DATA NOTE

The genome sequence of a parasitoid wasp, Ichneumon xanthorius Forster, 1771 [version 1; peer review: 3 approved]

University of Oxford and Wytham Woods Genome Acquisition Lab, Gavin Broad1, Darwin Tree of Life Barcoding collective, Wellcome Sanger Institute Tree of Life programme, Wellcome Sanger Institute Scientific Operations: DNA Pipelines, Tree of Life Core Informatics collective, Darwin Tree of Life Consortium

1Department of Life Sciences, Natural History Museum, London, UK

Abstract
We present a genome assembly from an individual female Ichneumon xanthorius (Arthropoda; Insecta; Hymenoptera; Ichneumonidae). The genome sequence is 315 megabases in span. The majority of the assembly (82.64%) is scaffolded into 12 chromosomal pseudomolecules. Gene annotation of this assembly on Ensembl has identified 10,622 protein coding genes.

Keywords
Ichneumon xanthorius, genome sequence, chromosomal, Hymenoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✔ ✔ ✔

version 1 10 Feb 2022

1. Xinhai Ye1, Shanghai Institute for Advanced Study, Zhejiang University, Hangzhou, China
2. James B. Whitfield1, University of Illinois at Urbana-Champaign, Urbana, USA
3. Gaelen Burke, University of Georgia, Athens, USA

Any reports and responses or comments on the article can be found at the end of the article.
Species taxonomy
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea; Ichneumonidae; Ichneumoninae; Ichneumon; *Ichneumon xanthorius* Forster, 1771 (NCBI:txid2795680).

Background

*Ichneumon xanthorius* is an idiobiont endoparasitoid of Lepidoptera, ovipositing in the host pupa, arresting its development, consuming it entirely and pupating within the host pupal shell. It has been reared from pupae of several species of *Noctua* Linnaeus and *Xestia* Hübner (Lepidoptera: Noctuidae) in experiments where females were presented with potential hosts (*Hinz & Horstmann, 2007*); although the natural host range is poorly known, it will be limited to noctuid moths with larvae which feed low in the vegetation and pupate in the spring. This is a univoltine species, with females active post-hibernation mainly in April and May and then the next generation from July to September, sometimes into October, before spending the winter in concealed locations, such as under bark. Males are seen from mid-June to late August, mostly in July (data from *iRecord*; requires registration) and do not over-winter. The species is widely distributed across Europe, North Africa, the Middle East and into Central Asia. In Britain, *I. xanthorius* seems to be most frequent in southern England but has also been widely recorded in Scotland, Wales and Ireland (*Broad, 2016*; *O’Connor et al. 2007*; data from *iRecord*). Found mainly in open areas, including gardens, and often seen on flowers, especially umbels.

To our knowledge, this is the first chromosomal genome produced for an ichneumonid wasp. The Ichneumonoidea, or Darwin Wasps, comprise one of the great radiations of metazoan life, with over 25,000 described (and many more undescribed) species attacking a huge variety of (mostly) holometabolous insects (*Broad et al., 2018*; *Klopfstein et al., 2019*). Genomic data will help us uncover some of the adaptations that have enabled this success.

Genome sequence report

The genome was sequenced from a single female *I. xanthorius* (*Figure 1*) collected from Wytham Woods, Oxfordshire (biological vice-county: Berkshire), UK (latitude 51.770, longitude -1.331). A total of 55-fold coverage in Pacific Biosciences single-molecule long reads and 62-fold coverage in 10X Genomics read clouds were generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 85 missing/misjoins and removed 1 haplotypic duplication, reducing the assembly size by 0.05% and scaffold number by 32.13%, and increasing the scaffold N50 by 57.52%.

