affect the synthesis of oils (Yan et al., 2021). In addition, scientists have also used QTL analysis to find many genes and candidate genes related to fatty acid composition. This also shows that the genetic mechanism that controls the types and proportions of fatty acids is really complicated (Wang et al., 2015).

Brassica napus is widely distributed around the world and is an important oil crop. Rapeseed has a high oil content and a wide range of uses. It can be used as edible oil, animal feed, and as a raw material for the production of biofuels (Wang et al., 2015). Many kinds of fatty acids can be extracted from the seeds of *Brassica napus*, so they can be used in many different fields, especially in biodiesel, where Brassica napus has a particularly important use. Biodiesel is a renewable energy source that can reduce human dependence on traditional fossil fuels (Wang et al., 2015). In order to improve the quality and yield of rapeseed oil, scientists have put a lot of effort into genetic engineering and breeding. In a 2022 study, Fenyk's research team found that by increasing the expression of certain synthetic enzymes in rapeseed plants, rapeseed can accumulate more oil and change its lipid metabolism.

This review mainly summarizes the various factors that control the composition of fatty acids in *Brassica napus*. The article will focus on the effects of genetic factors, biochemical processes, and hormones on the synthesis and accumulation of fatty acids. The article will also mention the research progress in recent years in QTL positioning, genome-wide association analysis (GWAS) and transcriptome analysis. These research results have helped us identify many important genes related to fatty acid metabolism and their regulatory networks. In addition, the article will also talk about some emerging technologies, such as acetylation modification, which can effectively affect the metabolism of oleic acid and bring new ways to improve rapeseed. By integrating these latest research results, we hope that this article can point out the problems that have not yet been solved, and provide some reference and help for further improving the oil quality and economic value of *Brassica napus* in the future.

2 Fatty acid biosynthesis pathway in *Brassica napus*

2.1 Overview of de novo fatty acid synthesis in plastids

In the seeds of *Brassica napus*, there is a small structure called a "plastid". Fatty acids are usually initially synthesized in the plastid during seed development. One of the raw materials for synthesizing fatty acids is phosphoenolpyruvate (PEP), which is transported into the plastid and enters the fatty acid manufacturing process. PEP can provide carbon and some energy (such as ATP), which are the raw materials required for the initial synthesis of fatty acids, so this process is critical. A transport protein called PPT helps PEP enter the plastid, and it is active in the cell in the early stages of embryonic development (Kubis et al., 2004).

2.2 Key enzymes involved in fatty acid elongation and desaturation

In the later stages of fatty acid synthesis, several important enzymes are involved. First, the "elongation" process of fatty acids is initiated by an enzyme called acetyl-CoA carboxylase. This enzyme can convert acetyl-CoA into malonyl-CoA, which is the first step in fatty acid elongation (Slabas et al., 2001). Next, the fatty acid synthase complex will continue to catalyze a series of reactions to make the carbon chain of fatty acids longer. Then comes the process of adding double bonds to the fatty acid chain, which is called "desaturation". This step is mainly completed by desaturase (FAD). They can convert saturated fatty acids into unsaturated fatty acids. For example, the enzyme FAD5 can convert oleic acid into linoleic acid (Gacek et al., 2017). Other studies have found that if an enzyme called PDAT1 is expressed more in plants, the composition of fatty acids will change, thereby changing the proportion of unsaturated fatty acids (Fenyk et al., 2022).

2.3 The role of lipid transport and storage in fatty acid metabolism

After fatty acid synthesis is completed, the transportation and storage of fatty acids are also very important steps. In *Brassica napus*, fatty acids are usually assembled into triacylglycerol (TAG) molecules, which is the main form of fat storage in seeds. The "Kennedy pathway" can put very long-chain fatty acids (VLCFAs) into TAG molecules, which is the key to this storage process. Among them, glycerol-3-phosphate acyltransferase is mainly at work (Taylor et al., 1992). In addition to the same cell structure, fatty acids are also transported to different cell structures, so transportation between cell structures is also very important, especially lipid transfer from plastids to endoplasmic reticulum (ER). This transport must go through the process for the final assembly and storage of lipids. However, the specific mechanism in this regard is still not clear (He et al., 2020).

