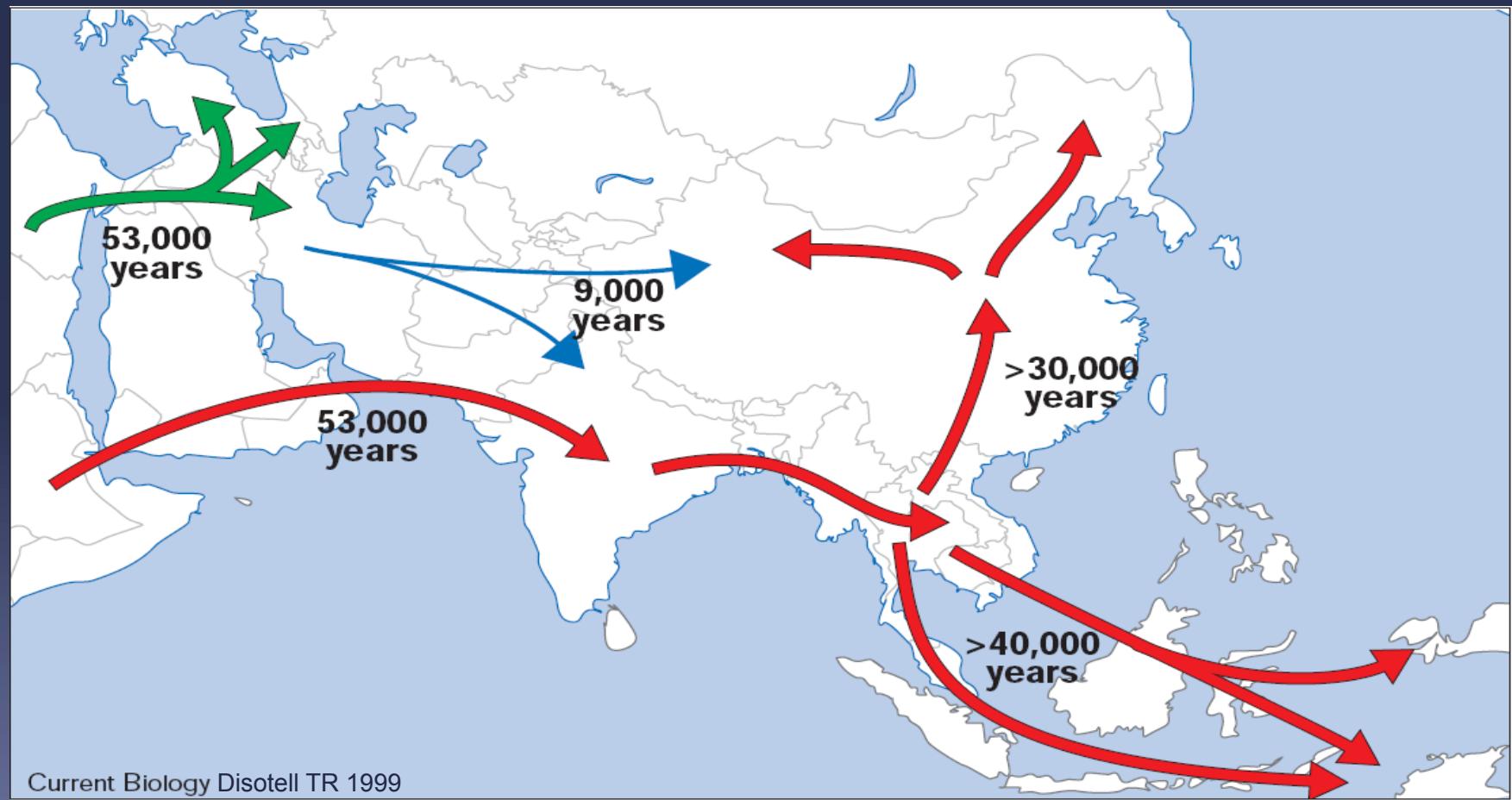


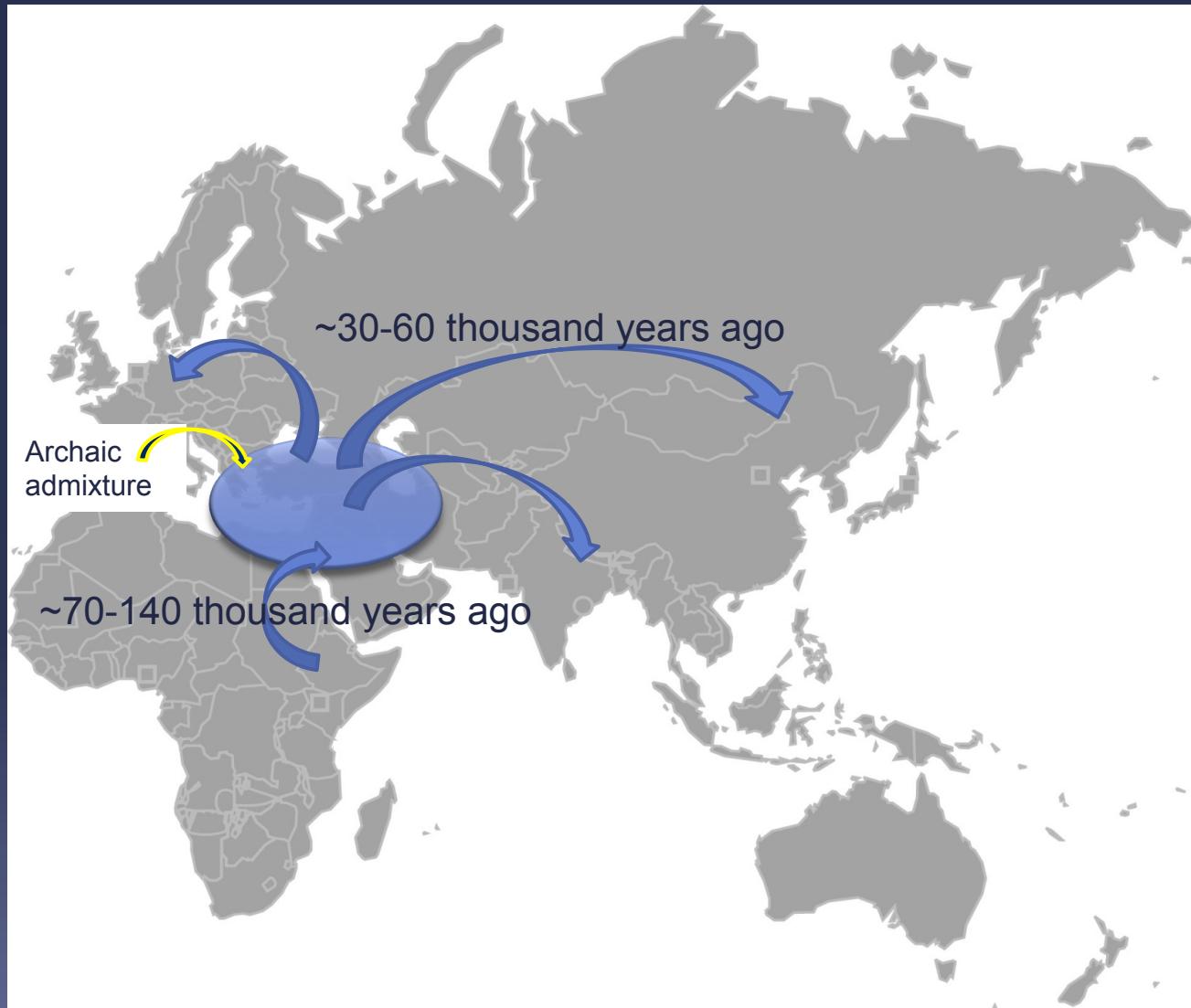
The peopling of Eurasia and the delayed expansion hypothesis

