

Repeated DNA sequences in genomes of species of the genus *Linum*

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Key words: genus *Linum*, flax genome, high-throughput sequencing, repeatome, 30-chromosome flaxes

Motivation and Aim: Members of different sections of the genus *Linum* are characterized by wide variability in size, morphology and number of chromosomes in karyotypes [1]. Since such variability is largely determined by the amount and composition of repeated sequences, we conducted a comparative study of the repeatomes of species from 4 sections forming a clade of blue-flowered flaxes.

Methods and Algorithms: Based on the results of high-throughput genome sequencing performed in this study, as well as available WGS data, bioinformatic analysis of repeated sequences from 12 flax samples was carried out [2].

Results: It was found that the genomes of closely related species, which have a similar karyotype structure, are also similar in the repeatome composition. In contrast, the repeatomes of karyologically distinct species differ significantly. No similar tandem-organized repeats have been identified, with the exception of one common repeat for 16- and 30-chromosome species of the sect. *Linum*. A number of mobile element families have been identified in genomes of all species, among which *Athila*, *Ty3/gypsy* LTR retrotransposon, was the most abundant. Genomes of 30-chromosome members of the sect. *Linum*, including the cultivated species *L. usitatissimum*, differ noticeably from other species by unusually high number of satellite DNA families, as well as their relative content.

Conclusion: Trends in decreasing the content of dispersed DNA repeats and increasing the content of satellite DNA during the evolution of blue-flowered flax genomes have been revealed. The extremely high content of satellite DNA in the genomes of 30-chromosome flaxes is probably due to their allotetraploid origin. The phylogenetic relationships between the investigated flax species, established on the basis of the similarity of the repeatomes, are in good agreement with the data obtained earlier with the help of other phylogenetic markers.

Acknowledgements: Supported by the RFBR (16-04-01239) and the Program of fundamental research for state academies for 2013–2020 years (Task 0103-2014-0008 Subprogram No. 53 General genetics).

References

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