3 Genetic regulation of fatty acid composition

3.1 Overview of genes regulating fatty acid biosynthesis

In *Brassica napus*, the synthesis of fatty acids is controlled by many genes, and the process is quite complicated. Studies have found some key regulatory genes, such as *FATB* and *FAD5*. They correspond to two enzymes, fatty acyl ACP thioesterase B and fatty acid desaturase, which are very important for the synthesis of oleic acid and linoleic acid (Gacek et al., 2017). There are also some genes, such as *BnaA6.RGA* and *BnaC7.RGA*, which are "brakes" of gibberellin (GA) signals, that is, they inhibit the action of GA. These genes interact with transcription factors such as BnaLEC1s, thereby affecting the proportion and type of fatty acids (Yan et al., 2021). Using the method of genome-wide association analysis (GWAS), scientists have also found more locations and genes related to fatty acid content and composition, such as LACS9, KCR1 and FAB1 (Qu et al., 2017; Gazave et al., 2020) (Figure 1).

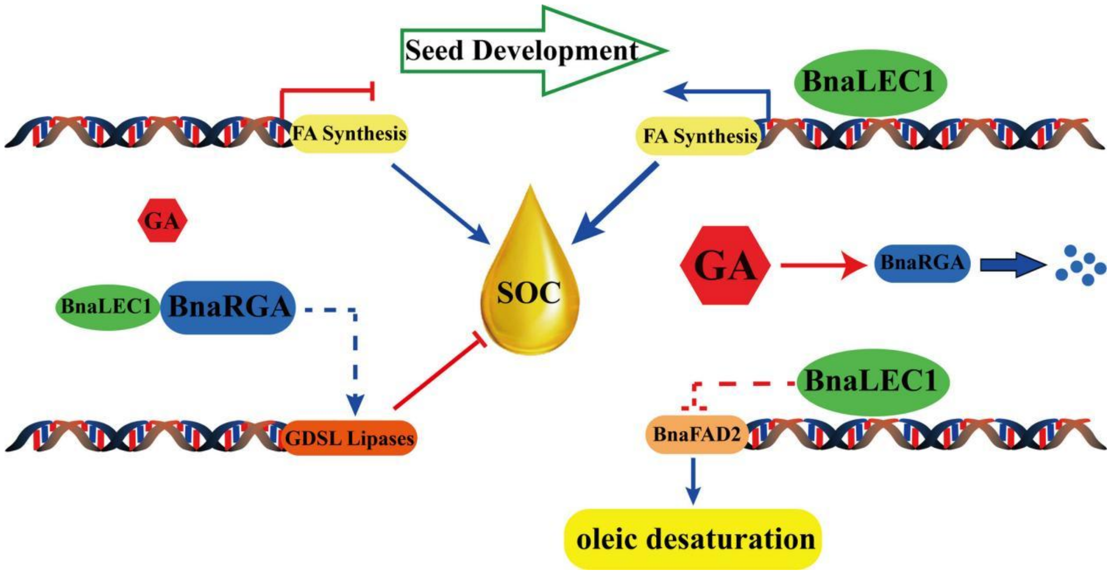


Figure 1 Working model for the regulatory mechanism of BnaRGAs in the SOC and FAs composition. At the early stage of seed development, the GA remains a low level, BnaRGAs form a complex with BnaLEC1s and block their DNA-binding capacity, leading to repressed fatty acid synthesis. In addition, BnaRGAs activate the expression of GDSL lipases, which further represses SOC accumulation. During seed development, GA levels gradually increase, which triggers the degradation of BnaRGAs to relieve their repression of BnaLEC1s. Simultaneously, BnaLEC1s activate the expression of FA-related genes to promote FA biosynthesis. By contrast, the expression of BnaFAD2 is repressed by BnaLEC1s. The resulting reduction in FAD2 activity leads to reduced oleic desaturation, thereby facilitating the accumulation of oleic acid and reducing the level of linoleic acid (Adopted from Yan et al., 2021)

