

Foot feathering birds flock genetically together

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Although chicken and pigeon diverged more than 89 million years ago, a new study was able to find in both species the exact same number of loci and exact same number of genes. Credit: Chiara Bortoluzzi, Wageningen University

Like trains running on separate but parallel tracks, sometimes the forces of evolution can affect different species running along these tracks in very similar ways.

Take the evolution of a simple trait found in birds: foot feathering.

Lead researcher Chiara Bortoluzzi and colleagues at Wageningen University in the Netherlands, investigated the genetic basis of foot feathering, a phenotype that is observed in certain breeds of chicken.

"Foot feathering is an interesting case since, although it is a very recognizable trait that can be very easily selected to fixation in breeds, it is in fact not a monogenic trait, caused by a [single gene](#)," said Bortoluzzi.

The trait, known scientifically as ptilopody, can be observed in domesticated and wild avian species and is characterized by the partial or complete development of feathers on the skin of the ankles and feet.

Previous work had demonstrated that regulatory mutations in the genes Tbx5 and Pitx1 contribute to foot feathering in domesticated breeds of pigeon. Bortoluzzi wanted to investigate whether similar mutations might also be contributing to foot feathering in chickens, and if so, if also the same pathways might be altered by the same regulatory mechanisms.

Parallel evolution is known as the independent development of similar

phenotypic traits in separate but related lineages. In other words, when faced to adapt, nature can go to the same genetic toolbox to come up with new solutions.

Now, in the advanced online edition of the journal *Molecular Biology and Evolution*, Bortoluzzi and co-authors report that indeed, similar mutations in the same set of genes are affecting similar molecular pathways contributing to foot feathering in domesticated chickens.

To perform their study, they used a combination of genome wide analysis, followed by comparative genomics and gene expression analysis. DNA of 169 samples from 87 traditional chicken breeds was used for whole-genome sequencing analysis, followed by tissues and gene expression analysis.

While demonstrating that genetic variants at *Tbx5* and *Pitx1* are major contributors to foot feathering, strikingly, the authors identified a 17,000 base-pair long genetic deletion near *Pitx1*. This deletion removes the same exact region in pigeons with foot feathering. Thus, not only are the same genes involved in foot feathering phenotypes in pigeons and chickens, but the nature of the mutations is also very much the same, at least in the case of *Pitx1*.

"It is really amazing to see that, although [chicken](#) and pigeon diverged more than 89 million years ago we were able to find in both species the exact same number of loci and exact same number of genes," said Bortoluzzi. "This similarity is even more striking and remarkable as a similar deletion at one of the loci has the same outcome in regulating gene expression."

The manuscript provides strong evidences that foot feathering has evolved by parallel evolution in chickens and pigeons.

"The interesting aspect is that [foot](#) feathering can also be observed in avian wild species, including snowy owl, golden eagle, and rock ptarmigan," said Bortoluzzi. "In these wild raptor and boreal species, ptilopody has entirely evolved by natural selection. However, the occurrence of the phenotype suggests us that the same underlying [genes](#) and mutations can evolve in different species under different types of selection and selection pressure. It would be very interesting to further validate this hypothesis in future studies on both wild and domesticated avian [species](#)."

More information: Chiara Bortoluzzi et al, Parallel genetic origin of foot feathering in birds, *Molecular Biology and Evolution* (2020). [DOI: 10.1093/molbev/msaa092](#)

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