

SUPPLEMENTAL FIGURES

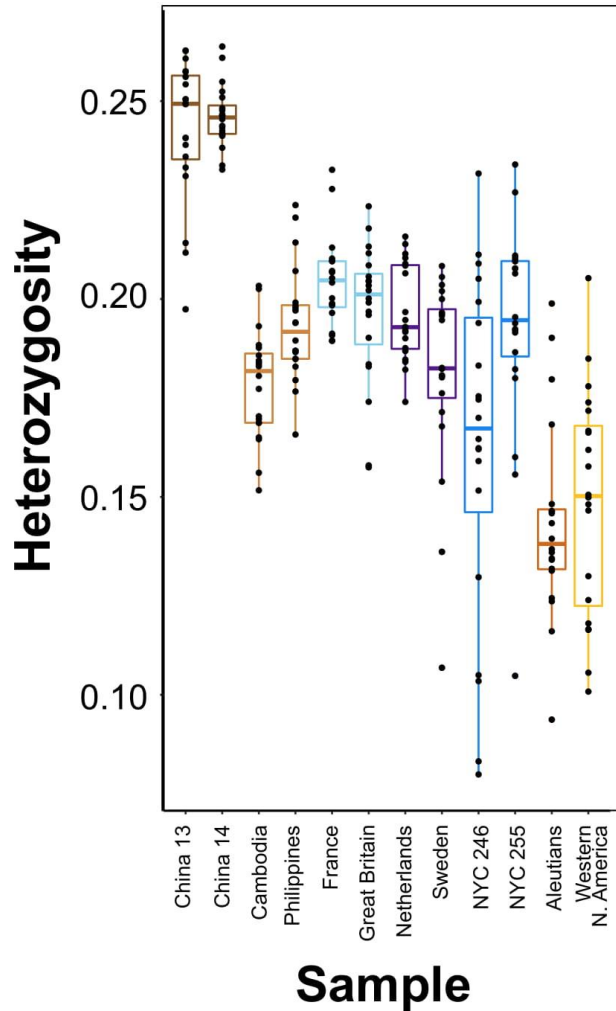


Figure S1- Heterozygosity measured on each chromosome ($n=20$) for each of 12 brown rat samples. A box and whisker plot of mean chromosomal heterozygosity was overlaid the point estimates where colors indicate genomic cluster assignment. Additional details of sample locations available in Table S1. Each evolutionary cluster was represented by a different color: *eastern China*- dark brown; *SE Asia*- light brown; *Aleutian*- orange; *Western North America*- yellow; *Northern Europe*- purple; *Western Europe*- light blue; and *Expansion*- medium blue.