3.2 Transcription factors affecting fatty acid metabolism

Transcription factors are "dispatchers" that play a directing role in the step of gene "expression". They are also very critical for fatty acid metabolism. BnaLEC1s is an important transcription factor that can turn on many genes related to oil synthesis. But its activity is also affected by factors such as BnaRGAs (Yan et al., 2021). There are also some transcription factors from soybeans, such as GmDof4 and GmDof11. If they are expressed more in *Brassica napus*, they can regulate genes such as *FAB2* and *FAD2*, thereby significantly increasing the oleic acid content (Sun et al., 2018). In addition, the researchers also found that if a zinc finger protein family gene called BnTT1 is "silenced" and does not work, it will affect the expression of a large number of fatty acid synthesis-related genes, and ultimately lead to changes in fatty acid composition (Lian et al., 2017) (Figure 2).

3.3 The role of epigenetics and post-transcriptional regulation

In addition to the genes themselves, some "epigenetic" mechanisms also affect the composition of fatty acids. Studies have found that a regulatory SNP called rSNP affects the binding ability of transcription factors, thereby changing the expression of fatty acid-related genes (Klees et al., 2021). These rSNPs affect a variety of transcription factors, such as DOF, MYB, NAC and TCP families. These transcription factors are important for regulating gene expression in different tissues (Klees et al., 2021). In addition, "post-transcriptional regulation" is also involved in regulation. Experiments have shown that if the antisense method is used to reduce the expression of certain lipid synthesis enzymes, not only will the enzyme be reduced, but the activity, translation or transcription of other related components will also be affected, which indicates that there is a very complex regulatory network behind it (Slabas et al., 2001).

4.Environmental Influences on Fatty Acid Profiles

4.1 Impact of temperature, light, and soil conditions on fatty acid composition

Temperature, light and soil conditions all have a significant impact on the fatty acid ratio of *Brassica napus*, among which the effect of temperature is particularly significant. When the night temperature is relatively low (LNT), the oleic acid content in the seeds will decrease, while the erucic acid content will increase. Compared with rapeseed plants grown under low night temperatures (20/18 ℃), rapeseed plants grown under low night temperatures (20/13 ℃) have 9% less oleic acid and 10% more erucic acid (Mi et al., 2023) (Figure 2). In addition to the fatty acid ratio, low temperature also affects the membrane lipids in rapeseed plants. This phenomenon is more common in the endoplasmic reticulum (ER). Low temperature will increase the content of unsaturated fatty acids and phosphatidylethanolamine (PtdEtn) (Tasseva et al., 2004). These environmental changes will affect the expression of some genes related to fatty acid synthesis, such as SAD, ECR and KCS, which will be expressed more under low temperatures (Mi et al., 2023).

4.2 Interaction between abiotic stress and metabolic pathways

In addition to climatic and environmental factors, abiotic stresses such as temperature difference and salinity can also affect the synthesis of fatty acids in rapeseed. Abiotic stresses and metabolic pathways interact with each other to change the composition of fatty acids in rapeseed. Cold stress will increase the lipid content in the endoplasmic reticulum, affect the fluidity of the cell membrane, and change the expression of genes that control the synthesis of fatty acids and phospholipids (Tasseva et al., 2004). Salinity and cadmium stress can also affect the expression of FAD genes, which are very important for maintaining oil quality. Under the influence of salt stress, genes such as ADS4.1 and FAD7.4 are expressed more strongly, and they are effective genes for stress resistance (Xu et al., 2019).

4.3 Strategies to reduce environmental impacts through breeding

In order to reduce the impact of the environment on fatty acid composition, researchers have conducted research on breeding to improve rapeseed, mainly including gene adjustment and screening for more stress-resistant varieties. Fenyk et al. (2022) found that when key enzymes (such as PDAT1) in rapeseed are expressed more, lipid metabolism can be changed and oil accumulation can be increased. But the negative impact is that it may reduce the degree of unsaturation of fatty acids. Yan et al. (2021) studied and adjusted genes involved in gibberellin (GA) signal transduction (such as BnaRGA). These genes are related to BnaLEC1s transcription factors. Together, they can increase the oil content of seeds and change the fatty acid ratio. Some new biotechnologies are also gradually emerging, such as genome editing technology without genetic modification and the use of nanoparticles to deliver genes. These new methods may help researchers breed cabbage rapeseed varieties that are more adaptable to the climate and have better fatty acids (Lohani et al., 2020).

