DATA NOTE

The genome sequence of the common wasp, *Vespula vulgaris* (Linnaeus, 1758) [version 1; peer review: 3 approved with reservations]

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Abstract

We present a genome assembly from an individual female *Vespula vulgaris* (the common wasp; Arthropoda; Insecta; Hymenoptera; Vespidae). The genome sequence is 188 megabases in span. The majority of the assembly is scaffolded into 25 chromosomal pseudomolecules.

Keywords

Vespula vulgaris, common wasp, genome sequence, chromosomal

This article is included in the [Tree of Life](#) gateway.

Open Peer Review

Approval Status ? ? ?

	1	2	3
version 1			
14 Sep 2021	view	view	view

1. **Seirian Sumner** , University College London, London, UK
Emeline Favreau, University College London, London, UK
2. **Jean-Michel Drezen** , CNRS-Université de Tours, Parc de Grandmont, France
3. **Rodolpho S. T. Menezes** , Universidade de São Paulo, Bandeirantes, Ribeirão Preto, Brazil

Any reports and responses or comments on the article can be found at the end of the article.

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Author roles: Crowley LM: Investigation, Resources, Writing – Original Draft Preparation;

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Species taxonomy

Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespula; *Vespula vulgaris* (Linnaeus, 1758) (NCBI:txid7454).

Introduction

The Common wasp, *Vespula vulgaris*, is one of the most widespread species of social wasp in the UK. This species is eusocial, living in colonies with a reproductive queen, sterile workers and reproductive males. Colonies are annual in the UK, typically producing up to around 10,000 workers (Archer, 1981). Nests are commonly constructed underground, particularly within old rodent holes, but can also be frequently found in aerial situations such as roof spaces, sheds, outhouses etc. Nests are constructed out of a paper-like substance produced from macerated wood fibres mixed with saliva. The nest consists of hexagonal cells arranged into combs, covered by a nest envelope. The nest envelope of this species is yellow to brown in colour due to the mix of partially rotted wood used to make the pulp.

Overwintered queens emerge from early March, found a nest around May, and produce the first workers from early June (Archer, 2008). Worker numbers build up throughout the summer, with males and new queens produced around September. Nests usually last until late October, although exceptionally, some may last through the winter to February.

This species is a generalist predator, with workers preying on a wide range of insect and other arthropod species, which are killed, butchered and malaxated before being carried back to the nest to be fed to the developing brood. Adults feed on carbohydrate rich substances including nectar, sap, honeydew and secretions from the larvae. The propensity of adults to visit flowers, particularly shallow blooms, means this species may act as an important pollinator. We note the recent production of a high-quality genome assembly for *V. vulgaris* and two other species of this genus (Harrop *et al.*, 2020), and believe the sequence described here, generated as part of the Darwin Tree of Life project, will further aid understanding of the biology and ecology of the common wasp.

Genome sequence report

The genome was sequenced from a single female *V. vulgaris* collected from Wytham Woods, Oxfordshire, UK (latitude 51.774, longitude -1.332). A total of 87-fold coverage in Pacific Biosciences single-molecule long reads and 190-fold coverage in 10X Genomics read clouds were generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 18 missing/misjoins, reducing the assembly length by 0.001% and the scaffold number by 34.15%, and increasing the scaffold N50 by 2.74%. The final assembly has a total length of 188 Mb in 28 sequence scaffolds with a scaffold N50 of 9 Mb (Table 1). Of the assembly sequence, 99.5% was assigned to 25 chromosomal-level scaffolds (numbered by sequence length)

Table 1. Genome data for *Vespula vulgaris*, iyVesVulg1.1.

Project accession data	
Assembly identifier	iyVesVulg1.1
Species	<i>Vespula vulgaris</i>
Specimen	iyVesVulg1
NCBI taxonomy ID	NCBI:txid7454
BioProject	PRJEB43808
BioSample ID	SAMEA7520502
Isolate information	Female, head/thorax
Raw data accessions	
PacificBiosciences SEQUEL II	ERR6635597
10X Genomics Illumina	ERR6054669-ERR6054672
Hi-C Illumina	ERR6054673-ERR6054675
Illumina PolyA RNA-Seq	ERR6286719
Genome assembly	
Assembly accession	GCA_905475345.1
Accession of alternate haplotype	GCA_905404185.1
Span (Mb)	188
Number of contigs	50
Contig N50 length (Mb)	9
Number of scaffolds	28
Scaffold N50 length (Mb)	9
Longest scaffold (Mb)	20
BUSCO* genome score	C:96.4%[S:96.1%,D:0.3%],F:0.8%,M:2.8%,n:5991

*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/Vespula%20vulgaris/dataset/CAJQFS01/busco>.

