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Single-cell DNA methylation analysis of chicken diplotene oocytes

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Motivation and Aim: Recent advancements in single-cell genomic studies have opened up a variety of possibilities for investigating developmental processes. Such techniques allowed studying of DNA methylation dynamics during oogenesis in mammals [1, 2]. However, the way in which epigenetic profile changes throughout avian oogenesis is still unknown. In this study, we conducted a bisulfite sequencing for chicken oocyte nuclei in early and late diplotene stages.

Results: Our results showed that DNA methylation level decreases on late diplotene stage. Overall methylation levels for both stages are lower in comparison to somatic cells but higher than methylation levels in sperm. We also discovered that regions with low methylation levels in early diplotene nuclei undergo even further demethylation in the later stage and these regions are related to low-methylated regions in sperm.

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References

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