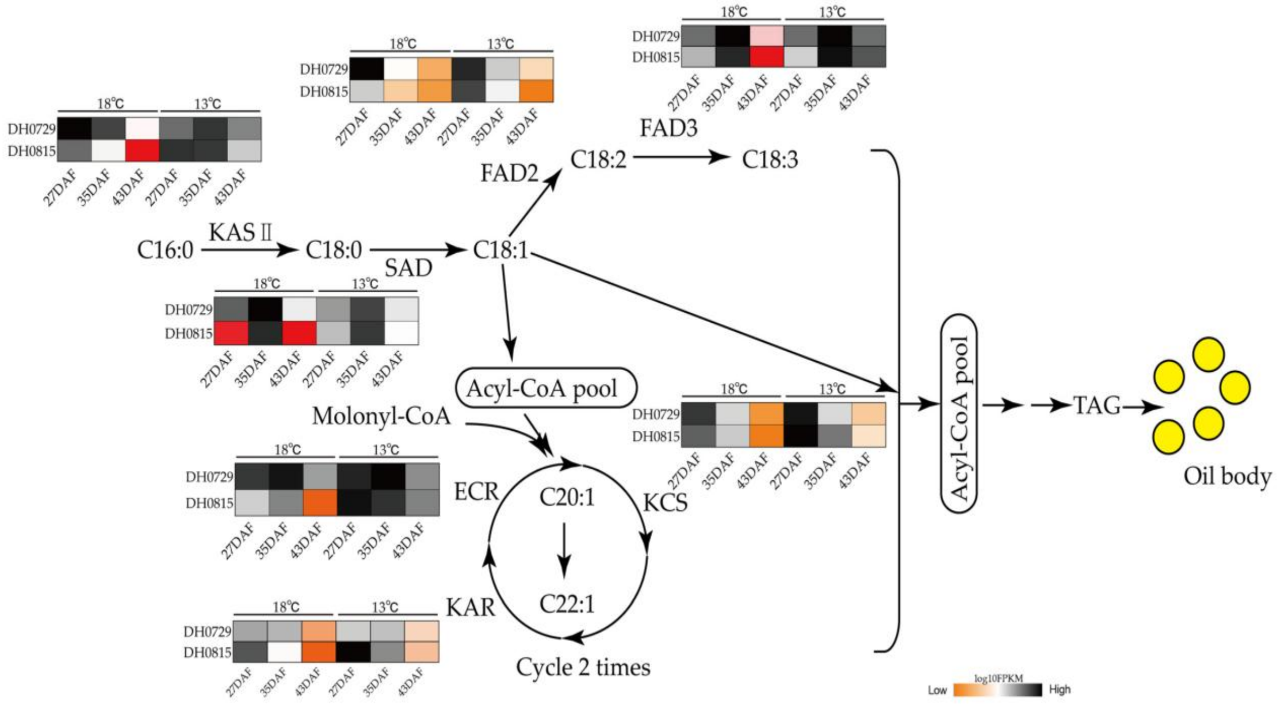


Figure 2 Effects of nighttime temperature on fatty acid metabolism in *Brassica napus* developing seeds (Mi et al., 2023)

5 Biotechnological Interventions to Modify Fatty Acid Composition

5.1 CRISPR/Cas9-mediated genome editing in *B. napus*

CRISPR/Cas9 is a tool that can precisely modify genes. Using CRISPR/Cas9 technology to change the way fatty acids are synthesized in *Brassica napus* is a good way to improve oil quality and the economic value of seeds. The principle of this technology is to "inactivate" or adjust certain genes that affect fatty acid synthesis. For example, the BnaRGAs gene blocks the signal transmission of gibberellin (GA), but this gibberellin (GA) signal is important for oil synthesis. In a 2021 study, Yan et al. found that if these genes are suppressed, the oil content of rapeseed seeds will increase and the proportion of fatty acids will change, with an increase in oleic acid and a decrease in linoleic acid.

