

Supplementary data for the manuscript

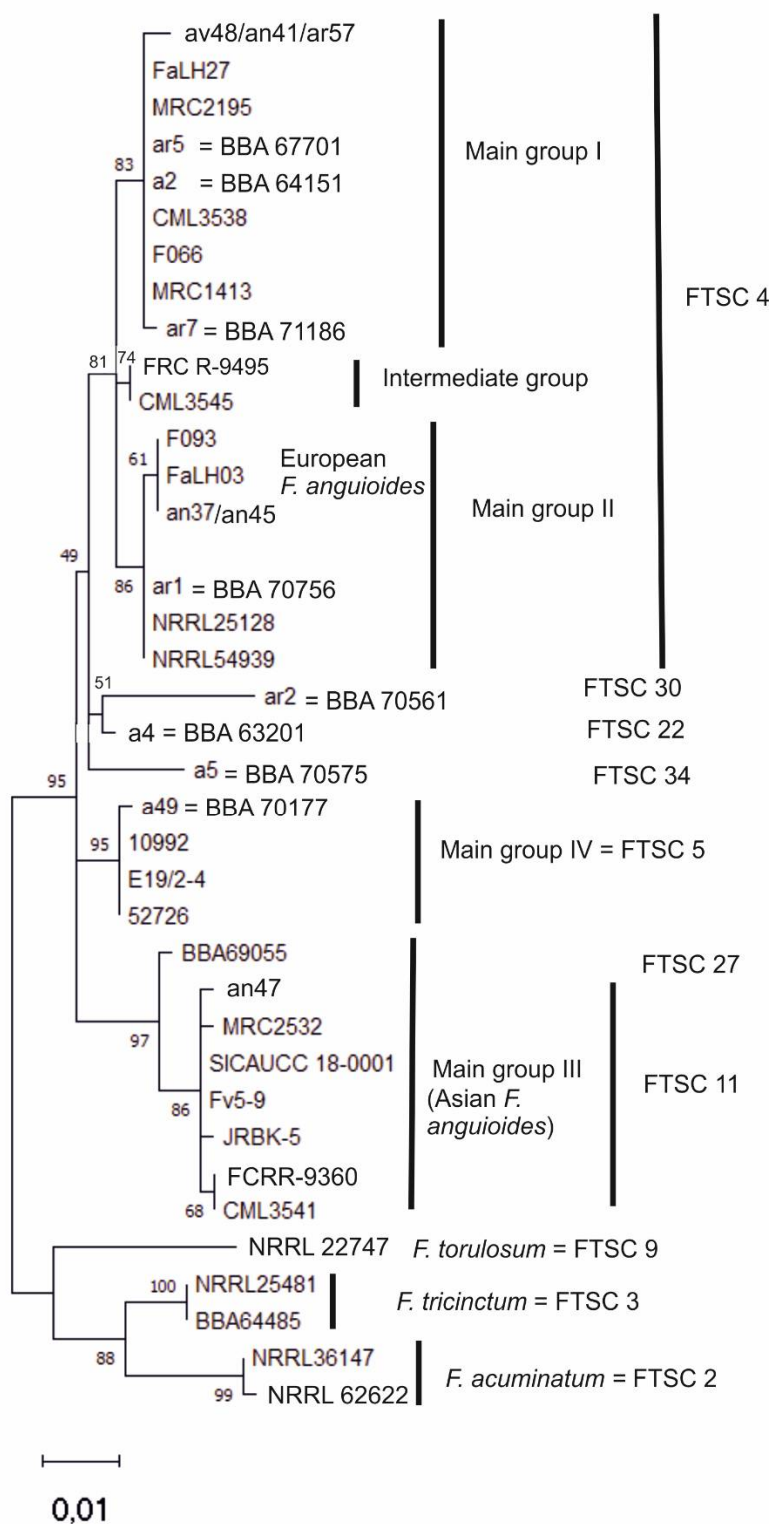
**Molecular variation within *Fusarium avenaceum* and related species**

