**Supplementary Information**

**Τhe complete mitochondrial genome of *Bactrocera carambolae* (Diptera: Tephritidae): genome description and phylogenetic implications**

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**Supplementary Table S1.** List of the complete mitogenome sequences used in the present study. Species names, abbreviation used, GenBank accession numbers and references are given.

|  |  |  |
| --- | --- | --- |
| Species | GenBank  Accession number | Reference |
| *Bactrocera dorsalis* | NC\_008748 | [53] |
| *Bactrocera dorsalis* | DQ917577 | *-* |
| *Bactrocera dorsalis* | KM244662 | [93] |
| *Bactrocera dorsalis (B. `syn. papayae’)* | DQ917578 | *-* |
| *Bactrocera dorsalis (B. `syn. philippinensis'*) | DQ995281 | *-* |
| *Bactrocera dorsalis (B. `syn. invadens’)* | KX534207 | [82] |
| *Bactrocera dorsalis* | KT343905 | Present study |
| *Bactrocera dorsalis (B. `syn. invadens’)* | MN104220 | Present study |
| *Bactrocera dorsalis (B. `syn. philippinensis'*) | MG916968 | Present study |
| *Bactrocera carambolae* | NC\_009772 | *-* |
| *Bactrocera carambolae (M5)* | MN104218 | Present study |
| *Bactrocera carambolae (M8)* | MN104219 | Present study |
| *Bactrocera carambolae (S2)* | MN104217 | Present study |
| *Bactrocera correcta* | NC\_018787 | [83] |
| *Bactrocera zonata* | NC\_027725 | [54] |
| *Bactrocera arecae* | NC\_028327 | [55] |
| *Bactrocera tryoni* | NC\_014611 | [52] |
| *Bactrocera melastomatos* | NC\_029467 | [56] |
| *Bactrocera latifrons* | NC\_029466 | [56] |
| *Bactrocera umbrosa* | NC\_029468 | [56] |
| *Bactrocera ritsemai* | NC\_037723 | [62] |
| *Bactrocera limbifera* | NC\_037722 | [63] |
| *Bactrocera oleae* | NC\_005333 | [51] |
| *Bactrocera biguttula* | MK293875 | [92] |
| *Bactrocera minax* | NC\_014402 | [81] |
| *Bactrocera tsuneonis* | NC\_038164 | [64] |
| *Ceratitis capitata* | NC\_000857 | [94] |

**Supplementary Table S2.** List of the primers used for the amplification of the mitogenomesof the *Bactrocera carambolae* and *Bactrocera dorsalis* specimens.Numbers in primer names indicate the exact primer position in the *B. dorsalis* mtDNA sequence (NC\_008748). F: forward primer, R: reverse primer.

|  |  |  |
| --- | --- | --- |
| **Primer name** | **Sequence 5′-3′** | **Amplicon size** (bp) |
| **Bd 317 F**  **Bd 846 R** | GAACCCTAATCACTGTATCCTC | 530 |
| TTCACTTGCTTGTATGGCTGC |
| **Bd 757 F**  **Bd 1623 R** | GACTTAATCAAACTTCTCTGCG | 867 |
| GATGTTCCTACTATTCCTGCTC |
| **Bd 1507 F**  **Bd 2293 R** | GTCTATCGCCTAAACTTCAGC | 787 |
| GGAAATTATCCCGAATCCTGG |
| **Bd 2160 F**  **Bd 3056 R** | CAGACCGAAACTTAAATACTTCC | 897 |
| GAGGTAGTTCTGAATAACTGTG |
| **Bd 2850 F**  **Bd 3656 R** | CAGACTATCCAGATGCTTACAC | 807 |
| CTACCTTTACACCTAAGGCTG |
| **Bd 3518 F**  **Bd 4251 R** | GAATTAGCAACAGACGGATTCC | 734 |
| CGTGAGGGTATTAATCAGTAGG |
| **Bd 3968 F**  **Bd 4650 R** | TTTGGTGCCTCAAATAGCCC | 683 |
| AGAGTAAGTAATAAATGTCCTGC |
| **Bd 4508 F**  **Bd 5137 R** | GCTCACCTAGTACCTCAAGGAACC | 630 |
| CAATGGCTGGAGATAAACTTCTGTGG |
| **Bd 5014 F**  **Bd 5814 R** | CTACACACCTTACCTGTAACATTAGG | 801 |
| GTGAAGAAGACTTGGGATCAAATCC |
| **Bd 5627 F**  **Bd 6439 R** | GACTTCCAATCATAAGGTCTAC | 812 |
| GCTTAAAATAGAGCATAACACTG |
| **Bd 6220 F**  **Bd 7014 R** | CTCCAATTAAGGAAGTATGACG | 795 |
| GACTGTCTGTTATTCTTTTCGG |
| **Bd 6906 F**  **Bd 7746 R** | TATACCTCGCAATATAACTCAACC | 841 |
| TAATCGGATTGGGGATGTGG |
| **Bd 7554 F**  **Bd 8350 R** | TATAGCAGCAGGTAATCAAGAAG | 797 |
| TTAGAGGGGGTAAGATTCGTG |
| **Bd 8198 F**  **Bd 8978 R** | AACCTCATTTCATTGACACCAC | 781 |
| CCTAAGGCTCATGTTGAAGC |
| **Bd 8774 F**  **Bd 9681 R** | AAGCCTTTAAATCAGTTTGACGC | 908 |
| GAGTATGTGAAGGTGCTTTGG |
| **Bd 9533 F**  **Bd 10317 R** | CACCATTCATAAAACAAATAGGAC | 785 |
| AATGCGGCAATTAGTGTAGTAG |
| **Bd 10073 F**  **Bd 10859 R** | ATAAATCACCCCTTAGCAATAGG | 787 |
| GATCCGTAGTAGATCCCACG |
| **Bd 10711 F**  **Bd 11431 R** | GCAGACATCAACTTAGCATTC | 721 |
| AGAGGACTAGGGCAATTACC |
| **Bd 11204 F**  **Bd 12077 R** | ACCCCTACTTCTCATACAAGG | 874 |
| GTGAATCGGAGTTAGTTTCTGG |
| **Bd 11861 F**  **Bd 12620 R** | TAACGAAAACGAGGTAAAGTCCC | 760 |
| TTTTGGAACGGAAGGTTCTAGG |
| **Bd 12529 F**  **Bd 13213 R** | CGCATCACAAAAAGGTTGAGG | 685 |
| AGACGAGAAGACCCTATAAATC |
| **Bd 13004 F**  **Bd 13929 R** | TCTCCAAAAAAATTACGCTGTTATCCC | 926 |
| ATTGTACCTTGTGTATCAGGGTTTATC |
| **Bd 13621 F**  **Bd 14518 R** | GCTAATTCTAAGCATACATTTTATATTACC | 898 |
| CTGTAATTGATAATCCACGATGAACC |
| **Bd 14226 F**  **Bd 14801 R** | ACCTTAATAGCAAGAGCGACG | 576 |
| CTAAATTTGTGCCAGCAGCC |
| **Bd 14605 F**  **Bd 15135 R** | CATTTTAAATAATAGGGTATCTAATCCTAG | 531 |
| TTAATGAAAAACGGTATATTACTTAGGG |
| **Bd 14894 F**  **Bd 15850 R** | AGCAAAAATACACGCAAAAACTTAC | 957 |
| TTTATACTTACATTTAAGTGGTGTATG |
| **Bd 15706 F**  **Bd 472 R** | AATTCTCGGAAATGTCTATATTGG | 682 |
| CTGCTGAGGCTATGGCTTG |

