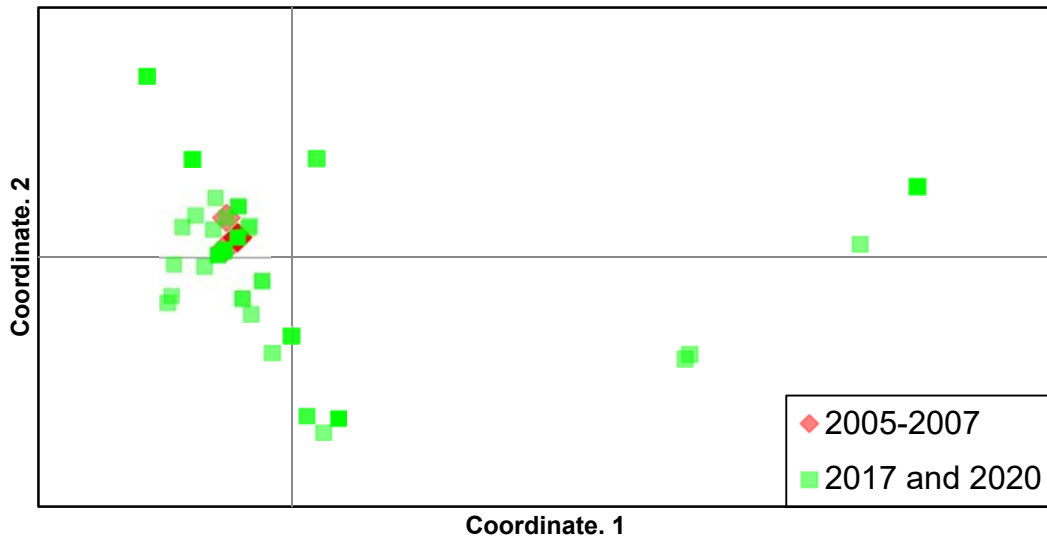


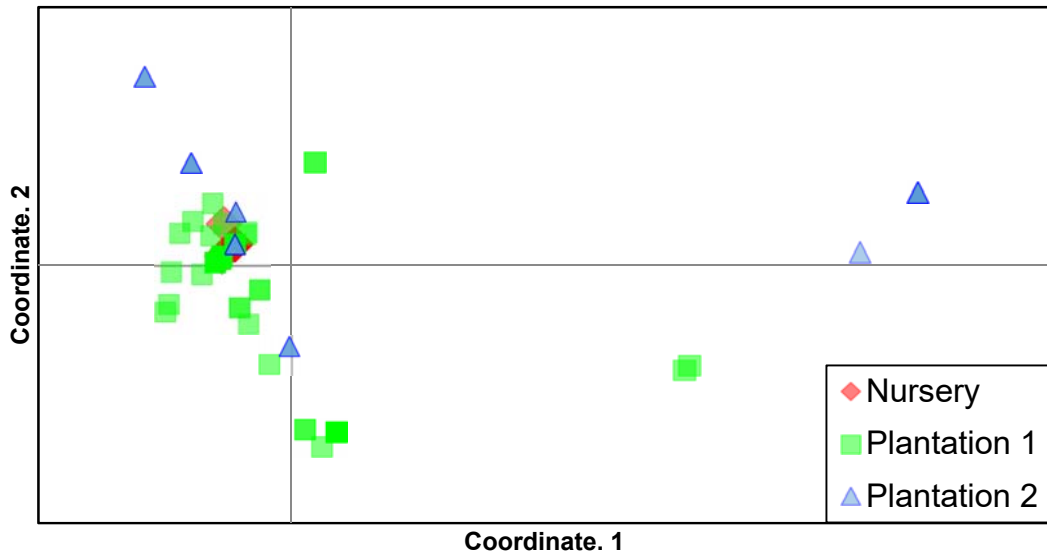
Supplementary Figure 1. A) Scatter plot obtained from the Principal Coordinate Analysis (PCoA) of the multilocus haplotypes identified among the 136 isolates of *Fusarium circinatum* examined. Coordinates 1 and 2, explained 89.31% and 8.26% of the total variance, respectively, with the total cumulative proportion of variation explained by the first 3 coordinates equalling 98.98%. Three different groups of isolates were preliminarily identified and named Clusters 1-3. **B)** STRUCTURE-based Bayesian modelling, with an optimal K of 3.

