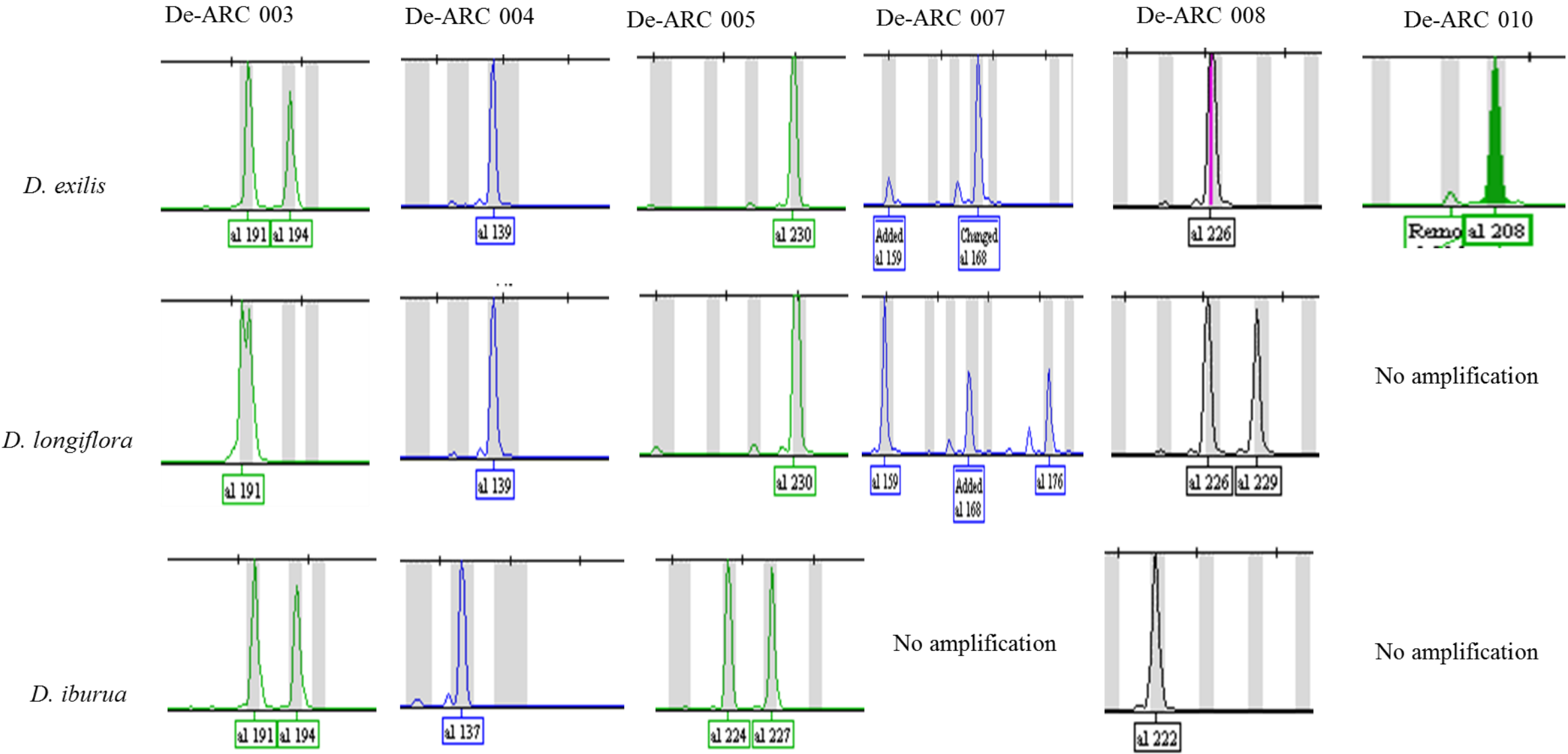


Figure S1: Raw data from SSR markers visualized with GeneMapper 5.0. software (Applied Biosystems) for *D. exilis*, *D. longiflora*, and *D. iburua*.



