



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



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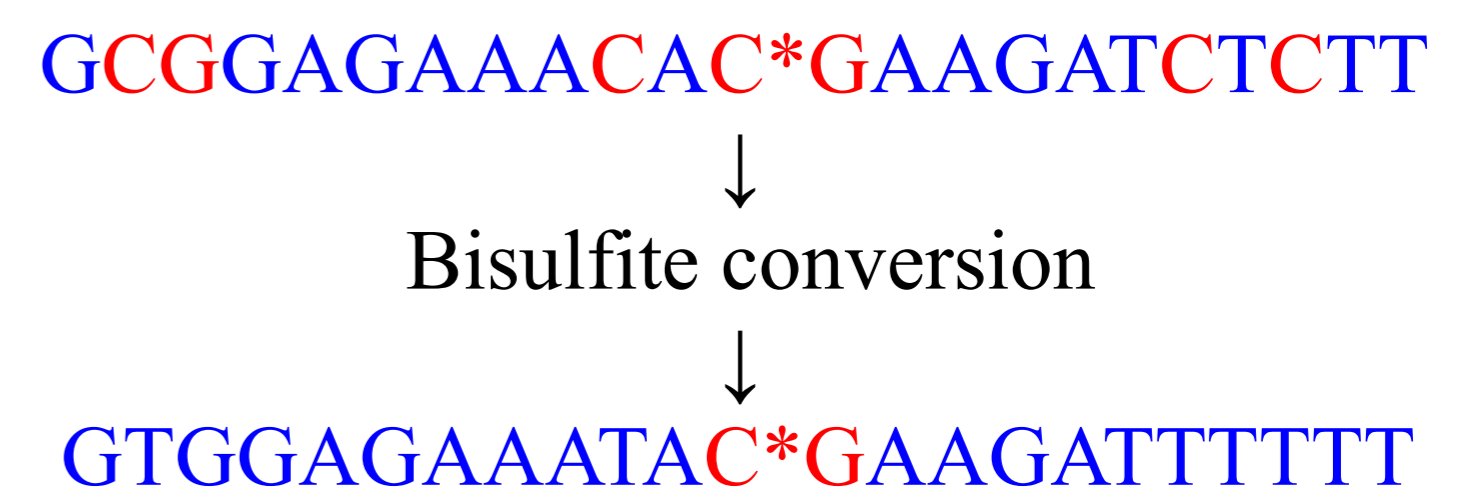
## Background

Domestication has given rise to large physiological and behavioural changes in our animals. Many genetic mechanisms behind these changes have been studied, but new focus lie on epigenetics and DNA methylation. Could these DNA modifications be stable enough to affect domestication?

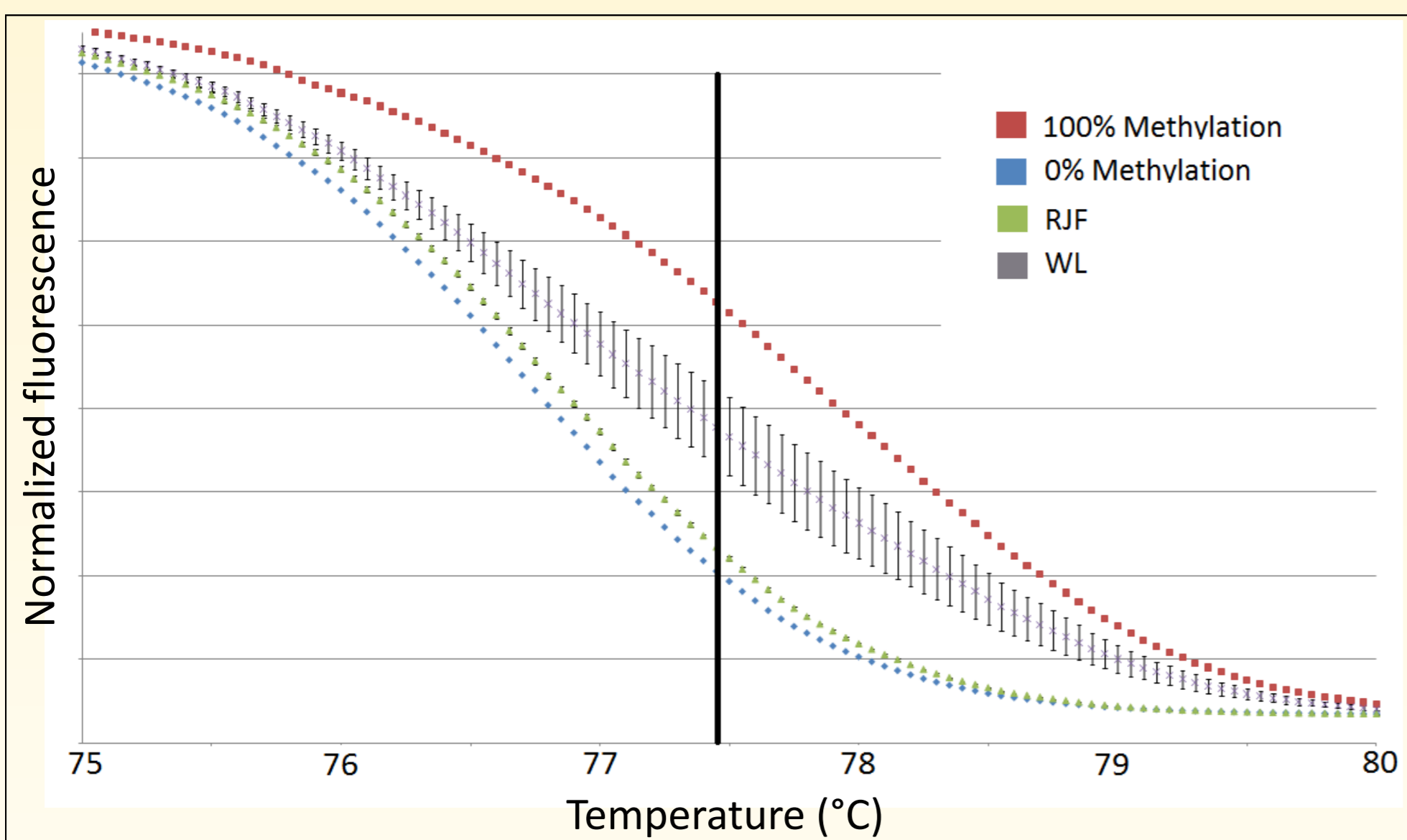
The **aim** of this study was to investigate methylation differences between White Leghorns (WL) and Red Junglefowl (RJF) using methylation-sensitive high-resolution melting (MSHRM)

