Into Thin Air and Back: Deer Mouse Study Examines High-Altitude Adaptation

Life has adapted to all sorts of extreme environments on Earth, among them, animals such as the deer mouse, shimmying and shivering about, and having to squeeze enough energy from the cold, thin air to fuel their bodies and survive.

Now, Scott et al. (2015) have examined the underlying muscle physiology from a group of highland and lowland deer mice. Deer mice were chosen because they exhibit the most extreme altitude range of any North American mammal, occurring below sea levels in Death Valley to more than 4,300 m high in the mountains.

The research team took mice native to high- or low-altitude habitats, and after rearing the lab, measured the population differences in the mice, as well as their offspring. Many muscle physiology traits tended to show heritable differences between populations, whereas many were more plastic, changing with acclimation to a new altitude environment.

These differences were associated with changes in the expression of a number of genes involved in energy metabolism, muscle plasticity, vascular development, and cellular stress. At the intracellular level, genes that influence the proliferation of the powerhouses of the cell, mitochondria, were also more highly expressed in highland mice. Together these genetic changes resulted in increasing the oxidative capacity and blood supply to skeletal muscle, where rivers and tributaries of blood vessels and capillaries serve to enrich and energize skeletal muscle.

The results add to the growing knowledge and underlying mechanisms of fitness-related physiological performance under hypoxic conditions.

Reference

Scott GR, Elogio TS, Lui MA, Storz JF, Cheviron ZA. 2015. Adaptive modifications of muscle phenotype in high-altitude deer mice are associated with evolved changes in gene regulation. *Mol Biol Evol.* 32(8):1962–1976.

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doi:10.1093/molbev/msv100

Advance Access publication May 22, 2015

Most Comprehensive Study to Date Reveals Evolutionary History of Citrus

Citrus fruits—delectable oranges, lemons, limes, kumquats, and grapefruits—are among the most important commercially cultivated fruit trees in the world, yet little is known of the origin of the citrus species and the history of its domestication.

Now, Carbonell-Caballero et al. (2015) have performed the largest and most detailed genomic analysis on 30 species of *Citrus*, representing 34 citrus genotypes, and used chloroplast genomic data to reconstruct its evolutionary history.

Overall, the results confirm a monophyletic origin—a single common ancestor—that gave rise to all citrus fruit. Another result from the study was the remarkable level of heteroplasmy, or hybridization seen, an event that the authors showed occurred frequently in Citrus evolution.

The *Citrus* evolutionary tree is made of three main branches: The citron/Australian species, the pummelo/micrantha, and the papeda/mandarins. The Citrus ancestors were generated in a succession of speciation events occurring between 7.5 and 6.3 Ma, followed by a second radiation (5.0–3.7 Ma) that separated citrons from Australian species, and finally, Micrantha from Pummelos and Papedas from mandarins. Further radiation of Fortunella, sour and sweet oranges, lemons, and mandarins took place later (1.5–0.2 Ma).

On a finer scale, the group also identified six genes that may be general hotspots of natural genetic variation in Citrus. Advantageous mutations for adaptation were detected in four of these genes, matK, ndhF, ycf1, and ccsA. In particular, matK and ndhF were thought to help the Australian varieties adapt to hotter and drier climates whereas ccsA represents the emergence of mandarins.

"This new phylogeny based on chloroplast genomes provides an accurate description of the evolution of the genus citrus and clears up years of ambiguities derived from previous proposals based on one or a few nuclear or chloroplast genes," said corresponding author Joaquin Dopazo.

Reference

Carbonell-Caballero J, Alonso R, Ibañez V, Terol J, Talon M, Dopazo J. 2015. A phylogenetic analysis of 34 chloroplast genomes elucidates the relationships between wild and domestic species within the genus. *Citrus. Mol Biol Evol.* 32(8):2015–2035.

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doi:10.1093/molbev/msv101

Advance Access publication May 22, 2015