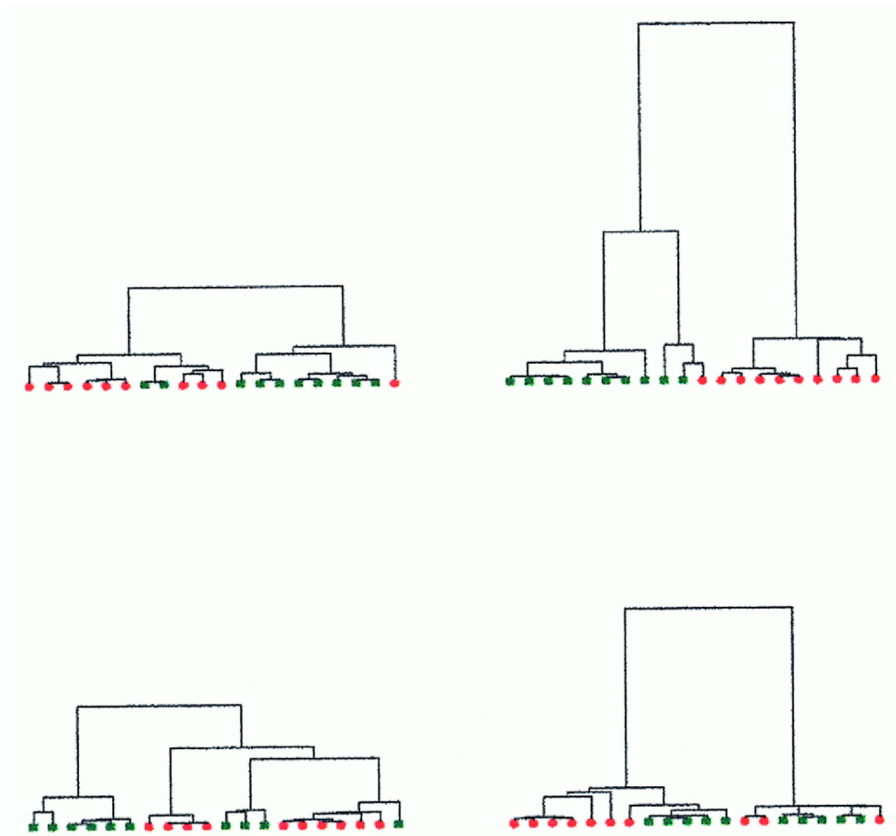


To: Journal Club
From: Harpending
Re: mtDNA

As a followup to our brief discussion today I dug up this figure:



These are gene trees of 20 genes drawn from two populations that exchange one migrant every two generations, that is they are approaching being different species. The red genes are from one population, the green from another. The population histories are exactly the same: the differences reflect random noise from one locus to the next.

Two things to notice:

- a. The trees vary a lot in total depth, and it doesn't tell us much if we know it about one locus, like for example when mitochondrial Eve lived.

b. Even if we could reconstruct the gene trees perfectly, we would still not know there were two populations because the reds and greens are mixed up with each other in the tree. The upper right tree comes closest to giving us the correct demography.

I have reading the Bandelt group paper, several times. I can't for the life of me understand why we want to know any of that stuff. Even when they do say something substantive it comes out not quite right. Consider this:

Thus, if A2, B2, C1, and D1 entered the Americas without variation in the coding region – in other words, each with only a single (successful) founder sequence (the root haplotype), their entry into the Americas would have occurred right after the peak of the Last Glacial Maximum (LGM, centered at ~21.0 kya and extending from 19.0 to at least 23.0 kya [41]), or slightly earlier, so that a coastal (Pacific) route would have been the only option during such glacial periods.

In other words, “if we assume that x is true then y shows that x is true”.

Henry