

Supplementary Figures

Figure S1: The histogram built from 1000 stochastic MCMC permutation simulations shows the variance of our sample (solid diamond) could still be randomly obtained.

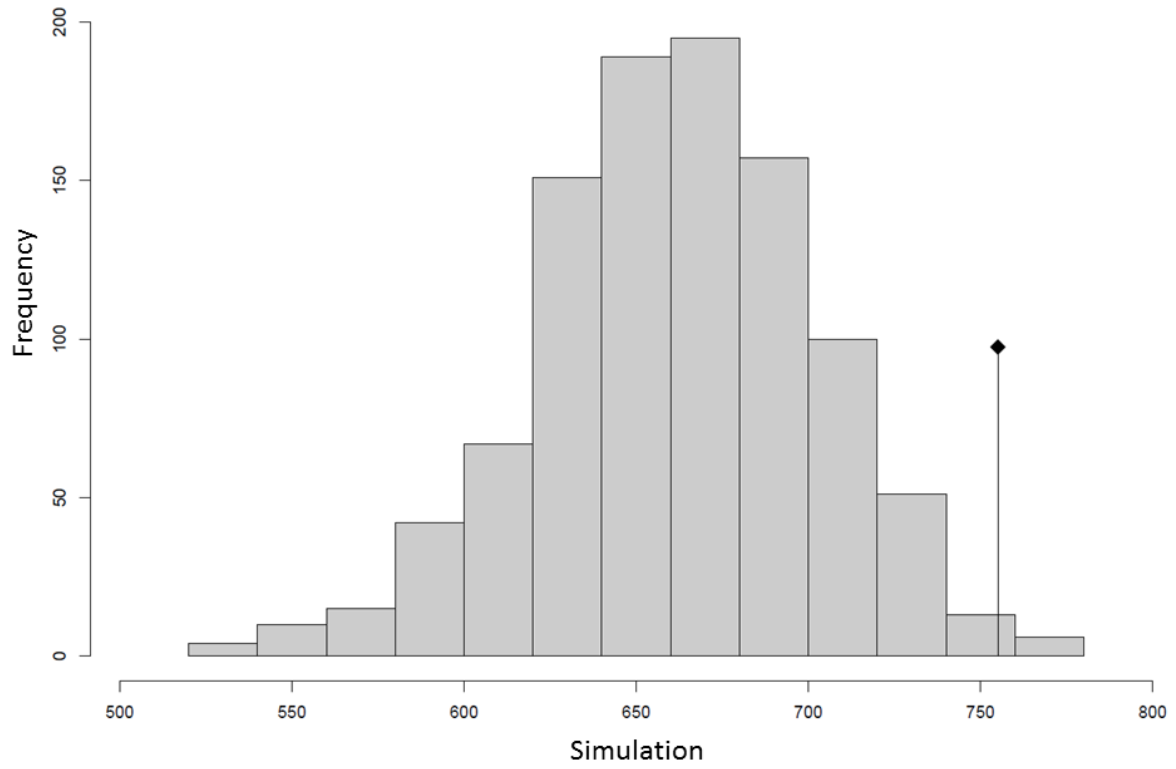


Figure S2: Result of the factor correspondence analysis (FCA) with the most informative factor (FC1) against A) the second most informative factor (FC2), or B) the third informative factor (FC3). The percentage of the variance explained by the factor is shown in parentheses. CNP = central North Pacific; ETP = eastern Tropical Pacific; GM = Gulf of Mexico; CS = Caribbean Sea.

