Data Article

Complete mitogenome data from a European specimen of *Ostrinia scapulalis* (Walker, 1859) (Lepidoptera, Pyraloidea, Crambidae, Pyraustinae)

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**ABSTRACT**

We present an assembly and annotation of the mitogenome of a European specimen of the Adzuki bean borer, *Ostrinia scapulalis* (Walker, 1859). The data were obtained by combining WGS data issue of a de novo and a previously published sequence library (Gschloessl et al., 2018). We also provide the phylogenetic positioning of the mitogenome within the *Ostrinia* genus, the *Crambidae* family and with more distant Lepidoptera species.

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Specifications Table

| Subject          | Insect Science                                      |
|------------------|-----------------------------------------------------|
| Specific subject area | Lepidoptera, Crambidae, Mitogenomics               |
| Type of data     |                                                     |

- FASTQ: DNA sequence reads
- FASTA: mitochondrial genome assembly
- GFF: mitogenome gene annotations
- TABLE: gene annotations, base composition, Lepidoptera species used for phylogenetic analysis
- FIGURE: mitogenomic circular map, AT-rich region sequence, phylogenetic tree

How data were acquired
Whole-genome shotgun sequencing on Illumina NextSeq 500 v2 platform using the paired-end protocol (2 × 150 base pairs (bp)).

Data format
Raw sequence reads and analysed (assembled and annotated) mitogenome.

Parameters for data collection
Genomic DNA was extracted from one Ostrinia scapulalis larva using the DNeasy Tissue Kit from Qiagen (Hilden, Germany). A 2 × 150bp shot-gun paired-end library with an insert size of 300bp was generated and sequenced by LGC Genomics GmbH (Berlin, Germany) on an Illumina NextSeq 500 v2 platform.

Description of data collection
The Ostrinia scapulalis mitogenome was assembled with MITObim v1.9. Genomic regions were annotated with MITOS v2. The circular mitochondrial genome map was generated with OGDRAW. Multiple sequence alignments were generated separately for each protein-coding and rRNA gene with MAFFT v7.471. Phylogenetic trees were built on the concatenated gene alignments with PHYML v3.0 and MrBayes v3.2.7a and visualized with FigTree v1.4.4.

Data source location
Samples were collected in 2015 near Abbeville/France (50°8’13.57”N; 1°50’23.62”E).

Data accessibility
Repository name: NCBI BioProject
Data identification number: PRJNA637835
Direct URL to data: http://www.ncbi.nlm.nih.gov/bioproject/637835
Repository name: NCBI Genbank
Data identification number: MT801073
Direct URL to data: http://www.ncbi.nlm.nih.gov/nuccore/MT801073

Value of the Data

- This data represents the mitogenome of a European specimen of Ostrinia scapulalis.
- The data can benefit to researchers working on Lepidoptera evolution and higher systematics.
- The present data can be used for phylogenetic studies of Lepidoptera mitogenomes especially for getting deeper insights in diversification dynamics of Ostrinia species.

1. Data Description

The O. scapulalis (hereafter named OSCA) mitogenome had a size of 15,305 bp and an A+T content of 80.9%. All 38 genetic regions commonly known for arthropod mitogenomes [2] were identified (Supplementary GFF annotation file): 13 protein-coding genes, 22 tRNA and 2 rRNA (12S rRNA and 16S rRNA) genes, and one A+T-rich control region. The gene order and the composition of start on stop codons of the protein-coding genes corresponded to those observed for other Ostrinia spp. [3,4] and Crambidae [5] mitogenomes. Fifteen intergenic spacer regions (see Table 1: positive intergenic nucleotide values) of a total length of 341 bp were identified.
Table 1
Gene features of the O. scapulalis mitogenome.