De-ARC 011

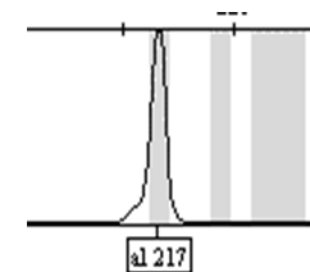
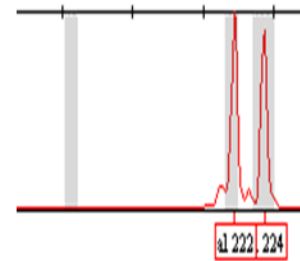
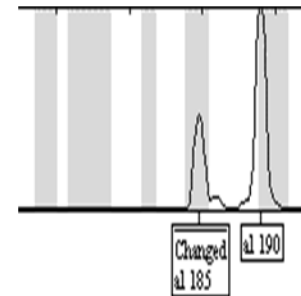
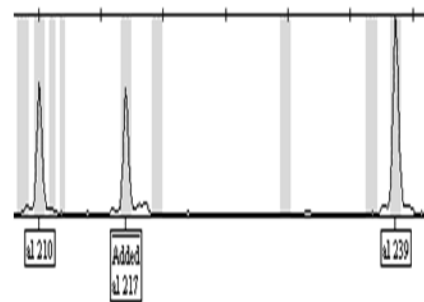
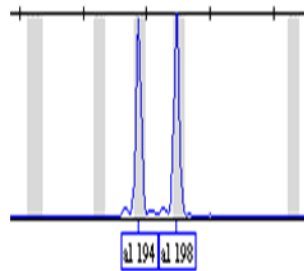
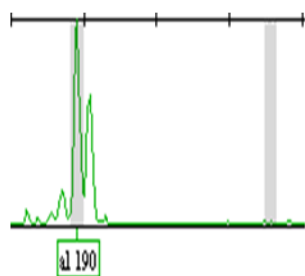
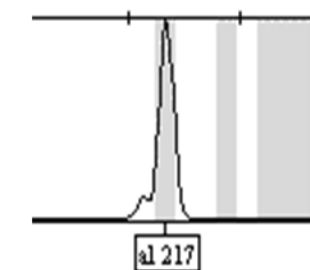
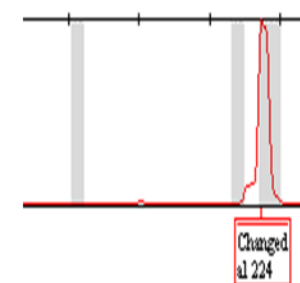
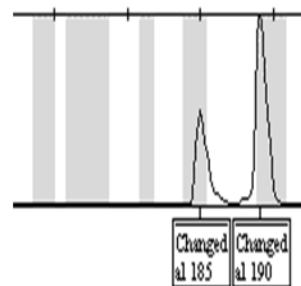
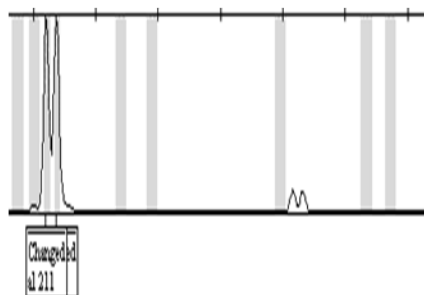
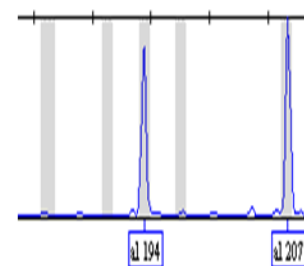
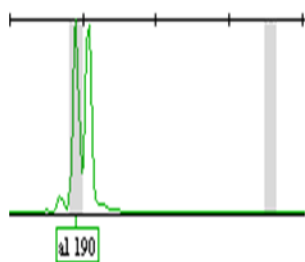
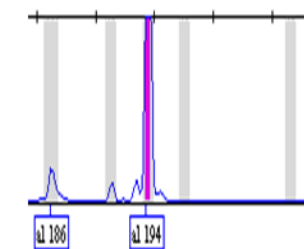
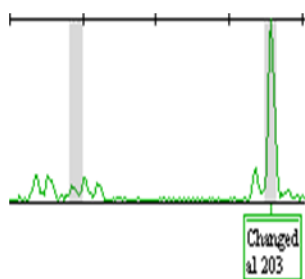
De-ARC 013

