

Research Status of Molecular Biology in Flax

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Abstract: Flax is a kind of worldwide fiber and oil crops, and it has a very important role in economic crop production in the world. With the development of molecular biology techniques, the research of flax molecular level has a very big breakthrough. But, flax molecular biology researches are less reported due to the later starting. This paper summarized the latest research progress of molecular biology of flax, including molecular marker technology, construction of genetic map, gene engineering and omics researches, in order to provide the reference to understand the development and research status for flax molecular breeding researchers.

Key words: flax, molecular biology, genetic map, genetic engineering

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Introduction

Flax (*Linum usitatissimum* L.) is an annual self-pollinated crop (-370 MB genome size), originated in central Asia and Mediterranean regions, Mesopotamia, Asia and Egypt. Flax cultivation has been 5 000 years' history, which is a kind of important oil and fiber crop, known as "fiber queen" (Ragupathy *et al.*, 2011). Flax fiber, as a natural fiber, to be a part of the flax having the highest value, is one of the important materials for the spinning industry. The fabric of flax has many good qualities and unique advantages, such as antibacterial, beautiful, cool, anti bacteria to eliminate static electricity, etc. With the favour of people all over the world, it is currently a fashion in the international market, especially in the United States, Western Europe, Japan, South Korea and other developed countries. The flax fabrics and their products are important export products, as an

important raw material of textile industry in China, which are of great significance to boost the local economy.

Molecular biology is at the molecular level of biological research. Through the study of structure, function and biological macromolecular biosynthesis, etc., we aimed to clarify the essence of life, so as to make known the whole life of the biological process. Since 1950s, the research frontiers of molecular biology had been a biological and growing point. Molecular biology has penetrated into almost all the fields of biology, from certain DNA is the carrier of genetic information to life phenomenon of molecular regulation, which becomes an important part in the field of life science. The paper gave a brief overview of the flax molecular biology research progress in order to provide references for researchers to understand the research status in flax molecular marker technology, the construction of a genetic map, genetic engineering and flax omics researches.

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Molecular Marker Technology in Flax

Molecular markers, generally refers to DNA molecular markers, is an individual or the nucleotide sequence of genetic material in the genome difference among population on the basis of genetic markers, with some differences in characteristics of DNA fragments, which reflected the differences between genomic DNA directly. DNA molecular marker technology is born and developed on the basis of the development of molecular biology, and has been successfully applied to a variety of animal and plant molecular genetic map construction, genetic diversity analysis and germplasm identification, genetic relationship identification, gene mapping of important agronomic traits, transgenic animal and plant identification and marker-assisted selection breeding, etc., has made remarkable achievements, and has broad application prospects. At present, the less application of molecular marker technology is used in flax, RAPD (Random Amplified Polymorphism DNA), AFLP (Amplification Fragment Length Polymorphism), SSR (Simple Sequence Repeat) and SRAP (Sequence Related Amplification Polymorphism) markers are used mainly in flax researches.

RAPD marker

RAPD technology was founded in 1990 by Black *et al.* (1992), which can be used to detect the entire genome DNA polymorphism by using PCR technology. The technology is widely used in flax molecular biology analysis due to the simple and fast inspection speed, less dosage of DNA samples, and does not depend on the species specificity and genome structure, a set of primers can be used for different biological genome analyses, and the characteristics of the low costs of development. Huang (2009) optimized the system of flax RAPD reaction system, screened 12 polymorphic primers with high repeatability from 70 primers using three typical flax varieties, analyzed the flax germplasm genetic diversity using RAPD

technique, which laid a foundation for the molecular identification of flax (Huang, 2011). Deng *et al.* (2011) obtained 206 polymorphism bands from 25 random primers on 10 flax varieties from different countries and regions in genetic diversity of RAPD analysis. Fu (2002) is analyzed the genetic relationship of 12 germplasm on behalf of the seven flax varieties by RAPD primer, provided the evidence that *L. angustifolium* as cultivated ancestors hypothesis from the molecular level. Yang *et al.* (2011) screened a polymorphic primer OPP02 from 240 random primers to identify the disease-resistant gene, which proved OPP02792 was closely linkaged to the resistance of powdery mildew gene by cloning, recycling and sequencing. Gao *et al.* (2007) obtained three different segments S62, S135 and G06 related to the dominant nuclear male sterility in flax on the genetic background of similar sibling hybrid isolated 17 fertile plants and sterile plant flax with RAPD molecular markers.

AFLP marker

AFLP marker technology is based on PCR (Polymerase Chain Reaction) and RFLP markers, and it uses PCR technology of genome DNA double enzyme to cut pieces for selective amplification. This technique can economically, quickly and effectively generate a large number of molecular markers, rich polymorphism markers and evenly throughout the genome, codominant inheritance, repeatability and comparability, tag information study without any prior knowledge of genome sequences, so it is widely used in flax before the genome sequencing. Bo *et al.* (2003) found the specific belt linkaged to the blight resistant gene with AFLP analysis, the genetic distance between them was 5.2 cM in F2 gene pool which generated from the cross between JIN YA 7 and JIN YA10. Vromans *et al.* (2011) studied the genetic diversity of 110 flax resources comes from all over the world and a wild relatives *L. bienne* flax resources with AFLP marker technique. Li *et al.* (2011) analyzed 85 flax materials by using AFLP markers, 168 polymorphic

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