Testis Size Matters for Genome Evolution

In many primates, females mate with multiple partners, causing an often-intense competition among males to pass along their DNA to be king of the genome as well as the jungle.

Alex Wong (2014) used a published sequence data set from 55 species of primates to test for a correlation between molecular evolutionary rates across a genome (substitution rates) and testes weights, used in the study as a proxy for increased sperm production and competition. It is widely thought that the production of increased numbers of sperm results from more rounds of cell division—and with more cell division, more mutations arise during sperm production.

“In general, the speed of genome evolution is higher for species in which males have large testes in comparison to species in which males have small testes,” said Wong. “This finding helps us to understand why genomes evolve at different rates in different species, and has implications for our understanding of the relationship between female mate choice and the overall fitness of a population.”

Wong applied a sophisticated evolutionary method to detect a correlation between testes size and substitution rate in primates and found a positive correlation when accounting for other confounding factors. This finding could provide support for the general prediction that sperm competition should result in higher substitution rates as a consequence of higher spermatogenic activity in species that mate with more than one male.

“The current finding of covariance between sperm competition intensity and substitution rates adds to a growing body of knowledge concerning the sources of substitution rate variation,” said Wong. “The extent to which this covariance is widespread is not yet clear; application of robust comparative methods to large phylogenetic data sets in other taxa, such as birds and insects, will help to establish its generality.”

Reference


Joseph Caspermeyer*, 1

1 MBE Press Office

*Corresponding author: E-mail: MBEpress@gmail.com.

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Study Yields “Genghis Khan” of Brown Bears, New Understanding of Brown and Polar Bear Evolution

Male bears are seemingly always on the prowl, roaming much greater distances than females, particularly for mating. For bear evolution, studying the paternally inherited Y chromosome is therefore a rich source to trace both the geographic dispersal and genetic differences between bear species.

By mining the genome of a recently sequenced polar bear, researchers Bidon et al. (2014) developed Y chromosome-specific markers and analyzed several regions of the Y chromosome from a broad geographic sample of 130 brown and polar bears. They also included a continuous 390,000-bp long stretch of genomic Y chromosomal region available in brown, polar, and black bear genomes to gain a better understanding of the paternal signature of bear evolution.

They found evidence of extensive male gene flow that has led to the distribution of some brown bear Y chromosomes across incredibly large geographic distances, with two brown bears as far away as Norway and the Alaskan ABC islands carrying very similar Y chromosomes. This implies that one male brown bear lineage has spread across most of the brown bear’s distribution range. “This pattern in brown bears covers even larger geographic areas than analogous findings from humans, where the Y-chromosomal lineage of Genghis Khan, founder of the Mongol Empire, was spread across much of Asia,” said Tobias Bidon and Frank Hailer, lead authors of the study.

Because their data consistently showed that black, brown, and polar bears carry highly distinct Y chromosome lineages, the researchers also estimated the timing of split between the male lineages of brown and polar bears. The obtained time estimate for the speciation event of brown and polar bears is ~0.4–1.1 Ma. This is significantly older than previous estimates based on mtDNA, confirming recent observations from autosomal markers that brown and polar bears from a genetic point of view represent highly distinct species. The study also shows that dispersing males connect the enigmatic brown bear population of the Alaskan ABC-islands to the North American mainland and that the resulting movement of genes is substantial enough to maintain high genetic variability within this island population.

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