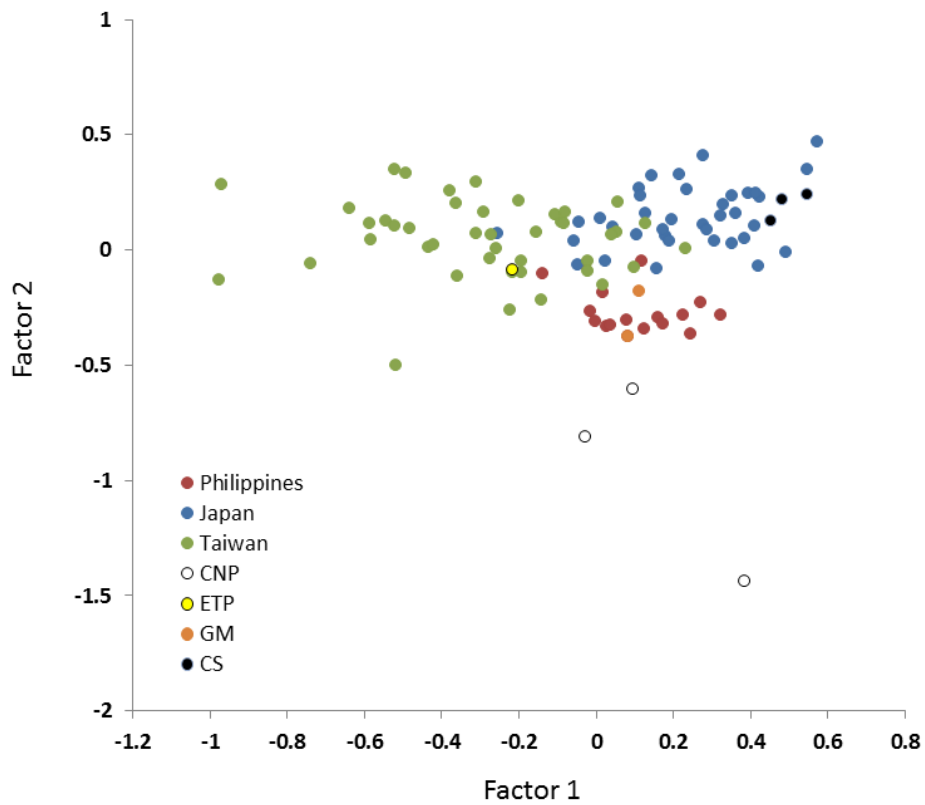


Figure S3: Posterior group membership assignment based on DAPC classification. Each row represents one individual; the heat colour represents the individual's membership probabilities (red = 1, white = 0); blue crosses represent the original cluster (geographic groups) as indicated in columns.

