

Discordant evolution of cellular genomes in peas (*Pisum* L.) as evidenced from complete sequences of plastid genomes and partial sequences of mitochondrial genomes

V.S. Bogdanova¹, A.V. Mglinets¹, N.V. Shatskaya¹, O.E. Kosterin^{1, 2*}, V.I. Solovyev^{1, 2}, G.V. Vasiliev¹

¹ Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

² Novosibirsk State University, Novosibirsk, Russia

* e-mail: kosterin@bionet.nsc.ru

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Motivation and Aim: The genus *Pisum* L. (Fabaceae) includes an important crop, the pea (*Pisum sativum* L.) and its wild relatives, the genetic diversity of which can be used for crop improvement. At the same time wild peas are a good model for studying microevolutionary phenomena. Earlier we revealed among them a principal concordant divergence of genes from the three cellular genomes [1], later data appeared suggesting a more complicated evolutionary history [2]. To clarify this we carried out an analysis of organellar genomes rather than single markers.

Methods and Algorithms: The plastid genome and a mitochondrial genome fragment were sequenced using the Ion Torrent platform in 16 wild and 3 cultivated accessions representing pea genetic diversity. The genomes were assembled with MIRA4 program, visualized with the Tablet software and checked manually. Phylogenetic analysis was carried out with Bayesian MCMC using of BEAST 1.8.4 software

Results: Phylogenetic reconstructions based on the plastid genome, a mitochondrial genome fragment, and a nuclear gene for the histone H1 subtype 5, updated with phenotypic information, evidenced for at least four events of introgression of organellar genomes through hybridisation of diverged evolutionary lines in the course of the genus evolution. One of the cases concerned introgression of plastid genome and three other cases introgression of mitochondrial genome from a distinct evolutionary lineage, as judged from the phylogenetic pattern revealed from the nuclear gene *His5*. A plastid genome intermediate between the consensuses of the common pea *P. sativum* L. and its distant wild relative, *P. fulvum* Sibth and Smith was revealed, and accession Pe 013 of wild pea from Tokat Province of Turkey was nominated as a 'missing link' between the mentioned species.

Conclusion: Discordant evolution of the three cellular genomes because of introgression may be widespread in plant microevolution and should not be underestimated in reconstruction of phyletic relationships.

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References

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