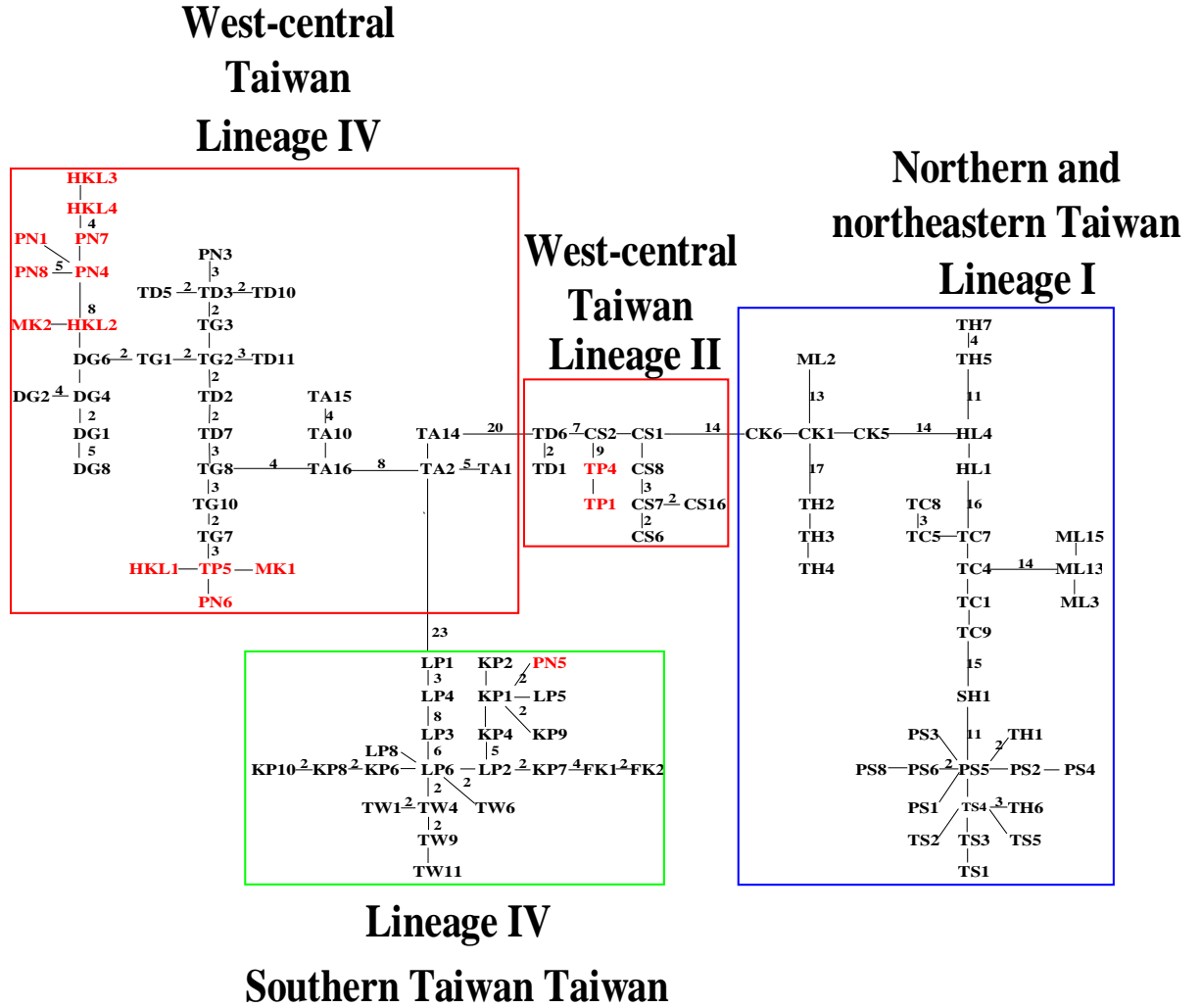
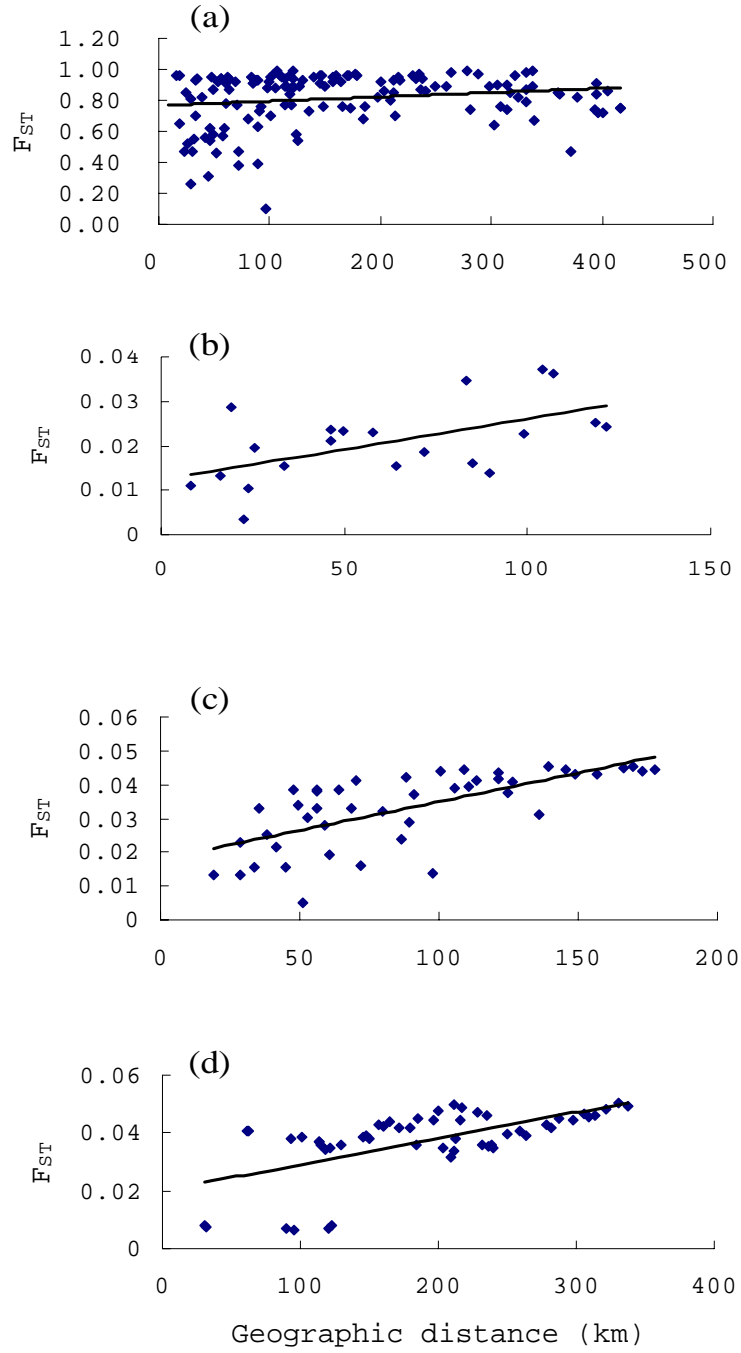


**Fig.7.** Neighbour-joining (NJ) tree based on mtDNA 16S+COI sequences with bootstrap values (NJ/ MP/ ML, respectively) shown adjacent to corresponding four lineages. Haplotypes from eastern populations and Mulan River are represented by triangles and circles, respectively. Haplotypes are coded as in Table 1. "—", bootstrap value < 50. N, NE, northern and northeastern Taiwan; WC, west-central Taiwan; S, southern Taiwan.



**Fig. 8.** Minimum-spanning network based on mutations between haplotypes obtained from 20 populations and including one population of Mulan River from China. Each line without any number represents a single mutational change that interconnects two haplotypes. The number beside solid line is the number of multiple steps that interconnect two haplotypes. Haplotypes are presented by sampling locality codes, as showed in Table 1.



**Fig. 9.** Pairwise  $F_{ST}$  values among populations plotted against their straight-line geographical distances (km) and the corresponding regression line for all populations and three different regional populations. (a), all population in Taiwan ( $R^2=0.032$ ); (b), northern Taiwan ( $R^2=0.462$ ); (c) west-central Taiwan ( $R^2=0.476$ ); (d) southern Taiwan ( $R^2=0.384$ ).