The final assembly has a total length of 315 Mb in 150 sequence scaffolds with a scaffold N50 of 20.1 Mb (*Table 1*). Of the assembly sequence, 82.64% was assigned to 12 chromosomal-level scaffolds (numbered by sequence length) (*Figure 2–Figure 5; Table 2*). The orientation of chromosome 10, region 1.08–1.74 Mb cannot be determined from available data. The assembly has a BUSCO v5.1.2 (*Manni et al., 2021*) completeness of

![Figure 1. Image of the *IchXant1* specimen taken during preservation and processing.](image-url)
Table 1. Genome data for *Ichneumon xanthorius*, iyIchXant1.1.

| **Project accession data** |     |
|---------------------------|-----|
| Assembly identifier       | iyIchXant1.1 |
| Species                   | *Ichneumon xanthorius* |
| Specimen                  | iyIchXant1 |
| NCBI taxonomy ID          | NCBI:txid2795680 |
| BioProject                | PRJEB46331 |
| BioSample ID              | SAMEA7746465 |
| Isolate information       | Female, head/thorax |

| **Raw data accessions** |     |
|-------------------------|-----|
| PacificBiosciences SEQUEL II | ERR6808013 |
| 10X Genomics Illumina    | ERR6688586-ERR6688589 |
| Hi-C Illumina           | ERR6688585 |

| **Genome assembly** |     |
|---------------------|-----|
| Assembly accession  | GCA_910589235.1 |
| Accession of alternate haplotype | GCA_910589515.1 |
| Span (Mb)            | 230 |
| Number of contigs    | 214 |
| Contig N50 length (Mb) | 3 |
| Number of scaffolds  | 106 |
| Scaffold N50 length (Mb) | 10 |
| Longest scaffold (Mb) | 25 |
| BUSCO* genome score  | C:95.5%(S:95.2%, D:0.4%), F:1.4%, M:3.1%, n:5991 |

| **Genome annotation** |     |
|-----------------------|-----|
| Number of protein-coding genes | 10,622 |
| Average length of coding sequence (bp) | 1,454.23 |
| Average number of exons per transcript | 6.14 |
| Average exon size (bp) | 279.63 |
| Average intron size (bp) | 1,109.68 |

*BUSCO scores based on the hymenoptera_odb10 BUSCO set using v5.1.2. C=complete [S=single copy, D=duplicated], F=fragmented, M=missing, n=number of orthologues in comparison. A full set of BUSCO scores is available at [https://blobtoolkit.genomehubs.org/view/iyIchXant1.1/dataset/CAKJD01/busc](https://blobtoolkit.genomehubs.org/view/iyIchXant1.1/dataset/CAKJD01/busc).

95.5% (single 95.2%, duplicated 0.4%) using the hymenoptera_odb10 reference set (n=5991). While not fully phased, the assembly deposited is of one haplotype. Contigs corresponding to the second haplotype have also been deposited.

**Genome annotation report**
The iyIchXant1.1 genome has been annotated using the Ensembl rapid annotation pipeline (Table 1; [https://rapid.ensembl.org/Ichneumon_xanthorius_GCA_917499995.1/](https://rapid.ensembl.org/Ichneumon_xanthorius_GCA_917499995.1/)). The resulting annotation includes 17,487 transcribed mRNAs from 10,622 protein-coding and 1,584 non-coding genes. There are 1.49 coding transcripts per gene and 6.14 exons per transcript.

**Methods**
Sample acquisition and DNA extraction
A single female *I. xanthorius* was collected from Wytham Woods, Oxfordshire, UK (latitude 51.774, longitude -1.332) by Liam Crowley, University of Oxford, using a net. The sample...
Figure 2. Genome assembly of *Ichneumon xanthorius*, iyIchXant1.1: metrics. The BlobToolKit Snailplot shows N50 metrics and BUSCO gene completeness. The main plot is divided into 1,000 size-ordered bins around the circumference with each bin representing 0.1% of the 314,990,913 bp assembly. The distribution of scaffold lengths is shown in dark grey with the plot radius scaled to the longest scaffold present in the assembly (27,402,130 bp, shown in red). Orange and pale-orange arcs show the N50 and N90 scaffold lengths (20,145,675 and 1,060,478 bp), respectively. The pale grey spiral shows the cumulative scaffold count on a log scale with white scale lines showing successive orders of magnitude. The blue and pale-blue area around the outside of the plot shows the distribution of GC, AT and N percentages in the same bins as the inner plot. A summary of complete, fragmented, duplicated and missing BUSCO genes in the hymenoptera_odb10 set is shown in the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/iyIchXant1.1/dataset/CAKJTD01/snail.

was identified by Gavin Broad, Natural History Museum, and snap-frozen on dry ice.