(Figure 1–Figure 4; Table 2). The assembly has a BUSCO (Simão *et al.*, 2015) v5.1.2 completeness of 96.4% using the hymenoptera_odb10 reference set. While not fully phased, the assembly deposited is of one haplotype. Contigs corresponding to the second haplotype have also been deposited.

Methods

A single female *V. vulgaris* was collected from Wytham Woods, Oxfordshire, UK (latitude 51.774, longitude -1.332) by Liam Crowley, University of Oxford, using a net. The sample was snap-frozen using dry ice and stored in a CoolRack.

DNA was extracted from head/thorax tissue of iyVesVulg1 at the Wellcome Sanger Institute (WSI) Scientific Operations

Figure 1. Genome assembly of *Vespula vulgaris*, iyVesVulg1.1: metrics. The BlobToolKit Snailplot shows N50 metrics and BUSCO gene completeness. An interactive version of this figure is available at <https://blobtoolkit.genomehubs.org/view/Vespula%20vulgaris/dataset/CAJQFS01/snail>.

core from the whole organism using the Qiagen MagAttract HMW DNA kit, according to the manufacturer's instructions. RNA (also from the whole organism) was extracted in the Tree of Life Laboratory at the WSI using TRIzol, according to the manufacturer's instructions. RNA was then eluted from the same tissue in 50 µl RNase-free water and its concentration RNA assessed using a Nanodrop spectrophotometer and Qubit Fluorometer using the Qubit

RNA Broad-Range (BR) Assay kit. Analysis of the integrity of the RNA was done using Agilent RNA 6000 Pico Kit and Eukaryotic Total RNA assay. A further sample from the same tissue was prepped for Hi-C sequencing in the Tree of Life Laboratory using the Arima v2.0 kit.

Pacific Biosciences HiFi circular consensus and 10X Genomics read cloud sequencing libraries were constructed according

Figure 2. Genome assembly of *Vespula vulgaris*, iyVesVulg1.1: 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/Vespula%20vulgaris/dataset/CAJQFS01/blob>.

to the manufacturers' instructions. Sequencing was performed by the Scientific Operations core at the Wellcome Sanger Institute on Pacific Biosciences SEQUEL II and Illumina HiSeq X instruments. Hi-C data were sequenced on HiSeq X.

Assembly was carried out with Hifiasm (Cheng *et al.*, 2021). Haplotypic duplication was identified and removed with purge_dups (Guan *et al.*, 2020). One round of polishing was

performed by aligning 10X Genomics read data to the assembly with longranger align, calling variants with freebayes (Garrison & Marth, 2012). The assembly was then scaffolded with Hi-C data (Rao *et al.*, 2014) was carried out with SALSA2 (Ghurye *et al.*, 2019). The assembly was checked for contamination and corrected using the gEVAL system (Chow *et al.*, 2016) as described previously (Howe *et al.*, 2021). Manual curation was performed using gEVAL, HiGlass

Figure 3. Genome assembly of *Vespa vulgaris*, iyVesVulg1.1: cumulative sequence. BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the busco genes taxrule. An interactive version of this figure is available at <https://blobtoolkit.genomehubs.org/view/Vespa%20vulgaris/dataset/CAJQFS01/cumulative>.

(Kerpedjiev *et al.*, 2018) and Pretext. The mitochondrial genome was assembled with MitoHiFi (Uliano-Silva *et al.*, 2021). The genome was analysed and BUSCO scores generated within the BlobToolKit environment (Challis *et al.*, 2020). Table 3 contains a list of all software tool versions used, where appropriate.

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

Figure 4. Genome assembly of *Vespula vulgaris*, iyVesVulg1.1: Hi-C contact map. Hi-C contact map of the iyVesVulg1.1 assembly, visualised in HiGlass.

Table 2. Chromosomal pseudomolecules in the genome assembly of *Vespula vulgaris*, iyVesVulg1.1.

INSDC accession	Chromosome	Size (Mb)	GC%
FR997668.1	1	20.09	35.3
FR997669.1	2	19.27	36.3
FR997670.1	3	13.10	35.2
FR997671.1	4	10.43	34.6
FR997672.1	5	9.59	35.2
FR997673.1	6	9.17	35
FR997674.1	7	9.11	34.5
FR997675.1	8	8.75	33.9
FR997676.1	9	8.61	35.1
FR997677.1	10	8.52	35
FR997678.1	11	7.65	33.9
FR997679.1	12	5.68	34.2
FR997680.1	13	5.44	33.1

INSDC accession	Chromosome	Size (Mb)	GC%
FR997681.1	14	5.26	33.9
FR997682.1	15	5.21	34.7
FR997683.1	16	5.04	33.9
FR997684.1	17	5.02	33.4
FR997685.1	18	4.57	33.2
FR997686.1	19	4.38	33.4
FR997687.1	20	4.13	33.4
FR997688.1	21	4.10	33.4
FR997689.1	22	4.07	35.8
FR997690.1	23	3.95	34
FR997691.1	24	3.41	33
FR997692.1	25	2.61	30.7
FR997693.1	MT	0.02	17.2
-	Unplaced	1.01	37.8

Table 3. Software tools used.