Chad Huff

The peopling of Eurasia



The delayed-expansion hypothesis

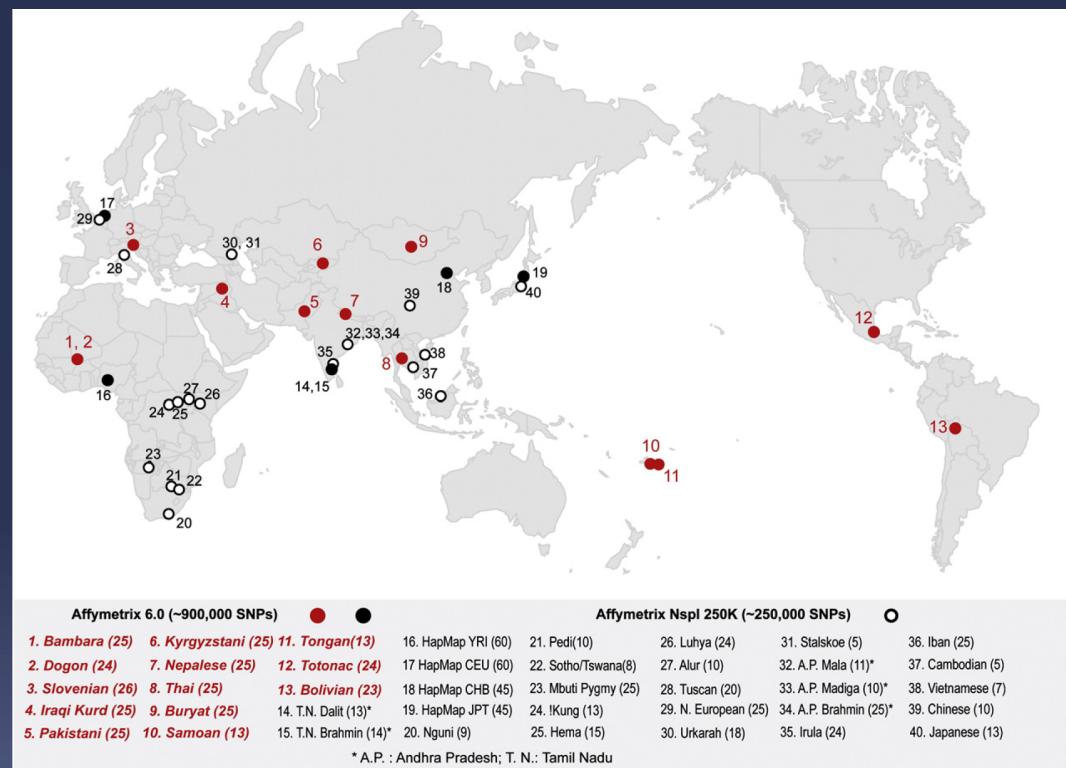


Datasets

One 100 kb region on Chr12 (ENr123) sequenced in 814 individuals from 12 populations.



250,000 SNPs genotyped in 850 individuals from 40 populations



Xing et al., 2010. Genome Biology.
“Sequence data”

Xing et al., 2010. Genome Research.
“Microarray data”