| Gene (anticodon) | Start | Stop | Strand | Size | Intergenic nucleotides | Start/stop codon |
|------------------|-------|------|--------|------|------------------------|------------------|
| trnM(cac)        | 1     | 68   | +      | 68   | –1                     |                  |
| trnl(gat)        | 68    | 135  | +      | 68   | 0                      |                  |
| trnQ(ttg)        | 136   | 204  | –      | 69   | 92                     |                  |
| ND2              | 297   | 1289 | +      | 993  | –15                    | ATT/TAA          |
| trnW(tca)        | 1275  | 1341 | +      | 67   | –8                     |                  |
| trnC(gca)        | 1334  | 1398 | –      | 65   | 0                      |                  |
| trnG(gta)        | 1399  | 1465 | –      | 67   | 8                      |                  |
| COX1             | 1474  | 3009 | +      | 1536 | –5                     |                  |
| trnL2(taa)       | 3005  | 3071 | +      | 67   | 48                     |                  |
| COX2             | 3120  | 3788 | +      | 669  | –35                    | ATA/TAA          |
| trnK(ttt)        | 3754  | 3824 | +      | 71   | –1                     |                  |
| trnD(gtc)        | 3824  | 3892 | +      | 69   | 0                      |                  |
| ATP8             | 3893  | 4054 | +      | 162  | –7                     | ATA/TAA          |
| ATP6             | 4048  | 4722 | +      | 675  | –1                     | ATG/TAA          |
| COX3             | 4722  | 5513 | +      | 792  | 2                      | ATC/TAA          |
| trnG(tcc)        | 5516  | 5582 | +      | 67   | 0                      |                  |
| ND3              | 5583  | 5936 | +      | 354  | 10                     |                  |
| trnA(tgc)        | 5947  | 6013 | +      | 67   | –1                     |                  |
| trnK(tgg)        | 6013  | 6077 | +      | 65   | –1                     |                  |
| trnN(gtt)        | 6077  | 6143 | +      | 67   | 2                      |                  |
| trnS1(gct)       | 6146  | 6211 | +      | 66   | 1                      |                  |
| trnE(ttc)        | 6213  | 6279 | +      | 67   | –2                     |                  |
| trnF(gaa)        | 6278  | 6346 | –      | 69   | –17                    |                  |
| ND5              | 6330  | 8057 | –      | 1728 | 24                     | ATA/TAA          |
| trnH(gtg)        | 8082  | 8148 | –      | 67   | –1                     |                  |
| ND4              | 8148  | 9488 | –      | 1341 | 7                      | ATG/TAA          |
| ND4L             | 9496  | 9739 | –      | 294  | 9                      | ATG/TAA          |
| trnT(tgt)        | 9799  | 9865 | +      | 67   | 0                      |                  |
| trnP(tgg)        | 9866  | 9930 | –      | 65   | 32                     |                  |
| ND6              | 9963  | 10,469 | +      | 507  | –1                     | ATA/TAA          |
| CYTB             | 10,469 | 11,817 | +      | 1149 | –1                     | ATG/TAA          |
| trn52(tga)       | 11,617 | 11,684 | +      | 68   | 38                     |                  |
| ND1              | 11,723 | 12,661 | –      | 939  | 1                      | ATG/TAG          |
| trnL1(tag)       | 12,663 | 12,730 | –      | 68   | 21                     |                  |
| 16S rRNA         | 12,752 | 14,023 | –      | 1272 | 46                     |                  |
| trnV(tac)        | 14,070 | 14,135 | –      | 66   | 0                      |                  |
| 12S rRNA         | 14,136 | 14,914 | –      | 779  | 0                      |                  |
| A+T-rich region  | 14,915 | 15,305 | –      | 391  | 0                      |                  |

The gene names, the coordinates, the orientation, the size, the gene overlaps/intergenic spacers (column 6) and the start/stop codons of the O. scapulalis mitogenome are listed.

Table 2
Base composition and skewness indices for each specific gene region of the O. scapulalis mitogenome.