Software tool	Version	Source
Hifiasm	0.12	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	1.0	https://github.com/marcelauliano/MitoHiFi
gEVAL	N/A	Chow et al., 2016
HiGlass	1.11.6	Kerpedjiev et al., 2018
PretextView	0.1.x	https://github.com/wtsi-hpag/PretextView
BlobToolKit	2.6.1	Challis et al., 2020

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.

Data availability

European Nucleotide Archive: *Vespula vulgaris* (common wasp). Accession number PRJEB43808; <https://identifiers.org/ena.embl:PRJEB43808>.

The genome sequence is released openly for reuse. The *V. vulgaris* 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. The genome will be annotated using the RNA-Seq data and presented through the [Ensembl](#) pipeline at the European Bioinformatics Institute. Raw data and assembly accession identifiers are reported in [Table 1](#).

Acknowledgements

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Members of the Darwin Tree of Life Barcoding collective are listed here: <https://doi.org/10.5281/zenodo.4893704>.

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Members of the Tree of Life Core Informatics collective are listed here: <https://doi.org/10.5281/zenodo.5013542>.

Members of the Darwin Tree of Life Consortium are listed here: <https://doi.org/10.5281/zenodo.4783559>.

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[Publisher Full Text](#)

Open Peer Review

Current Peer Review Status: ? ? ?

Version 1

Reviewer Report 06 January 2022

<https://doi.org/10.21956/wellcomeopenres.19012.r47289>

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Rodolpho S. T. Menezes

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The manuscript by Crowley *et al.* present a genome assembly from a female *Vespula vulgaris*. The genome sequence is 188 megabases in span, a very similar result found by Harrop *et al.* (2020)¹. Overall the manuscript presents an advance in the genomic field of social wasps. The methodology is thorough and explained and the figures are well constructed. However, I think the authors should compare their results with the assembled genomes from the three *Vespula* species, specially *Vespula vulgaris* as reported by Harrop *et al.*, (2020)¹. Thus, considering a comparative context will better justify the genome sequence of two individuals of the same species.

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[Publisher Full Text](#)

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

Partly

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: Cytogenetics, phylogenomics, and phylogeography.

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, however I have significant reservations, as outlined above.

Reviewer Report 21 December 2021

<https://doi.org/10.21956/wellcomeopenres.19012.r47264>

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Jean-Michel Drezen

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The genome report of the common wasp *Vespula vulgaris* begins with an introduction describing the natural history of the wasp, followed by technical aspects of genome sequencing performed to obtain high-quality genome chromosome scale assembly. The introduction is well written and will be of interest for a broad audience, whereas the detailed protocol and figures will be understood only by specialists in genomics, which is acceptable if it is a clear choice to do so for these short papers, if not more explanations are needed in the figure legends and methods part. The genome obtained is of high quality and the most important point of the protocol are described. However, some points could be improved.

In the introduction the exclusive reference to the UK fauna seems a little surprising since the original geographical distribution of this species is Eurasia from UK to China, it should be stated somewhere, the wasp is not an endemic species of UK! It is also noteworthy that this species has also been recorded as an invasive pest in different parts of the world such as South America, Australia and New Zealand and may have a strong impact on local fauna because of its proliferation in these areas of invasion (Lester and Beggs, 2019¹).

I understand that the genome note should be very concise but this accurate natural history could have been written as well centuries ago and some references to current research themes on wasps would be of interest for example the study of venom components, of high recombination rates in Hymenoptera, the evolution of sociality, behavior (Herrera et al. 2020²; Sirviö et al., 2013³; etc...)

Few genomes from Hymenoptera have been obtained at the chromosomal scale and this an important achievement, however this is the second one for this species, as appropriately noted. A comparison between the two genomes obtained, at least at first glance, would be of interest, in particular the repetitive sequences (including transposable elements) recovered in obtained genomes may vary depending on the technical approach used.

Figure 1: The meaning of colored circle in the middle of the figure using most of the space available is difficult to understand. It provides almost no additional information since the important numbers are already indicated in "scaffold statistics", "scale", "busco" and "composition". I would reorganize the figure to give more space to the important data by reducing the size of this circle, it could be the size of the green one (Busco).

Figure 2: Some explanations on the principle of blobtool (what distribution of GC content and coverage might tell?) and what is shown on the y axis is required for non-specialists to understand something. As it stands only researcher deeply involved in genomics can make something of this figure. At what might correspond the circles having different GC proportion (lower with higher coverage and higher with similar coverage)? Some words are required in the legend to help non-specialists.

