Brief Communications

A Pleistocene Population X-plosion?

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In two recent papers, Kaessmann et al. presented DNA sequence data from the X chromosome (Xq13.3) of 30 chimpanzees and 69 humans (Kaessmann et al. 1999a; Kaessmann et al. 1999b). These data bear on two longstanding questions involving late Pleistocene demographic history: (1) whether the long-term demography of humans is characterized by explosive population growth, and (2) whether chimps show population growth coinciding temporally with growth in humans.

Some genetic loci, such as mitochondrial DNA sequences (Rogers 1995), autosomal microsatellites (Kimmel et al. 1998), and microsatellites on the Y chromosome (Pritchard et al. 1999), have been taken as support for an explosion in human population size; other data have not (Harris and Hey 1999). However, most of the data showing no evidence of a population increase have been gathered from nuclear sequences of functional importance, making them vulnerable to the effects of natural selection (Kaessmann et al. 1999b). Xq13.3 provides the first substantial noncoding nuclear genetic sequence data useful for the evaluation of historical demography. The additional chimp data are pertinent to discussions of whether human demographic expansion was caused by generalized historical events affecting many species, such as global climate changes, or by human-specific factors, such as technological innovations.

In their analysis of Xq13.3 diversity in humans, Kaessmann et al. found that a test of Tajima's D (Tajima 1989), which compares the total number of variable nucleotide positions in a sample of sequences with the mean pairwise difference, fails to reject the hypothesis of constant population size. However, two lines of evidence suggest that the data are consistent with a population expansion.

First, the application of Fu's F_s test (Fu 1997), which compares the relative abundance of alleles at different frequencies in a sample and is more

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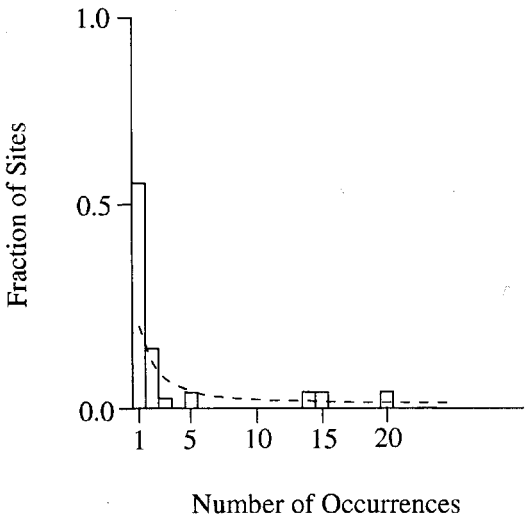

Figure 1. Frequency spectrum of mutations in human Xq13.3 sequences. Dashed line represents theoretical expectation under the hypothesis of no growth.

sensitive to population growth than D, yields a value of -7.570, rejecting the hypothesis of demographic stationarity at the 5% significance level. The negative value of F_s indicates that more low-frequency variants are observed than are expected—a deviation reflected in a graphical comparison of observed data to theoretical expectations under constant size (Figure 1).

Second, the application of Rogers' method for estimating historical demographic parameters, which analyzes the distribution of pairwise nucleotide differences among sampled sequences, yields $\hat{\theta}_0 = 0.646$, and $\hat{\tau} = 2.423$ (Rogers 1995). Under a two-epoch "sudden change" model of population history, which makes the simple assumption that a population changed instantaneously from an ancient population size to the modern one, $\hat{\theta}_0 = 2N_0\mu$ provides an estimate of ancient population size N_0 (measured as the number of X chromosomes), and $\hat{\tau} = 2\mu t$ provides an estimate of the length of time t (measured in generations) that has passed since the size change occurred (Rogers 1995). N_0 and t can be obtained by letting μ equal the product of the nucleotide substitution rate (per site per year), the number of nucleotides in the sequence, and the number of years per generation. Under the nucleotide substitution rate of 10^{-9} per site per year proposed by Kaessmann et al. (1999a), a sequence length of 10,000 nucleotides, and a 20-year generation time, $\hat{\theta}_0$, and $\hat{\tau}$ point to a rise in human populations from an initial effective size of around 1600 X chromosomes (roughly 1000 people), approximately 120,000 years before present. The confidence interval around both of these estimates is likely to be broad.

Xq13.3 sequences in chimps are more ambiguous: $F_s = -6.637$ for all chimps together, and -3.671 for West African chimps alone, failing marginally to reject stationarity. Neither constant size nor growth can be excluded.

In summary, Xq13.3 data from chimps are complex and ambiguous, but they do not appear to show evidence of a major Pleistocene expansion. However, F_s rejects the hypothesis that human population size has been constant, and $\hat{\theta}_0$ and $\hat{\tau}$ are in general agreement with earlier findings of population growth based on autosomal microsatellites, microsatellites on the Y chromosome, and mitochondrial DNA (Kimmel et al. 1998; Pritchard et al. 1999; Rogers 1995). Xq13.3 sequences can be added to the list of loci supporting a late Pleistocene population explosion in humans.

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