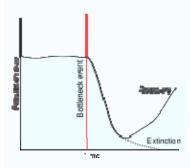
# **Population bottleneck**

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Population bottleneck and recovery or extinction

A **population bottleneck** (or **genetic bottleneck**) is an <u>evolutionary</u> event in which a significant percentage of a population or species is killed or otherwise prevented from reproducing, and the population is reduced by 50% or more, often by several <u>orders of magnitude</u>. [1]

Population bottlenecks increase <u>genetic drift</u>, as the rate of drift is inversely proportional to the population size. They also increase <u>inbreeding</u> due to the reduced pool of possible mates (see <u>small population size</u>).

A slightly different sort of genetic bottleneck can occur if a small group becomes reproductively separated from the main population. This is called a <u>founder effect</u>.

### **Examples**

#### Humans

Human <u>mitochondrial DNA</u> (inherited only from one's mother) and <u>Y chromosome</u> DNA (from one's father) show <u>coalescence</u> at around 140,000 and 60,000 years ago respectively. In other words, all living humans' <u>female line ancestry</u> trace back to a single female (<u>Mitochondrial Eve</u>) at around 140,000 years ago. Via the <u>male line</u>, all humans can trace their ancestry back to a single male (<u>Y-chromosomal Adam</u>) at around 60,000 years ago. [2]

However, such coalescence is genetically expected and does not, in itself, indicate a population bottleneck, because mitochondrial DNA and Y-chromosome are only a small part of the entire genome, and are atypical in that they are inherited exclusively through the mother or through the father, respectively. Most genes in the genome are inherited from either father or mother, thus can be traced back in time via either matrilinear or patrilinear ancestry. [3] Research on many (but not necessarily most) genes find different

coalescence points from 2 million years ago to 60,000 years ago when different genes are considered, thus disproving of the existence of more recent extreme bottlenecks (i.e. a single breeding pair). [4][5]

But this is not inconsistent with the <u>Toba catastrophe theory</u> which suggests that a bottleneck of the human population occurred ca. 70,000 years ago, positing that the human population was reduced to a c.15,000 individuals<sup>[5]</sup> when the <u>Toba supervolcano</u> in <u>Indonesia</u> erupted and triggered a major <u>environmental</u> change. The theory is based on geological evidences of sudden climate change, and on coalescence evidences of some genes (including mitochondrial DNA, Y-chromosome and some nuclear genes)<sup>[6]</sup> and the relatively low level of genetic variation with humans.<sup>[5]</sup> On the other hand, in <u>2000</u>, a *Molecular Biology and Evolution* paper suggested a transplanting model or a 'long bottleneck' to account for the limited genetic variation, rather than a catastrophic environmental change.<sup>[7]</sup>

#### **Animals**

Year	American bison (est)
Before <u>1492</u>	60,000,000
1890	750
2000	360,000

<u>Wisent</u>, also called European bison, faced extinction in the early <u>20th century</u>. The animals living today are all descended from 12 individuals and they have extremely low genetic variation, which may be beginning to affect the reproductive ability of bulls (Luenser et al., 2005). The population of <u>American Bison</u> fell due to overhunting, nearly leading to extinction around the year 1890 and has since begun to recover (see table).

A classic example of a population bottleneck is that of the <u>Northern Elephant Seals</u>, whose population fell to about 30 in the 1890s although it now numbers in the tens of thousands. Another example are <u>Cheetahs</u>, which are so closely related to each other that <u>skin grafts</u> from one cheetah to another do not provoke <u>immune responses</u>, thus suggesting an extreme population bottleneck in the past. Another largely bottlenecked

species is the <u>Golden Hamster</u>, of which the vast majority are descended from a single litter found in the <u>Syrian</u> desert around <u>1930</u>.

According to a paper published in 2002, the <u>genome</u> of the <u>Giant Panda</u> shows evidence of a severe bottleneck that took place about 43,000 years ago. [8] There is also evidence of at least one primate species that suffered from a bottleneck around this time scale.

Sometimes further deductions can be inferred from an observed population bottleneck. Among the <u>Galápagos Islands</u> giant tortoises, themselves a prime example of a bottleneck, the comparatively large population on the slopes of Alcedo volcano is significantly less diverse than four other tortoise populations on the same island. Researchers' DNA analysis dates the bottleneck around 88,000 years before present (<u>YBP</u>), according to a notice in *Science*, <u>October 3</u>, <u>2003</u>. About 100,000 YBP the volcano erupted violently, burying much of the tortoise habitat deep in pumice and ash.

## Population bottlenecks in evolutionary theory

As a population becomes smaller, genetic drift plays a bigger role in speciation. A land animal like a brown bear might find itself locally reduced to a few dozen pairs on an Arctic island. That likely happened as the last Ice Age came to an end, and the Bering land bridge receded into the sea. In that circumstance, a beneficial trait appearing in an alpha male or two may change the color, size, swimming ability, cold resistance, or aggressiveness of the group in just a few generations. This would be an example of punctuated equilibrium.

### Minimum viable population size

In <u>conservation biology</u>, <u>minimum viable population</u> size (MVP) helps to determine the <u>effective population size</u> when a population is at risk for <u>extinction</u> (Gilpin and Soulé, 1986 and Soulé, 1987). There is considerable debate about the value of the MVP.