

MITOCHONDRIAL DNA EDITING IN POTATO

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Mutations in mtDNA and/or nuclear-mitochondrial interactions can affect crop morphology and physiology, resulting in cytoplasmic male sterility (CMS), flower abnormalities, and differences in performance of reciprocal hybrids. However, the conventional and biotechnological tools available so far were largely insufficient and/or inefficient to uncover the direct and indirect role of mitochondrial genes in such interactions.

Genome editing of higher plant mitochondria has recently been shown in animal systems and in a few crops with considerable success as well as some limitations. In particular, CRISPR/Cas technology is not practicable due to unknown ways to import sgRNAs in cytoplasmic organelles. Hence, in order to understand the role of orfs with unknown function on male fertility and the agronomic performance of interspecific *Solanum* spp. hybrids, we used, for the first time in potato, two TALE-based approaches: one based on the *FokI* nuclease (mitoTALEN) and one more on targeted base editing by the DddA cytidine deaminase (TALECD). Both methods were effective in our hands, resulting in homoplasmic deletions of varying magnitude with the former and base substitutions leading to premature stop codons with the latter.

We will discuss the efficacy and efficiency of such novel approaches to purposely edit cytoplasmic genomes in plants, a hitherto difficult target

to achieve, with the aim to induce precise modifications for genetic studies and breeding as well.