DOI 10.18699/BioGenEvo-2018-15

Polymorphism in genes related to fatty acid composition in *Linum usitatissimum*

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Key words: fatty acids, FAD genes, SAD genes, polymorphism, flax, *Linum usitatissimum*

Motivation and Aim: Flax (*Linum usitatissimum* L.) is highly recommended in human health because of its alpha-linolenic acid (ALA) content, as it has been reported that the ALA component of flax oil (omega-3 fatty acid) improves bone and cardio-vascular health [1]. Fatty acid (FA) biosynthesis in flax involves several consecutive steps governed by different gene families, such as stearoyl-acyl carrier protein desaturase (SAD) genes and FA desaturase (FAD) genes [2]. Despite the fact that these genes were identified, information on their polymorphism is restricted. Therefore, the aim of our study was to determine polymorphism of *SAD* and *FAD* genes in flax by sequencing these genes from 192 flax genotypes with different composition of FAs.

Methods and Algorithms: Seeds were obtained from the All-Russian Research Institute for Flax. DNA was isolated from 5-day-old seedlings using a CTAB method. We designed the primers for amplification of target genes by MethyMer and prepared DNA libraries using a two-stage PCR. We analyzed the concentration of obtained libraries on Qubit 2.0 fluorometer and their quality – on Agilent 2100 Bioanalyzer. Sequencing of *FAD* and *SAD* genes was performed on Illumina platform. For bioinformatics analysis, CLC Genomics Workbench was used. Obtained reads were mapped on reference sequences of *SAD* and *FAD* genes for polymorphism identification.

Results: High-throughput sequencing of *SAD* and *FAD* genes from 192 flax genotypes with diverse FA composition was performed. High coverage of DNA sequences was achieved, we obtained no less than 3000 reads for each sample. This therefore enabled the accurate assessment of levels of polymorphism and the identification of single nucleotide polymorphisms (SNPs).

Conclusion: High-throughput sequencing can be successfully used to analyze the level of polymorphism of flax desaturase genes. Identified SNPs will assist in estimation of genetic diversity, phylogenetic analysis, identification of functional polymorphisms, and marker-assisted selection.

Acknowledgements: This work was performed within the framework of the Program of fundamental research for state academies for 2013-2020 years (No. 01201363819) and was funded by RFBR according to the research project 17-29-08036.

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