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## Comparative analyses of NA genome in Zea maize

Mitochondrial genomes are perhaps the most unusual sequences to annotate, due to the common characteristic of expedient change within the genome. Only six (mtDNA) genomes have been sequenced. It has been observed that functions of mitochondria are conserved across various species, but similarities between functions differ when comparing the mtDNA genomes in size, gene, content, organization, and gene expression. This study compared the NA genome sequence within Zea to show similarities and differences in sequences in relation to other mtDNA genomes such as *oryza*, *marchantia*, *NB*, *beta*, *arabidopsis*, and *reclinomonas*. Effectively identifying homologous sequences in genomes based on similarity between a reference plant genome and other plant mtDNA sequences was computed by using Multipip. MultipipMaker computes alignments of 2 or more DNA sequences. The alignments are seen as "percent identity plots," and it holds linear order of the reference genomes displaying on the horizontal axis. Analyses of the NA genome shows that mitochondrial genome size varies within Zea maize, and is due primarily to large repetitive regions of DNA sequences. High levels of sequence conservation are seen within both coding and intergenic regions of the Zea mitochondrial genotypes.