De-ARC 014

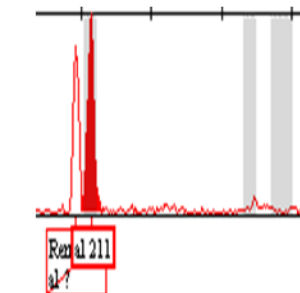
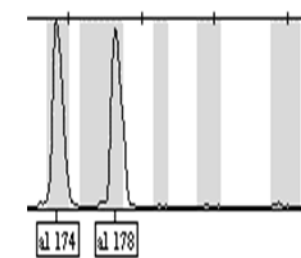
De-ARC 015

De-ARC 016

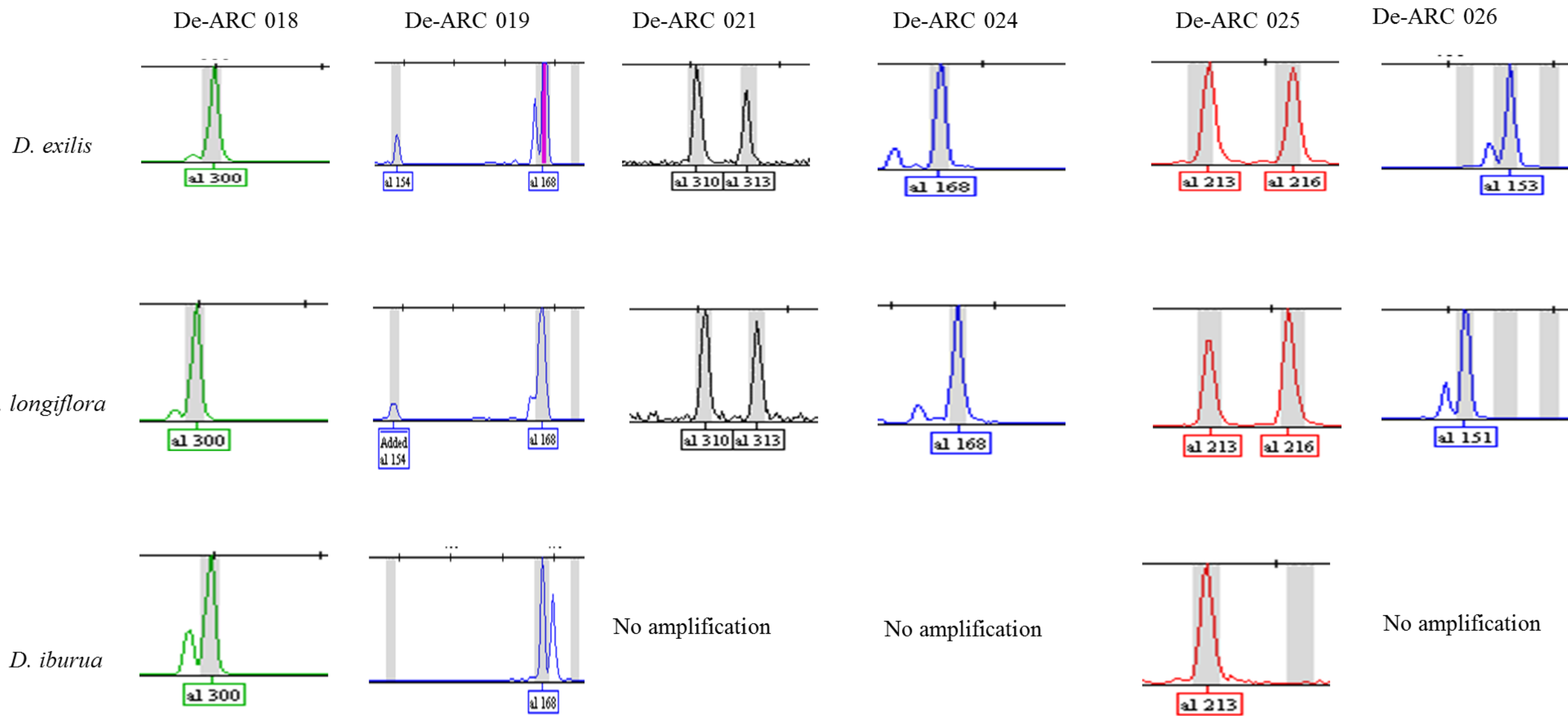
De-ARC 017

*D. exilis**D. longiflora**D. iburua*

No amplification