DNA was extracted at the Tree of Life laboratory, Wellcome Sanger Institute. The iyIchXant1 sample was weighed and dissected on dry ice with tissue set aside for Hi-C sequencing. Thorax tissue was disrupted using a Nippi Powermasher fitted with a BioMasher pestle. Fragment size analysis of 0.01–0.5 ng of DNA was then performed using an Agilent FemtoPulse. High molecular weight (HMW) DNA was extracted.
using the Qiagen MagAttract HMW DNA extraction kit. Low molecular weight DNA was removed from a 200-ng aliquot of extracted DNA using 0.8X AMPure XP purification kit prior to 10X Chromium sequencing; a minimum of 50 ng DNA was submitted for 10X sequencing. HMW DNA was sheared into an average fragment size between 12–20 kb in a Megaruptor 3 system with speed setting 30. Sheared DNA was purified by solid-phase reversible immobilisation using AMPure PB beads with a 1.8X ratio of beads to sample to remove the shorter fragments and concentrate the DNA sample.

Figure 3. Genome assembly of *Ichneumon xanthorius*, iyIchXant1.1. GC coverage. BlobToolKit GC-coverage plot. Scaffolds are coloured by phylum. Circles are sized in proportion to scaffold length. Histograms show the distribution of scaffold length sum along each axis. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view iyIchXant1.1/dataset/CAKJTD01/blob.
The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer and Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system.

**Sequencing**

Pacific Biosciences HiFi circular consensus and 10X Genomics read cloud sequencing libraries were constructed according to the manufacturers’ instructions. Sequencing was performed by the Scientific Operations core at the Wellcome Sanger...
Table 2. Chromosomal pseudomolecules in the genome assembly of *Ichneumon xanthorius*, iyIchXant1.1.

| INSDC accession | Chromosome | Size (Mb) | GC%  |
|-----------------|------------|-----------|------|
| OU824200.1      | 1          | 27.40     | 42.3 |
| OU824201.1      | 2          | 23.86     | 43.0 |
| OU824202.1      | 3          | 25.76     | 43.5 |
| OU824203.1      | 4          | 24.20     | 43.3 |
| OU824204.1      | 5          | 20.15     | 42.5 |
| OU824205.1      | 6          | 18.22     | 42.9 |
| OU824206.1      | 7          | 21.55     | 44.0 |
| OU824207.1      | 8          | 18.38     | 42.1 |
| OU824208.1      | 9          | 20.52     | 42.9 |
| OU824209.1      | 10         | 17.22     | 40.4 |
| OU824210.1      | 11         | 15.71     | 42.2 |
| OU824211.1      | 12         | 13.19     | 43.2 |
| OU824212.1      | MT         | 0.02      | 15.7 |
| -               | Unplaced   | 68.81     | 43.3 |

Figure 5. Genome assembly of *Ichneumon xanthorius*, iyIchXant1.1: Hi-C contact map. Hi-C contact map of the iyIchXant1.1 assembly, visualised in HiGlass. Chromosomes are shown in size order from left to right and top to bottom.
Institute on Pacific Biosciences SEQUEL II and Illumina NovaSeq 6000 instruments. Hi-C data were generated from head tissue using the Arima v2.0 kit and sequenced on an Illumina NovaSeq 6000 instrument.

