

The genomes of peregrine and saker falcons throw lights on evolution of a predatory lifestyle

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In a collaborative study published online in *Nature Genetics*, researchers from Cardiff University, BGI, International Wildlife Consultants, Ltd., and Abu Dhabi Falcon Hospital, have completed the genome sequencing and analysis of two iconic falcons, the peregrine (*Falco peregrinus*) and saker (*Falco cherrug*). The work provides an invaluable resource for the deep understanding of the adaptive evolution in raptors and the genetic basis of their wide distribution.

Peregrine and saker falcons are widespread, and their unique morphological, physiological and behavioral adaptations make them successful hunters. The peregrine is renowned as the world's fastest animal, and the falcon is the national emblem of United Arab Emirate. In recent decades, peregrine and saker falcons have been listed as endangered due to rapid population declines caused by a wide range of factors including environmental change, overharvesting for falconry, habitat loss and bioaccumulation of pesticides (e.g. DDT, PCBs).

In this study, researchers focused on the evolutionary basis of predatory adaptations underlying peregrine and saker. They conducted [whole genome sequencing](#) and assembled the high quality ~1.2 Gb reference genomes for each falcon species. Phylogenetic analysis suggested that the two falcon species might diverged 2.1 million years ago.

Comparing with chicken and [zebra finch](#), researchers found the

transposable element composition of falcons was most similar to that of zebra finch. Large segmental duplications in falcons are less frequent than that in chicken and zebra finch, and comprise less than 1% of both falcon genomes. They also found that a gene expansion in the olfactory receptor γ -c clade in chicken and zebra finch is not present in falcons, possibly reflecting their reliance on vision for locating prey.

Observing genome-wide [rapid evolution](#) for both falcons, chicken, zebra finch and turkey, researchers found that the nervous system, olfaction and [sodium ion](#) trans-*port* have evolved rapidly in falcons, and also the evolutionary novelties in beak development related genes of falcons and saker-unique arid-adaptation related genes.

Shenkai Pan, bioinformatics expert from BGI, said, "The two falcon genomes are the first predatory bird genome published. The data presented in this study will advance our understanding of the [adaptive evolution](#) of raptors as well as aid the conservation of endangered falcon species."

Provided by BGI Shenzhen

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