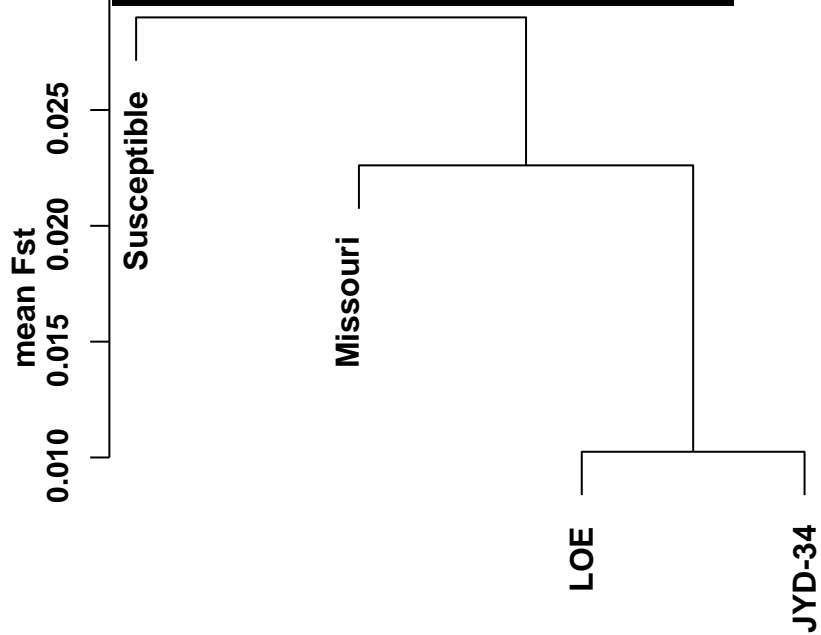
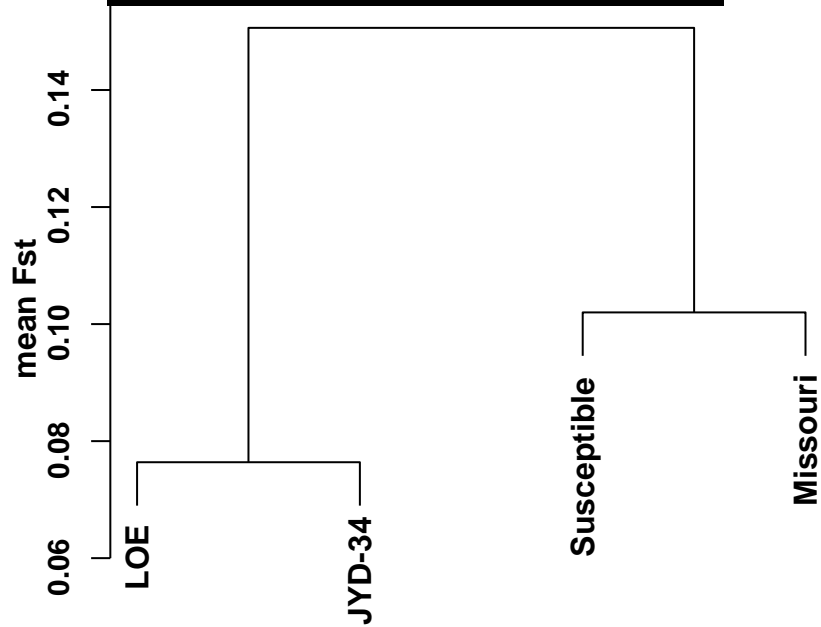