## Methods

- »Gene promoter regions were selected from expression and methylation array data.
- »Bisulfite conversion of unmethylated cytosine residues.
- »MSHRM in order to detect potential nucleotide differences.

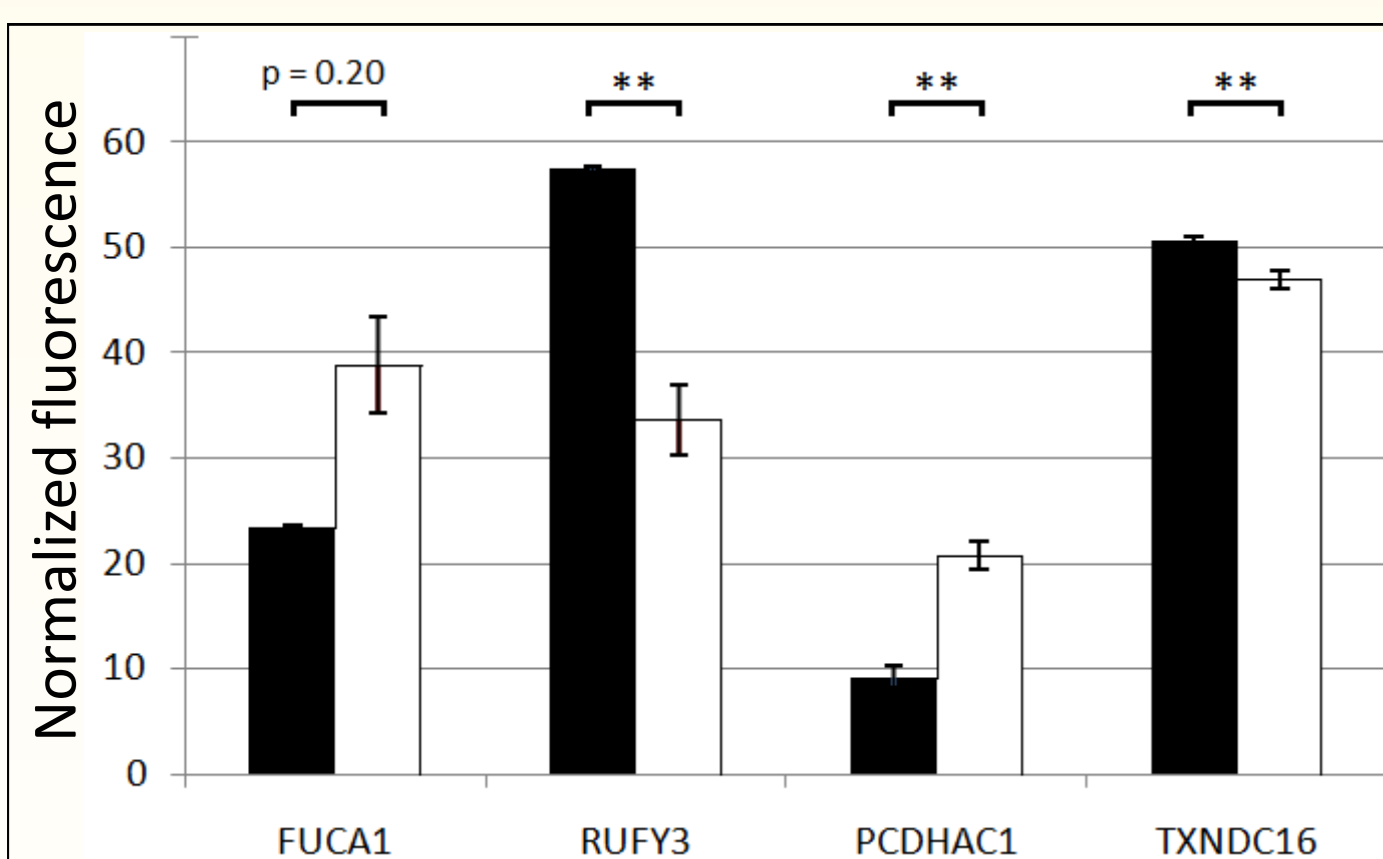


\* marks a methylation



## Results

All investigated genes showed significantly different methylation, or trends towards it, between races. White Leghorns displayed more variation than Red Junglefowl for two of the four investigated genes, which might indicate non-fixed epialleles.



↑ Melting curve for gene *FUCA1*

← Methylation differences for the four genes, in *Cerebellum*

## Conclusion

The methylation differences studied here were comparable to previous methylation array data.

The differences between RJF and WL indicate that epigenetic factors could be a part of domestication.

## Prospect

Methylations could explain some phenotypical differences, and with more generations the inheritance of such differences could be assessed. Dietary changes could also affect both behaviour and methylation, and provide a new approach in looking at the origin of behavioural changes.

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