

Genomic sequences of two iconic falconry birds - Peregrine and Saker Falcons- successfully decoded

December 16 2011

A group of scientists from United Kingdom (UK), China and United Arab Emirates (UAE) jointly announced the complete sequencing of peregrine and saker falcons genomes at the 2nd International Festival of Falconry held in Al Ain, UAE. The study is a part of Falcon Genome Project, launched and funded by the Environment Agency – Abu Dhabi (EAD) in this January. The results will enable biologists to better study the basic biology and genetics of falcons and provide new insights into understanding the origin and populations of these species.

Two particular species of birds, peregrine and saker falcons, are widespread but heavily exploited birds of prey that exhibit migratory habit and are popular hunting falcons commonly found in the country. In particular, the saker is the national bird of United Arab Emirate. In the past century, the two falcons have been listed as endangered species with population decline, caused by a wide range of factors including migration obstacles, environmental changes, habitat loss, use of pesticides (e.g. DDT, PCBs), among others. In the late 1990s, the peregrine has been successfully removed from the endangered species list through the increased recovery efforts, but the saker is still facing this challenge.

Since this January, researchers from UK, [China](#) and UAE have been working together to conduct the genomic studies of peregrine and saker falcons, aiming to identify the genome sequences of the two species and

enhance their future conservation to face the unforeseen challenge of the rapid changing environments and human activities. Abu Dhabi's Falcon Hospital (ADFH) provided the blood samples collected from male specimens of [peregrine](#) and saker falcons, and BGI were responsible for sequencing these samples on its large-scale next-generation sequencing platforms and producing high-quality data output. The bioinformatics analysis is conducted by the scientists from the School of Biosciences, Cardiff University (UK) and BGI.

Dr. Ning Li, CEO of BGI Europe, said, "The complete [genome](#) sequencing of the two falcons will lay a solid scientific foundation for identifying the origin and populations of falcons and accelerating the selective breeding of high-quality varieties. We believe we will make more breakthroughs in this project to help researchers better protect these endangered species."

"This study will open the door to an unparalleled understanding of falcon biology and help us to manage and conserve wild [falcon](#) stocks in the future" said Dr Andrew Dixon, Head of Research at International Wildlife Consultants Ltd (IWC).

Provided by BGI Shenzhen

Citation: Genomic sequences of two iconic falconry birds - Peregrine and Saker Falcons- successfully decoded (2011, December 16) retrieved 20 April 2024 from <https://phys.org/news/2011-12-genomic-sequences-iconic-falconry-birds.html>

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