5.2 Overexpression and silencing of key regulatory genes

Overexpressing some genes or silencing some genes is also an effective way to improve the fatty acid ratio of rapeseed. For example, there are two common transcription factors GmDof4 and GmDof11 in soybeans. After overexpressing them in *Brassica napus*, the oleic acid content will increase significantly, while the linoleic acid and linolenic acid contents will decrease relatively. GmDof4 can activate the FAB2 gene, while GmDof11 inhibits FAD2. Both processes affect the fatty acid synthesis pathway (Sun et al., 2018). In 2022, Fenyk et al. overexpressed the PDAT1 enzyme in Arabidopsis thaliana in rapeseed and found that the oil accumulation mode changed and the fatty acid composition also changed. However, it is worth mentioning that although this approach changes the fatty acid ratio, the oil content of the seeds may decrease slightly and the proportion of unsaturated fatty acids will also decrease.

5.3 Role of metabolic engineering in optimizing fatty acid profiles

Metabolic engineering refers to making some overall adjustments to the metabolic pathways within the plant so that it can produce what we need more efficiently. In *Brassica napus*, this method has been used to optimize the composition of fatty acids. In 2022, Jia's team acetylated the BnaACP3 gene, successfully making oleic acid less likely to be converted into linoleic acid, and ultimately accumulating more oleic acid. In addition, through genome-wide association studies (GWAS), scientists have also found genes such as FATB and FAD5, which are closely related to fatty acid synthesis and can serve as important targets in future metabolic engineering (Gacek et al., 2017; Gazave et al., 2020).

6. Integration of Omics Approaches

6.1 Genomic tools for identifying fatty acid-associated genes

There are now many genomic tools that can help us understand the genetic mechanisms of fatty acid composition in B. napus more comprehensively. Genome-wide association studies (GWAS) are a relatively important tool that can help find out which genes are related to fatty acid traits. A study used GWS to find a set of loci on chromosome A05 that affect oleic acid and linoleic acid content using 91 205 SNPs (single nucleotide polymorphisms). Among them, FATB and FAD5 genes are two of the more important regulatory factors (Gacek et al., 2017). In 2020, another study by the Gazave team found 53 SNP loci associated with 24 fatty acid traits. These loci involve 12 candidate genes, many of which are related to the acyl lipid pathway. A new 3-ketoacyl-CoA thiolase (KAT) homologous gene was also discovered in the study.

6.2 The role of transcriptomics and proteomics in understanding pathway regulation

Transcriptomics and proteomics studies have given us a deeper understanding of the regulation of fatty acid synthesis. By analyzing gene expression during seed development in *Brassica napus*, the study found that many regulatory mechanisms are similar to those in Arabidopsis, especially in fatty acid and starch metabolism (Niu et al., 2009). In addition, a microarray analysis comparing high-oleic acid and low-oleic acid varieties found differences in the expression of 562 genes. Among them are some key genes, such as pyruvate kinase and acyl lipid desaturase (Guan et al., 2011). Proteomics studies also tell us that post-translational modifications such as acetylation also affect fatty acid synthesis. For example, when BnaACP3 is acetylated, it can change the metabolic rate of oleic acid (Jia et al., 2022). These studies show that to understand the changes in fatty acid composition, we must not only look at the gene level, but also look at proteins and their modifications.

6.3 Application of metabolomics in lipid profile and biosynthesis

Metabolomics is a powerful method for studying the types and synthesis of fatty acids. For example, scientists used a mass spectrometry imaging technique called MALDI-MSI to analyze the distribution of lipids in *Brassica napus* seeds. The results showed that the types and contents of lipids in different tissue regions were different, indicating that lipid synthesis may be "zonal regulated" (Lu et al., 2018). Metabolomics has also been used to compare the differences in lipid synthesis between leaves and seeds. The study found several key genes that are directly involved in the synthesis of various fatty acids and triacylglycerols (TAGs) (Chen et al., 2015). These findings show that lipid metabolism is very complex. To truly understand how it works, it is necessary to combine metabolomics data with other omics information to fully understand how fatty acids are synthesized and regulated.

