Evolution and the Single-Pair Bottleneck

A Population-Genetic Test of the Literal Ark Model

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Abstract

The flood narrative in Genesis records that most terrestrial animals boarded the ark as single breeding pairs, with a smaller set of clean animals boarding in sevens. Read literally, this places nearly every living terrestrial lineage through a founding event of one diploid pair roughly 4,500 years ago, followed by dispersal from a single region, the mountains of Ararat in the Middle East, in what is now Turkey. This paper evaluates that scenario against two well established bodies of population genetics: the genetics of small and inbred populations, and the theory of founder effects during range expansion. An effective size of about two produces severe and predictable consequences, rising inbreeding, loss of genetic variation, and a risk of mutational meltdown. A single geographic origin further predicts a radial decline of genetic diversity away from the point of release and a nested, serial founder structure centered on the mountains of Ararat. The observed distribution of terrestrial diversity does not show this pattern; it shows deep, geographically structured radiations and coalescence times that greatly exceed a few thousand years. I close by stating two falsifiable challenges that a literal ark model must meet: to demonstrate the founder effect and inbreeding signatures of a recent single pair bottleneck, and to demonstrate the expected radiation outward from the region where the ark is said to have come to rest.

Keywords: *founder effect, inbreeding depression, genetic drift, mutational meltdown, serial founder effect, biogeography, phylogeography*

1. Introduction

The flood account in Genesis specifies the composition of the animals taken aboard the ark. In the general instruction, pairs of every kind of land animal and bird are to be preserved, a male and its mate (Genesis 6:19 to 20). A second instruction distinguishes clean from unclean animals, directing that clean animals and birds be taken in larger numbers, commonly read as seven or seven pairs, while unclean animals are taken as single pairs (Genesis 7:2 to 3). Whatever the precise count for the clean minority, the dominant literal reading places the great majority of terrestrial kinds through a founding event of exactly one breeding pair.

Stated in the language of population genetics, this is a strong and testable claim. It asserts a recent founding date, on the order of 4,500 years before the present under standard young life chronologies, an extreme founding bottleneck of a single diploid pair for most lineages, and a single geographic point of release, the mountains of Ararat, where the ark is said to have come to rest (Genesis 8:4), in the Middle East, in what is now Turkey. Each of these properties, recency, a single pair, and a single place of origin, generates predictions that can be tested against the genetics of living populations and against the geographic distribution of diversity.

In what follows I set aside the geophysical questions surrounding the flood itself and restrict attention to population genetics and biogeography. I first examine the immediate genetic consequences of an effective population size near two, the domain of inbreeding and genetic drift. I then turn to what a single geographic origin predicts for the spread of diversity across the continents, and I compare that prediction with the pattern actually observed. I address the objections most likely to be raised from a creationist perspective, and I conclude with two challenges framed as positive predictions the model must satisfy.

2. Inbreeding load, drift load, and the limits genetic drift

An effective population size near two carries immediate and well characterized genetic consequences. With so few founders, the inbreeding coefficient rises steeply in the first generations, and inbreeding depression, the loss of fitness that accompanies increased homozygosity of deleterious recessive alleles, is among the best documented phenomena in population biology (Charlesworth & Charlesworth, 1987; Keller & Waller, 2002). Inbreeding depression is not a marginal effect; in wild populations it reduces survival, fertility, and resistance to disease and environmental stress (Hedrick & Kalinowski, 2000). Genetic variation itself scales with population size across wildlife, so the smallest populations are also the least variable and the least able to respond to new selective pressures (Frankham, 1996).

Beyond inbreeding, a very small population is exposed to genetic drift so strong that selection struggles to counter it. Mildly deleterious mutations that selection would ordinarily remove can instead drift to fixation, and as they accumulate they lower mean fitness, which further reduces population size, which in turn strengthens drift. This self reinforcing decline is the process known as mutational meltdown (Lynch, Conery, & Bürger, 1995). Genetic factors of this kind are not merely theoretical worries confined to the smallest populations; they are implicated in real declines toward extinction (Spielman, Brook, & Frankham, 2004).

3. Radiation and migration

A single geographic origin makes strong and specific predictions about how diversity should be arranged across space. When a population spreads outward from one source, it does so as a sequence of colonization steps, and each newly founded population is established by only a sample of the population that gave rise to it. Because every step is a subsample, alleles are lost at each frontier and are rarely regained, so genetic diversity does not remain constant across the range. It declines steadily with distance from the point of origin. Populations near the source retain the fullest diversity, populations at the far edges of the expansion are the most genetically depleted, and the diversity found at any distant site tends to be a nested subset of the diversity present closer to the origin. This distance decay of heterozygosity, and the nested, serial structure that accompanies it, is a direct and general consequence of range expansion from a single starting point. It is simply how diversity behaves when a lineage radiates outward from one place. The founder-effect numbers have been published based on population genetics simulations toward ~5,000 (Lande 1995), and then later Traill et al. 2007 who put the minimum viable population near 4,000. The most recent publication is from Frankham et al. 2014 who revised the rule again to 100/1000.

