Improvement of the assembly of heterozygous genomes of non-model organisms, a case study of the genomes of two Spodoptera frugiperda host strains
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Improvement of the assembly of heterozygous genomes of non-model organisms, a case study of the genomes of two Spodoptera frugiperda host strains

Motivation: Some heterozygous regions have a significant divergence between the two haplotypes and the assembly process can lead to the construction of two different contigs, instead of one consensus sequence.

Objective: Set up a strategy to detect and correct false duplications in already-built assemblies.

APPLICATION: Spodoptera frugiperda genomes

Comparison of 2 Spodoptera strains: the genome of the Spodoptera frugiperda “rice variant” has been sequenced and assembled with Platanus, and annotated with the help of Maker. The comparison of the two draft sequences leads to the identification of about 16,000 pairs of orthologous genes, and thousands of segmental rearrangements (deletions, duplications or inversions).