

Supplementary File 1

Interspecific comparison of exon positions in four genes associated with the *MAT1* locus of three *Teratosphaeria* species

The exon positions of the *Teratosphaeria destructans* *MAT1-1-1*, *MAT1-1-10*, *MAT1-2-1* and *MAT1-2-12* genes were investigated and compared to the positions of these exons in *T. gauchensis* and *T. zuluensis* (Fig. S1). The *MAT1-1-1* gene had four and the *MAT1-1-10* three exons, whereas *T. zuluensis* and *T. gauchensis* had four exons in both of these genes (Fig. S1). The second *MAT1-1-10* exon of *T. gauchensis* and *T. zuluensis* was not predicted in *T. destructans* (Fig. S1). The *MAT1-2-1* gene had three exons and two introns (Fig. S1), which were conserved in all three *Teratosphaeria* species. The *MAT1-2-12* gene that was predicted in *T. destructans* contained two exons, whereas *T. gauchensis* and *T. zuluensis* harboured two additional exons at the end of this gene (Fig. S1). The last stop codon position of *MAT1-2-12* in *T. destructans* was absent in the other two *Teratosphaeria* species, although their stop codon occurred in *T. destructans*. Additionally, the “GT” intron signal of the final *T. gauchensis* and *T. zuluensis* intron was absent in *T. destructans*. These explain the differences in gene prediction between the species, but the true size of this gene and the number of exons remains uncertain, since mRNA data are not available for any of these species.

Nucleotide identity between *T. destructans* and closely related *Teratosphaeria* species was ca. 90% and 84% for the respective *MAT1-1-1* and *MAT1-2-1* genes. Protein identities for the *MAT1-1-1* and *MAT1-2-1* alignments were 89% and 77%, respectively.

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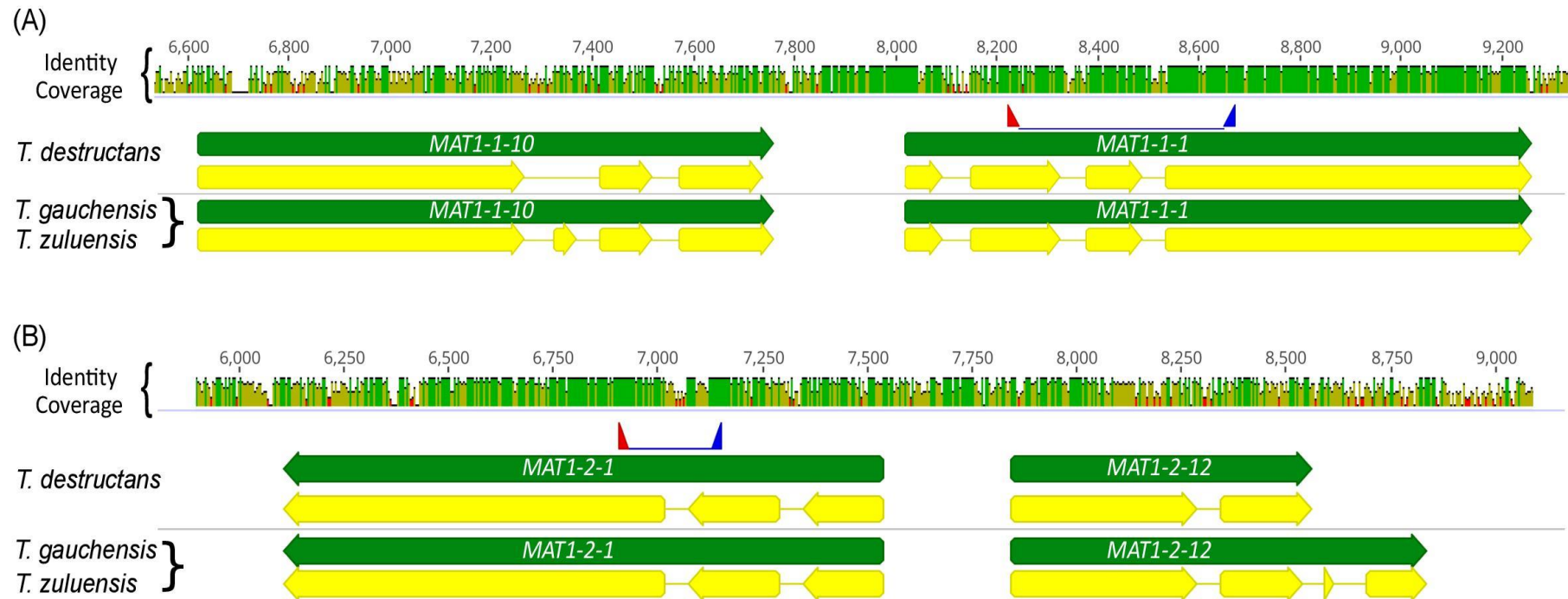


Figure S1. Exon positions of genes in the *MAT1-1* (A) and *MAT1-2* (B) loci of *Teratosphaeria destructans*, *T. zuluensis* and *T. gauchensis*. Exons (yellow arrows) are indicated beneath the *MAT* genes (green arrows). The position of primer pairs T_Ma1-F and T_Ma1-R (on *MAT1-1-1*) and TdMAT2_1 and TdMAT2_2 (on *MAT1-2-1*) are indicated with red and blue triangles. The identity coverage between the species are indicated above the genes.