100 = you need about **100 effectively breeding individuals** in the short term to reduce the danger of inbreeding depression.

1000 = you need about **1000 effectively breeding individuals** long term to keep enough genetic diversity for the population to keep adapting over time.

Apply this to the flood account. If the terrestrial animals of the world descend from pairs released together at the mountains of Ararat about 4,500 years ago and dispersed outward from that one region, then the same logic yields clear and shared expectations. Genetic diversity should decline in a roughly radial fashion with distance from the Middle East, and this gradient should appear again and again across many unrelated groups, because all of them expanded from the same place at the same time. Phylogenies should be shallow, with a recent common origin and a compressed, nearly simultaneous branching near the root. The genomes of populations should carry serial founder signatures aligned along the dispersal corridors leading out of the Middle East, and the youngest, most genetically depleted populations should sit at the geographic extremes, in Australia, the Americas, and the remote islands of the Pacific.

The observed distribution of terrestrial diversity does not match these expectations on any point. There is no shared radial gradient of decreasing diversity centered on the Middle East and repeated across taxa. Instead, groups show deep, geographically structured radiations rooted in particular regions and continents, with the marsupials of Australia, the endemic faunas of the Neotropics, and the isolated radiations of oceanic archipelagos standing as familiar examples. Phylogeographic structure runs deep rather than shallow, and the coalescence times of lineages within and among these groups routinely extend far beyond a few thousand years (Avise, 2000; Hewitt, 2000). Rather than a young, star-like radiation emanating from Ararat, the map of life records old, regionally anchored divergence. The physical difficulty of migration compounds the genetic mismatch, since animals would have had to cross oceans and reach isolated landmasses within a few thousand years while leaving no genetic trail of that transit through the Middle East and beyond.

4. Anticipated objections

Creationists commonly hold that the created kinds diversified rapidly after the flood, so a radiation outward from the landing site is, on this view, expected rather than surprising. The point is fair as far as it goes, but it does not remove the difficulty; it sharpens it. If the fauna radiated from the mountains of Ararat, then the radiation should carry the geographic fingerprint of that origin, a diversity gradient that decays away from the Middle East and a serial founder structure shared across the many lineages that left from the same place. It is precisely this Ararat centered signature that is missing. The radiations we observe are anchored in many different regions rather than in one, and they do not nest outward from a single Middle Eastern source. Predicting rapid radiation is not enough; the model must predict a radiation with the specific geometry that a single origin requires, and that geometry is absent.

A second objection holds that the depth of coalescence and the geographic structure were simply created that way, that lineages were designed at the outset known as created heterozygosity. This argument does not engage the pattern that requires explanation, namely that it cannot explain the pattern of diversity we see like evolution can. The full weight of the coalescence evidence deserves separate and detailed treatment, and I reserve it for a dedicated paper; here it is enough to note that appealing to created depth neither answers the observed structure nor removes the burden of accounting for it.

5. Conclusion: two challenges

A literal reading of the flood account is a testable hypothesis about the recent history of terrestrial life, and it predicts definite signatures in the genetics of populations and in the geography of diversity. Stated as positive predictions, the model implies two things that should be found and are not.

The first challenge concerns founder effects and inbreeding. If most terrestrial lineages passed through a single pair about 4,500 years ago, then living populations across independent lineages should carry the genetic marks of that event, the signatures of an extreme and recent bottleneck, elevated inbreeding, sharply reduced variation traceable to a handful of founders, and the load profile expected of a lineage that passed through so narrow a filter. The biblical model needs to demonstrate these founder effects and inbreeding signatures directly and across the board, not in a single favorable case but as the shared inheritance of terrestrial life. The genetics of living populations does not present that uniform recent bottleneck; it presents variation and structure far richer and far older than a single pair a few thousand years ago can supply.

The second challenge concerns radiation from the landing site. If the animals of the world dispersed from the mountains of Ararat, then their diversity should be arranged as a radiation outward from that region, a decline of diversity with distance from the Middle East and a serial founder structure shared across taxa and centered on the place where the ark is said to have come to rest. The biblical model needs to

demonstrate these radiation events from that origin. The observed biogeography shows no such center. The diversity gradients, the deep and regionally anchored radiations, and the depth of coalescence across terrestrial life are inconsistent with a single recent origin in the mountains of Ararat.

Until the model produces positive evidence for these predicted founder effect, inbreeding, and radiation signatures, the population genetic and biogeographic record stands against a literal single pair ark bottleneck. The burden it faces is not rhetorical but evidential: to show, in the genetics of living populations and on the map of their diversity, the very fingerprints that a recent founding from one pair in one place would necessarily leave.

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