Evidence for Eurasian bottleneck(s): Mitochondrial Mismatch Distributions

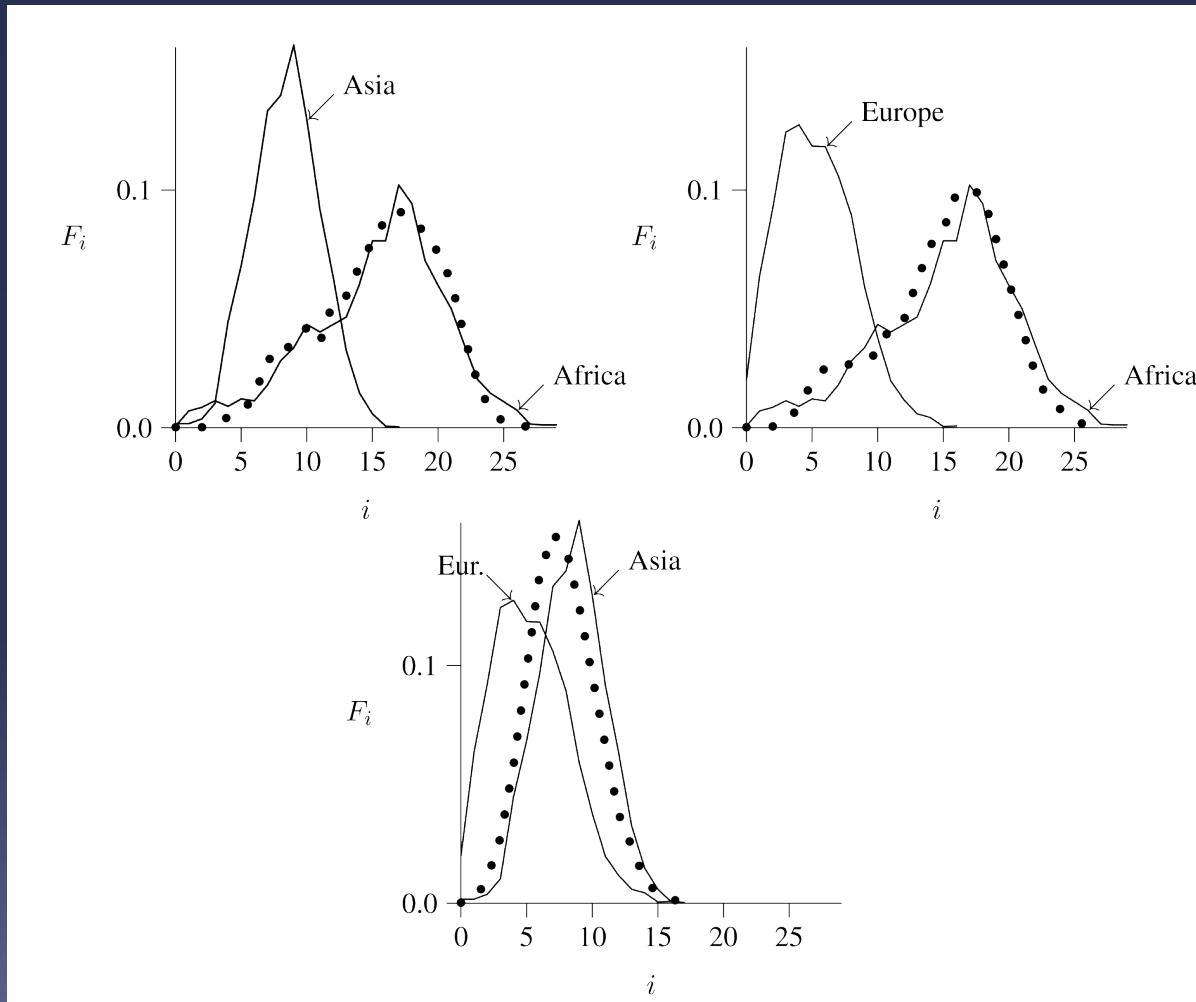


Figure 7.13: Mitochondrial Mismatch Distributions

Evidence for Eurasian bottleneck(s): Site frequency spectra

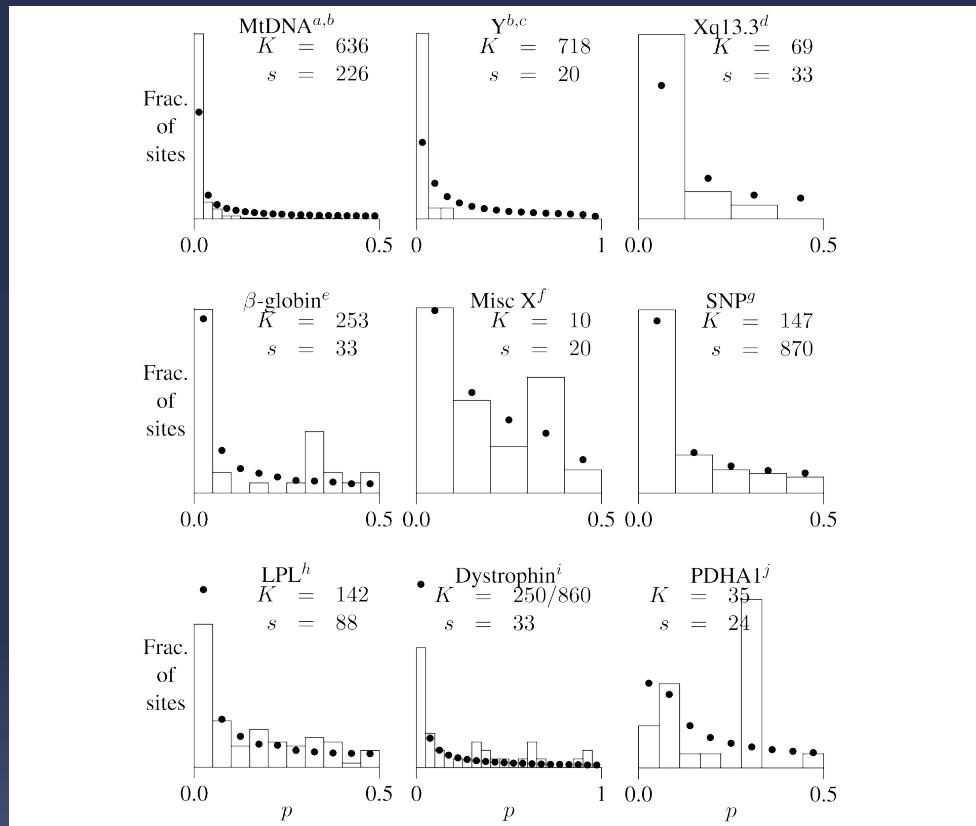
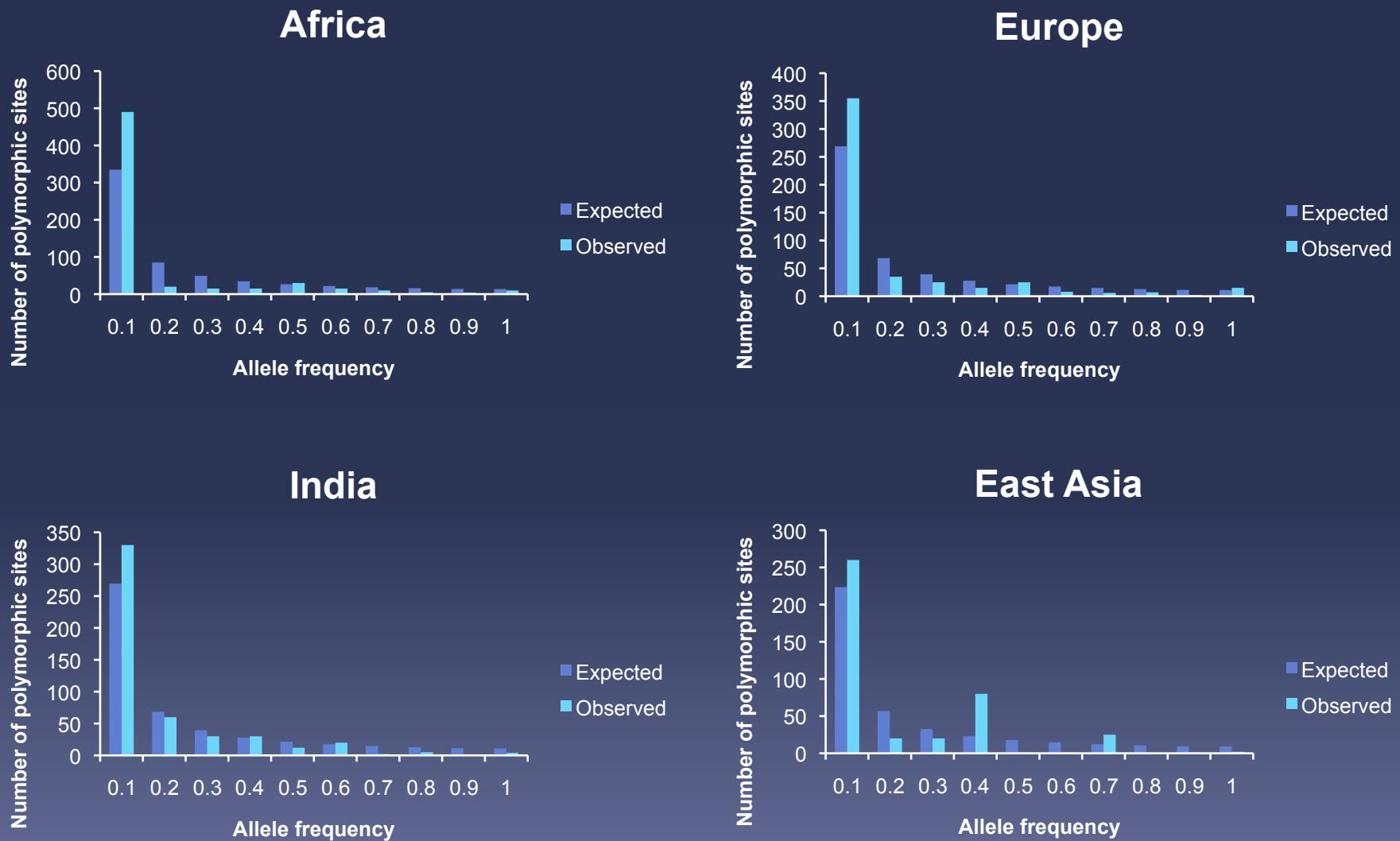
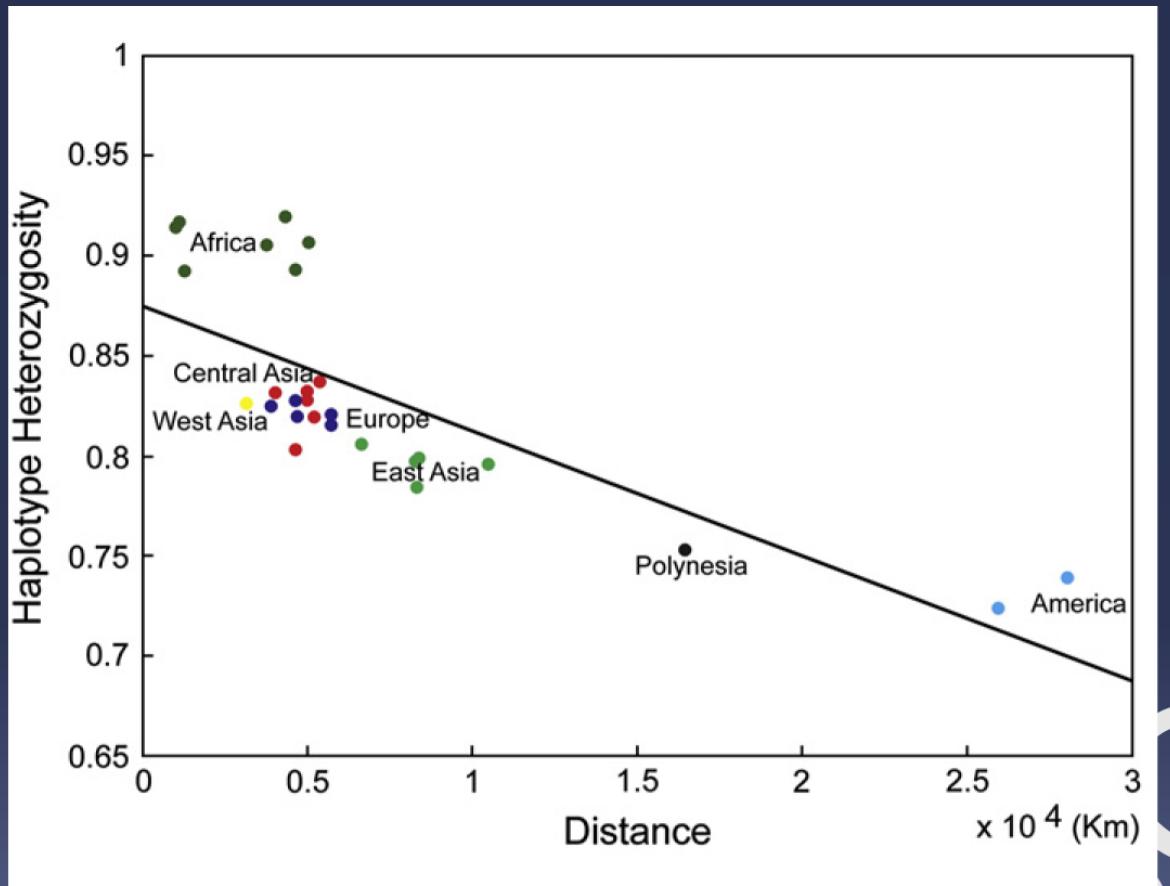