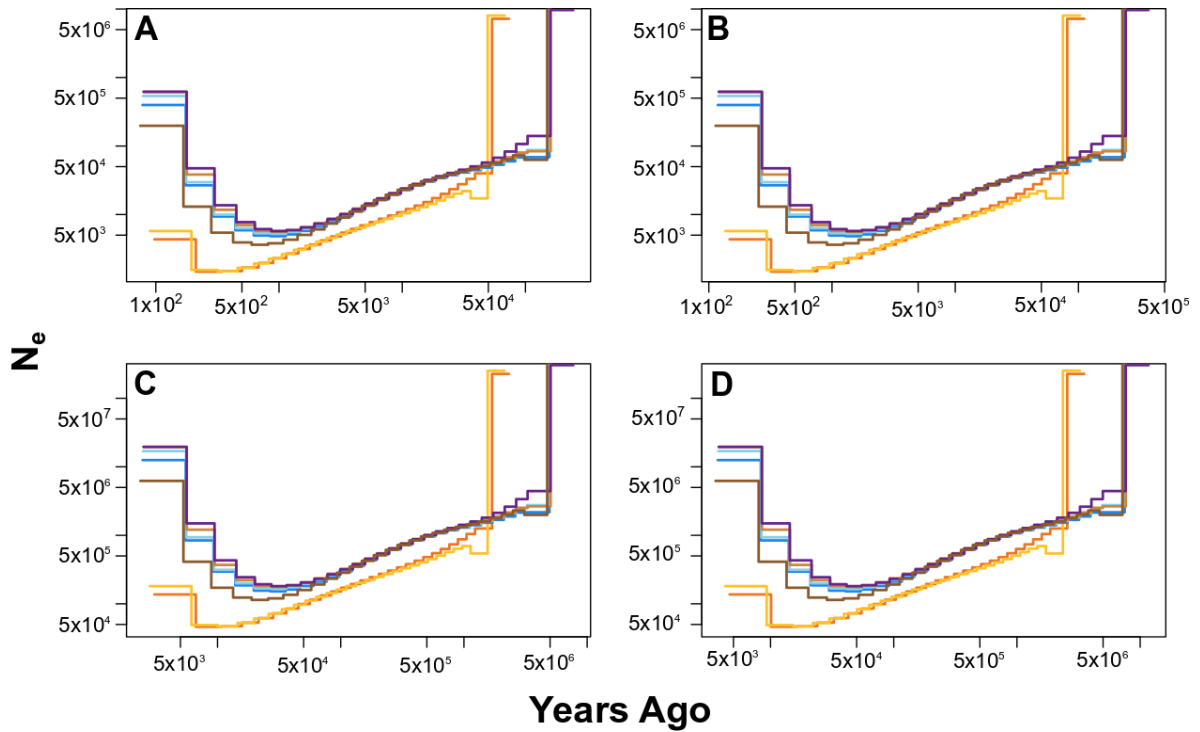


Figure S2- MSMC plots with varied mutation rate (μ) and generation time. In panels A and B, the estimated μ from our coalescent model (9.29×10^{-8}) was used, while panels C and D use the rate of 2.96×10^{-9} from Deinum *et al.* (2015). Panels A and C used a mutation rate of 3 generations per year, where panels B and D used 2 generations per year. Panel A was presented as Figure 2 in the main text. Each evolutionary cluster was represented by a different color: *eastern China*- dark brown; *SE Asia*- light brown; *Aleutian*- orange; *Western North America*- yellow; *Northern Europe*- purple; *Western Europe*- light blue; and *Expansion*- medium blue.

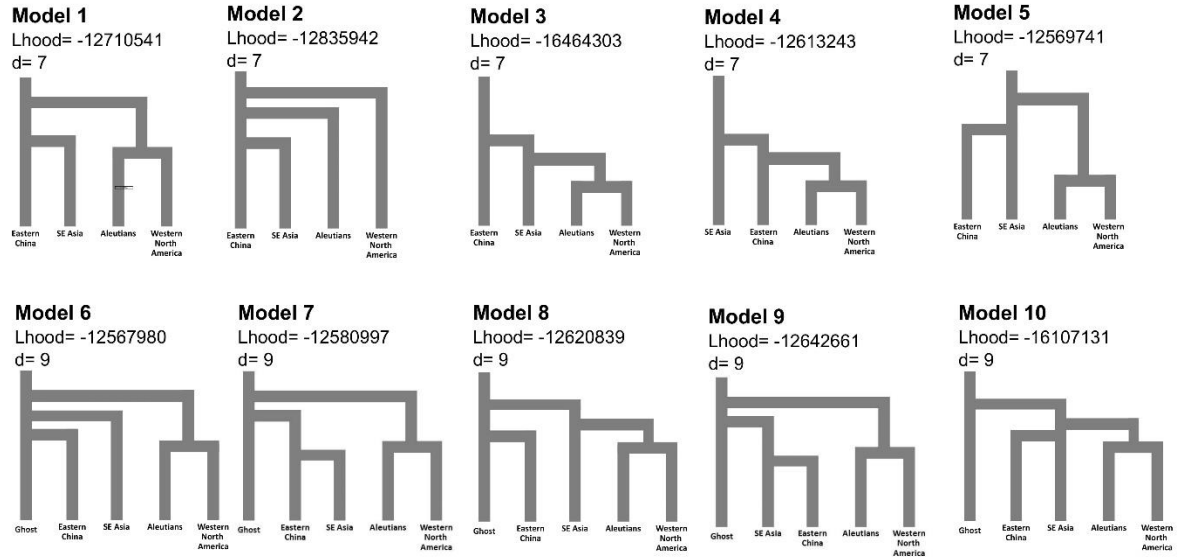


Figure S3- Topology, likelihood (Lhood), and number of parameters estimated (d) for 10 four- or five-population scenarios used to select topological relationships between *eastern China*, *SE Asia*, *Aleutian*, and *Western North America* evolutionary clusters. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -12567980 for Model 6.

