Supplementary figures

Figure legends

Fig. S1. Alignment of sequences representing all the alleles observed in the AF12 microsatellite marker. Some of these alleles were only observed in a single isolate and had to be sequenced to confirm that the length variation between the alleles are due to a step-wise mutation in the microsatellite region. The represented alignment confirms this. Alignment was performed in CLC Bio Main Workbench v. 6 (CLC Bio, www.clcbio.com).

Fig. S2. Plot data, generated using Clumpak (Kopelman et al., 2015), of the K against ΔK values to determine the most likely number of genetic clusters (K) all the isolates can be grouped in. The optimal K value is the value with the biggest rate of variation when comparing the LnP(D) to successive K-values. This result was used for a final population structure analysis in STRUCTURE v2.2.

Figures

Fig. S1

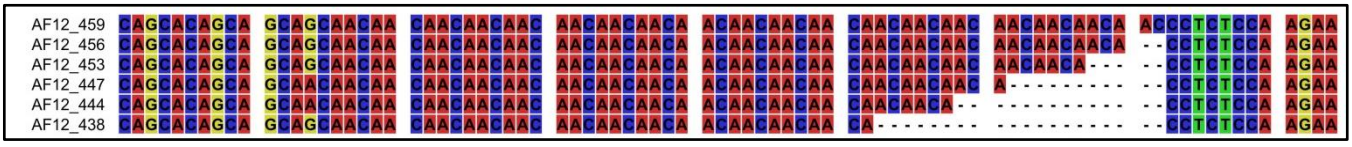
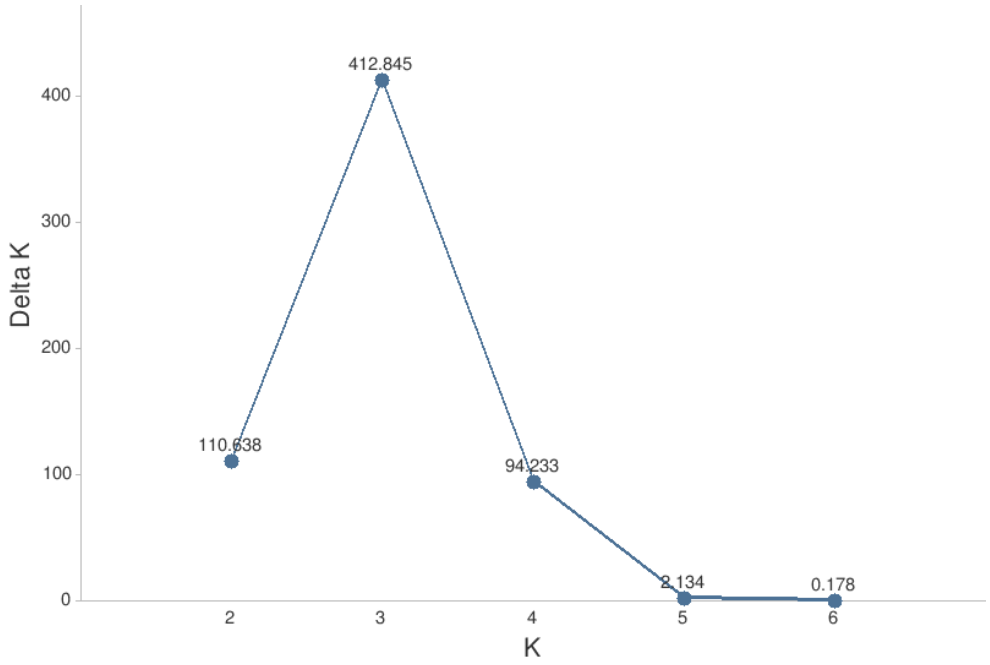


Fig. S2


412.845
110.638
94.233
2.134
0.178
Delta K
400
300
200
100
0
2
3
4
5
6
K