

Consecutive chromatin loops in *Dictyostelium discoideum*

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Motivation and Aim: Previous analysis of Hi-C maps [1] showed the absence of TADs at 2 kb resolution, bright points of enriched contacts are visible. The loops have been noted to cover more than half of the *Dictyostelium* genome, have a median size of 20 kb, and their positions are highly conserved, with over 90 % of anchors overlap between stages. Moreover, some loops are stand-alone, but more than half of them are consecutive; their comparative analysis is the aim of this study.

Methods and Algorithms: Data were obtained from Hi-C and RNA-seq experiments at 0, 2, 5, and 8 hours after fasting induction. The public ChIP-seq and ATAC-seq datasets [2] were downloaded from Sequence Read Archive (SRA) with accession number SRP269799.

Results: It was shown that the level of expression within the loop significantly exceeds that within the boundaries of the loops, and the loops are also characterized by a convergent arrangement of genes around the bases of the loops, thus loops in *Dictyostelium* are probably formed by transcription itself similarly to what was shown previously for mouse [3]. Further analysis revealed loop heterogeneity in terms of expression levels and active chromatin marker signal.

Conclusion: Together with previous results, this suggests a possible extrusion mechanism for loop formation in *Dictyostelium discoideum*, with extrusion termination dependent on transcriptional activity. However, the regulatory role of the loops is not excluded, and additional analyzes are required to test this hypothesis.

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References

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