Figure 4: Same remark - it may worth writing that each square corresponds to a chromosome.

In the Methods section it is not clear which tissue was used for RNA extraction is it head/thorax (indicated in the first sentence) or the whole body, as indicated in the second sentence?

It would be useful for the reader to know how many genes are included in the hymenoptera_odb10 reference set since the result of Busco depends on the hymenoptera orthologous genes which is not stable yet and might decrease as more genomes get sequenced, in principle all highly conserved hymenopteran genes should be recovered in a chromosomal scale genome. For example, testing a Busco set of 1658 genes we recovered more than 99% orthologues in the parasitoid wasp *C. congregata* genome (Gauthier *et al.*, 2021⁴ (my paper)). Either some of the genes in the Busco set used are not highly conserved and should not be included in the set used or the genome is not complete regarding gene content.

It is a general practice to check for contamination but insect genomes may contain insertions of virus sequences (Gasmi *et al.*, 2015⁵ (my paper)) or of bacterial genomes (Wolbachia, Klasson *et al.*, 2014⁶) that are deleted after checking for "alien sequences", although they are actual part of the genome. How the approach used here (Geval) is dealing with this problem?

References

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chromosome four of *Drosophila ananassae*. *BMC Genomics*. 2014; **15**: 1097 [PubMed Abstract](#) | [Publisher Full Text](#)

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?

No

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

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Insect viruses, polydnviruses, parastoid wasps genomics, evolution

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, however I have significant reservations, as outlined above.

Reviewer Report 05 November 2021

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Summary

The genome report of the common wasp *Vespula vulgaris* includes a short, to the point natural history description (level of sociality, life cycle, ecology), followed by the protocols (one wasp, long-read sequencing, Hi-C) to obtain the high-quality genome assembly. We commend the efforts to produce long-reads and a near-chromosomal-level assembly from a single female wasp *Vespula vulgaris*. As a result of state-of-the-art sequencing methods, the assembly contains an expected high amount of complete protein-coding genes (BUSCO score) and 28 scaffolds within the range of chromosome count previously found in *Vespula* species, including this species (Harrop et al 2020). The readily availability of the high-quality assembly will help the wasp research community to produce more informed comparative analyses. At the time of this publication, there are few

wasp genomes assembled at chromosomal level, thus the rationale for assembling this genome is well described.

Comments:

1. A reference that details the ecosystem services of this wasp as pollinator and predator/regulator of insect populations could be included e.g. Brock *et al.* (2021)¹.
2. The authors note, correctly, that this is not the first high quality genome sequence for this species, but it is the first for a UK representative. There is little/no comparison of this genome with the previously published one; this may be beyond the scope of a short genome report like this.
3. DNA for both PacBio and Hi-C sequencing, as well as RNA sequencing was all obtained from the sample single individual. Sequencing DNA from a single diploid individual is preferable as it reduces heterozygosity; however, a male would have been even better, as hymenopteran males are haploid. Was the female a queen or worker? This should be stated as it could be useful for future population genetics studies.
4. Information on the amount of sequencing conducted (e.g. number of reads) appears to be missing.
5. RNA appears to have been obtained from a whole body, although this is not entirely clear; e.g. it could be that the single female was cut in half and half used for DNA and half for RNA. This wouldn't matter for the DNA sequencing but it could affect the repertoire of genes represented in the RNA sample, e.g. if some organs were present in one half but not the other. Future work might consider adding brood types and males to the RNA pool to improve annotations.
6. To make the article reproducible, the report would need to include a link to the bioinformatics steps taken and code used. Table 3 list the software tools used, but there is no description of specific options used for each step, for instance whether hifiiasm was used with the Hi-C integration or freebayes options. Here is a Wellcome Open research example on Github: https://github.com/SimonAB/Gonzalez-Jimenez_MIRS
7. In the Methods, the mitochondrial method is mentioned. Is it available? If so, where?
8. Figure 1: the scales of the circle are difficult to understand: what is the visual difference between 190M and 20M? Also, what is the purple rectangle on 190M?
9. Figure 2: The legend font size is quite small to read.
10. Figure 4: There are several dots on the Hi-C contact map that could be indicative of mis-assembly or TAD loci. Have you investigated it?
11. Typo: Remove 2nd 'was' from this sentence: The assembly was then scaffolded with Hi-C data (Rao *et al.*, 2014) **was** carried out with SALSA2 (Ghurye *et al.*, 2019).

References

1. Brock RE, Cini A, Sumner S: Ecosystem services provided by aculeate wasps. *Biol Rev Camb Philos Soc.* **96** (4): 1645-1675 [PubMed Abstract](#) | [Publisher Full Text](#)

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?

Partly

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

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Social wasps; social evolution & behaviour; sociogenomics

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however we have significant reservations, as outlined above.