

Supplementary File 2

Intron sequences in *MAT1-1-1* and *MAT1-2-1*

The positions of the *Teratosphaeria gauchensis* and *T. zuluensis* *MAT1-1-1* and *MAT1-2-1* introns were investigated in comparison to the position of these introns in representative Capnodiales species (Fig. S1a and S1b). The sequence of each *Teratosphaeria* intron was also interrogated to identify the 5' donor (GURWGU), 3' acceptor (WNYAG) and branch site (lariat) (RCURAY) sequence motifs as described by Kupfer *et al.* (2004) (Fig. S2 and S3).

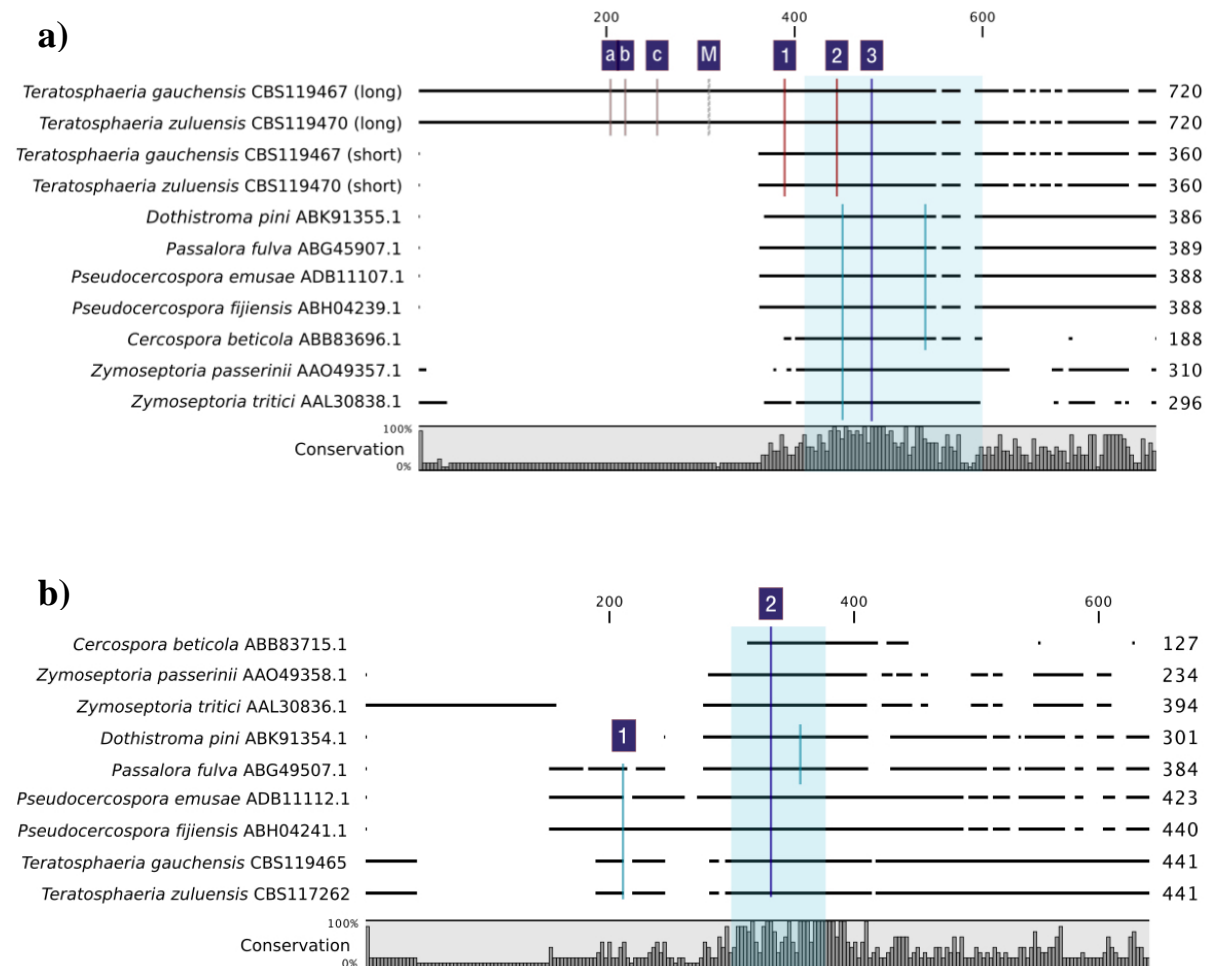


Fig. S1 (caption on next page)

Figure S1. Alignment of the (a) *MAT1-1-1* and (b) *MAT1-2-1* proteins of *Teratosphaeria gauchensis*, *T. zuluensis* and representative Capnodiales species. The initial long *MAT1-1-1* predictions, without N-terminal homology to other *MAT1-1-1* proteins, are include in (a). Vertical lines represent intron positions; boxed numbers correspond to *Teratosphaeria* introns analysed in Fig. S2. Grey = introns in the non-homologous region of the long *MAT1-1-1* gene, red = *Teratosphaeria*-specific intron position, navy = intron position shared between all studied Capnodiales species, light blue = intron position shared in a subset of Capnodiales species. The conserved domain in each protein is shaded. Numbers at the end of each line represent protein length, whereas alignment length is provided above each figure. GenBank® accession numbers follow after the species names of the Capnodiales representatives.

