

Supplementary File 3

Homology between hypothetical *MAT* proteins

The hypothetical *MAT* proteins predicted in the *MAT1-1* and *MAT1-2* idiomorphs of *Teratosphaeria gauchensis* and *T. zuluensis* were compared to the *MATORFs* previously described from *Cercospora*, *Passalora* and *Pseudocercospora*. Local tBLASTn searches revealed similarity between the two *MATORF2* genes in *C. beticola*, *Ps. eumusae*, the *MAT ORF1-1-2* in *Pa. fulva* and the hypothetical *MAT* protein predicted in the *Teratosphaeria MAT1-1* idiomorph (*MAT1-1-10*). Similarly, the hypothetical *MAT* protein in the *Teratosphaeria MAT1-2* idiomorph (*MAT1-2-12*) was found to be homologous to the *MATORF1* genes of *C. beticola* and *Ps. eumusae* and *ORF1-2-2* of *Pa. fulva*. Overall protein identity and similarity between *Teratosphaeria* and the other two species was low, but positions with high levels of conservation were apparent (Table S1). Figure S3a and S3b present the alignment of these accessory *MAT* proteins, highlighting conserved positions.

Table S1. Statistics of the alignment between the hypothetical *MAT* proteins of *Teratosphaeria* and the accessory *MAT* proteins of *Cercospora beticola*, *Passalora fulva* and *Pseudocercospora eumusae*.

| | <i>MAT1-1</i> hypothetical protein | <i>MAT1-2</i> hypothetical protein |
|--|--|--|
| Nucleotide identity¹ | 29.8 – 33.2 % | 24.0 - 37.1 % |
| Amino acid identity | 12.8 - 17.5 % | 12.9 - 17.6 % |
| Amino acid similarity | 29.1 - 34.3 % | 25.6 - 31.3 % |
| Residues with 100 % conservation² | 18 (4.6 %) | 11 (3.3 %) |
| Residues with 70-90% conservation² | 58 (14.8 %) | 25 (7.5 %) |
| Residues that differ between the two groups³ | 30 (7.6 %) | 6 (1.8 %) |
| Total residues in alignment | 393 | 335 |

¹ Based on alignment of coding sequences (CDS)

² Based on protein alignment

³ Amino acid residues conserved in *Teratosphaeria* and in the Capnodiales, but not between the two

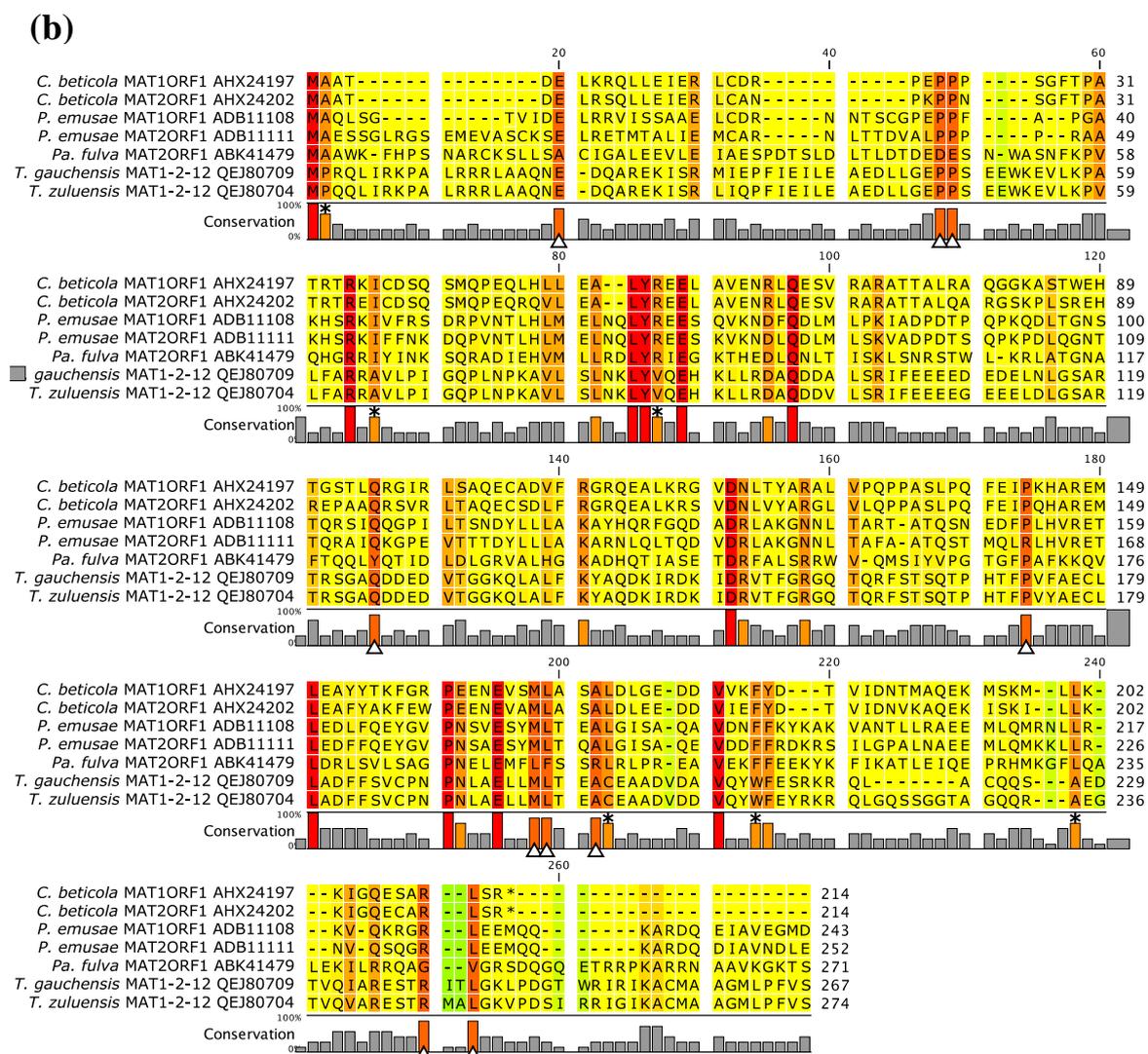


Figure S3. Amino acid alignment of the hypothetical ORFs predicted in the *MAT1-1* (a) and *MAT1-2* (b) idiomorphs of *Teratosphaeria* with the “MATORF” proteins of *Cercospora beticola*, *Passalora fulva* and *Pseudocercospora eumusae*. The alignment is coloured according to the percentage identity of the amino acids at each position: green = ≤ 30 %; yellow / light orange = 21 – 59 %; orange = 60 – 99 %; red = 100%. Positions with ≥ 70 % identity are also coloured in the conservation bar plot. Further, positions with a mismatch in only of the species is indicated by white arrows. Asterisks indicate positions where different amino acids are conserved in *Teratosphaeria* compared to the other three species.