Sexual practice of polygyny skews genetic variability

September 26 2008

Researchers have found DNA evidence that polygyny, the practice among males of siring children with multiple female partners at the same time or successively, has led to an excess of genetic diversity on the X chromosome relative to the autosomes. Details are published Sep. 26 in the open-access journal *PLoS Genetics.*

Women have been more successful on average in passing their genes on to the next
generation. "This is because a few males have fathered children with multiple females, which occurs at the expense of other less successful males", says Dr. Michael Hammer, ARL Division of Biotechnology at the University of Arizona.

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children with multiple female partners at the same time or successively, has led to an excess of genetic diversity on the X chromosome relative to the autosomes. Details are published September 26 in the open-access journal *PLoS Genetics*.

The X chromosome is present in two copies in females and a single copy in males. The autosomes, which are inherited equally by both sexes from each parent, are expected to have more genetic diversity than the X chromosome in a population with an equal number of breeding males and females.

The article examines potential demographic and evolutionary forces that have led to higher than expected genetic variation on the X chromosome. The research team measured levels of neutral polymorphism at 40 independent loci on the X chromosome and autosomes in ninety humans representing six populations, including: Biaka (Central African Republic), Mandenka (Senegal), San (Namibia), French Basque, Han Chinese and Melanesians (Papua New Guinea). The group contrasted alternative explanations for the higher observed levels of X-linked (versus autosomal) diversity.

Background selection, changes in population size and sex-specific migration were
all discounted as contributors to the observed patterns of genetic variability. Only the process of polygyny could by itself account for the sex ratio skew and resulting patterns of genomic variation. By this process, fewer unique male genes are being passed into the next generation.

The group's research highlights how unseen, sex-biased forces have shaped genomic patterns of variability. Over the long-term, the findings may provide lessons on the dynamics of beneficial mutations on different chromosomes as they sweep through the population.

Citation: Hammer MF, Mendez FL, Cox MP, Woerner AE, Wall JD (2008) Sex-Biased Evolutionary Forces Shape Genomic Patterns of Human Diversity. PLoS Genet 4(9): e1000202. doi:10.1371/journal.pgen.1000202
dx.plos.org/10.1371/journal.pgen.1000202

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