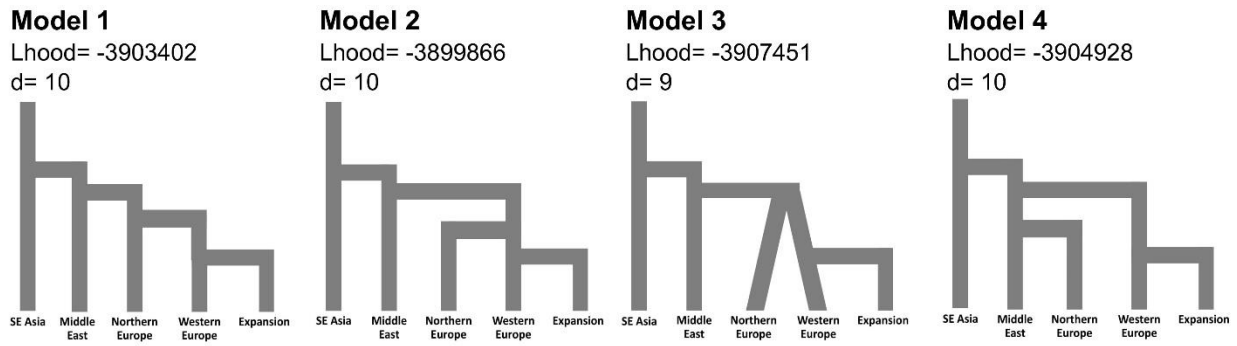


Figure S4- Topology, likelihood (Lhood), and number of parameters estimated (d) for four five-population scenarios used to identify the regional topological relationships between *SE Asia*, an unsampled population likely in the Middle East, *Northern Europe*, *Western Europe*, and *Western Europe-Expansion* populations. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -3899866. Model 2 had the highest likelihood of the four scenarios tested.

