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# Chromatin loops are involved in spatial organization of replication in budding yeast

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*Motivation and Aim*: The loop extrusion model explains the formation of loop-like structures and topologically associating domains in the chromatin. According to the model, SMC complexes extrude DNA thread to form a loop, while two CTCF molecules occupy loop boundaries and constrain the extrusion [1]. However, CTCF-encoding gene appears only in Bilateria, while loop-like structures are observed in the older taxa [2]. Therefore, alternative mechanisms for the determination of the loop boundaries must exist.

*Methods and Algorithms*: We processed the multi-omic data for *Saccharomyces cerevisia*e to annotate positions of loops, estimate the expression rate of genes located in loop boundaries, and study the distribution of histone modifications and replication-related proteins around loops.

*Results*: The profiling of ChIP-seq signal revealed enrichment of Orc-6, Mcm-7, and Rif1 proteins near loop boundaries. All three are known to be responsible for the initialization and/or maintenance of the replication process [3, 4]. Besides, we found characteristic patterns around loop boundaries for histones modifications H3K4me1, H3K4me3, and H3K9ac which were reported to participate in resolving transcription-replication conflict in previous studies [5, 6]. BrdU-seq data demonstrated that newly synthesized DNA is likely placed inside loops rather than at the loop boundaries.

*Conclusion*: The concept of loop-like organization of replication factories in the nucleus was proposed previously by Guillou et al. [7]. Our findings support this idea indicating that the replication machinery might determine the positions of the loop boundaries. But more studies are needed to confirm positions of active replication origins and whether newly-appeared loops in late S phase are formed by extruded DNA undergoing the replication process.

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