Subsequent assignment of isolates to these different genetic backgrounds yielded three distinct assemblages of isolates, the makeup of which corresponds to those identified previously (**A**).

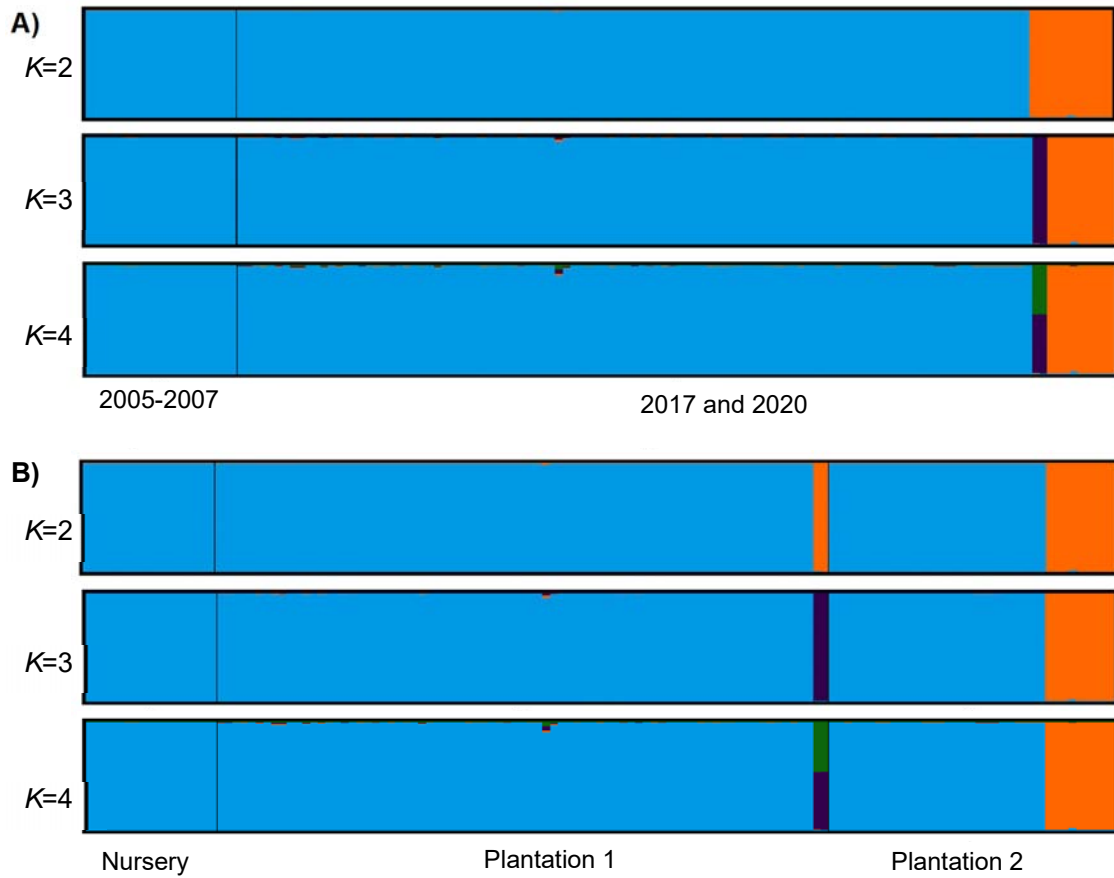
Sampling date (PCoA)



