

# Inherited epigenetics produced record fast evolution

February 29 2012

---



Per Jensen, professor of ethology at Linköping University, shows how extensive changes in chickens' genome have occurred through epigenetics. Credit: Vibeke Mathiesen

The domestication of chickens has given rise to rapid and extensive changes in genome function. A research team at Linköping University in Sweden has established that the changes are heritable, although they do not affect the DNA structure.

Humans kept Red Junglefowl as livestock about 8000 years ago.

Evolutionarily speaking, the sudden emergence of an enormous variety of domestic fowl of different colours, shapes and sizes has occurred in record time. The traditional Darwinian explanation is that over thousands of years, people have bred properties that have arisen through random, spontaneous mutations in the chickens' genes.

Linköping zoologists, with Daniel Nätt and Per Jensen at the forefront, demonstrate in their study that so-called epigenetic factors play a greater role than previously thought. The study was published in the high-ranking journal *BMC Genomics*.

They studied how individual patterns of gene activity in the brain were different for modern laying [chickens](#) than the original form of the species, the red jungle fowl. Furthermore they discovered hundreds of genes in which the activity was markedly different.

Degrees of a kind of epigenetic modification, DNA methylation, were measured in several thousand genes. This is a chemical alteration of the DNA molecule that can affect gene expression, but unlike a mutation it does not appear in the DNA structure. The results show clear differences in hundreds of genes.

Researchers also examined whether the epigenetic differences were hereditary. The answer was yes; the chickens inherited both methylation and gene activity from their parentages. After eight generations of cross breeding the two types of chickens, the differences were still evident.

The results suggest that [domestication](#) has led to epigenetic changes. For more than 70 % of the genes, domesticated chickens retained a higher degree of methylation. Since methylation is a much faster process than random mutations, and may occur as a result of stress and other experiences, this may explain how variation within a species can increase so dramatically in just a short time. Nätt and Jensen's research may lead

to a review of the important foundations for the theory of [evolution](#).

**More information:** Heritable genome-wide variation of gene expression and promoter methylation between wild and domesticated chickens by Daniel Nätt, Carl-Johan Rubin, Dominic Wright, Martin Johnsson, Johan Belteky, Leif Andersson and Per Jensen. *BMC Genomics* 13:59, February 2012.

Provided by Linköping University

Citation: Inherited epigenetics produced record fast evolution (2012, February 29) retrieved 25 April 2024 from <https://phys.org/news/2012-02-inherited-epigenetics-fast-evolution.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.