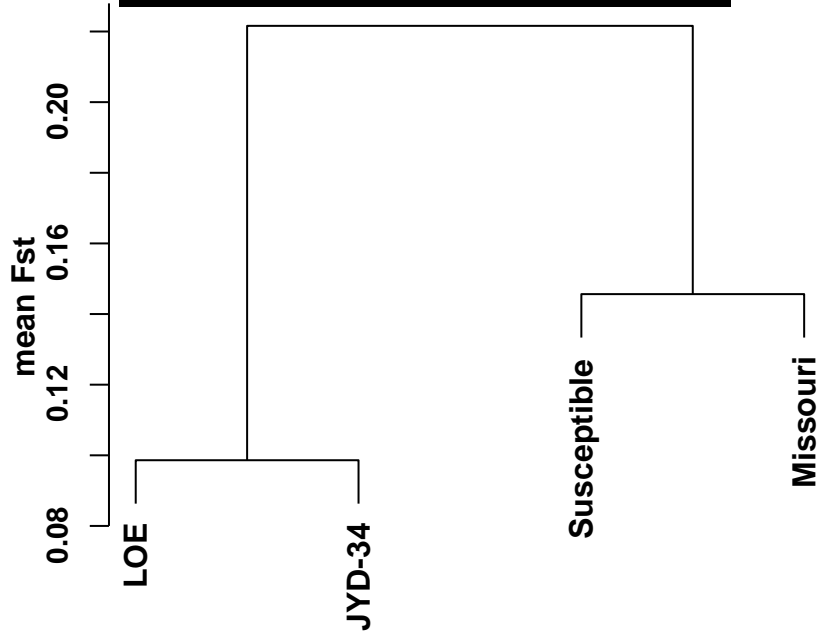
1602137 SNPs with FST at least 0



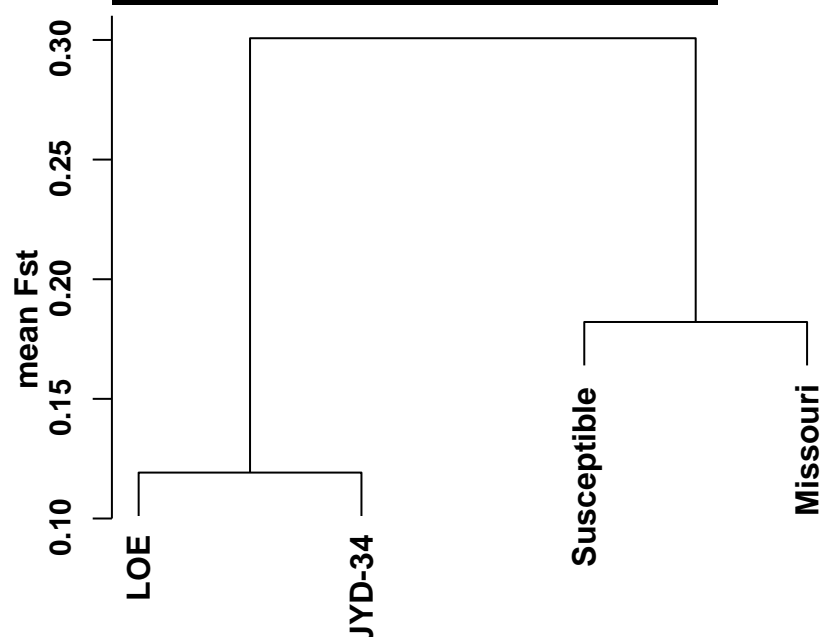
137454 SNPs with FST at least 0.1



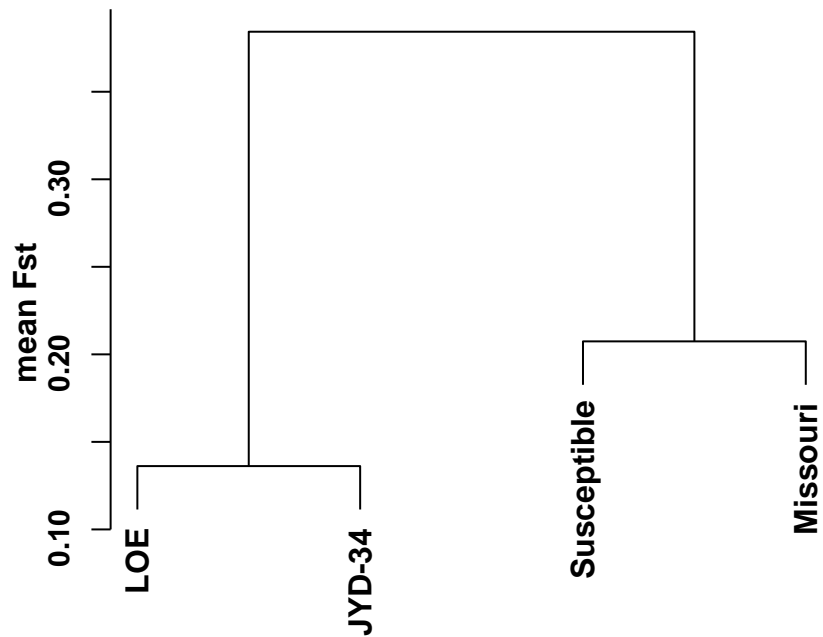
64983 SNPs with FST at least 0.2



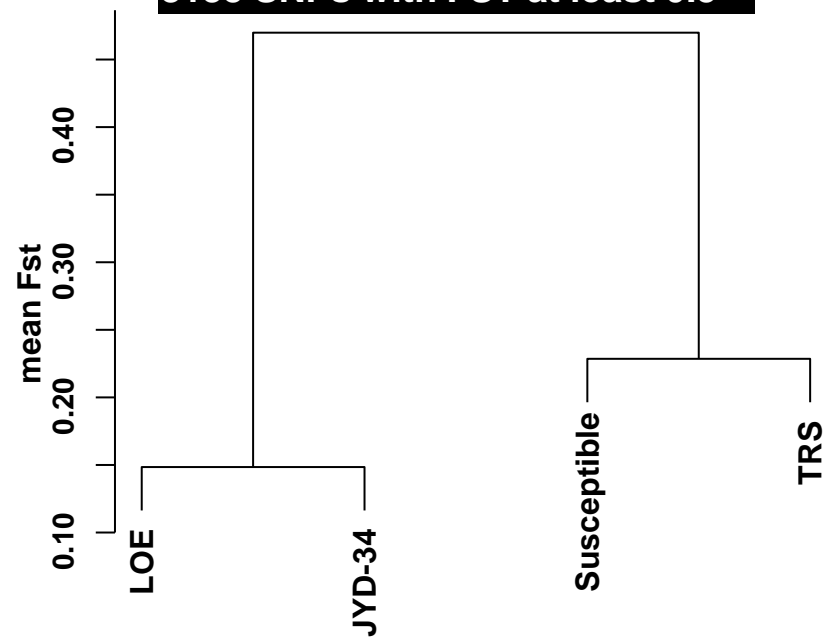
31254 SNPs with FST at least 0.3



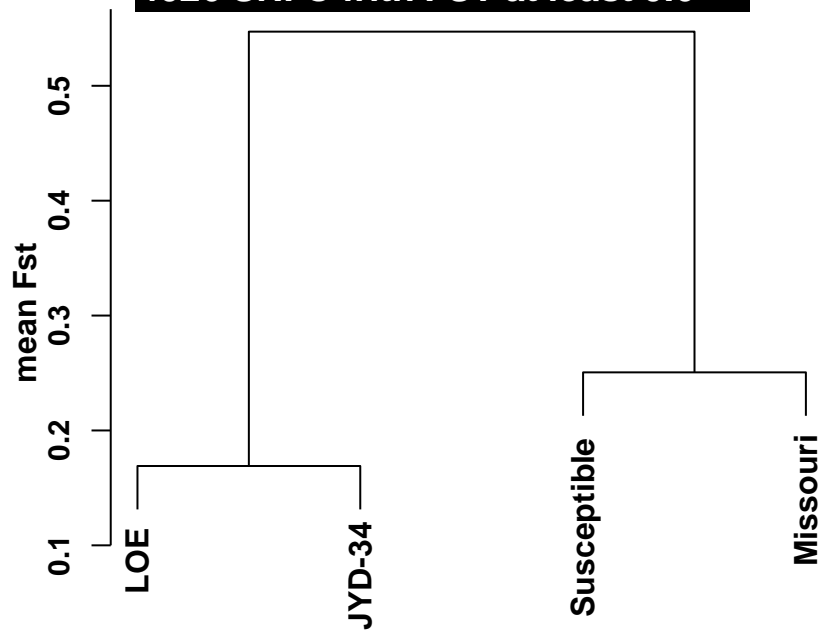
15970 SNPs with FST at least 0.4



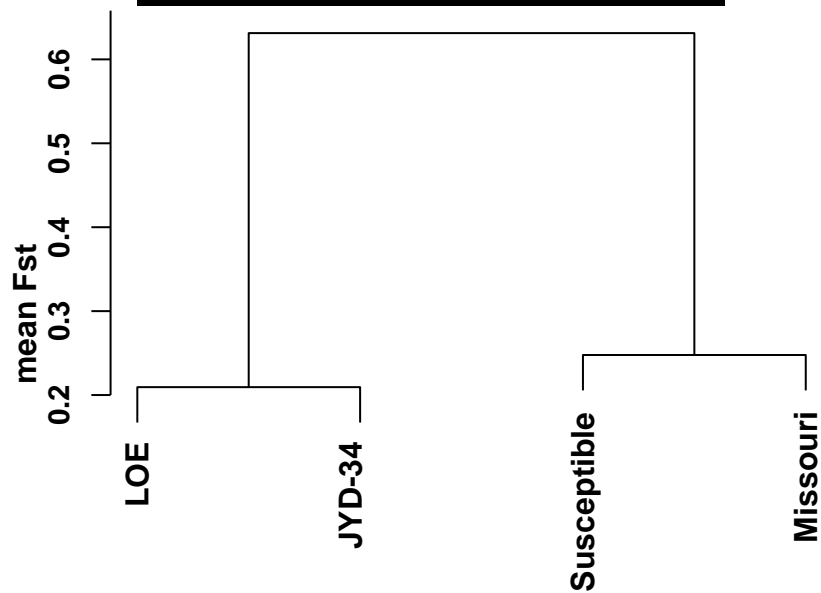
8135 SNPs with FST at least 0.5

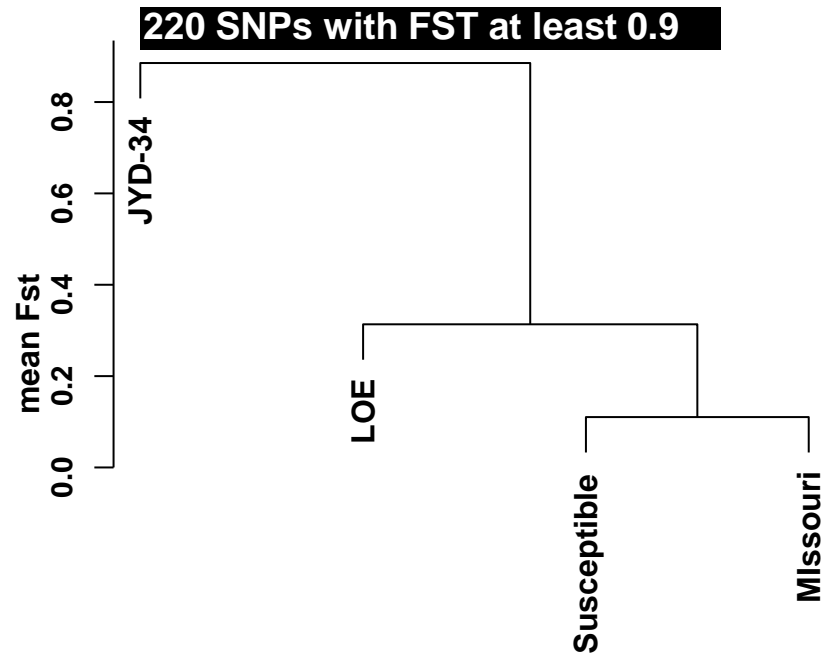
