New Phytologist Supporting Information

Article title: Homologous recombination and retention of a single form of most genes shape the highly chimeric mitochondrial genome of a cybrid plant

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Article acceptance date: 14 October 2014

The following Supporting Information is available for this article:

Fig. S1 Dot-plot comparisons of mitochondrial genomes.

Fig. S2 Total read depth of the cybrid Nt(+Hn) mitochondrial contigs.

Fig. S3 Partial nucleotide sequence of the cybrid cox1 gene cDNA.

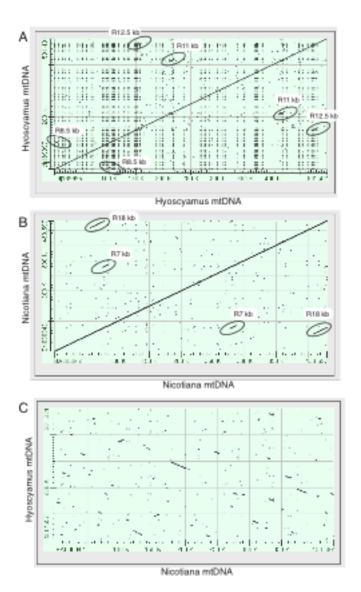


Fig. S1 Dot-plot comparisons of mitochondrial genomes. (A–C) Self-self dot-plot analysis of the mitochondrial genomes of *H. niger* (A) and *N. tabacum* (B), conducted to visualize repeats (ovals surround the largest repeats, which are labeled by 'R', followed by their lengths in kb). (C) Dot-plot comparison of the mitochondrial genomes of *H. niger* and *N. tabacum*, conducted to visualize regions of shared synteny.

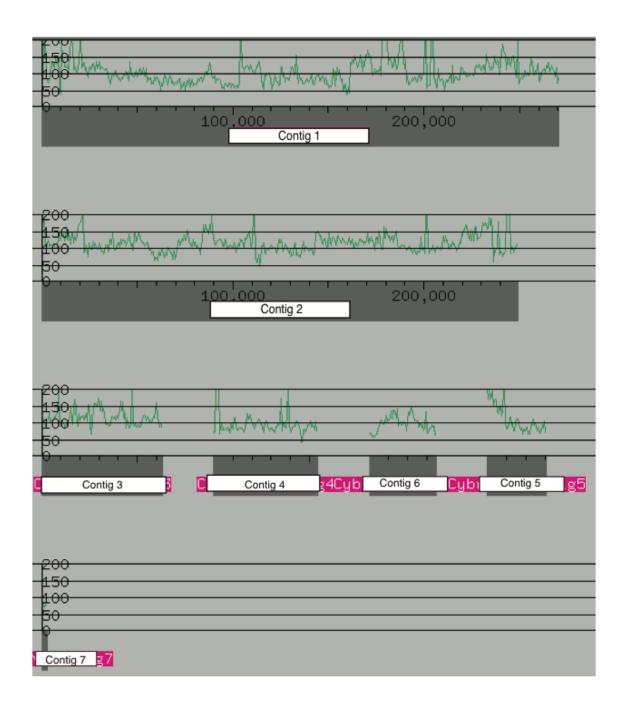


Fig. S2 Total read depth of the cybrid Nt(+Hn) mitochondrial contigs. A total of \sim 780,000 reads matched the mitochondrial assembly. The average total read depth was 107 reads.

Fig. S3 Partial nucleotide sequence of the cybrid cox1 gene cDNA. RNA edited sites are in red and marked with the letter 'E' below them. Sites corresponding to the co- conversion tract (CCT) are in green and underlined. The intron has been spliced out and the intron insertion site is indicated with an arrowhead.