| Type               | Size [bp] | A%  | G%  | T%  | C%  | A+T% | AT skew | GC skew |
|--------------------|-----------|-----|-----|-----|-----|------|---------|---------|
| Entire mitogenome  | 15,305    | 41.7| 7.7 | 39.2| 11.4| 80.9 | 0.031   | –0.197  |
| Protein-coding genes| 11,139    | 34.5| 10.8| 44.9| 9.9 | 79.4 | –0.131  | 0.045   |
| tRNA               | 1480      | 41.7| 10.8| 39.9| 7.6 | 81.6 | 0.022   | 0.172   |
| rRNA               | 2051      | 41.7| 9.9 | 43.4| 4.9 | 85.1 | –0.021  | 0.338   |
| A+T-rich region    | 391       | 42.7| 2.0 | 49.6| 5.6 | 92.3 | –0.075  | –0.467  |

which ranged from 1 to 92 bp with the longest being located between the trnQ and ND2 genes. Furthermore, region overlaps (see Table 1: negative intergenic nucleotide values) of 1 to 35 bp could be observed for fifteen gene pairs. More annotation details can be found in Table 1 and are also represented as mitogenome map in Fig. 1. Base compositions, AT and GC skews to each genomic region type are shown in Table 2. The tRNA secondary structures showed the typical
Fig. 1. Map of the *Ostrinia scapulalis* mitogenome generated with OGDRAW. Annotated genes are highlighted.

clover-leaf except for trnS1 in which the dihydouridine (DHU) arm was replaced by an unstable loop (Supplementary Fig. 1). The characteristics of the A+T-rich region are shown in Fig. 2. Finally, we built a phylogeny based on 63 lepidopteran mitogenomes (including the generated OSCA mitogenome, Table 3), with a focus on Pyraloidea (Fig. 3 and Supplementary Fig. 2).

2. Experimental Design, Materials and Methods

2.1. DNA sampling and sequencing

*Ostrinia scapulalis* larval samples were collected in 2015 from a stem of mugwort in North of France (50° 8’13.57″N; 1°50’23.62″E). Genomic DNA was extracted from one larva using the DNeasy Tissue Kit from Qiagen (Hilden, Germany) according to the manufacturer’s protocol. Subsequently, a 2×150 bp shot-gun paired-end library with an insert size of 300 bp, was generated using the DNA extract and sequenced by LGC Genomics GmbH (Berlin, Germany) on
Table 3

Lepidoptera mitogenomes which were used to build the phylogenetic trees. For *Ostrinia* spp. the countries are also given in which the samples were taken.