Genome assembly
Assembly was carried out with Hifiasm (Cheng et al., 2021). Haplotypic duplication was identified and removed with purge_dups (Guan et al., 2020). Scaffolding with Hi-C data (Rao et al., 2014) was carried out with SALSA2 (Ghurye et al., 2019). The Hi-C scaffolds were polished with the 10X Genomics Illumina data by aligning to the assembly with longranger align, calling variants with freebayes (Garrison & Marth, 2012). One round of the Illumina polishing was applied. The mitochondrial genome was assembled with MitoHiFi (Uliano-Silva et al., 2021), which performed annotation using MitoFinder (Allio et al., 2020). The assembly was checked for contamination as described previously (Howe et al., 2021). Manual curation (Howe et al., 2021) was performed using HiGlass (Kerpedjieva et al., 2018) and Pretext. The genome was analysed within the BlobToolKit environment (Challis et al., 2020). Table 3 contains a list of all software tool versions used, where appropriate.

Genome annotation
The Ensembl gene annotation system (Aken et al., 2016) was used to generate annotation for the Ichneumon xanthurius assembly (GCA_917499995.1). Annotation was created primarily through alignment of transcriptomic data to the genome, with gap filling via protein to-genome alignments of a select set of proteins from UniProt (PMID: 30395287).

Ethics/compliance issues
The materials that have contributed to this genome note have been supplied by a Darwin Tree of Life Partner. The submission of materials by a Darwin Tree of Life Partner is subject to the Darwin Tree of Life Project Sampling Code of Practice. By agreeing with and signing up to the Sampling Code of Practice, the Darwin Tree of Life Partner agrees they will meet the legal and ethical requirements and standards set out within this document in respect of all samples acquired for, and supplied to, the Darwin Tree of Life Project. Each transfer of samples is further undertaken according to a Research Collaboration Agreement or Material Transfer Agreement entered into by the Darwin Tree of Life Partner, Genome Research Limited (operating as the Wellcome Sanger Institute), and in some circumstances other Darwin Tree of Life collaborators.

Table 3. Software tools used.

| Software tool  | Version | Source                                   |
|----------------|---------|------------------------------------------|
| Hifiasm        | 0.15.3  | Cheng et al., 2021                       |
| purge_dups     | 1.2.3   | Guan et al., 2020                        |
| SALSA2         | 2.2     | Ghurye et al., 2019                      |
| longranger align | 2.2.2 | https://support.10xgenomics.com/genome-exome/software/pipelines/latest/advanced/other-pipelines |
| freebayes      | v1.3.1-17-gaa2ace8 | Garrison & Marth, 2012 |
| MitoHiFi       | 2       | https://github.com/marcelauliano/MitoHiFi |
| HiGlass        | 1.11.6  | Kerpedjieva et al., 2018                 |
| PretextView    | 0.0.4   | https://github.com/wtsi-hpag/PretextView |
| BlobToolKit    | 2.6.4   | Challis et al., 2020                     |

Data availability
European Nucleotide Archive: Ichneumon xanthurius. Accession number PRJEB46331; https://identifiers.org/ena.embl/RJEB46331.

The genome sequence is released openly for reuse. The I. xanthurius genome sequencing initiative is part of the Darwin Tree of Life (DTol) project. All raw sequence data and the assembly have been deposited in INSDC databases. Raw data and assembly accession identifiers are reported in Table 1.

Author information
Members of the University of Oxford and Wytham Woods Genome Acquisition Lab are listed here: https://doi.org/10.5281/zenodo.5746938.

Members of the Darwin Tree of Life Barcoding collective are listed here: https://doi.org/10.5281/zenodo.5744972.

Members of the Wellcome Sanger Institute Tree of Life programme are listed here: https://doi.org/10.5281/zenodo.5744840.

Members of Wellcome Sanger Institute Scientific Operations: DNA Pipelines collective are listed here: https://doi.org/10.5281/zenodo.5746904.

Members of the Tree of Life Core Informatics collective are listed here: https://doi.org/10.5281/zenodo.5743293.

