Researchers use phylogenetics to untangle convergent adaptation in birds

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Researchers from Skoltech and their colleagues have shown that adaptation to similar environments hardly involves similar genomic positions when species are distantly related. The team investigated

recurrent adaptations of wildlife birds' mitochondria to high altitude, migration, diving, wintering, and flight. Repeatable substitutions are rather a coincidence than adaptation, which confirms the scientific opinion that distant species "choose" different ways of similar trait evolution. The paper was published in the journal *Genome Biology and Evolution*.

If an organism wants to survive in unusual conditions, such as oxygen starvation typical for high altitudes or elevation of metabolism rate due to extreme temperatures, it has to adapt. If different species meet similar environment conditions, they will adapt independently and could even do it by same substitutions in identical genomic positions—this is called single-position molecular convergence.

"Convergent evolution is one of most fascinating topics of evolutionary biology: from a practical point of view, it helps to find particular genomic positions associated with adaptation; from a more theoretical one, it shows how repeatable evolution is. Yet detection of adaptive convergent single-position mutations is known to be hard, especially in phylogenetically distant species: scientists continue to argue about whether it is possible at all," Skoltech Ph.D. graduate Valentina Burskaia says.

Burskaia, Professor Georgii Bazykin and their colleagues designed an unusually large dataset of 415 species in which similar traits appear independently dozens of times. The dataset allowed them to examine the problem deeply, as previous attempts to detect convergent single-nucleotide mutations in phylogenetically distant species were often limited by few numbers of convergent phenotype acquisitions.

"Mitochondrial genome was chosen for the study as it is small and thus sequenced for many species, yet full of extremely important genes. Mitochondrial genes are responsible for hypoxia and metabolism level

tuning: this guided our selection of phenotypic traits of interest," Burskaia notes.

The team looked at birds who live at high altitudes and diving birds (likely to face hypoxia). To study adaptations which affect metabolism rate changes, scientists considered four groups of species: birds with outstanding flight abilities, long-distance migrants, flightless birds and wintering birds. By running powerful phylogenetic methods, where species are placed on a "tree" and coincident changes in phenotype and genotype are counted, the researchers were able to show that the majority of convergence events can be explained by random coincidences rather than adaptation.

The study, being conceptually close to recent attempts to search for single-position convergences in echolocating bats and marine mammals, confirms that evolutionary landscape at between-order distances is too different for single-position adaptive convergence.

More information: Valentina Burskaia et al, Convergent adaptation in mitochondria of phylogenetically distant birds: does it exist?, *Genome Biology and Evolution* (2021). DOI: 10.1093/gbe/evab113

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