



Supplementary Fig. 2.

a) Neighbour-joining tree among *S. rubrovittatus* local populations constructed based on F_{ST} using mitochondrial *COI* sequences.

Uppercase character indicates one of three clusters (N, S and K) identified in Bayesian clustering analysis (BAPS program).

b) Consensus tree among *S. rubrovittatus* local populations based on Cavalli-Sforza & Edwards' (1967) chord distances derived

from allele frequencies at six microsatellite loci (NJ method of tree construction). Bootstraps over 40% are indicated. Uppercase

character indicates one of three clusters (N, S and K) identified in Bayesian clustering analysis (BAPS program).

c) Genetic distance tree among *S. rubrovittatus* local populations constructed using combined mitochondrial *COI* and six

microsatellite data. Bootstraps over 40% are indicated. Uppercase character indicates one of three clusters (N, S and K) identified

in Bayesian clustering analysis (BAPS program).