Members of the Darwin Tree of Life Consortium are listed here: https://doi.org/10.5281/zenodo.5638618.
References

Aken BL, Ayling S, Barrell D, et al.: The Ensembl gene annotation system. Database (Oxford). 2016; 2016: baw093.
PubMed Abstract | Publisher Full Text | Free Full Text

Allio R, Schomaker-Bastos A, Romiguier J, et al.: MitoFinder: Efficient Automated Large-Scale Extraction of Mitogenomic Data in Target Enrichment Phylogenomics. Mol Ecol Resour. 2020; 20(4): 892–905.
PubMed Abstract | Publisher Full Text | Free Full Text

Broad GR: Checklist of British and Irish Hymenoptera - Ichneumonidae. Biodivers Data J. 2016; (4): e9042.
PubMed Abstract | Publisher Full Text | Free Full Text

Challis R, Richards E, Rajan J, et al.: BlobToolKit - Interactive Quality Assessment of Genome Assemblies. G3 (Bethesda). 2020; 10(4): 1361–74.
PubMed Abstract | Publisher Full Text | Free Full Text

Cheng H, Concepcion GT, Feng X, et al.: Haplotype-Resolved de Novo Assembly Using Phased Assembly Graphs with Hifiasm. Nat Methods. 2021; 18(2): 170–75.
PubMed Abstract | Publisher Full Text | Free Full Text

Garrison E, Marth G: Haplotype-Based Variant Detection from Short-Read Sequencing. arXiv: 1207.3907. 2012.
Reference Source

Ghurye J, Rhee A, Walenz BP, et al.: Integrating Hi-C Links with Assembly Graphs for Chromosome-Scale Assembly. PloS Comput Biol. 2019; 15(8): e1007273.
PubMed Abstract | Publisher Full Text | Free Full Text

Guan D, McCarthy SA, Wood J, et al.: Identifying and Removing Haplotypic Duplication in Primary Genome Assemblies. Bioinformatics. 2020; 36(9): 2896–98.
PubMed Abstract | Publisher Full Text | Free Full Text

Hinz R, Horstmann K: Über Wirtsbeziehungen Europäischer Ichneumon-Arten. (On the Host Relationships of European Species of Ichneumon Linnaeus (Insecta, Hymenoptera, Ichneumonidae, Ichneumoninae).) Spixiana. 2007; 30(1): 39–63.
Reference Source

Howe K, Chow W, Collins J, et al.: Significantly Improving the Quality of Genome Assemblies through Curation. GigaScience. 2021; 10(1): giaa153.
PubMed Abstract | Publisher Full Text | Free Full Text

Kerpedjiev P, Abdennur N, Lekschas F, et al.: HiGlass: Web-Based Visual Exploration and Analysis of Genome Interaction Maps. Genome Biol. 2018; 19(1): 125.
PubMed Abstract | Publisher Full Text | Free Full Text

Klopfstein S, Santos BF, Shaw MR, et al.: Entomological Communications. Entomological Communications. 2019; 1: e01006–e01006.
Manni M, Berkeley MR, Seppey M, et al.: BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. Mol Biol Evol. 2021; 38(10): 4647–54.
PubMed Abstract | Publisher Full Text | Free Full Text

O’Connor JP, Nash R, Fitton MG: A Catalogue of the Irish Ichneumonidae (Hymenoptera: Ichneumoninae), Irish Biogeographical Society, 2007.
Reference Source

Rao SSP, Huntley MH, Durand NC, et al.: A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. Cell. 2014; 159(7): 1665–80.
PubMed Abstract | Publisher Full Text | Free Full Text

Uliano-Silva M, Nunes JGF, Krasheninnikova K, et al.: marcelauliano/MitoHiFi: mitohifi_v2.0. 2021.
Publisher Full Text
Open Peer Review

Current Peer Review Status: ✔ ✔ ✔

Reviewer Report 05 April 2022

https://doi.org/10.21956/wellcomeopenres.19565.r49264

© 2022 Burke G. This is an open access peer review report distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Gaelen Burke
Department of Entomology, University of Georgia, Athens, GA, USA

