

Diversity of CRISPR arrays identified into plant mitochondrial genomes

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Mitochondrial genome of plants is much bigger than that of animals or fungi, and stores many noncoding sequences of non-mitochondrial origin. Moreover, mitochondrial genome of higher plants is actively involved in horizontal gene transfer processes where it can act both as a donor and a gene acceptor. In this work we identified many CRISPR-like arrays in number of mitochondrial genomes of higher plants. These CRISPR-like arrays are widespread among species and include agricultural (*Vitis vinifera*, *Beta vulgaris*, *Daucus carota*, *Vicia faba*), wild types (*Zea luxurians*) model plants (*Arabidopsis thaliana*), and even liverworts (*Treubia lacunose*, *Marchantia polymorpha*). Existence of such elements may be associated with mobile genetic elements (MGEs) presence or defense against DNA of foreign origin (including MGEs). Some of mitochondrial genomes contain dozens of CRISPR-like arrays: *Cucumis sativus* – 57, *Ophioglossum californicum* – 42, *Cucurbita pepo* – 36, *Cycas taitungensis* – 20. We suggest that CRISPR arrays were transferred to mitochondrial genomes during evolution probably from ancestor of *Alphaproteobacteria* host, which is probably a sister group to *Asgardarchaeota* (which possess CRISPR-Cas system). Due to the existence of mitoviruses, that infect mitochondria directly, evolution of plants led to the need for the CRISPR-Cas system to maintain the immunity of mitochondria. The mechanism of discovered CRISPR-like system might be different of those in Bacteria and Archaea, so our next step is to identify CRISPR associated proteins in mitochondrial and nuclear genomes of higher plants.