DATA NOTE

The genome sequence of the European turtle dove, *Streptopelia turtur* Linnaeus 1758 [version 1; peer review: 1 approved]

Jenny C. Dunn ¹, Keith C. Hamer², Antony J. Morris ³, Philip V. Grice⁴, Michelle Smith⁵, Craig Corton⁵, Karen Oliver⁵, Jason Skelton⁵, Emma Betteridge⁵, Jale Dolucan ^{5,6}, Michael A. Quail⁵, Shane A. McCarthy^{5,7}, Marcela Uliano-Silva⁵, Kerstin Howe ⁵, James Torrance ⁵, William Chow⁵, Sarah Pelan ⁵, Ying Sims⁵, Richard Challis ⁵, Jonathan Threlfall ⁵, Daniel Mead ^{5,8}, Mark Blaxter ⁵

¹University of Lincoln, Lincoln, LN6 7TS, UK

²School of Biology, University of Leeds, Leeds, LS2 9JT, UK

³Centre for Conservation Science, Royal Society for the Protection of Birds, Sandy, Bedfordshire, SG19 2DL, UK

⁴Natural England, Peterborough, PE1 1NG, UK

⁵Wellcome Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK

⁶Achilles Therapeutics plc, London, W6 8PW, UK

⁷Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, UK

⁸Owlstone Medical, Cambridge, CB4 0GJ, UK

V1 First published: 27 Jul 2021, 6:191
<https://doi.org/10.12688/wellcomeopenres.17060.1>
Latest published: 27 Jul 2021, 6:191
<https://doi.org/10.12688/wellcomeopenres.17060.1>

Abstract

We present a genome assembly from an individual female *Streptopelia turtur* (the European turtle dove; Chordata; Aves; Columbidae). The genome sequence is 1.18 gigabases in span. The majority of the assembly is scaffolded into 35 chromosomal pseudomolecules, with the W and Z sex chromosomes assembled.

Keywords

Streptopelia turtur, European turtle dove, genome sequence, chromosomal

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

Open Peer Review

Approval Status

1

version 1

27 Jul 2021

[view](#)

1. **Noor D. White** , National Institutes of Health, Bethesda, USA

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

Corresponding author: Mark Blaxter (mark.blaxter@sanger.ac.uk)

Author roles: **Dunn JC:** Data Curation, Formal Analysis, Investigation, Resources, Writing – Review & Editing; **Hamer KC:** Data Curation, Formal Analysis, Investigation, Resources, Writing – Review & Editing; **Morris AJ:** Data Curation, Formal Analysis, Investigation, Resources, Writing – Review & Editing; **Grice PV:** Data Curation, Funding Acquisition, Investigation, Resources, Writing – Review & Editing; **Smith M:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Corton C:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Oliver K:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Skelton J:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Betteridge E:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Dolucan J:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Quail MA:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **McCarthy SA:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Uliano-Silva M:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Howe K:** Formal Analysis, Investigation, Methodology, Software, Supervision, Validation, Writing – Review & Editing; **Torrance J:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Chow W:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Pelan S:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Sims Y:** Formal Analysis, Investigation, Methodology, Software, Validation, Writing – Review & Editing; **Challis R:** Formal Analysis, Methodology, Software, Validation, Visualization, Writing – Review & Editing; **Threlfall J:** Project Administration, Writing – Original Draft Preparation, Writing – Review & Editing; **Mead D:** Conceptualization, Investigation, Project Administration, Writing – Review & Editing; **Blaxter M:** Conceptualization, Data Curation, Funding Acquisition, Supervision, Writing – Review & Editing

Competing interests: Jonathan Threlfall was employed by F1000 Research Limited until January 2021.

Grant information: This work was supported by Wellcome through core funding to the Wellcome Sanger Institute (206194) and the Darwin Tree of Life Discretionary Award (218328). SMcC is supported by Wellcome (207492). Sample collection was jointly funded by the Royal Society for the Protection of Birds and Natural England under the Action for Birds in England (AfBiE) scheme.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Copyright: © 2021 Dunn JC *et al.* This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

How to cite this article: Dunn JC, Hamer KC, Morris AJ *et al.* **The genome sequence of the European turtle dove, *Streptopelia turtur* Linnaeus 1758 [version 1; peer review: 1 approved]** Wellcome Open Research 2021, 6:191

<https://doi.org/10.12688/wellcomeopenres.17060.1>

First published: 27 Jul 2021, 6:191 <https://doi.org/10.12688/wellcomeopenres.17060.1>

Species taxonomy

Eukaryota; Metazoa; Chordata; Aves; Columbiformes; Columbidae; Streptopelia; *Streptopelia turtur* Linnaeus 1758 (NCBI:txid177155).

