DATA NOTE

The genome sequence of the seven-spotted ladybird,
Coccinella septempunctata Linnaeus, 1758 [version 1; peer review: 2 approved]

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Abstract
We present a genome assembly from an individual female Coccinella septempunctata (the seven-spotted ladybird; Arthropoda; Insecta; Coleoptera; Coccinellidae). The genome sequence is 399 megabases in span. The majority (99.96%) of the assembly is scaffolded into 9 chromosomal pseudomolecules, with the X sex chromosome assembled.

Keywords
Coccinella septempunctata, seven-spotted ladybird, genome sequence, chromosomal

This article is included in the Tree of Life gateway.
Species taxonomy
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Coccinellidae; Coccinellinae; Coccinellini; Coccinella; Coccinella septempunctata Linnaeus, 1758 (NCBI:txid41139).

Background
The 7-spot ladybird, Coccinella septempunctata Linnaeus, 1758, is an iconic species of ladybird and one of the most common in the UK and across Europe. It is widespread and abundant throughout its native range of Europe, Asia and North Africa, although its distribution trend in the UK is decreasing (Roy & Brown, 2018). It can be found across a wide range of habitats including gardens and agricultural land. Adults are large (5–8 mm), conspicuously marked species with vivid red elytra marked with 7 black spots. The head, pronotum and legs are black. The scarce 7-spot ladybird, Coccinella magnifica, is very similar, but can be distinguished by its larger black spots, and additional pair of white markings below the legs on the underside. The 7-spot ladybird is a predatory species, feeding on a wide range of aphid species both as a larva and as an adult. It overwinters as an adult in among foliage, dead plant material and leaf litter. The broad geographic success of this species may be underpinned by its ecological plasticity based on both genetic and phenotypic polymorphisms (Hodek et al., 2013). It has been repeatedly introduced to North America as a biological control agent against aphids in agricultural systems.

Genome sequence report
The genome was sequenced from one female C. septempunctata (Figure 1) collected from Wytham Farm, Oxfordshire (biological vice-county: Berkshire), UK (latitude 51.779, longitude -0.317). A total of 76-fold coverage in Pacific Biosciences single-molecule long reads and 89-fold coverage in 10X Genomics read clouds were generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 78 missing/misjoins and removed 10 haplotypic duplications, reducing the assembly length by 2.60% and the scaffold number by 70.37%, and increasing the scaffold N50 by 49.73%.

The final assembly has a total length of 399 Mb in 24 sequence scaffolds with a scaffold N50 of 41.4 Mb (Table 1). The majority, 99.96%, of the assembly sequence was assigned to 10 chromosomal-level scaffolds, representing 9 autosomes (numbered by sequence length), and the X sex chromosome (Figure 2–Figure 5; Table 2). There is a repeat that is shared between chromosomes X and 9 that could be slightly differently distributed between the two. The assembly has a BUSCO v5.1.2 (Manni et al., 2021) completeness of 97.5% (single 96.4%, duplicated 1.0%) using the endopterygota_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
Sample acquisition and nucleic acid extraction
A single female C. septempunctata was collected from Wytham Farm, Oxfordshire (biological vice-county: Berkshire), UK...
(latitude 51.779, longitude -0.317) by Liam Crowley, University of Oxford, using a pooter. The sample was identified by the same individual and snap-frozen on dry ice.

DNA was extracted from the whole organism of *icOcyOlen1* at the Wellcome Sanger Institute (WSI) Scientific Operations core from the whole organism using the Qiagen MagAttract HMW DNA kit, according to the manufacturer’s instructions. Following this, further DNA was extracted for a PacBio top-up.

Tissue was cryogenically disrupted to a fine powder using a Covaris cryoPREP Automated Dry Pulveriser, receiving multiple impacts. Fragment size analysis of 0.01-0.5 ng of DNA was then performed using an Agilent FemtoPulse. High molecular weight (HMW) DNA was again extracted using the Qiagen MagAttract HMW DNA extraction kit. 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. 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 DNA sequencing libraries were constructed according 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 generated using

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**Figure 3. Genome assembly of Coccinella septempunctata, icCocSept1.1: 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/icCocSept1.1/dataset/CAJRAZ01/blob](https://blobtoolkit.genomehubs.org/view/icCocSept1.1/dataset/CAJRAZ01/blob).
the Arima v2 Hi-C kit and sequenced on an Illumina NovaSeq 6000 instrument.

**Genome assembly**

Assembly was carried out with HiCanu (Nurk *et al.*, 2020); 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) using SALSA2 (Ghurye *et al.*, 2019). The assembly was checked for contamination and corrected.
Table 3. Software tools used.

| Software tool          | Version | Source                              |
|------------------------|---------|-------------------------------------|
| HiCanu                 | 2.1     | Nurk et al., 2020                   |
| purge_dups             | 1.2.3   | Guan et al., 2020                   |
| SALSA2                 | 2.2     | Ghurye et al., 2019                 |
| longranger align       | 2.2     | https://support.10xgenomics.com/genome-exome/software/pipelines/latest/advanced/other-pipelines |
| freebayes              | 1.3.1-17-gaa2ace8 | Garrison & Marth, 2012 |
| MitoHiFi               | 1.0     | Uliano-Silva et al., 2021           |
| gEVAL                  | N/A     | Chow et al., 2016                   |
| HiGlass                | 1.11.6  | Kerpedjiev et al., 2018             |
| PretexView             | 0.1.x   | https://github.com/wtsi-hpag/PretexView |
| BlobToolKit            | 2.6.2   | Challis et al., 2020                |

Figure 5. Genome assembly of *Coccinella septempunctata*, icCocSept1.1: Hi-C contact map. Hi-C contact map of the icCocSept1.1 assembly, visualised in HiGlass.

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, using the gEVAL system (Chow et al., 2016) as described previously (Howe et al., 2021). Manual curation (Howe et al., 2021) was performed using gEVAL, HiGlass (Kerpedjiev et al., 2018) and Pretext. The mitochondrial genome was assembled using 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 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.

Data availability
European Nucleotide Archive: Coccinella septempunctata (seven-spotted ladybird). Accession number PRJEB44834; https://identifiers.org/ena.embl/PRJEB44834

The genome sequence is released openly for reuse. The C. septempunctata 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 sequence is released openly for reuse. 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.

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

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Kerpedjiep P, Abdenour N, Lekchias F, et al.: HiGlass: Web-Based Visual
Open Peer Review

Current Peer Review Status: ✔️ ✔️

Version 1

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Jongsun Park
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The manuscript entitled "The genome sequence of the seven-spotted ladybird, Coccinella septempunctata Linnaeus, 1758" describe the whole genome sequence of C. septempunctata. All genomic data are properly available in the database and the figures which describe features of the whole genome assembly are properly drawn.

I'm not sure whether the author can also provide gene model of this genome or not because NCBI provides a number of transcripts. I think that just brief information of the gene model of this genome wiould be better for this manuscript.

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: Genomics, Comparative Genomics, Bioinformatics, Biodiversity informatics, Plant Taxonomy

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.
The is great genome assembly, of an important species, and I can easily find the data at NCBI and EBI - all of this is good.

My only tiny issue (and it is a tiny tiny issue) is that although the methods are described in the standard manner, and the software versions are used, there could be a better way - perhaps with a document showing example commands and a continuer to download the software - perhaps this needs to be a methods publication for this set of papers that really help a graduate student repeat the assembly?

Otherwise, a wonderful high quality assembly that has made entomology a better place.

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: Arthropod Genomics, Human Genomics, transcriptomics

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.

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