Genome and transcriptome analysis of the beet armyworm *Spodoptera exigua* reveals targets for pest control

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Supplementary files and descriptions provided via the Digital Repository Dryad

Supplementary Archive 1.

This archive contains all metadata of the genome project of *Spodoptera exigua* [Supplementary_Archive_1.zip: 271MB, md5sum:fff004653c3d2f19db4c23eb19950100]

- Spodoptera_exigua_assembly04.gff3: annotations and evidence alignments in GFF3 format.
- Spodoptera_exigua_assembly04.all.maker.transcripts.fasta: transcript sequences for MAKER produced gene annotations on all contigs
- Spodoptera_exigua_assembly04.all.maker.proteins.fasta: protein sequences for MAKER produced gene annotations on all contigs
- Spodoptera_exigua_assembly04.all.maker.augustus_masked.proteins.fasta: fasta file of ab-inito predicted protein sequences from program, masked means they filter/masking out the repetitive elements.
- Spodoptera_exigua_assembly04.all.maker.augustus_masked.transcripts.fasta: a fasta file of ab-inito predicted transcript sequences from program

Supplementary Archive 2.

This archive contains all files relevant to the phylogenetic analyses and the individual gene tree analyses. [Supplementary_Archive_2.zip: 12.1MB, md5sum:45f20e74f73824abf69b1cbd27bd6fae]

- FcC_supermatrix.fas: amino-acid alignment file comprising single copy complete BUSCOs for *S. exigua* and another 37 lepidopteran genome datasets
- Modelsel_.best_scheme.nex: corresponding partition file for the alignment file "FcC_supermatrix.fas" including selected models
- MG7_large_alignment.phy: amino-acid alignment file comprising the mg7 sequences of the extended dataset
- MG7_small_alignment.phy: amino-acid alignment file comprising the mg7 sequences of the reduced dataset
- Nuclearpore_alignment.phy: amino-acid alignment file comprising the nuclear pore complex sequences
- REPAT_alignment.phy: amino-acid alignment file comprising the REPAT sequences of the extended dataset
- REPAT_BetaRepat_alignment.phy: amino-acid alignment file comprising the βREPAT sequences of the reduced dataset
- Trypsins_alignment.phy: amino-acid alignment file comprising the trypsin sequences

Supplementary Archive 3.

This archive contains scripts / codes which have been used for assembly of the genome of *Spodoptera exigua* and the associated GO analysis [Supplementary_Archive_3.zip: 65KB, md5sum: 2a95fd3abb6b4df82bf8f8256b944e37]

- SEA program (Future Genomics Technologies BV, Leiden, The Netherlands) (Jansen et al. 2017)*
- Tulip v. 1.0.0 (Future Genomics Technologies BV, Leiden, The Netherlands) (Jansen et al. 2017)*
- R script for summarizing GO slim categories

*Jansen HJ, Liem M, Jong-Raadsen SA, Dufour S, Weltzien FA, Swinkels W, Koelewijn A, Palstra AP, Pelster B, Spaink HP et al. 2017. Rapid de novo assembly of the european eel genome from nanopore sequencing reads. Sci Rep. 7(1):7213.