Introduction

The European turtle dove, *Streptopelia turtur*, breeds throughout Europe, Central Asia, the Middle East and North Africa, overwintering in north Sub-Saharan Africa. Populations in the Atlantic archipelago of Britain and Ireland are primarily located in southern and eastern England. *S. turtur* populations are in rapid decline in the UK, having fallen by 98% between 1970 and 2018, making them critically endangered; they are also vulnerable to global extinction (Burns *et al.*, 2020). Several causes have been put forward for this collapse in population. Changes in farming practices and agricultural intensification in the UK have reduced the availability of wild plant seeds, increasing the reliance of *S. turtur* on anthropogenic seed sources (Browne & Aebischer, 2003); a negative association between nestling condition and consumption of seeds from anthropogenic sources has been reported, although this association was positive for adult birds (Dunn *et al.*, 2018). Additionally, infection with the protozoan parasite *Trichomonas gallinae* has been identified as a cause of death in adults and nestlings (Stockdale *et al.*, 2015). The length of breeding seasons and the number of breeding attempts of *S. turtur* have markedly reduced, meaning that fewer young are hatched each year (Browne & Aebischer, 2004). Large populations of migrating birds are also hunted in Mediterranean countries, such as France, Spain and Morocco, compounding this decline in numbers. The genome sequence described here

will be of utility to researchers assessing the vulnerability of *S. turtur* to parasitic infections, and to those interested in population genomics and supporting the numbers of this declining species.

Genome sequence report

The genome was sequenced from a blood sample collected from a single live female *S. turtur* during routine population health checks. A total of 34-fold coverage in Pacific Biosciences single-molecule long reads (N50 22 kb) and 45-fold coverage in 10X Genomics read clouds (from molecules with an estimated N50 of 34 kb) were generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. The Hi-C scaffolds were validated using BioNano Genomics long range restriction maps (106-fold effective coverage). Manual assembly curation corrected 54 missings/misjoins and removed 1 haplotypic duplication, reducing the scaffold number by 23.59%, increasing the scaffold N50 by 19.08% and decreasing the assembly length by 0.01%. The final assembly has a total length of 1.18 Gb in 357 sequence scaffolds with a scaffold N50 of 81.4 Mb (Table 1). The majority, 98.3%, of the assembly sequence was assigned to 35 chromosomal-level scaffolds representing 33 autosomes (numbered by synteny to the chicken, *Gallus gallus* domesticus: GCA_000002315.5), and the W and Z sex chromosomes (Figure 1–Figure 4; Table 2). The assembly has a BUSCO v5.1.2 (Simão *et al.*, 2015) completeness of 95.7% using the aves_odb10 reference set. While not fully phased, the assembly deposited is of one haplotype. Contigs corresponding to the second haplotype have also been deposited.

Table 1. Genome data for *Streptopelia turtur*, bStrTur1.2.

Project accession data	
Assembly identifier	bStrTur1.2
Species	<i>Streptopelia turtur</i>
Specimen	bStrTur1
NCBI taxonomy ID	NCBITxid:177155
BioProject	PRJEB32724
BioSample ID	SAMEA994735
Isolate information	Female, blood sample
Raw data accessions	
PacificBiosciences SEQUEL I	ERR3041797-ERR3041814
10X Genomics Illumina	ERR3229775, ERR3316037-ERR3316040
Hi-C Illumina	ERR4179379-ERR4179383
BioNano	ERZ1392829
Genome assembly	
Assembly accession	GCA_901699155.2
Accession of alternate haplotype	GCA_901699165.2

Genome assembly	
Span (Mb)	1,179
Number of contigs	1,246
Contig N50 length (Mb)	3.79
Number of scaffolds	311
Scaffold N50 length (Mb)	81.4
Longest scaffold (Mb)	222
BUSCO* genome score	C:95.7%[S:94.9%,D:0.8%],F:0.8%,M:3.5%, n:8338

*BUSCO scores based on the aves_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/Streptopelia%20turtur/dataset/CABFKC02/busco>.