**Supplementary Table S3.** List of the GenBank accession numbers of the *COI* and *ND4* partial sequences from *B. dorsalis* and *B. carambolae* used in the present study.

|  |  |  |
| --- | --- | --- |
| Sample id\* | GenBank Accession number | |
| ***COI*** | ***ND4*** |
| Bd 189 | KC446059 | KC446176 |
| Bd 200 | KC446064 | KC446181 |
| Bd 209 | KC446069 | KC446186 |
| Bd 224 | KC446074 | KC446191 |
| Bd 228 | KC446078 | KC446195 |
| Bd 400 | JX099639 | KC446216 |
| Bd 406 | JX099643 | KC446219 |
| Bd 411 | KC446099 | KC446220 |
| Bd 412 | KC446100 | KC446221 |
| Bd 416 | KC446103 | KC446224 |
| Bd 419 | KC446104 | KC446225 |
| Bd 580 | JX099650 | KC446226 |
| Bd 594 | JX099664 | KC446234 |
| Bd 744 | JX099708 | KC446239 |
| Bd 757 | JX099720 | KC446252 |
| Bd 771 | JX099726 | KC446258 |
| Bd 775 | JX099730 | KC446262 |
| Bd 798 | KC446122 | KC446281 |
| Bd 813 | JX099620 | KC446287 |
| Bd 1080 | KC446127 | KC446301 |
| Bd 1111 | KC446146 | KC446317 |
| Bd 1112 | JX099692 | KC446318 |
| Bd 1115 | KC446147 | KC446321 |
| Bd 1121 | KC446149 | KC446325 |
| Bd 1123 | JX099700 | KC446327 |
| Bd 1126 | KC446150 | KC446330 |
| Bd 1140 | JX099585 | KC446338 |
| Bd 1147 | JX099592 | KC446345 |
| Bd 1170 | JX099604 | KC446356 |
| Bd 1181 | JX099615 | KC446359 |
| Bd 1201 | JX099676 | KC446368 |
| Bd 1209 | JX099684 | KC446376 |
| Bd 1225 | JX099737 | KC446384 |
| Bd 1228 | JX099740 | KC446387 |
| Bd 1234 | JX099746 | KC446393 |
| Bd 1236 | JX099748 | KC446395 |
| Bd 1238 | JX099750 | KC446397 |
|  |  |  |

\*from Boykin et al. [24]

**Supplementary Figure S1**

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**Supplementary Figure S1.** Molecular Phylogenetic analysis by Maximum Likelihood method. Tree based on concatenated partial sequences of the *COI* and *ND4* genes of 38 *B. carambolae* and *B. dorsalis* specimens*.* *Bactrocera opiliae* and *Bactrocera occipitalis* were used as outgroups. The evolutionary history was inferred by using the Maximum Likelihood method based on the Hasegawa-Kishino-Yano model. Codon positions included were 1st+2nd+3rd. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the ones higher than 50 are presented. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (Scale bar = 0.005 substitutions per site). Asterisks indicate the sequences analyzed in the present study. Sequences’ accession numbers in Supplementary Tables S1 and S3.