Figure 6.1: Site frequency spectra. The open rectangles in each panel show observed spectra; the bold dots show the spectra expected under the infinite sites model with no selection and constant population size. K is the number of chromosomes sampled, s is the number of segregating sites, and p is the frequency of the mutant allele (where ancestral state could be determined) or the rarest allele (where ancestral state is unknown). Sources: ^a[13], ^b[9], ^c[31], ^d[15], ^e[8], ^f[21], ^g[7], ^h[4], ⁱ[39], ^j[10]

Evidence for Eurasian bottleneck(s): Site frequency spectra from sequence data



How large was the Eurasian bottleneck?



With a one generation bottleneck:

$$H_1 = (1 - 1/2N) H_0$$

$$H_1 = 0.82, H_0 = 0.91$$

Solving for N:

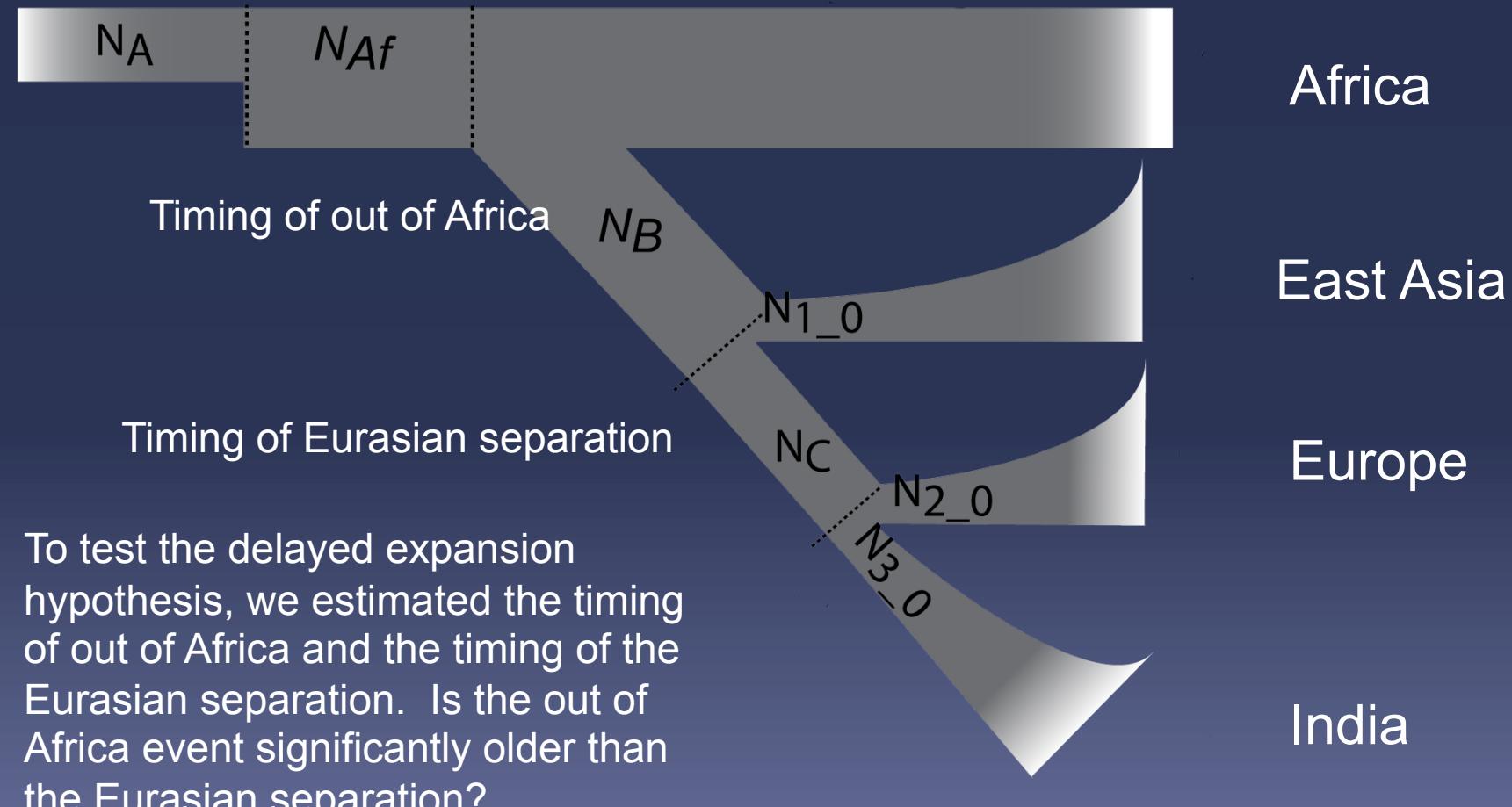
$$N = 5$$

This suggests a VERY small population founded Eurasia

Microarray data

- Average heterozygosity within Africa: 0.91
- Average heterozygosity immediately outside of Africa: 0.82