7 Case Study: Enhancing Oleic Acid Content in *Brassica napus*

7.1 Background: importance of oleic acid in human nutrition and industry

Oleic acid is a monounsaturated fatty acid that is highly valued for its health and industrial benefits. For humans, oleic acid helps protect heart health. It lowers “bad” cholesterol while increasing “good” cholesterol levels. Oils with high oleic acid content are also more durable and less likely to spoil. This makes it popular for cooking and food processing (Zhang et al., 2018). In addition, oleic acid can be used as a biodegradable lubricant and biofuel. These are more environmentally friendly (Gazave et al., 2020).

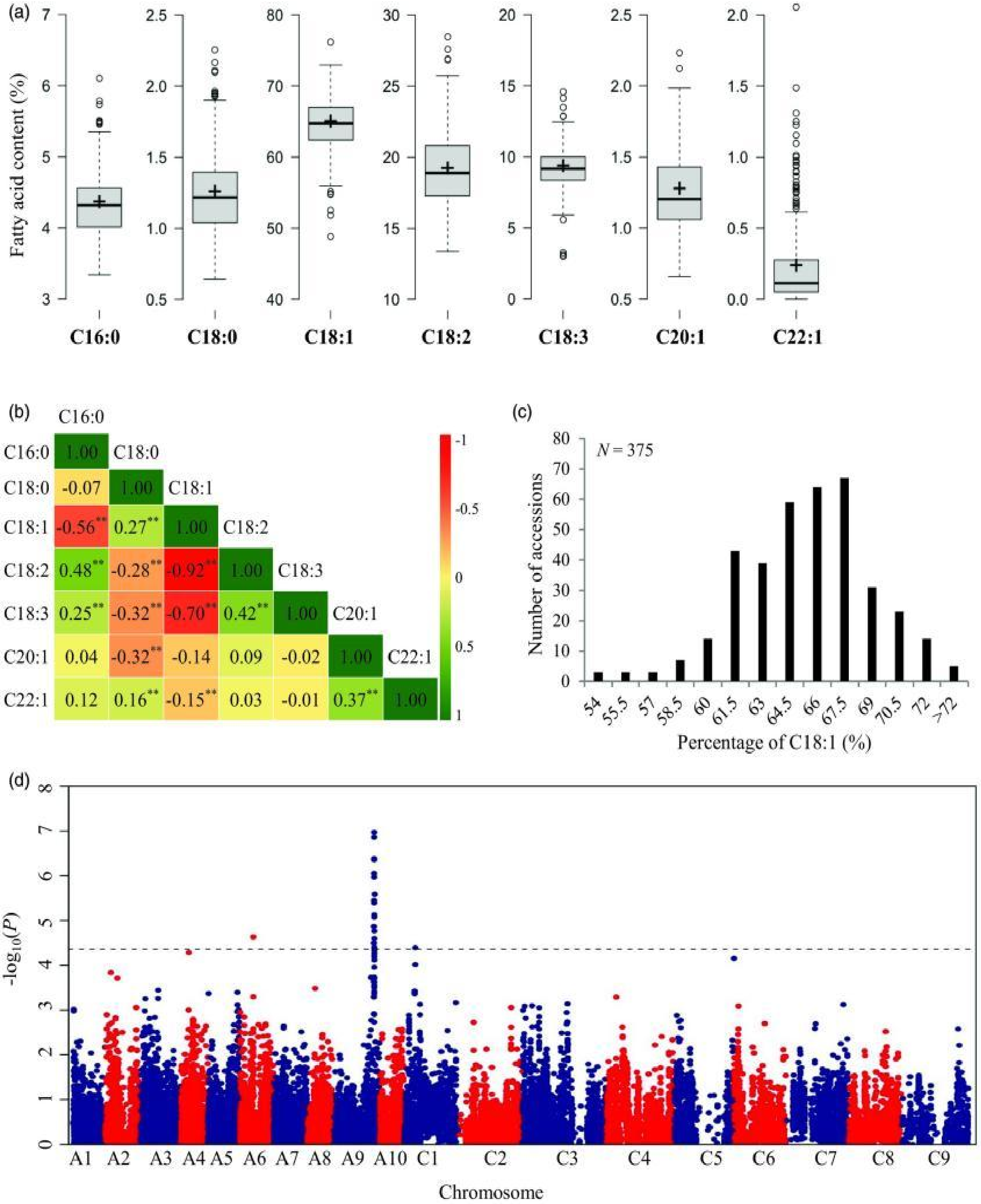
7.2 Genetic strategies to increase oleic acid content

