Figure S1. Genotype accumulation curve for 42 genotypes and 11 SSR loci produced using the function `genotype_curve` in *poppr* [78]. The horizontal axis represents the number of loci (NumLoci) randomly sampled without replacement up to n − 1 loci, the vertical axis shows the number of multilocus genotypes (MLG) observed, up to 31, the number of unique multilocus genotypes in the data set. The red dashed line represents 100% of the total observed multilocus genotypes. The curve reaches a plateau indicating the minimum number of markers covering all the genetic variance among samples, so that adding more markers to the analysis will not create very many new genotypes.