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# Oxford Nanopore Sequencing reveals complex mechanisms of repetitive DNA propagation in *Tribolium castaneum*

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## Abstract

The beetle *Tribolium castaneum* is a worldwide pest of stored products and representative of the most species-rich animal order on earth, the Coleoptera, and is the first sequenced beetle species. As its evolution is more representative of insects than that of *Drosophila melanogaster*, *T. castaneum* has become one of the most important models in the field of insect evolution, physiology and development. Even though experiments and sequencing analyses have shown that the *T. castaneum* genome is rich in different types of repetitive DNA sequences, most remain underrepresented in previous genome assembly versions, limiting analysis of their distribution, movement and rearrangement in the genome. The main obstacle to uncovering these properties of repetitive DNA is the relatively short read length used in conventional genome assembly pipelines. Therefore, we combined the results of Oxford Nanopore long-read sequencing with the existing reference genome to generate a new, high-quality genome assembly (TcasONT) of the model beetle *T. castaneum*. The resulting genome assembly is enriched by 50 Mb in the repetitive genome part, which corresponds to 25% of the estimated genome size of *T. castaneum*. Therefore, we utilized the expanded assembly to perform global and in-depth analyses of different classes of transposable elements (TEs), the abundant non-(peri)centromeric satellite DNA (satDNA) and their relationships. Although we found that TEs and satDNA often do not overlap, we showed there are specific cases where certain satDNA variants fuse with TEs to create a new repeat unit that can propagate independently in the genome or possibly by extrachromosomal circular DNA. Additionally, we have confirmed that the presence of both TEs and satDNA is not restricted to specific non-coding parts of the genome but rather propagates throughout euchromatin, suggesting an efficient mechanism by which repetitive DNA can have direct impact on gene regulation.

**Keywords:** oxford nanopore sequencing genome assembly

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