

High-throughput sequencing techniques to flax genetics and breeding: a systematic review

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Motivation and Aim: in recent years, DNA markers for flax (*Linum usitatissimum*) breeding have been actively used. Marker-assisted selection (MAS), as well as genomic selection and new generation sequencing (NGS), require extensive knowledge of flax genome. The aim of this analysis was to carry out systematic review on the application of NGS methods in flax genetics and breeding.

Methods and Algorithms: the search was performed in Scopus database by the different combinations of the following keywords (flax, linseed, marker, QTL, high throughput sequencing, genomic selection, GBS, GWAS, RNA-seq, miRNA-seq, resistance, fiber content, yield, fatty acid composition, tolerance) in article titles, abstracts and key-words.

Results: according to Scopus database, 304 articles described different flax breeding directions as fiber flax and linseed were revealed. The articles using NGS in flax (*Linum*) research increased from 2 in 2012 to 6 in 2018. A large number of SNPs were identified thereby and approbation of method “Genotyping by sequencing” on flax became possible. The obtained data was the basis for the identification of new economically valuable genes in flax by genome-wide association studies (GWAS) and for the genomic selection. The use of DNA markers in flax genetics and breeding is more advanced for linseed than fiber flax. For both crops technological properties (fatty acid composition for linseed and fiber quality for fiber flax) are among most frequently studied with DNA markers (45 and 16 articles respectively). Then, DNA markers for resistance genes are more frequently developed and used (25 and 11 articles respectively). The transcriptome and miRNA are mostly related with abiotic stress tolerance of flax (drought, salinity and imbalance of nutrients). However, the flax resistance to biotic factors was not widely presented in omics studies.

Conclusion: The fiber flax remains under-investigated in comparison with linseed in development and use of DNA markers diagnostic for economically valuable traits. Studies on flax quality and disease resistance are mainly focused on finding and tagging genomic loci determining these traits, while investigation of abiotic stress tolerance is focused on identification of metabolic networks and regulatory factors involved in tolerance, based on omics studies. The systematized results can be useful for flax geneticists and breeders.