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WHOLE TRANSCRIPTOME MAPPING REVEALS COMPLETE TRANSCRIPTION AND SIGNALS OF EUKARYOTIC PROCESSING IN PLANT MITOCHONDRIA

The plant chloroplast has become a vector to deliver transgenes. Recently, however, the mitochondrion has become a prospective target for plant genetic engineering. Transformation of mitochondria can result in synchronized expression of transgenes between all three plant genomes via interorganellar communication pathways within the cell, resulting in effective engineering of the whole plant cell factory. In addition, the mitochondrial genome (mitogenome) can shuffle genes between the chloroplast and the nuclear genome, making it a unique vector for transgenes, and of great potential to plant breeders. However, there is evidence that plastomes can be transferred across plant species boundaries by contact. As a result, understanding the plant mitochondrion is of paramount importance in identifying the risks of their use as transgenic vectors. Mitogenomes are known to have evolved from bacterial genomes and include operons and spliced genes. However, in this study, whole transcriptome mapping reveals indicators of eukaryotic processing never reported before in plant mitochondria, which will aid in our understanding of the mitogenome. The transcriptomic data of various plant and animal species available on NCBI were mapped to mitochondrial reference genomes. Mappings of reads to mitochondrial genomes revealed, for the first time, that selected monocot, dicot, non-seed plant, fungal and animal mitochondrial genomes were expressed in their entirety. Moreover, when poly-A selected transcript sets were mapped they were found to only cover part of the mitogenome. Thus mitochondrial transcripts may undergo eukaryotic-like processing that need to be further investigated. Overall, the plant mitochondrial genome shares many features with the size-relaxed nuclear genome.

Country or International Organization

South African Sugarcane Research Institute

Primary author: Dr RAMNATH, Lucretia (South African Sugarcane Research Institute)

Presenter: Dr RAMNATH, Lucretia (South African Sugarcane Research Institute)

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