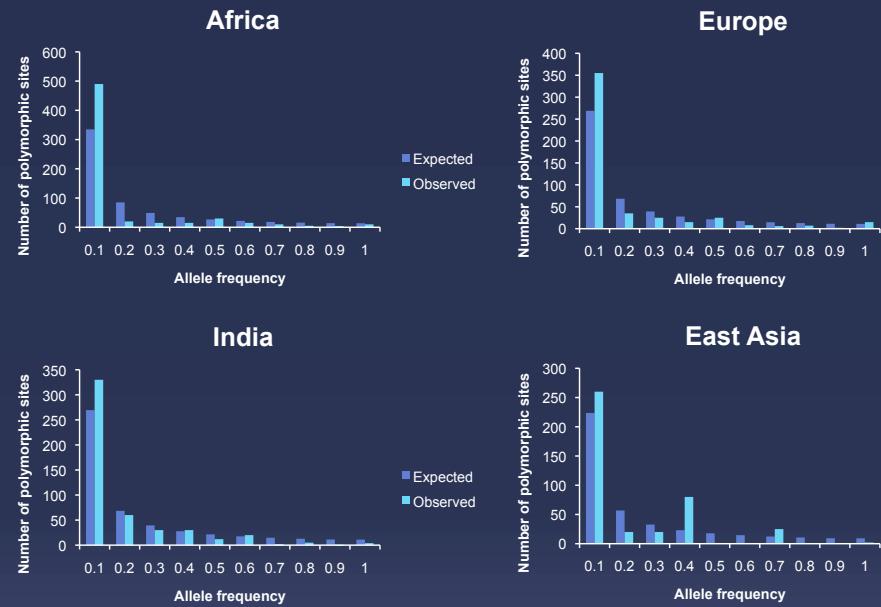
With a delayed expansion, the founding population size of Eurasia could have been much larger



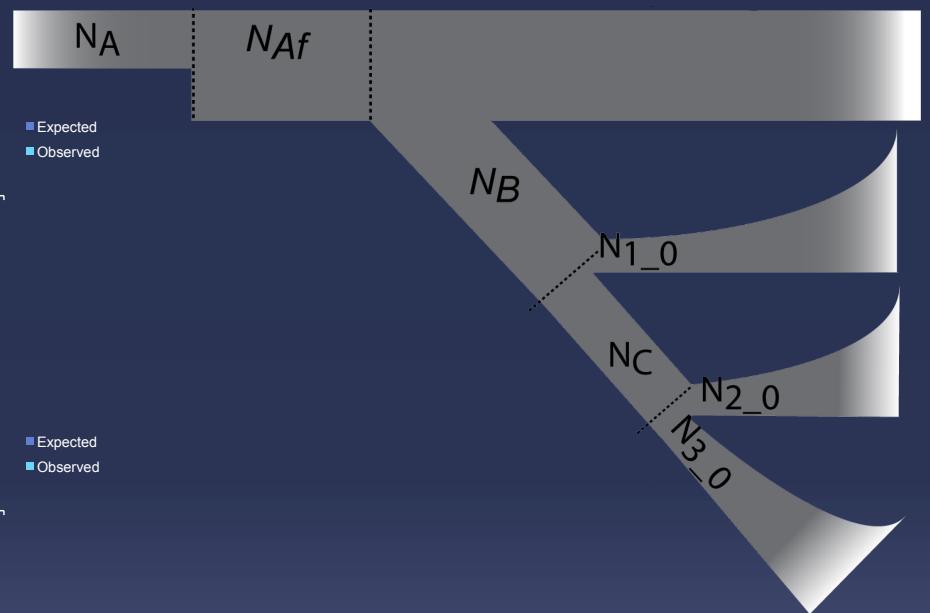
Inferring demographic history with dadi

dadi inputs

Site frequency spectra (sequence data)



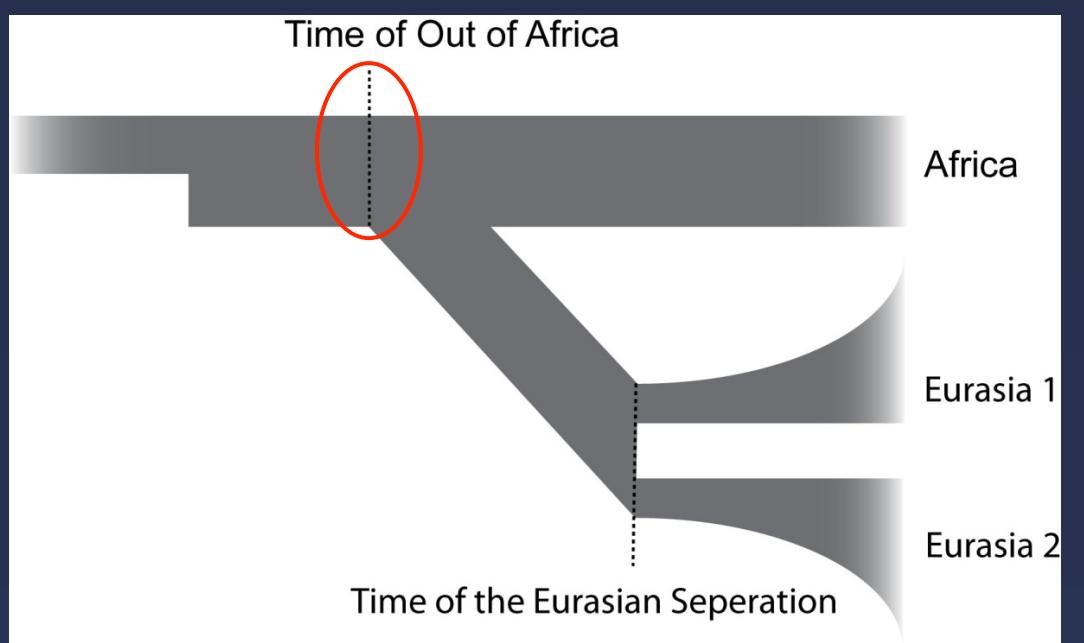
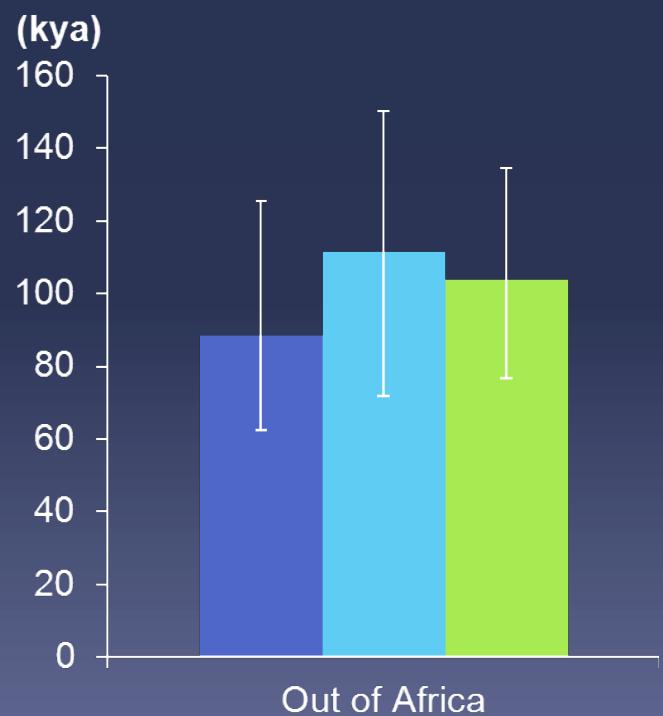
Model of demographic history



