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Funded by: Plant Genomics Internship @ MU

Comparison of regulatory regions in the mitochondrial genomes of grasses

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Regulation of transcription in plant mitochondria is not well understood. The recent sequencing of the mitochondrial genomes of 10 closely related grasses allowed a comparative analysis of regulatory regions. To look for conserved regions and potential "swapped" regulatory regions, we have performed a comparative analysis of the upstream and downstream regions of all of the protein-coding genes in the mitochondrial genomes of eleven grasses: five mitochondrial types of maize (two fertile and three cytoplasmic male sterile), three other taxa within the genus (*Zea mays ssp. parviglumis*, *Z. luxurians*, *Z. perennis*), two close relatives (*Tripsacum dactyloides*, *Sorghum bicolor*), and an outgroup, rice. These genomes contain an average of 35 protein-coding genes, composed of 40 transcriptional units. Our analyses examined 1000 base pairs (bp) upstream of the first exon of each transcriptional unit and 1000 bp downstream of its last exon. The reference genome was NB, the most common fertile maize mitochondrial genotype. Compared with the genes from NB, more than half of the mitochondrial genes in the other genomes contain sequences that flank different genes in NB; we refer to these as "swapped" regions. More than 25% of the translocated sequences are longer than 100 bp, and 21 are greater than 500 bp. The longer sequences are more likely to have a regulatory function. In addition, some of these regions were found multiple times: 12 of the translocated gene-flanking regions were found flanking five or more other genes; four had sequences that were flanking ten or more. Furthermore, in *Z. luxurians*, *Z. perennis* and *T. dactyloides*, the co-transcribed 18S and 5S ribosomal RNA genes have been translocated immediately upstream of the start of *cox1*, with the 5S rRNA 3' end only 80 bp from the start of *cox1* exon 1. This is a position that is difficult to rectify with the divergent transcriptional needs of the two types of genes.