| Super-family       | Family     | Subfamily      | Species              | Genbank no. |
|--------------------|------------|----------------|----------------------|-------------|
| Bombycoidea        | Bombycidae | Bombycinae     | *Bombyx mori*        | NC_002355  |
| Bombycoidea        | Saturniidae | Saturninae    | Acias selene         | NC_018133  |
| Bombycoidea        | Sphingidae | Sphinginae     | Manduca sexta        | NC_010266  |
| Geometroidea       | Geometridae | Ennominae     | Biston panterinaria  | NC_020804  |
| Geometroidea       | Geometridae | Ennominae     | Phthoronidia atrilineata | NC_010522 |
| Noctuoidea         | Erebidae   | Lymantriinae  | Lymantria dispar     | NC_012893  |
| Noctuoidea         | Noctuidae  | Noctuinae     | Spodoptera frugiperda| NC_027836  |
| Noctuoidea         | Notodontidae | Thaumetopoinea | *Ochrogaster lunifer* | NC_011128 |
| Papilionoidea      | Nymphalidae | Danainae      | Danaus plexippus     | NC_021452  |
| Papilionoidea      | Nymphalidae | Nymphalinae   | Melitaea cinxia      | NC_018029  |
| Papilionoidea      | Papilionidae | Papilioninae  | Papilio machaon      | NC_018047  |
| Pyraloidea         | Crambidae  | Crambinae     | Chilo auricilius     | NC_024644  |
| Pyraloidea         | Crambidae  | Crambinae     | Chilo sacchariphagus | NC_029716  |
| Pyraloidea         | Crambidae  | Crambinae     | Chilo suppressalis   | NC_015612  |
| Pyraloidea         | Crambidae  | Crambinae     | Diatraea saccharalis | NC_013274  |
| Pyraloidea         | Crambidae  | Crambinae     | Pseudargyria interruptella | NC_029751 |
| Pyraloidea         | Crambidae  | Evergestinae  | Evergestis junctalis | NC_030509  |
| Pyraloidea         | Crambidae  | Nymphalinae   | Ephesia interruptalis| NC_021756  |
| Pyraloidea         | Crambidae  | Nymphalinae   | Paracycroma distinctalis | NC_023471 |
| Pyraloidea         | Crambidae  | Nymphalinae   | Paracycroma prodigalis| NC_020094  |
| Pyraloidea         | Crambidae  | Nymphalinae   | Parapoxys crinalis   | NC_031151  |
| Pyraloidea         | Crambidae  | Pyraustinae   | Loxostege stictalis  | NC_027174  |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia furnacalis (China) | NC_003368 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia furnacalis (China) | MN793323 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia furnacalis (China) | MN747041 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia nubilalis (USA) | NC_003367 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia nubilalis (China) | MN793322 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia palustralis (South Korea) | MH574940 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia scapulalis (France) | MT810173 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia scapulalis (China) | NC_048887 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Ostrinia zealis (China) | NC_048888 |
| Pyraloidea         | Crambidae  | Pyraustinae   | Pyrausta despicata    | NC_046050  |
| Pyraloidea         | Crambidae  | Schoenobiinae | Sciraphaga incertula | NC_031329  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Cnaphalocrocis medinalis | NC_015985 |
| Pyraloidea         | Crambidae  | Spilomelinae  | Cydalima perspectalis | NC_042150 |
| Pyraloidea         | Crambidae  | Spilomelinae  | Dichrococ punctiferalis | NC_021389 |
| Pyraloidea         | Crambidae  | Spilomelinae  | Glyphodes pyloalis   | NC_025933  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Glyphodes quadrimaculalis | NC_022699 |
| Pyraloidea         | Crambidae  | Spilomelinae  | Haritolodes derogata | NC_029202  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Maruca testulalis    | NC_024283  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Maruca vitrata       | NC_024099  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Nomophila noctuella  | NC_025764  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Omiodes indicata     | NC_039177  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Palpita hypohomalia  | NC_039632  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Patania inferior     | NC_040973  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Pycnarnac lactiferalis| NC_033540 |
| Pyraloidea         | Crambidae  | Spilomelinae  | Spoladea recurvalis  | NC_027443  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Tyspanodes hylaps    | NC_025569  |
| Pyraloidea         | Crambidae  | Spilomelinae  | Tyspanodes striata   | NC_030510  |
| Pyraloidea         | Pyralidae  | Epipaschiniina | Lista haraldusalis   | NC_024535  |
| Pyraloidea         | Pyralidae  | Gallerinae    | Corycyra cephalonica | NC_016866  |
| Pyraloidea         | Pyralidae  | Gallerinae    | Galleria mellonella  | NC_028532  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Amyelois transiliata | NC_028443  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Ephesia elutella     | NC_039716  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Ephesia kuehniella   | NC_022476  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Euzophera pyriella   | NC_037175  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Meroperta pravella   | NC_035242  |
| Pyraloidea         | Pyralidae  | Phycitinae    | Plodia interpunctella| NC_027961  |
| Pyraloidea         | Pyralidae  | Pyralinae     | Endotrichia consocia | NC_037501  |
| Pyraloidea         | Pyralidae  | Pyralinae     | Hypsopygia regina    | NC_030508  |
| Pyraloidea         | Pyralidae  | Pyralinae     | Orthopygia glaucinalis| NC_047304 |
| Pyraloidea         | Pyralidae  | Pyralinae     | Pyralis farinalis     | NC_047303  |
an Illumina NextSeq 500 v2 platform. In total, 372,260,856 genomic reads were generated of which 306,203,188 remained after quality trimming with Trimmomatic v0.36 [6] (specific parameters were: PE -pred33, ILLUMINACLIP:$ADAPTERF:2:26:10 HEADCROP:5 LEADING:26 TRAILING:26 SLIDINGWINDOW:5:28 MINLEN:30, with $ADAPTERF containing all Illumina adapters and their reverse complement, respectively).