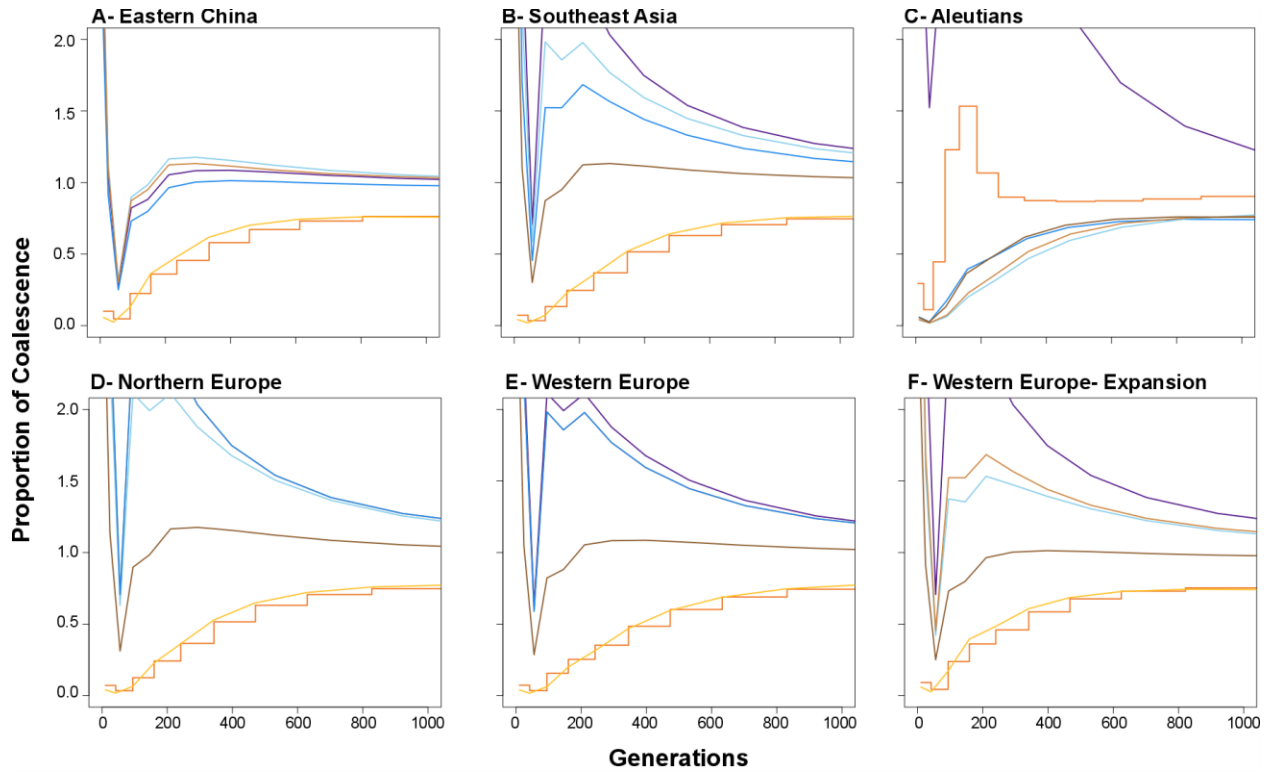


Figure S5- Curves of the proportion of population divergence between *eastern China* (A), *Southeast Asia* (B), *Aleutians* (C), *Northern Europe* (D), *Western Europe* (E), and the *Expansion* cluster (F) compared to the six other clusters indicated by line color (*eastern China*- dark brown; *SE Asia*- light brown; *Aleutian*- orange; *Western North America*- yellow; *Northern Europe*- purple; *Western Europe*- light blue; and *Expansion*- medium blue). We limited the temporal extent of the curves to the last 1000 generations (~ 333 years). Analysis was the cross-coalescence analyzed with MSMC2. The cross-coalescence can be estimated above one if there was more between cluster coalescence than within cluster coalescence, which appears in our data.

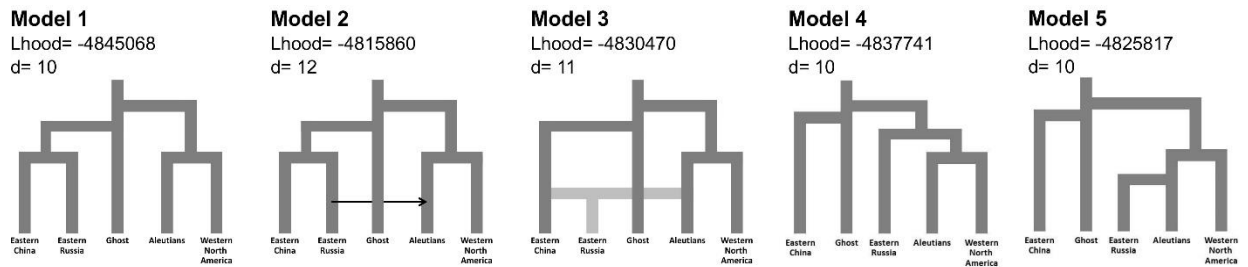


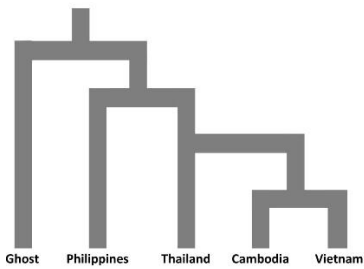
Figure S6- (top) Map of populations used for ddRADseq population modeling. (bottom) Topology, likelihood (Lhood), and number of parameters estimated (d) for five five-population scenarios used to identify the regional topological relationships between eastern China, eastern Russia, Aleutian, and Western North America populations. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -4815860. Model 2 had the highest likelihood of the five scenarios tested.



Model 1

Lhood= -1673287

d= 7



Model 2

Lhood= -1671886

d= 9

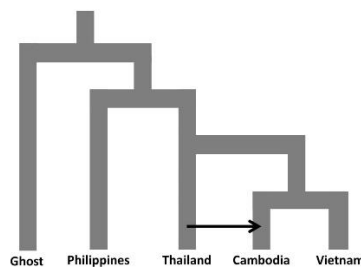
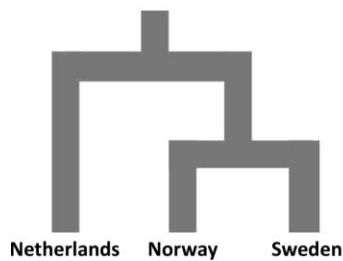


Figure S7- (top) Map of populations used for ddRADseq population modeling. (bottom) Topology, likelihood (Lhood), and number of parameters estimated (d) for two five-population scenarios used to identify the regional topological relationships within the *SE Asia* evolution cluster between the Philippines, Thailand, Cambodia, and Vietnam populations. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -1671886. Model 2 had the highest likelihood of the two scenarios tested.



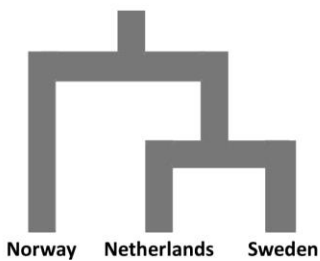
Model 1

Lhood= -895108
d= 5



Model 2

Lhood= -Infinity
d= 5



Model 3

Lhood= -896038
d= 5

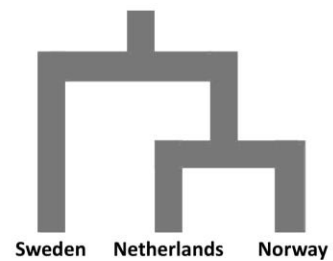
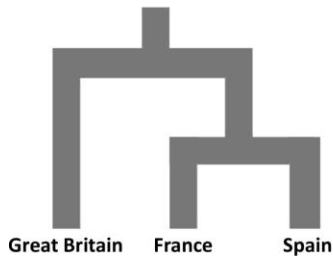


