

### **Additional file 5. Genetic transitive graphs.**

Graph connecting closely related mtDNA COI haplotypes. Clusters were identified using a graph approach where COI haplotype pairs are connected when being less genetically distant than a given threshold distance (Hamming distance) using the function ‘*gengraph*’ of the R package *adegenet* (Jombart *et al.* 2008). The Hamming distance cutoff is shown in the inset. Hamming distances between pairs of connected haplotypes are indicated by the numbers annotating the transitive graph edges. Colors indicate nuclear cluster membership for individuals sequenced in our study. The graph datasets labeled with a number (I and II) were subsequently analyzed with further divergence level using the same approach.

Reference:

Jombart T: **ADEGENET: a R package for the multivariate analysis of genetic markers.** *Bioinformatics* 2008, **24**(11):1403-1405.