No amplification



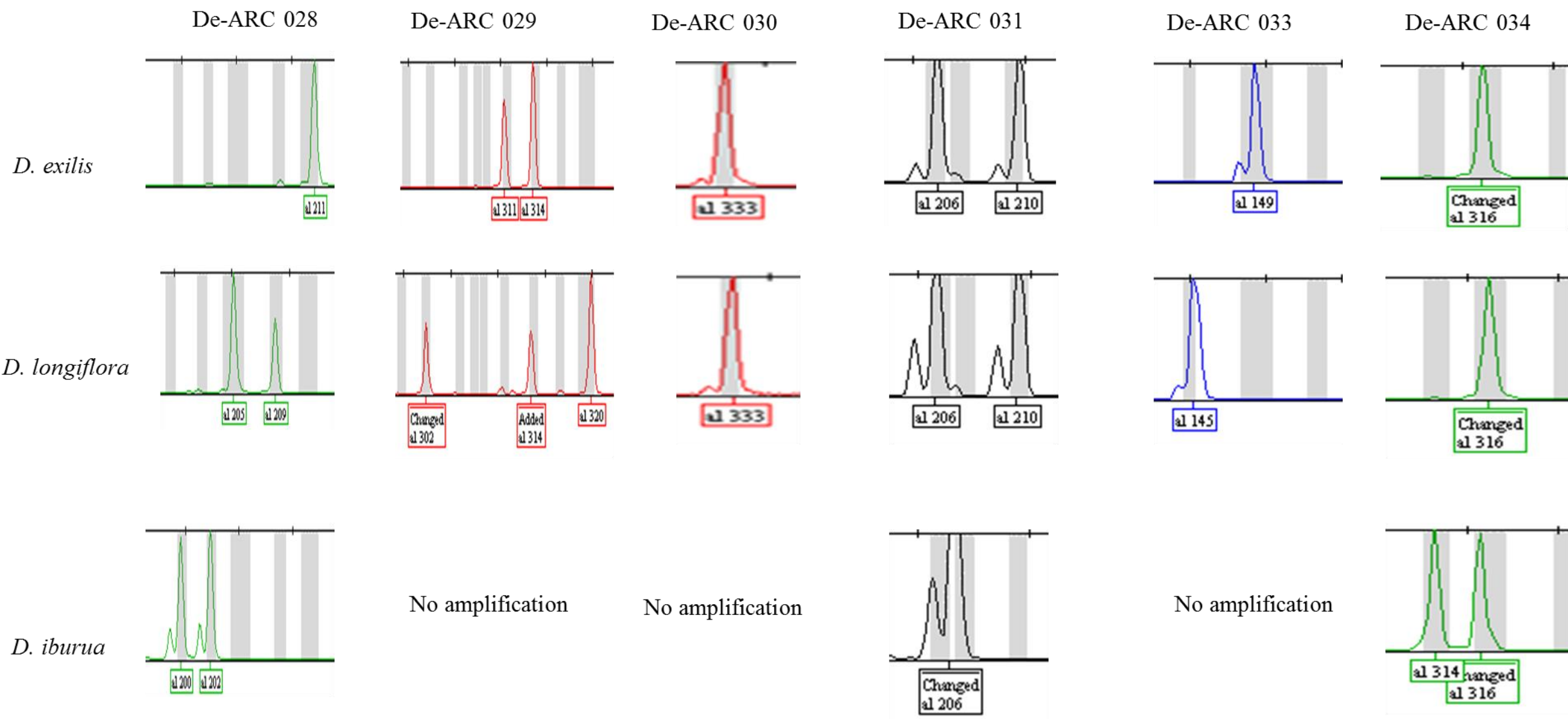


Figure S2: Genetic relationship and its pattern across species through a neighbor-joining tree based on 17 markers. The colors correspond to the species.