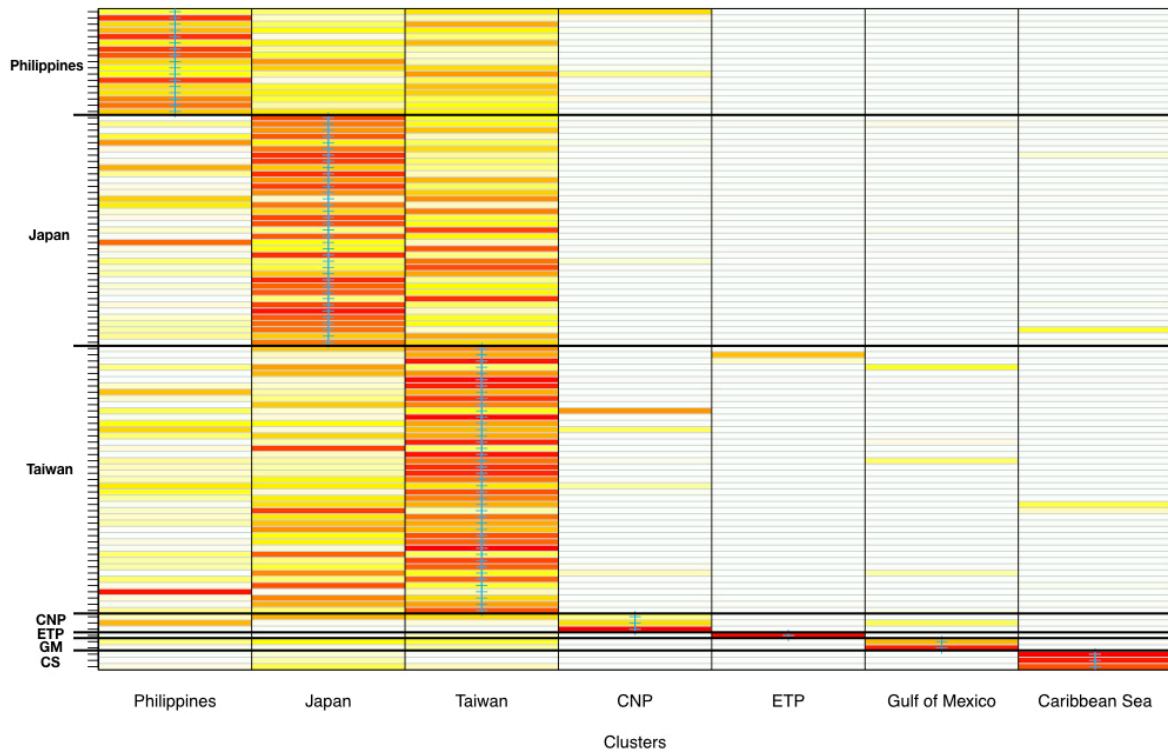
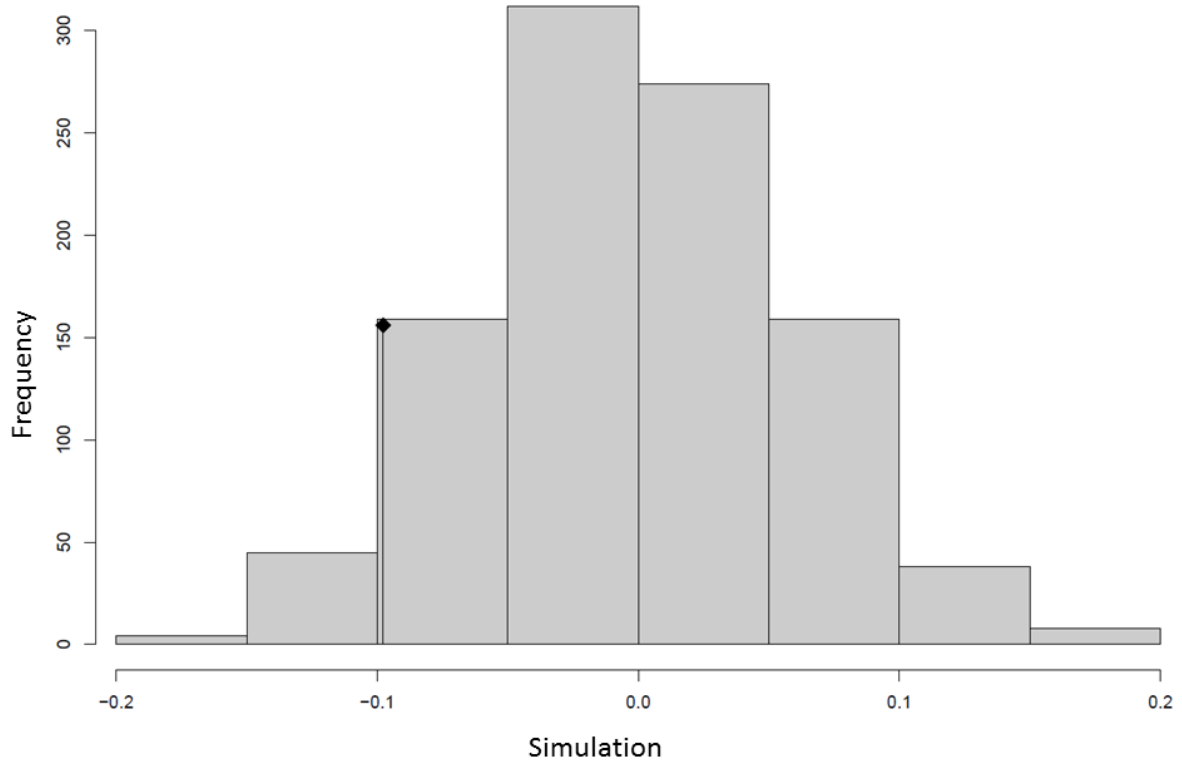


Figure S4: Histograms built from 1000 stochastic Monte-Carlo permutation simulations with genetic distance estimated using A) Nei's distance and B) Edwards' distance method. Solid diamond represents the observed value for our sample.