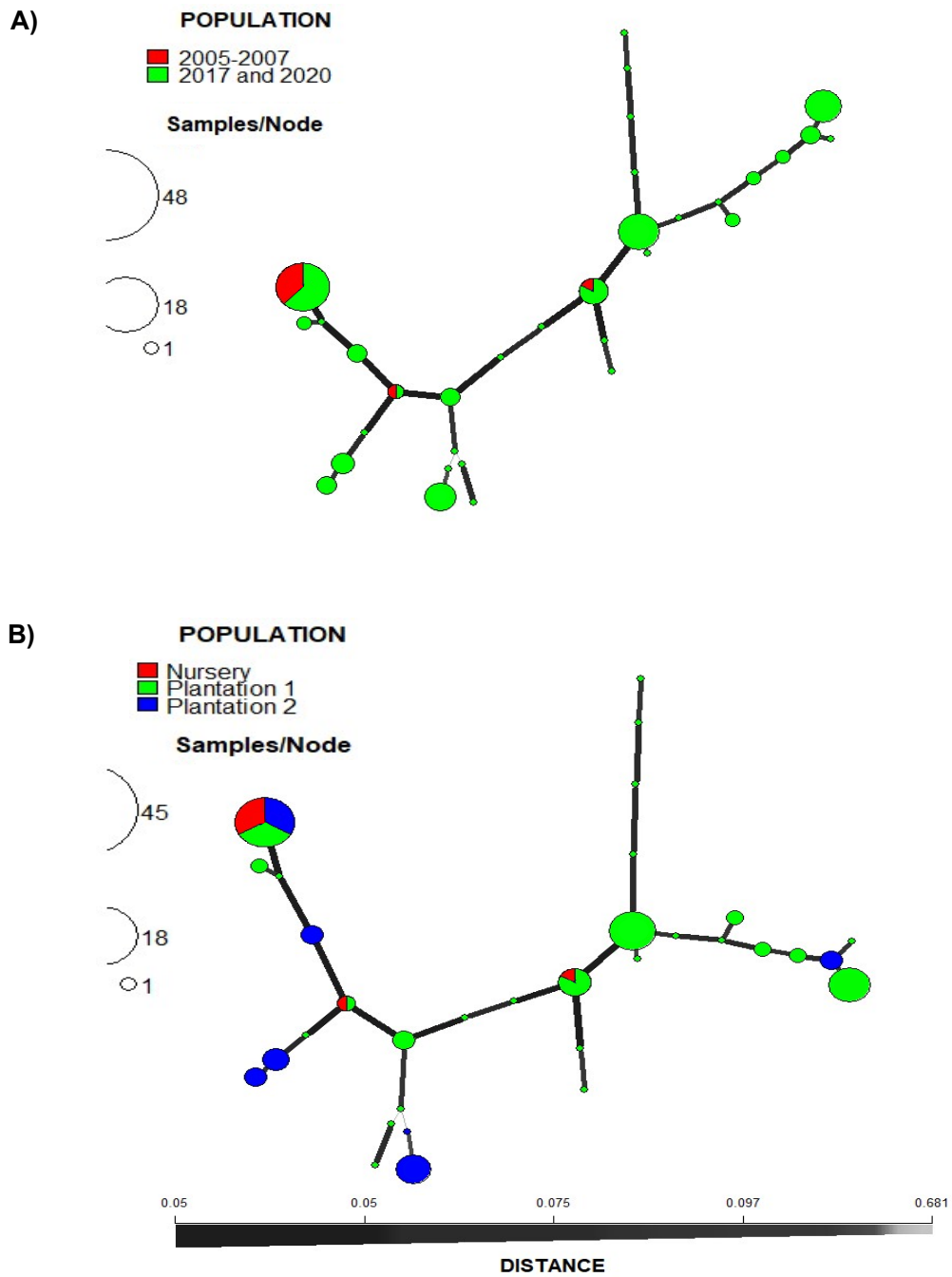
Samplig location (PCoA)



Supplementary Figure 2. PCoA displaying the relationships between individuals in the different collection groupings with relation to their respective collection subgroupings. The percentage of the variation explained by axis's 1, 2 and 3 are 89.31%, 8.26% and 1.41%, respectively. The total cumulative percentage of variation explained by the first 3 axes was 98.98%. The different Cluster assignments are colour coded with the number of respective individuals at each data point represented by its level of transparency/depth.



Supplementary Figure 3. STRUCTURE output for the *F. circinatum* collection groupings in relation to their collection subgroupings. The optimal number of suggested K 's were $K=2$ and $K=3$. The figures display the graphical interpretation of the best alignment whereby $K=2$, $K=3$, and $K=4$ when comparing (A) Sampling dates and (B) Sampling locations.



Supplementary Figure 4. Minimum-spanning network of the different collection groupings in relation to collection subgroupings. The collection subgroupings are represented by different coloured circles. The size of each of the circles or nodes is proportional to the number of multilocus haplotypes or samples in each node. The link between nodes represents a unique mutational event between haplotypes. The figures are as follows **A)** Collection date **B)** Collection location.