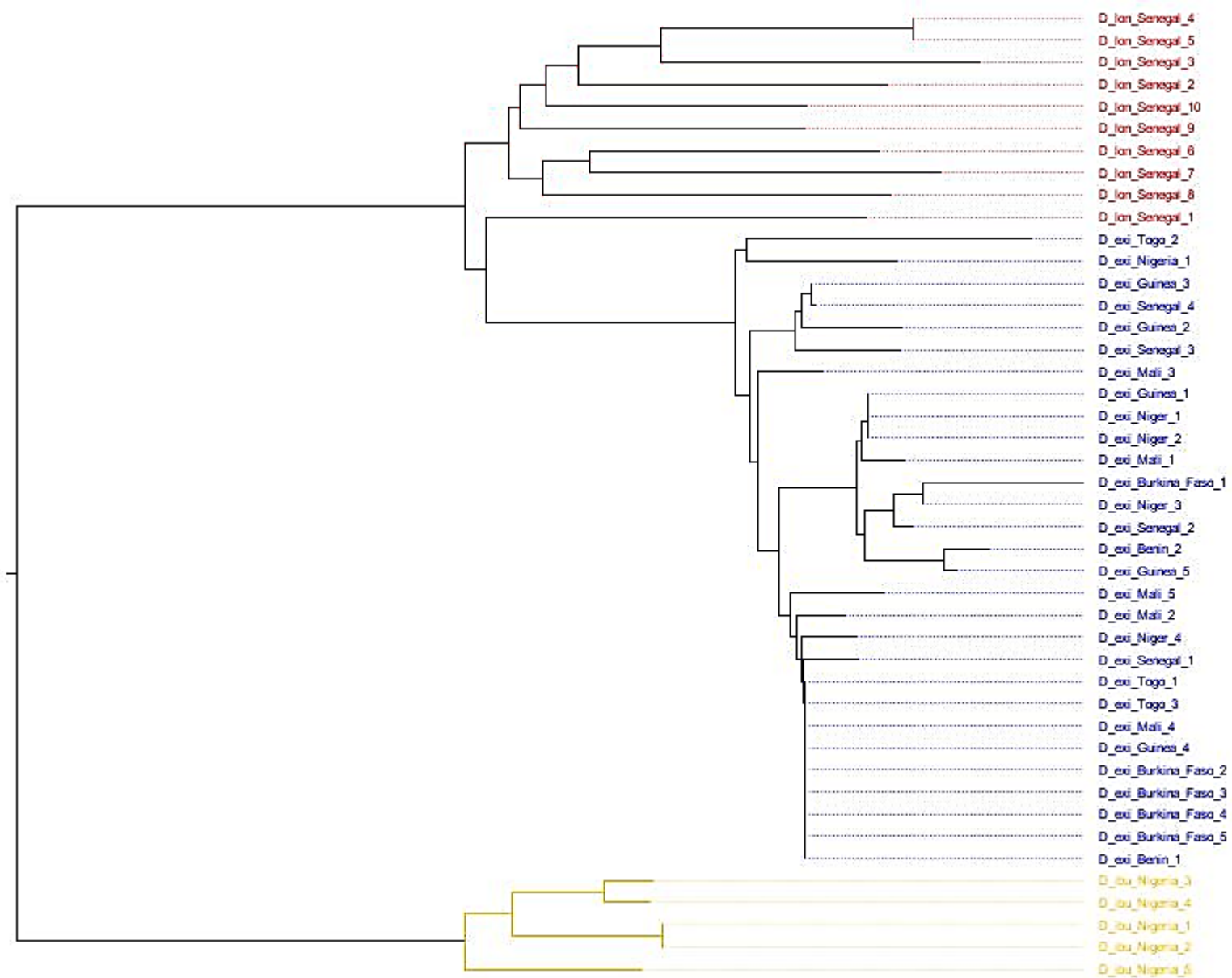


Figure S3: DAPC scatter plot for *Digitaria* accessions using the first two PCs. The inset indicates the number of PCs kept to describe the relationship between the clusters. The DAPC population numbers in each of the clusters correspond to group numbers of the neighbor-joining tree and the color corresponds to the color used in Figure 1.