Several genetic approaches have been used to increase the oleic acid content in *Brassica napus*. Overexpression of transcription factors: Studies have overexpressed two soybean transcription factors, GmDof4 and GmDof11, in *Brassica napus*, and found that the oleic acid content was significantly increased. GmDof4 can activate the FAB2 gene, while GmDof11 can inhibit FAD2. Both genes are closely related to the synthesis of fatty acids (Sun et al., 2018). Genome-wide association study (GWAS): Through GWAS, researchers have found several gene locations related to oleic acid content. For example, a new QTL was found on chromosome A9, which can increase oleic acid by 3%~5% (Zhao et al., 2019) (Figure 3).

In addition, studies have found related SNP sites on chromosomes A08 and C03 (Zhu et al., 2019). Regulatory role of transcription factors: Studies have found that a CCCH-type transcription factor called BnZFP1 is "positively regulated" for oleic acid. In other words, it can increase oleic acid. If BnZFP1 is expressed more in plants, the oleic acid content can be increased to 18.8% (Zhang et al., 2018). Acetylation modification: Recent studies have also found that acetylation modification of some proteins can also affect changes in oleic acid. For example, after BnaACP3 is acetylated, it becomes less likely to convert to linoleic acid, so oleic acid can be retained (Jia et al., 2022).

7.3 Success evaluation: field performance and economic impact

These genetic improvement methods have been tested in practice, and the results are good in terms of both field performance and economic returns. Field performance: Expressing more GmDof4 and GmDof11 in *Brassica napus* not only increases the oleic acid content, but also increases the total oil content in the seeds, making the plant more valuable for oil extraction (Sun et al., 2018). Similarly, plants with increased BnZFP1 expression also have higher oleic acid content and no negative impact on other growth characteristics (Zhang et al., 2018). Economic impact: High-oleic rapeseed is more expensive because it is nutritious and can be used in industry. Oil with high oleic acid content is less likely to spoil and can be stored longer, which can reduce the cost of spoilage and allow this oil to be used in more places (Zhang et al., 2018; Gazave et al., 2020). In addition, using this high oleic acid oil to make biofuel is a way to replace petroleum. This not only reduces environmental pollution, but also contributes to energy security (Gazave et al., 2020).



	C16:0	C18:0	C18:1	C18:2	C18:3	C20:1	C22:1
C16:0	1.00						
C18:0	-0.07	1.00					
C18:1	-0.56**	0.27**	1.00				
C18:2	0.48**	-0.28**	-0.92**	1.00			
C18:3	0.25**	-0.32**	-0.70**	0.42**	1.00		
C20:1	0.04	-0.32**	-0.14	0.09	-0.02	1.00	
C22:1	0.12	0.16**	-0.15**	0.03	-0.01	0.37**	1.00

Figure 3 Genome-wide association mapping for oleic acid (C18:1) content using an association panel of 375 *Brassica napus* accessions. (a) Box plot for fatty acid composition of the association panel. The middle line indicates the median; the plus sign indicates the mean; the box indicates the range of the 25-75th percentiles of the total data; the whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles; and the outer dots are outliers. (b) Distribution patterns of the C18:1 content in the 375 B. napus accessions. (c) Pairwise correlations for fatty acid composition. ** indicates correlations passed significance tests with *P*-values<0.01. (d) Manhattan plots for the GWAS of C18:1 content. The dashed horizontal line depicts the uniform significance threshold (−log101/23 168 = 4.36) (Adopted from Zhao et al., 2019)

8.Future Directions in Fatty Acid Regulation Research

8.1 Exploring new transcriptional regulators and their targets

Recent studies have found that some transcription factors play an important role in controlling rapeseed fatty acid synthesis. For example, DELLA proteins such as BnaA6.RGA and BnaC7.RGA are "repressors" in the process of fatty acid synthesis. They interact with other necessary transcription factors, such as BnaLEC1s, to affect oil synthesis (Yan et al., 2021). In addition, studies have also found that CCCH-type transcription factors such as BnZFP1 can increase oleic acid. It works by regulating a gene called DGAT1 (Zhang et al., 2018). These findings show that we can continue to look for new regulatory factors and their "targets", and perhaps find new ways to make rapeseed more productive.

