

The impact of *Zea mays* mitochondrial plasmids on the evolution of nuclear genes

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Motivation and Aim: Mitochondria of higher plants contain autonomously replicating linear and circular plasmids [1], with linear plasmids known to be able to insert into the mitogenome [2]. Due to the similarity of linear plasmids to mobile elements and known events of mitogenome insertions into the nuclear genome (NuMTs [3]), the investigation of the origin of mitochondrial plasmid insertions into the maize nuclear genome, their potential impact on the genome evolution and potential for construction of novel genome transformation systems are important yet unresolved problems. The aim of the current study is the detection and analysis of plasmid insertions in maize nuclear genomes.

Methods and Algorithms: Using BLAST software we searched for maize mitochondrial plasmid sequences (GenBank ID: X13704.1 (S3), J01426.1 (S2), X02451.1 (S1), M36398.1 (1.4 kb), NC_001400.1 (pBMSmt1.9, 1.9 kb)) in genomes of 24 maize inbred lines with chromosome-quality assemblies available at the MaizeGDB database (<https://www.maizegdb.org/>). Genome annotations of the B73 line (RefSeq ID GCF_902167145.1) were used for detailed analysis.

Results: Analysis of 24 genomes of maize inbred lines showed the presence of insertions of all linear and circular mitochondrial plasmids in the nuclear genome. This fact suggests that maize mitochondrial plasmids behave as MGEs with inter-organelle mobility. The median identity of the insertions was 95 %, indicating recent insertion events. Insertions contain homologous sequences to open reading frames (ORFs) and tRNAs, as well as full-length sequences for S3. The frequencies of insertions in the maize B73 reference genome vary across different genomic regions, overlapping with mobile genetic elements, pseudogenes, and introns of protein-coding genes, which may indicate their regulatory role. Phylogenetic analysis revealed distinct groups of nuclear genome tRNAs related to tRNAs introduced by plasmid S3 insertions.

Conclusion: As a result, we can conclude that maize mitochondrial plasmids, along with other MGEs, influenced the evolution of maize genes.

References

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