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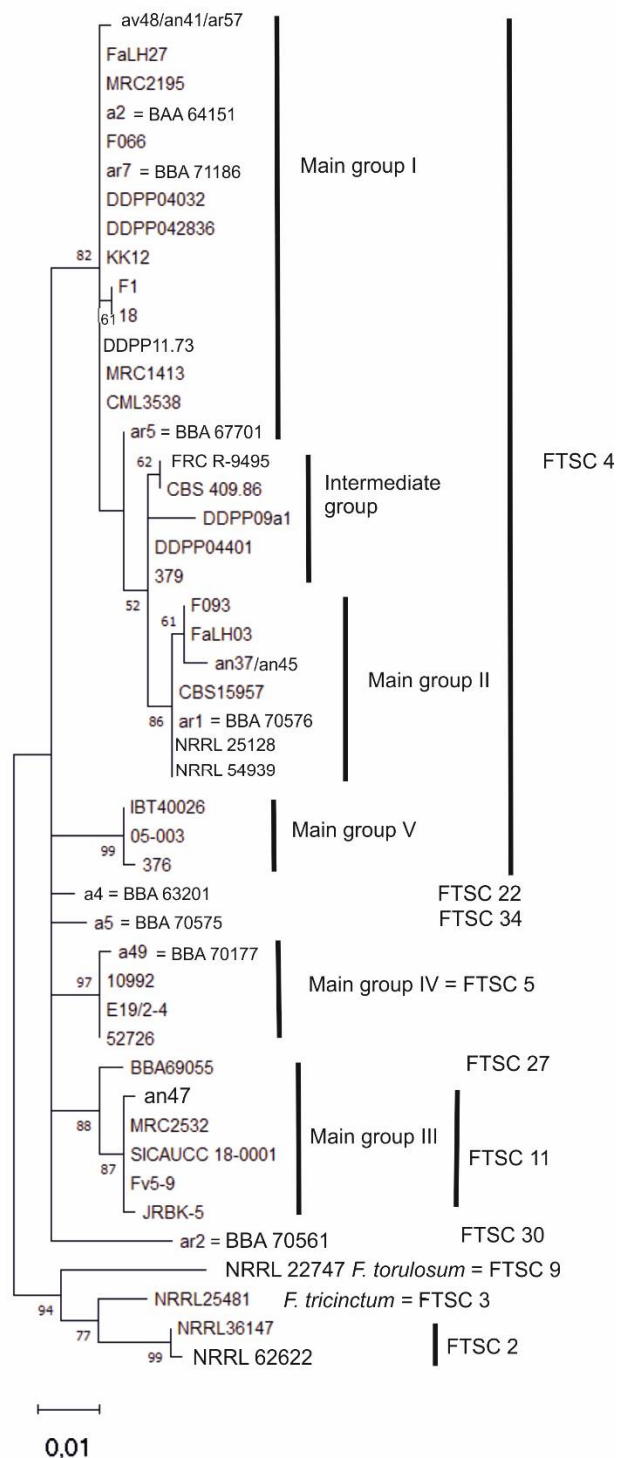
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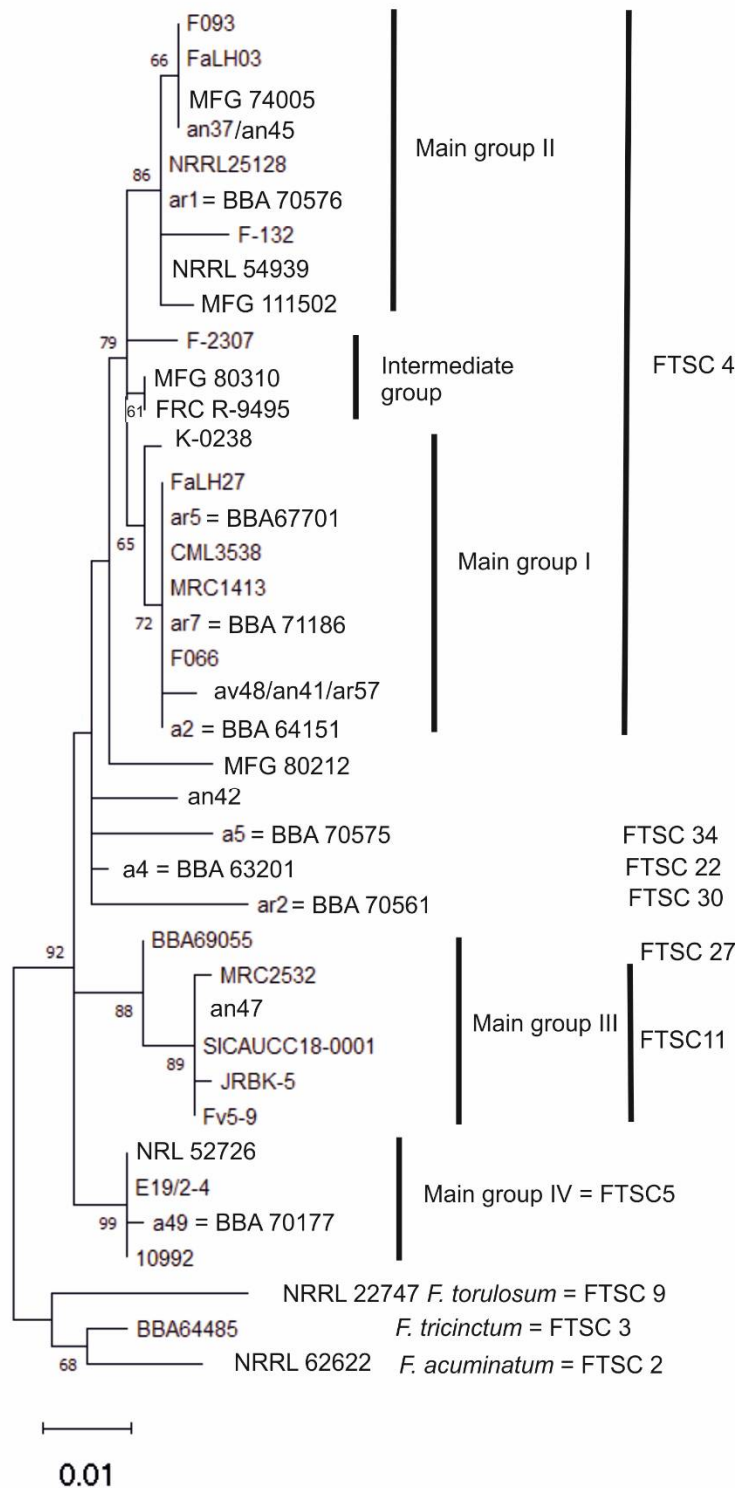
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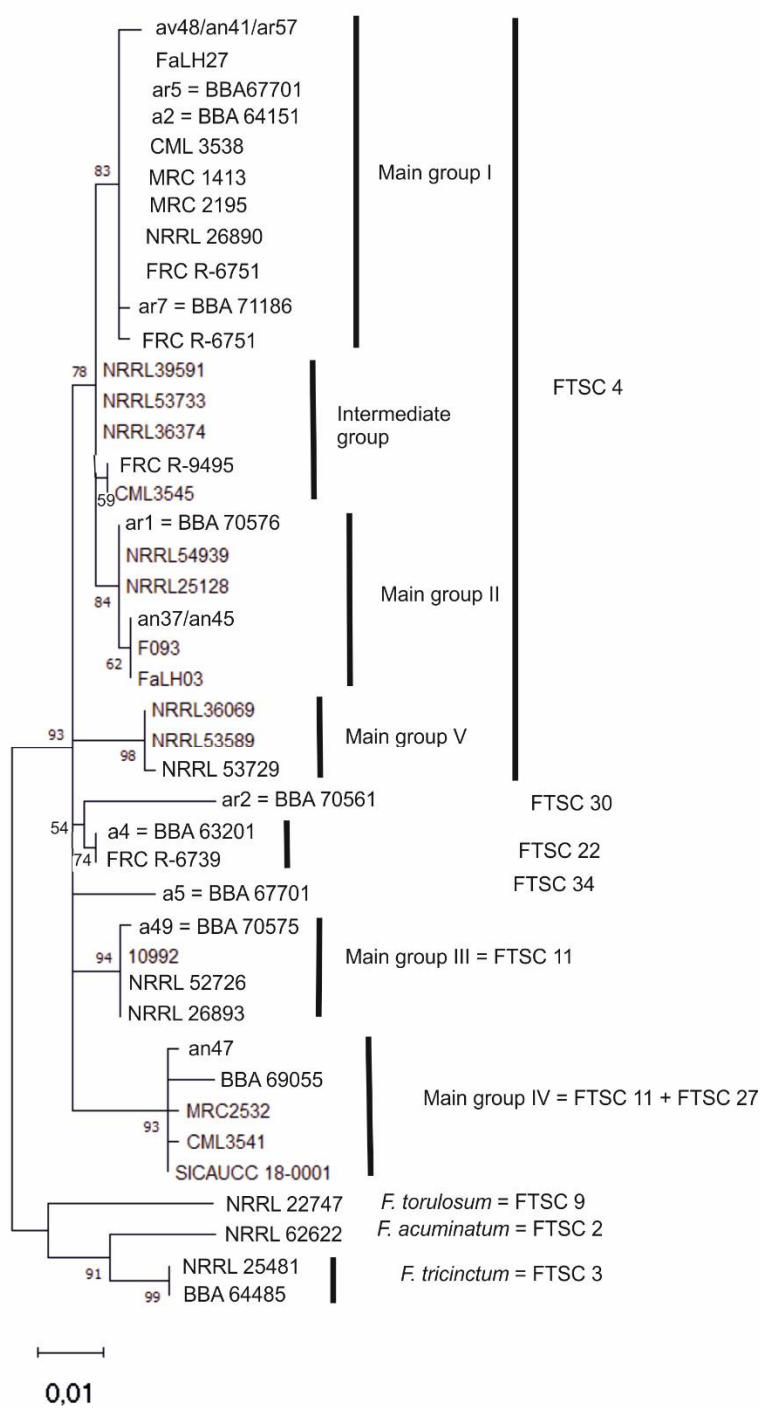
Supplementary Figure S1. Maximum likelihood consensus tree of *TEF1* sequences. Bootstrap values are indicated above nodes based on 500 pseudoreplicates of the data. Only branches present in more than 50% of the trees are shown. *Fusarium tricinctum* and *F. acuminatum* strains are outgroups.



