

Plant Genetics and Genomics: Crops and Models

Volume 23

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Plant Genetics and Genomics: Crops and Models book series provides current overviews and summaries of the state of the art in genetics and genomics for each of the important crop plants and genetic models for which such a volume does not now exist or is out of date.

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Genetics and Genomics of Linum

 Springer

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Preface

Flax (*Linum usitatissimum* L.) is one of the founding agricultural crops that was domesticated from the wild progenitor, commonly known as pale flax, by hunter-gatherers some 30,000 years ago. It has been selected either for the production of oil or for fiber. Fiber flax has been bred for its long, mainly unbranched stem containing long fibers. Linseed (or oil-seed flax) has been selected for short and highly branched plants to increase the number of flowers to maximize seed production. The health-related properties of flax in human and animal nutrition have opened an additional avenue for flax improvement. Modern flax breeding has the overall objectives to develop cultivars with increased fiber or seed yields, or improved health-related properties. Among the important characteristics are an improved adaptation and disease resistance to augment yields of the commercially important commodities. More than 40,000 accessions representing 54 *Linum* species are conserved in the gene banks around the world. These accessions provide an essential genetic resource for flax breeding and research, and this genetic resource has been partially characterized from cytogenetic, genetic, and genomic aspects. The new molecular genetic tools will make the flax germplasm more accessible to flax. The Canadian breeding program is presented as a model for how variety improvement has proceeded and the choice of which important characteristics need to be considered.

The initial molecular characterization of the flax germplasm was through molecular markers including isozymes, random amplified polymorphic DNAs (RAPDs), and restriction fragment length polymorphisms. The TUFGEN (Total Utilization of Flax Genomics) project has been a turning point for flax genomics resources with the development of the whole-genome sequence of CDC Bethune and the underpinning resources such as the datasets for BAC-end sequences and large-scale ESTs. The initial genome assembly has been refined by the inclusion of a range of techniques, including flax BNG optical map, the BAC physical map, and consensus genetic maps, resulting in a high-quality integrated genome. The assembly has resulted in chromosomes ranging from 15.6 to 29.4 Mb in size. However, the 15 pairs of chromosomes appear to be indistinguishable cytologically in size in spite of a twofold difference in DNA content.

The assembled genome sequence has been augmented by other molecular resources including the characterization of both coding and small RNA molecules. The transcriptomic analysis of the flax seed development will further the improvement of oil production and health-modulating phytochemicals of flax, which, along with the bast fiber, are arguably the most economically important traits in flax. The assembled genome sequence has also facilitated the theoretical identification of small RNA molecules as well as their physical identification.

Although there is more variation in the wild flax progenitor germplasm than in the cultivated varieties, chemical mutagenesis-derived mutant populations have been successfully used to identify important genes involved in cell wall formation among others. Flax is also amenable to transformation, and the development of the floral dip procedure for this species may facilitate other approaches to mutant production and increasing available variation. However, the issues with the transgenic flax, Triffid, and its unregulated escape into the commercial seed provide a cautionary tale for the development of genetically modified flax.

Some flax varieties have a particular characteristic, which is not known in other plant species, namely, the rapid modulation of its genome under certain growth conditions. The variation, with the generation of altered stable lines termed genotrophs, has been shown to occur within a specific defined subset of the genome. Understanding the mechanisms and characteristics of this genome compartment that appears to have the function of modifying the phenotype without the deleterious effects associated with a random mutagenesis makes it an interesting evolutionary mechanism. The plethora of molecular tools available allows this phenomenon to be understood at the molecular level, and potentially capable of manipulation.

The molecular resources available, the commercially important, and the health-related characteristics make flax an accessible interesting model system for understanding complex pathways while also providing the basis for improving the commercial attractiveness of the crop.

The development of the molecular resources for flax is directly attributable to the investment in the TUFGEN program and to the collaborations that were fostered, and continue to thrive, through the program.

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