

## Background

Domestication induces large physiological and behavioral changes in the animals put under that kind of selective pressure. One example is the chicken (*Gallus gallus*), that has evolved from wild Red Junglefowl to tame domesticated White Leghorns. New data indicate that the epigenome might have more of an effect than previously anticipated, and one mechanism that is of particular interest is DNA methylation.

## Aim

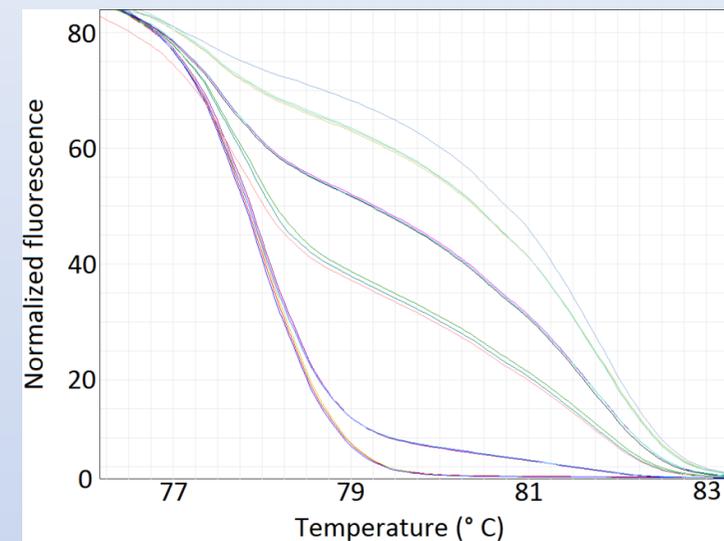
To investigate methylation differences between White Leghorn and Red Junglefowl using bisulfite conversion of DNA and methylation-sensitive high-resolution melting.

## Method

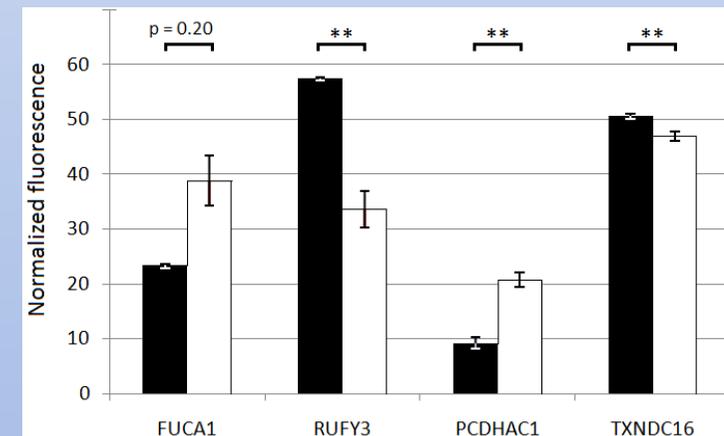
DNA was extracted from chicken brain tissue and negative and positive controls were prepared. Unmethylated cytosines were converted into to tyrosine using bisulfite treatment. Afterwards, the samples were analyzed using high-resolution melting. By melting DNA, sequence differences inherent in their genetic code can be detected as the DNA strands melt at different temperatures.

## Results

All investigated genes showed significantly different methylation, or trends towards it in both hypothalamus and cerebellum. These results compare with results from a previous study using a methylation array.



*A typical melting curve, here for the calibration series of PCDHAC1. The more methylated DNA samples will melt at higher temperatures than samples with low methylation.*



*Differences in methylation between WL (white bars) and RJF (black bars) for all four tested genes in cerebellum.*

## Conclusion

Methylation-sensitive high-resolution melting proves to be a valuable tool for methylation detection, and could here be used as confirmation of array studies. The findings indicate a larger epigenome variation in White Leghorns, which could imply that selection during domestication generated that variation and that the epialleles are not fixed.

## Future prospects

Besides looking at pure racial differences, studying specific changes in relation to stress is a field that could be expanded upon. Dietary changes affect differences in methylation, could this be interesting in relation to the feed our captive animals receive and how that makes them behave?

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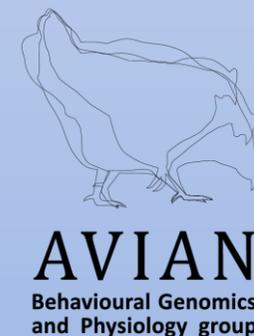
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DNA analysis of  
*Gallus gallus*:  
Do White Leghorn and Red  
Junglefowl differ in  
methylation?



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