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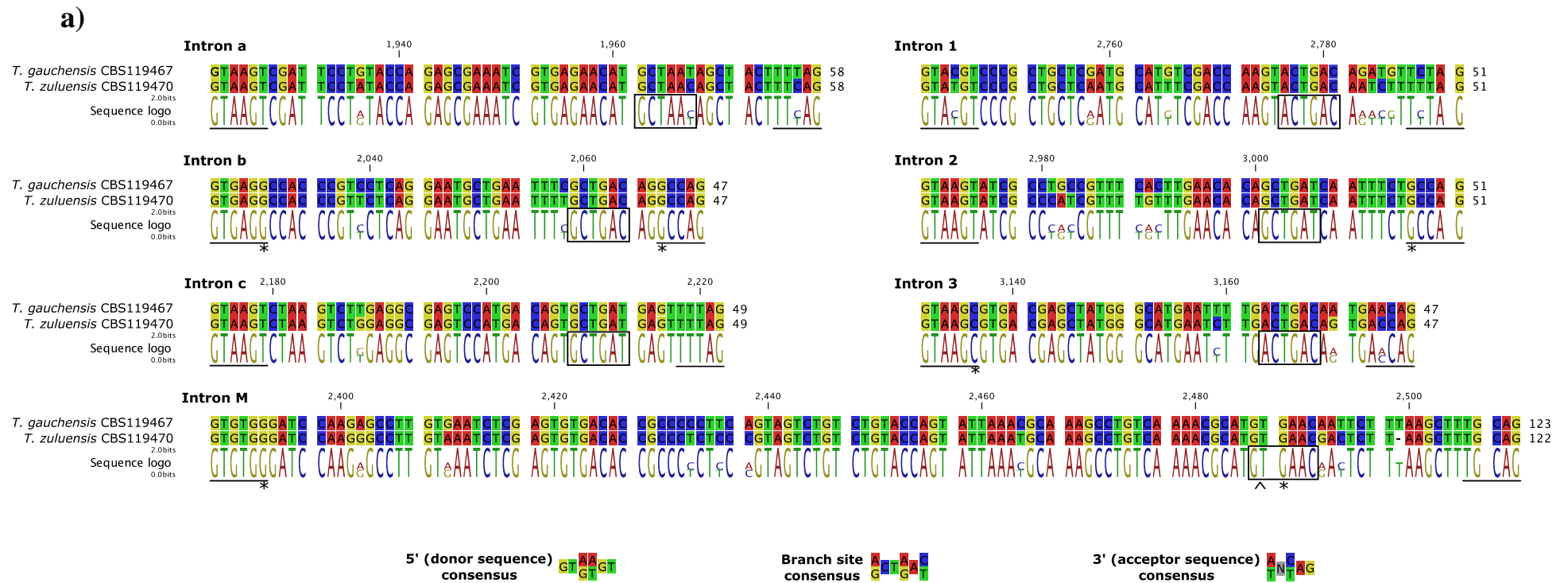


Fig. S2a (caption on next page)

b)

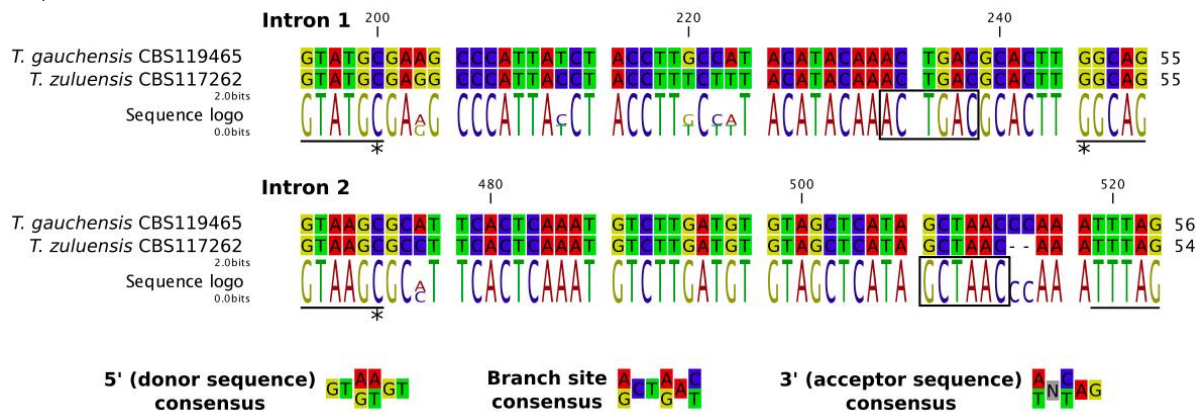


Figure S2. Intron sequences of the *Teratosphaeria gauchensis* and *T. zuluensis* (a) *MATI-1-1* and (b) *MATI-2-1* genes. The 5' donor and 3' acceptor sequence in each intron is underlined. Asterisks represent a mismatch to the fungal consensus (Kupfer *et al.*, 2004). The putative branch site (lariat) sequence is boxed. In intron "M", the putatively incorrect intron that merges *MATI-1-10* (*MATORF2*) with *MATI-1-1*, a branch site matching the fungal consensus is absent. The position of a possibly mutated branch site is indicated, with an asterisk and arrow highlighting mismatched nucleotides. Intron names refer to those indicated on Fig. S1.

References

Kupfer DM, Drabenstot SD, Buchanan KL, *et al.*, 2004. Introns and splicing elements of five diverse fungi. *Eukaryotic Cell* **3**, 1088-100.