A)



B)

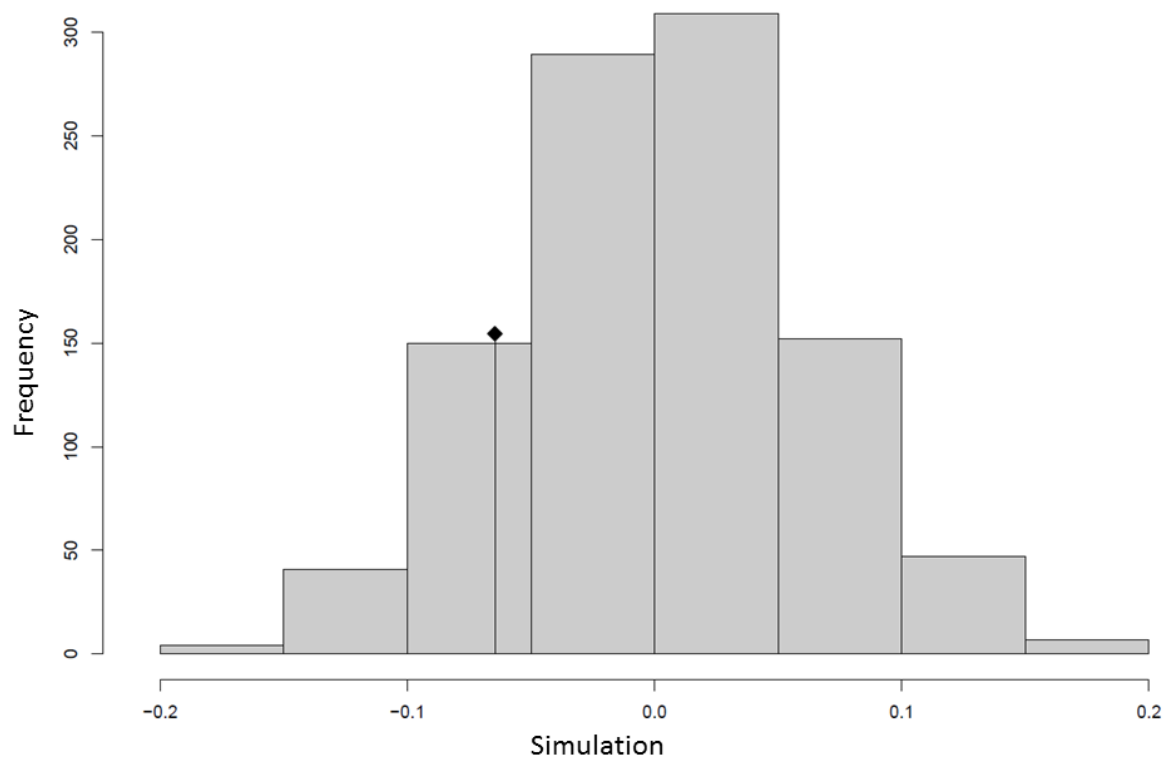
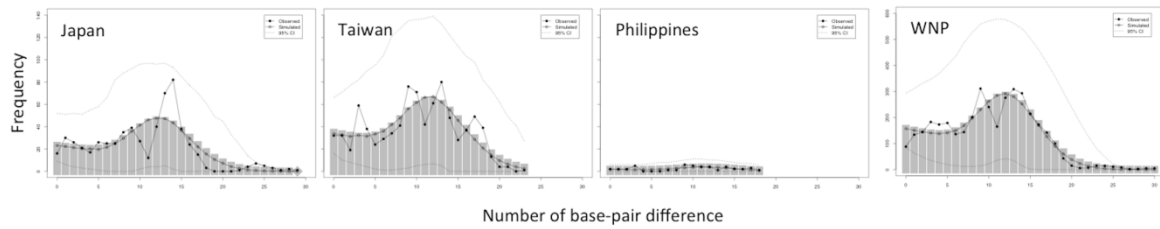


Figure S5: The observed and expected mismatch distributions under (A) demographic and (B) spatial expansion models. The vertical bars (in gray) indicate the model frequency in each scenario. Note the scale of frequency for Western North Pacific (WNP) is different from the other panels.

A: Under the demographic expansion model



B: Under the spatial expansion model