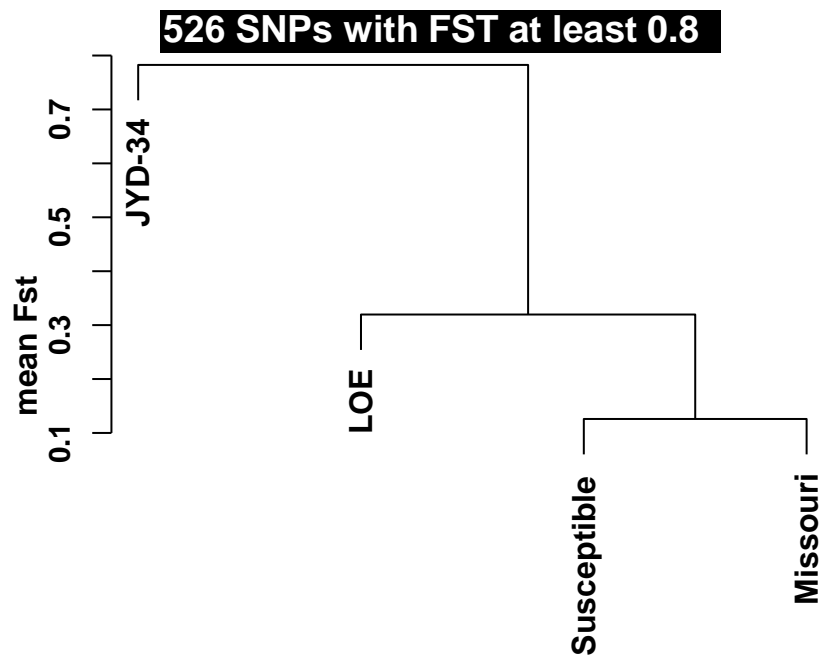


4026 SNPs with FST at least 0.6



1654 SNPs with FST at least 0.7





Additional file 1: Dendrogram visualization based on means F_{ST} . The dendrograms illustrate the divergence that exists between JYD-34 isolate and Missouri, Susceptible and LOE isolates, where $F_{ST} = 0$ means no divergence between two population and $F_{ST} = 1$ means complete divergence. In this analysis, for each SNP out of the total 1,602,137 SNPs, the F_{ST} corresponding to each of the different comparisons LOE/Susceptible; LOE/TRS; LOE/JYD; Susceptible/TRS; Susceptible/JYD; and TRS/JYD were calculated. If at least one of these comparisons had an F_{ST} value of 0.1 or greater, the corresponding SNP and the F_{ST} for each population comparison were retained in the analysis. Based on this criterion, 137,454 SNPs were kept to calculate the mean F_{ST} used in the distance matrix that allowed the construction of the dendrogram. Thresholds were progressively increased from 0 to 0.9.