8.2 Advanced breeding technology combining genomics and phenotypes

In order to further improve the fatty acid composition of *Brassica napus*, it is necessary to combine genomic information with external traits (i.e., "phenotype"). Using GWAS, several gene loci related to oleic acid and linoleic acid content were found on chromosome A05, including FATB and FAD5 genes (Gacek et al., 2017). In a 2017 study, Qu et al. used a 60K SNP chip of Brassica to find 62 regions related to various fatty acids and further understand the secrets of fatty acid synthesis. If these genetic data can be analyzed together with the actual performance of the plant, they can be used for more accurate breeding.

8.3 The role of artificial intelligence and machine learning in fatty acid pathway optimization

In recent years, emerging artificial intelligence (AI) and machine learning (ML) have great potential in optimizing fatty acid synthesis in *Brassica napus*. The widespread application of artificial intelligence (AI) and machine learning (ML) can help us process large amounts of genetic and phenotypic data, find the patterns in them, and predict the results under different gene combinations. Traits such as fatty acid content are particularly suitable for prediction using genetic data. In 2020, the Gazave team used a whole genome prediction model to analyze fatty acid traits, and the prediction results were highly accurate. With the help of AI and ML, scientists can find key genes faster and design better breeding strategies.

9 Conclusion

The fatty acid composition of *Brassica napus* involves multiple genes and biochemical processes. Two of the DELLA proteins, BnaA6.RGA and BnaC7.RGA, inhibit fatty acid synthesis by affecting another important transcription factor, BnaLEC1s. This means that adjusting the GA (gibberellin) signal can regulate the oil content and quality in seeds. Quantitative trait loci (QTL) analysis can also find many gene locations related to fatty acid metabolism, which can provide a complete genetic map for humans to understand the synthesis process of fatty acids in *Brassica napus*. Some other studies have also achieved good results: overexpressing the two transcription factors GmDof4 and GmDof11 in rapeseed plants can effectively increase the content of oleic acid, and it is feasible to improve oil quality through genetic engineering. On the other hand, genome-wide association studies (GWAS) have also discovered many key gene regions and candidate genes. These genes can be used as valuable targets in breeding.

To improve the fatty acid characteristics of *Brassica napus*, it is not enough to rely on one method alone. It is necessary to combine multiple technologies such as genetics, molecular biology, biochemistry and advanced breeding technology to maximize their functions. With the help of QTL positioning and GWAS tools, we can find genes and locations that play a key role in the process of fatty acid synthesis. And biochemical studies, such as overexpression of key enzymes such as PDAT1, also give us a clearer understanding of how oil accumulates. In recent years, the "acetylation modification" method has also shown potential in rapeseed fatty acid research. It can selectively increase the oleic acid content, and post-translational modification may also be a new means of regulating fatty acid metabolism. Combining these different methods, we can have a more comprehensive understanding of how fatty acids are synthesized, and we can also better cultivate new rapeseed varieties with better oil quality and higher yields.

In the future, there is still a lot of room for improving the fatty acid composition of *Brassica napus*. This will not only make rapeseed oil more nutritious, but also increase its market value. With the development of genetic engineering technology, we can now precisely modify key genes and regulatory pathways. This gives us the opportunity to breed new rapeseed varieties with high oleic acid and low linoleic acid. These changes are of great significance. They will not only bring healthier edible oil, but also produce more efficient biofuels, thereby reducing dependence on traditional energy. Moreover, the experience gained from studying rapeseed can also be applied to other oilseed crops, such as soybeans, peanuts or sunflowers. This makes the impact of this research even wider. Finally, to achieve these goals, continued collaboration between disciplines and the introduction of new technologies are needed. Only in this way can we truly meet the growing global demand for high-quality vegetable oils.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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