Adam, Eve, and Human Genetic Diversity

Has modern genetics disproven the idea of Adam and Eve? Could two individuals carry within them enough genetic variation to be the sole ancestors of today's diverse human population? Theoretical and empirical studies of genetic bottlenecks show that large diverse populations can be descended from a single couple. Commonly-used methods of reconstructing past human population sizes would not point to a single couple bottleneck even if it were true. There are a range of historical scenarios by which a single couple could be the sole progenitors of present day human genetic diversity.

Richard Buggs is Professor of Evolutionary Genomics at Queen Mary, University of London (QMUL) and a Senior Research Leader at Royal Botanic Gardens Kew. His research on genetics has been published in journals including *Nature, Current Biology* and *Evolution*. Much of his work takes methods developed for the analysis of the human genome and applies them to the genomes of trees. From 2013-2016 he led a twelve-week teaching module *Human Genetics and Genomics* for final year Biomedicine undergraduates at QMUL. He holds a doctorate from the University of Oxford and received his undergraduate education at the University of Cambridge, where he was elected Bateman Scholar at Trinity Hall and gained a first class Bachelor's degree in Natural Sciences.

- I. Defining a genetic Adam and Eve
 - A. Sole ancestors of all human beings
 - 1. All current human DNA variation:
 - a. Was contained in them
 - b. Or came via subsequent mutations
 - 2. The possibility of admixture from other lineages
 - B. As opposed to:
 - 1. A genealogical Adam and Eve
 - 2. A population
 - 3. A parable
- II. Naïve objections
 - A. "Humans are too diverse to have descended from one couple"
 - 1. A single couple can contain every possible base at each variable site

- 2. The problem is not the *level* but the *distribution* of diversity
- B. "Descent from one couple would be obvious from the data"
 - 1. Every pattern of genetic data can be explained by multiple scenarios
 - 2. One scenario does not emerge by simple Baconian induction
- C. "Reconstructions of past effective population sizes would show it"
 - 1. Estimates of past effective population size assume equilibrium
 - 2. Short, sharp bottlenecks are invisible to them
- III. The population genetics of bottlenecks
 - A. Theoretical studies
 - B. Empirical studies
- IV. The real issue is not whether but when a genetic Adam and Eve could have existed
 - A. African allele frequency spectra
 - B. Time to the most recent common ancestor estimates
- V. Scenarios to consider:
 - A. A bottleneck of two:
 - 1. over 500kya
 - 2. under 500kya with elevated mutation rates
 - 3. under 500kya with strong selection
 - 4. under 500kya with admixture from other lineages

- B. Bottleneck followed by exponential growth due to:
 - 1. Survival from pandemic
 - 2. Survival from natural disaster
 - 3. Migration to virgin territory
 - 4. God giving human soul to a single pair
 - 5. Creation

Suggested Readings:

Adam and Eve: a tested hypothesis? <u>https://natureecoevocommunity.nature.com/users/24561-richard-buggs/posts/22075-adam-and-eve-a-tested-hypothesis</u> Adam and Eve: lessons learned <u>https://natureecoevocommunity.nature.com/users/24561-richard-buggs/posts/32171-adam-and-eve-lessons-learned</u>

Adam and Eve: our ghostly ancestors? <u>https://natureecoevocommunity.nature.com/users/24561-richard-buggs/posts/61200-adam-and-eve-our-ghostly-ancestors</u>