This data note describes the genome sequence of Ichneumon xanthorius Forster. The genome has been sequenced from a single wasp and is assembled at a chromosomal level. The methodology is described adequately and was based on a PacBio HiFi long reads and scaffolding with a HiC chromatin contacts strategy. Based upon the assembly statistics, the high percentage of complete BUSCO genes and the blobplot that shows very consistent GC and coverage, the genome appears to be very high quality. The genome was annotated with the Ensembl pipeline. The genome size and number of genes, etc., are all similar to other parasitoid genomes currently in the literature. Overall, this genome sequence will be a very useful contribution to the community and to the diversity of genome sequences available from Darwin’s Wasps.

While another reviewer suggested an analysis to look for evidence of PDVs, I believe that is beyond the scope of this data note. Perhaps the authors could state whether this species was expected to have PDVs a priori in the introduction.

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.
**Reviewer Expertise:** Insect genomics, endogenous viruses

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

---

**Reviewer Report 05 April 2022**

https://doi.org/10.21956/wellcomeopenres.19565.r49269

© 2022 Whitfield J. This is an open access peer review report distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

James B. Whitfield
Department of Entomology, University of Illinois at Urbana-Champaign, Urbana, IL, USA

This genome report describes the genome sequence of the parasitic wasp, *Ichneumon xanthorius*, and represents the first chromosomal-level genome available for an ichneumonid wasp (the Ichneumonoidae is possibly the largest family of insects). The rationale for why this genome was targeted for sequencing is clearly, although minimally, laid out.

One briefly mentioned characteristic of the wasp that is of comparative interest is that it is an idiobiont endoparasitoid of host pupae. As an endoparasitoid, it is likely to have some strategy for evading the immune system of its host insect. Most genomic studies of endoparasitoids have been of koinobiont species that attack host larvae, and with associations with symbiotic viruses that are involved with these immunological interactions. It would thus be of interest whether this ichneumonid also possesses a similar virus, or whether it has some other battery of genes for host immune evasion. There are some known (published) core viral gene sequences from the viruses that are housed within other ichneumonid wasps (Campopleginae, Banchinae) that could be used as probes (although it is possible of course that if this wasp species does carry a virus, it might be too distantly related to the other viruses to recognize).

**Is the rationale for creating the dataset(s) clearly described?**
Yes

**Are the protocols appropriate and is the work technically sound?**
Yes

**Are sufficient details of methods and materials provided to allow replication by others?**
Yes

**Are the datasets clearly presented in a useable and accessible format?**
Yes

**Competing Interests:** No competing interests were disclosed.
Reviewer Expertise: Taxonomy and systematics of parasitoid wasps, comparative genomics of parasitoid viruses

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 17 March 2022

https://doi.org/10.21956/wellcomeopenres.19565.r49254

© 2022 Ye X. This is an open access peer review report distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Xinhai Ye

Institute of Insect Sciences, Shanghai Institute for Advanced Study, Zhejiang University, Hangzhou, China

This paper reports a chromosome-level genome of the ichneumonid wasp, *Ichneumon xanthorius*. This genomic resource will greatly facilitate future analyses of the evolution in parasitoid wasps. The sequencing strategies, related bioinformatic methods and genome information are clearly presented and I have only minor comments to the authors:

1. Parasitoid wasps in superfamily Ichneumonoidea often carry polydnaviruses (PDVs) as an important factor in parasitoid-host interaction, and PDV genomes are stably integrated into the genomes of parasitoid wasps. Therefore, I suggest that the authors indicate whether this species (*Ichneumon xanthorius*) carries PDVs, and this is very useful for the users of this genomic data.

2. Is there any experimental evidence (for example, chromosome staining) to support the 12 chromosomes assembled by SALSA2?

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a usable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics, Genome sequencing, Comparative genomics, Insect genomics,
Parasitoid wasp genomics, venom

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.