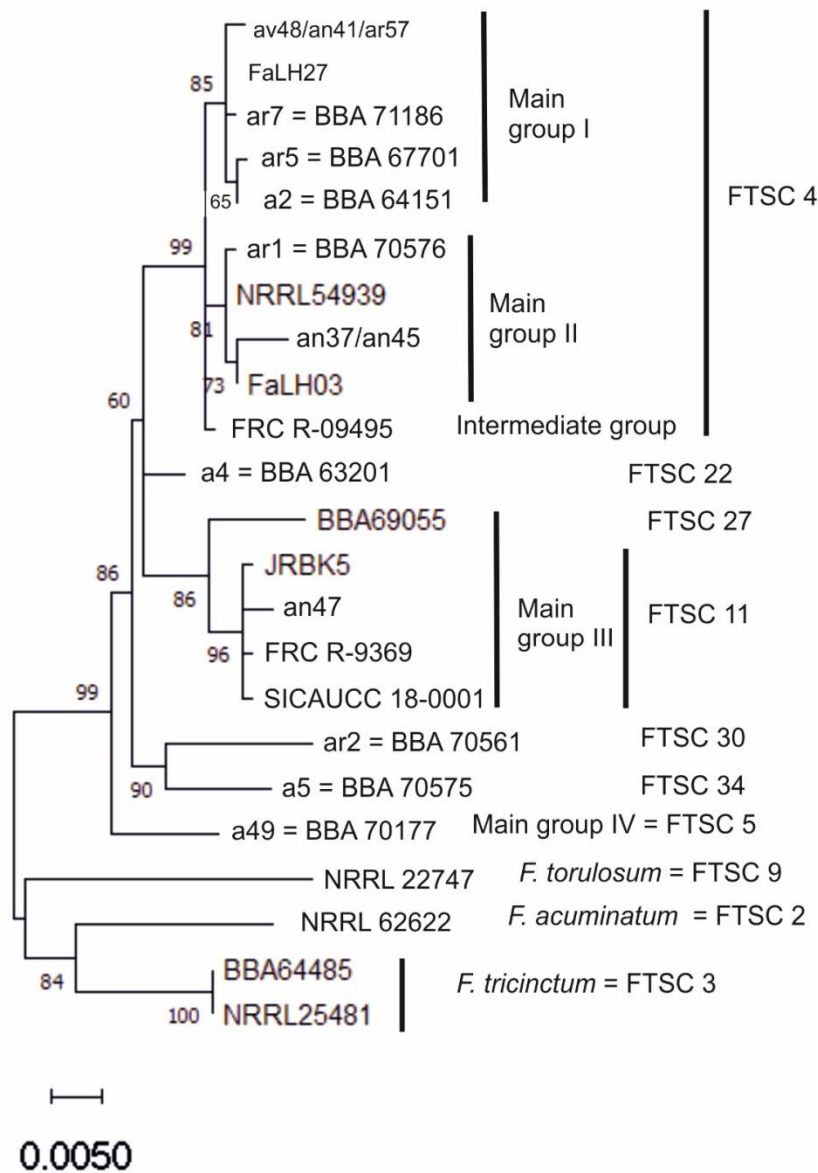
Supplementary Figure S2. Maximum likelihood consensus tree of *TEF1* sequences including strains of Kulik et al. (2011). Bootstrap values are indicated above nodes based on 500 pseudoreplicates of the data. Only branches present in more than 50% of the trees are shown. *Fusarium tricinatum* and *F. acuminatum* strains are outgroups.



Supplementary Figure S3. Maximum likelihood consensus tree of *TEF1* sequences including strains of Stakheev et al. (2016). Bootstrap values are indicated above nodes based on 500 pseudoreplicates of the data. Only branches present in more than 50% of the trees are shown. *Fusarium tricinctum* and *F. acuminatum* strains are outgroup.



Supplementary Figure S4. Maximum likelihood consensus tree of TEF1 sequences including strains of Laraba et al. (2022). Bootstrap values are indicated above nodes based on 500 pseudoreplicates of the data. Only branches present in more than 50% of the trees are shown. *Fusariumtricinctum* and *F. acuminatum* strains are outgroup.



Supplementary Figure S5. Maximum likelihood consensus tree for combined *TEF1* and *TUB2* sequences. Bootstrap values are indicated above nodes based on 500 pseudoreplicates of the data. Only branches present in more than 50% of the trees are shown. *Fusarium tricinctum* and *F. acuminatum* strains are outgroups.