2.2. Mitogenome assembly and feature analyses

The OSCA mitogenome was assembled in two steps as follows. First, the scaffolds of a previously published O. scapulalis genome draft [1], OSCA v1.2 (BioProject PRJNA390510), were searched for putative mitochondrion sequences by using blastn v2.2.28 [7] against the mitochondrial genome sequence of the closely related Asian corn borer Ostrinia furnacalis (Guenée) (NCBI
accession number NC_003368). Genome scaffolds with high quality mitochondrial hits were selected and assembled by LGC with CAP3 v2013 [8] into a mitogenome sequence of 14,864 bp. In a second step, this draft mitogenome was refined using MITObim v1.9 [9] (using the default k-mer size of 31 bp and the –pair parameter) and the Trimomatic-cleaned paired-end Illumina reads. Gene identification as well as tRNA structure prediction were carried out on the MITOS web server v2 [10], using as reference set ‘RefSeq 81 Metazoa’ and the genetic code ‘5’ for invertebrates. Nucleic base contents were determined with the wordcount program of the EMBOSS toolkit v6.6.0.0 [11]. AT/ GC skewness indices describing the genomic compositional asymmetry of a mitogenome or specific sequence region were calculated as: AT skew = [A−T] / [A+T] and GC skew = [G−C] / [G+C], where each base letter represents the respective base count. The circular map of the OSCA mitogenome was generated with the web tool OGDRAW v1.3.1 [12].

2.3. Phylogenetic analyses

In order to perform comparative analyses of O. scapulalis with other Lepidoptera the nucleotide sequences of the 13 PCGs and 2 rRNA genes of 63 mitogenomes - comprising 59 Lepidoptera species – (Table 3) were downloaded from the NCBI ‘nucleotide’ database (https://www.ncbi.nlm.nih.gov/nuccore, May 2020). Our taxon sampling was focused on the superfamilies Pyraloidea, encompassing 34 species belonging to the Crambidae (including O. scapulalis) and 13 species belonging to the Pyralidae. Regarding Ostrinia spp., we included in total nine mitogenomes belonging to five Ostrinia species. As outgroups we used 12 representative species of the lepidopteran superfamilies Bombycoidea, Geometroidea, Noctuoidea and Papilionoidea; based on the comprehensive study of Wahlberg et al. [13], we used the three Papilionoidea representatives to root our trees. The PCG and rRNA nucleotide sequences of all species were grouped into 15 gene–specific sequence sets. Each gene set was in separate globally aligned with the program MAFFT v7.471 [14] by applying the Needleman-Wunsch algorithm (mafft-ginsi for PCGs and mafft-qinsi for rRNA sequences) with a maximum of 1000 refinement iterations (–maxiterate 1000), leaving the other parameters set to their default value. Subsequently, for each species all gene–specific alignments were concatenated following the same gene order using in-house Python and Perl scripts.

Phylogenetic trees were generated with the PHYML web server v3.0 [15] and a local installation of MrBayes v3.2.7a [17]. PHYML was run using the Smart Model Selection [16] option with the Akaike Information Criterion and the tree searching method BIONJ being set and by applying 1000 bootstraps. Concerning the MrBayes analysis, a separate partition was set for each gene. For each partition the evolutionary model was set to the GTR substitution model (nst=6) with gamma-distributed rate variation (rates=invgamma) across sites and a proportion of invariable sites (GTR +I +Gamma). The standard nucleotide substitution model (nucmodel=4by4) was chosen and priors settings were left as by default. Trees were built using 100,000 samples (ngen=1,000,000, samplefreq=10). Further parameters were: printfreq=100, diagnfreq=1000, nchains=4, savebrlens=yes, starttree=random, startparams=reset, outgroup pamac (corresponding to Papilio machaon), sump burnin=25,000, sumt burnin=25,000. The phylogenetic tree was visualized using the program FigTree v1.4.4 [18].

CRediT Author Statement

BG conceived the study. RS led the ANR research program on European Ostrinia genomics. RS, PA, SN collected the samples in the field. SN, PA prepared the samples and extracted the DNA. BG was responsible for the bioinformatics analyses, i.e. improvement of the mitogenome assembly, annotation, characterization, comparative analyses. BG and GJK did the phylogenetic analyses. All authors wrote and approved the manuscript.
Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

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Supplementary Materials

Supplementary material associated with this article can be found, in the online version at doi:10.1016/j.dib.2020.106427.

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