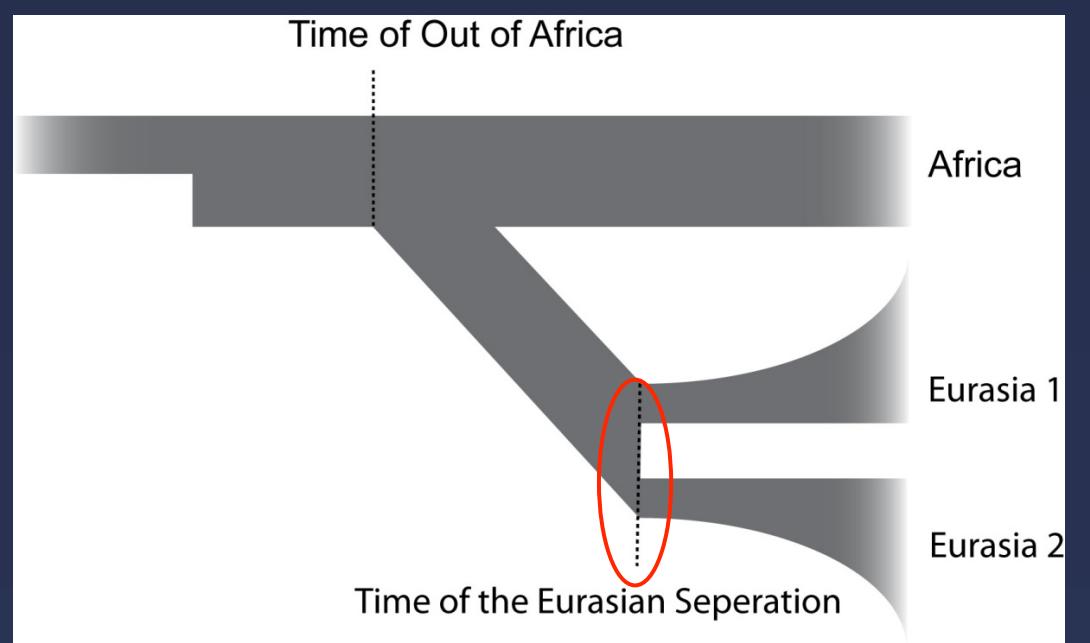
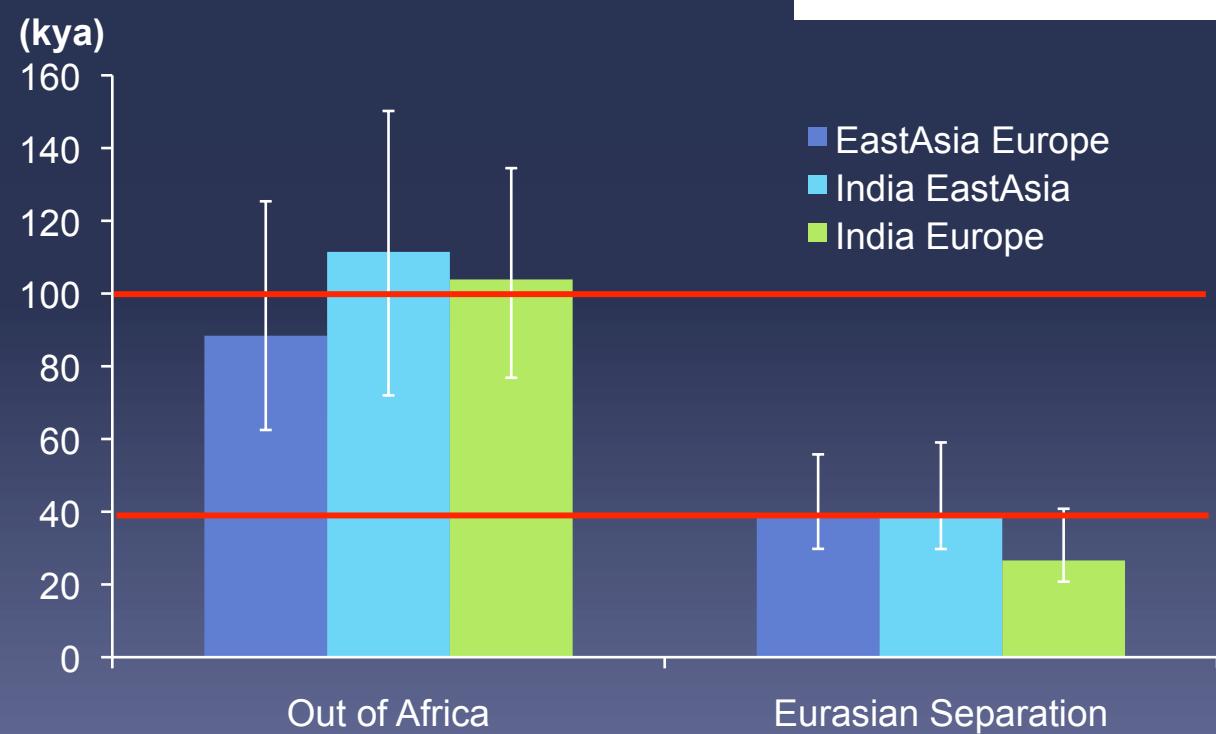
dadi output

