

A genetic and evolutionary perspective on foot feathering in a domestic avian species

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Abstract

Ever since Charles Darwin published *On the Origin of Species*, scientists have been fascinated with understanding the genetic basis of the astonishing trait variation in domesticated species. Domestic chicken (*Gallus gallus domesticus*) is an important model organism to investigate the molecular basis of trait variation, along with avian and vertebrate evolution. Since its domestication in South and South-East Asia, domestic chicken has been subjected for thousands of years to human-driven selection. Because of this strong artificial selection, domestic chickens nowadays display countless phenotypic variation in morphology, physiology, and behaviour. In this study, we focus on the feathered leg phenotype (*Pit*), a controversial trait observed in many chicken breeds of divergent origin and demographic history, as well as in some raptors and boreal birds. By mean of whole-genome sequencing data we were able to unravel the molecular mechanism underlying foot feathering. Our findings show that foot feathering is caused by a complex molecular mechanism that involves a structural variant affecting *Pitx1*, a gene involved in encoding hindlimb-specific transcript factor. Moreover the haplotype analysis indicate that foot feathered individuals share the same haplotype for the forelimb-specific transcription factor *Tbx5*. Comparative genomics was further used to shed light into the evolutionary history of the phenotype. We found that foot feathering is a clear example of a trait under parallel evolution in chicken and pigeon, as these two species share similar molecular mechanisms and selection pressure for foot feathering.