Figure S8- (top) Map of populations used for ddRADseq population modeling for both northern Europe (purple) and western Europe (blue) populations. (bottom) Topology, likelihood (Lhood), and number of parameters estimated (d) for three three-population scenarios used to identify the regional topological relationships within the *Northern Europe* evolution cluster between populations in the Netherlands, Sweden, and Norway. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -895108. Model 1 had the highest likelihood of the three scenarios tested. Note that Model 2 was considered impossible by the coalescent modeling.



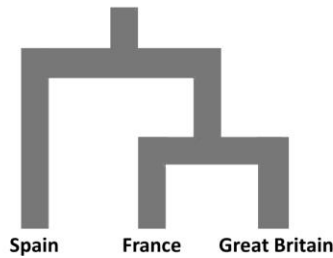
Model 1

Lhood= -523812
d= 5



Model 2

Lhood= -560827
d= 5



Model 3

Lhood= -548847
d= 5

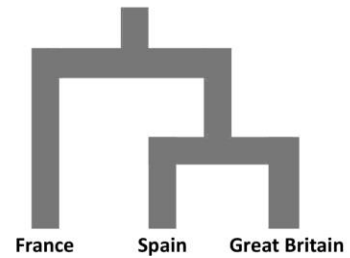


Figure S9- (top) Map of populations used for ddRADseq population modeling for both northern Europe (purple) and western Europe (blue) populations. (bottom) Topology, likelihood (Lhood), and number of parameters estimated (d) for three three-population scenarios used to identify the regional topological relationships within the *Western Europe* evolution cluster between the Great Britain, France, and Spain populations. The highest estimated likelihood following 50 independent runs of fastsimcoal2 was reported, where the maximum observed likelihood for these four clusters was -523812. Model 1 had the highest likelihood of the three scenarios tested.

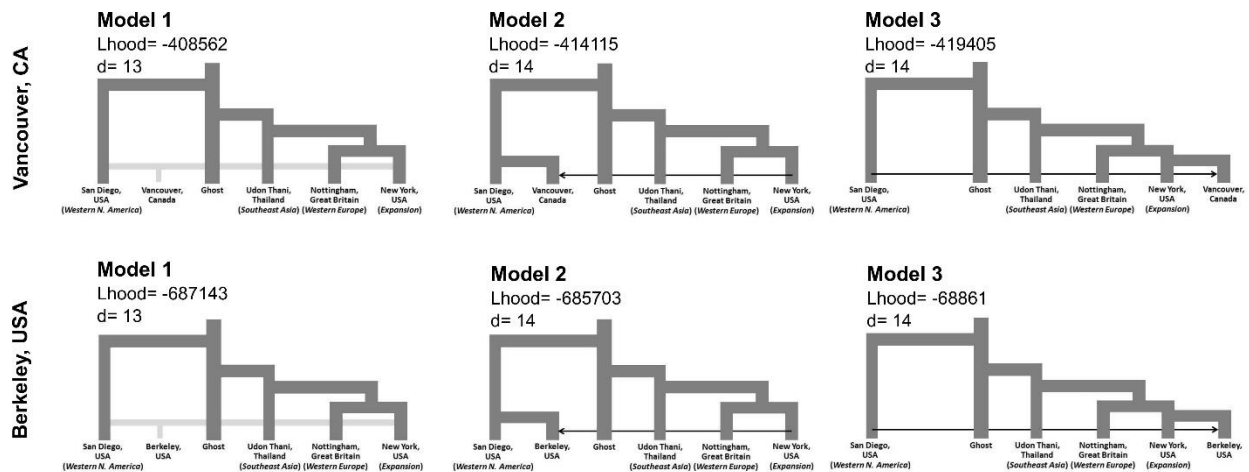


Figure S10- (top) Map of populations used for ddRADseq population modeling. (bottom) Topology, likelihood (Lhood), and number of parameters estimated (d) for three six-population models in Vancouver, Canada (top row) and Berkeley, USA (bottom row). All models contain the focal population; Udon Thani, Thailand (*SE Asia*); Nottingham, Great Britain (*Western Europe*); New York, USA (*Expansion*); San Diego, USA (*Western North America*); and an unsampled ancestral population. Models 1 and 2, respectively, were the best supported for Vancouver and Berkeley based upon the highest estimated likelihood from 50 independent runs of fastsimcoal2.