maximum likelihood estimates
for all parameters specified in the model

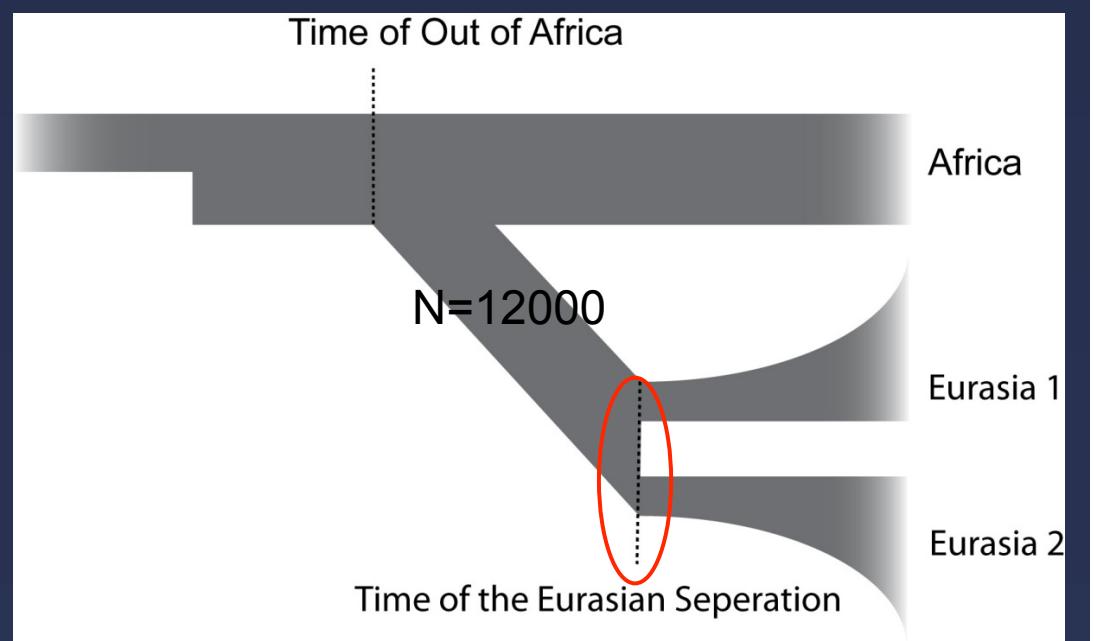
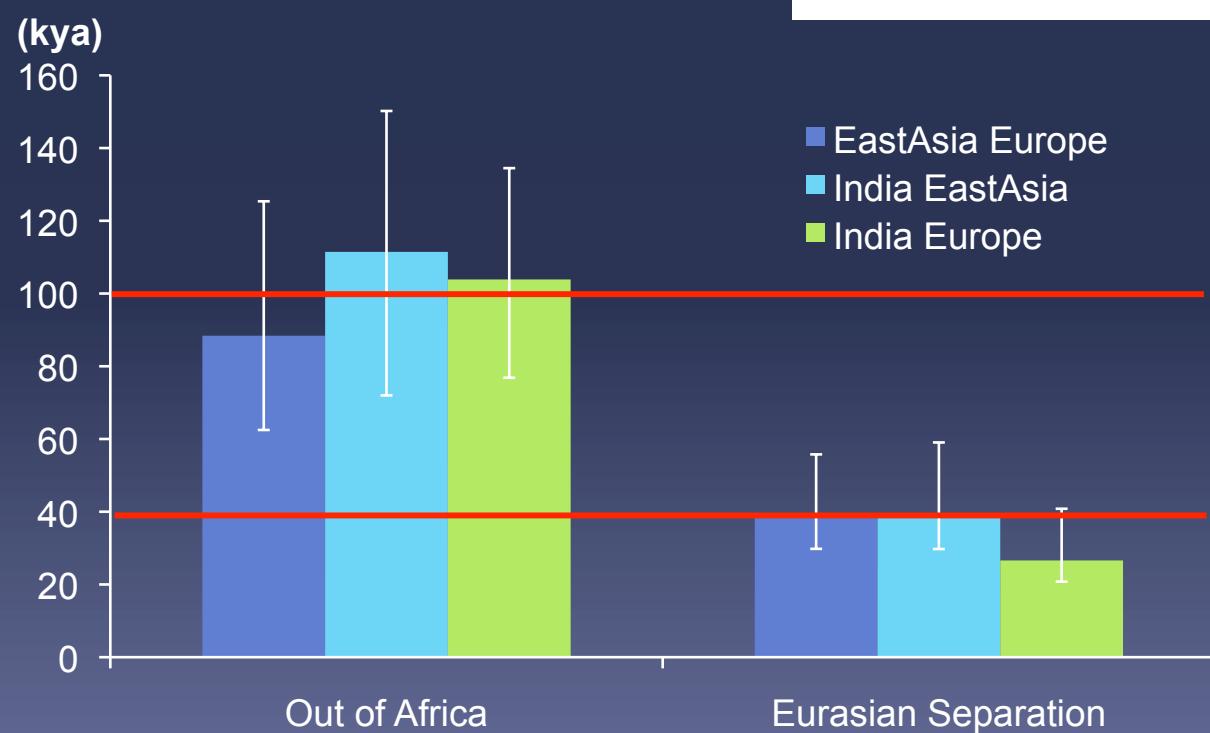
The timing of the peopling of Eurasia



The timing of the peopling of Eurasia



How large was the bottleneck?

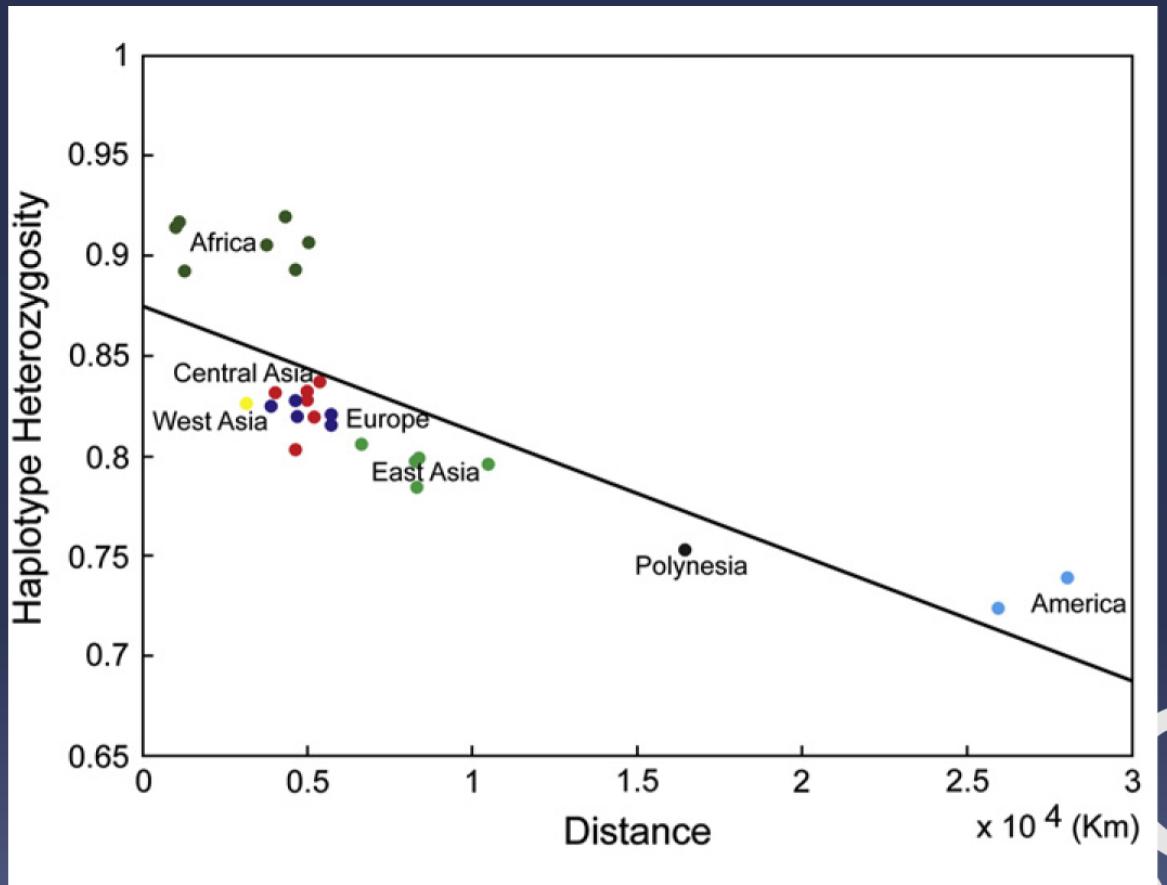


$t = 60,000$ years

or

$t = 2400$ generations

How large was the Eurasian bottleneck?



With a 2400 generation bottleneck and with $N=12000$:

$$H_1 = (1 - 1/2N)^{2400} H_0$$

$$H_0 = 0.91, N = 12000$$

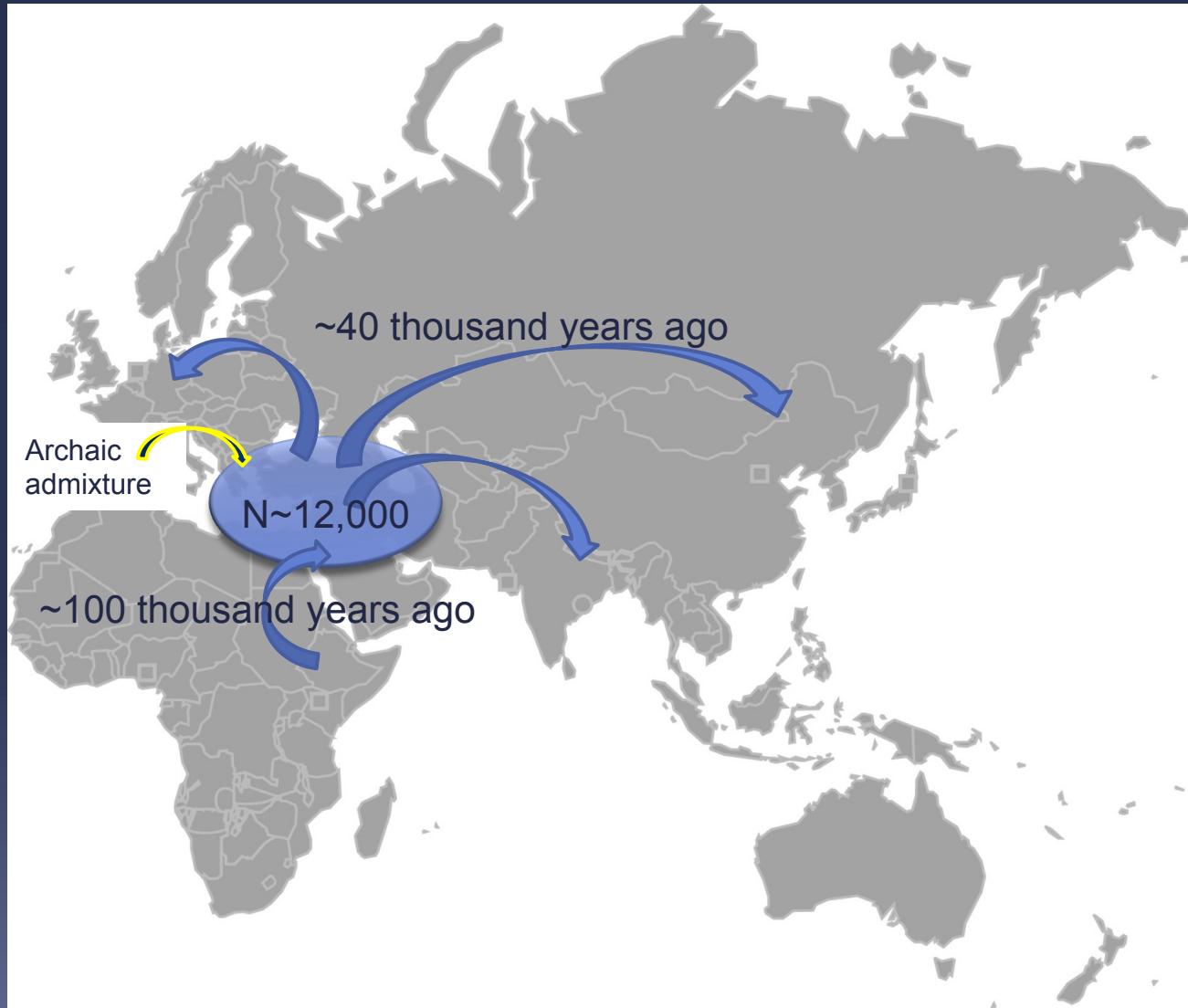
Solving for H_1 :

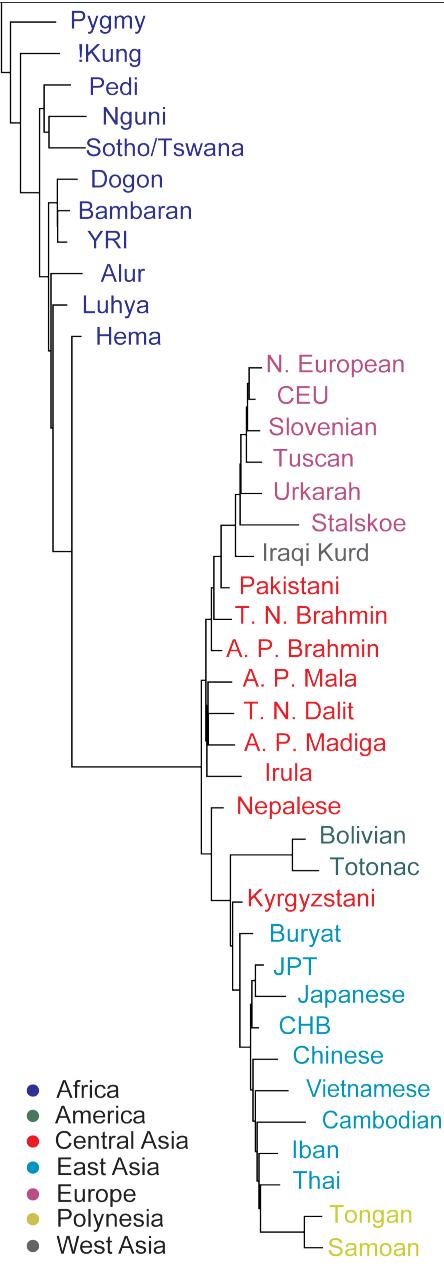
$$H_1 = 0.82, \text{ which equals our observed } H_1$$

Microarray data

- Average heterozygosity within Africa: 0.91
- Average heterozygosity immediately outside of Africa: 0.82

The delayed-expansion hypothesis





Neighbor joining tree
with microarray data

Evidence for a single Eurasian bottleneck: Shared history of genetic drift