Figure 1. Genome assembly of *Streptopelia turtur*, bStrTur1.2: 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/Streptopelia%20turtur/dataset/CABFKC02/snail>.

Methods

The European turtle dove specimen was taken from blood collected from a live bird during routine health checks of populations in Marks Tey, Essex, UK (latitude 51.874N, longitude 0.729E; grid reference TL8823). The sample was taken under Home Office (Animals Scientific Procedures Act, ASPA) licence

number PPL 7007641); the bird was caught and handled under a British Trust for Ornithology ringing license.

DNA was extracted using an agarose plug extraction from a blood sample following the BioNano Genomics Prep Blood and Cell Culture DNA Isolation Protocol. Pacific Biosciences

Figure 2. Genome assembly of *Streptopelia turtur*, bStrTur1.2: GC coverage. BlobToolKit GC-coverage plot. An interactive version of this figure is available at <https://blobtoolkit.genomehubs.org/view/Streptopelia%20turtur/dataset/CABFKC02/blob>.

(PacBio) CLR long read and 10X Genomics read cloud sequencing libraries were constructed according to manufacturers' instructions. Sequencing was performed by the Scientific Operations core at the Wellcome Sanger Institute on Pacific Biosciences SEQUEL I and Illumina HiSeq X instruments. Ultra-high molecular weight DNA was extracted using the BioNano Genomics Prep Animal Tissue DNA Isolation Soft Tissue Protocol and assessed by pulsed field gel and Qubit 2 fluorimetry. DNA was labeled for BioNano Genomics optical mapping following the BioNano Genomics Prep Direct Label and Stain (DLS) Protocol, and run on one Saphyr Optical Instrument chip flowcell (BioNano Genomics). Hi-C data were generated using the Arima Hi-C kit v1 by Arima Genomics, San Diego, USA, using the Illumina HiSeqX sequencing instrument.

Assembly was carried out following the Vertebrate Genome Project pipeline v1.6 (Rhie *et al.*, 2020) with Falcon-unzip (Chin *et al.*, 2016); haplotypic duplication was identified and

removed with purge_haplotigs (Roach *et al.*, 2018) and a first round of scaffolding carried out with 10X Genomics read clouds using scaff10x. Hybrid scaffolding was performed using the BioNano Genomics DLE-1 data and BioNano Solve. Scaffolding with Hi-C data (Rao *et al.*, 2014) was carried out with SALSA2 (Ghurye *et al.*, 2019). The Hi-C scaffolded assembly was polished with arrow using the PacBio data, then polished with the 10X Genomics Illumina data by aligning to the assembly with longranger align, calling variants with freebayes (Garrison & Marth, 2012) and applying homozygous non-reference edits using bcftools consensus. Two rounds of the Illumina polishing were applied. 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 evidence from BioNano Genomics (using the BioNano Access viewer), using HiGlass and Pretext. Figure 1–Figure 3 and BUSCO v5.1.2 scores were generated using BlobToolKit (Challis *et al.*, 2020). Table 3 gives version numbers of the software tools used in this work.

Figure 3. Genome assembly of *Streptopelia turtur*, bStrTur1.2: cumulative sequence. BlobToolKit cumulative sequence plot. An interactive version of this figure is available at <https://blobtoolkit.genomehubs.org/view/Streptopelia%20turtur/dataset/CABFKC02/cumulative>.

Figure 4. Genome assembly of *Streptopelia turtur*, bStrTur1.2: Hi-C contact map. Hi-C contact map of the bStrTur1 assembly, visualized in HiGlass (Kerpedjiev *et al.*, 2018).

Table 2. Chromosomal pseudomolecules in the genome assembly of *Streptopelia turtur*, bStrTur1.2.

INSDC accession	Chromosome	Size (Mb)	GC%
LR594551.2	1	222.12	0.40
LR594552.1	2	169.96	0.40
LR594553.2	3	126.22	0.40
LR594554.2	4	81.37	0.40
LR594556.1	5	70.85	0.41
LR594558.1	6	40.34	0.42
LR594557.1	7	42.93	0.41
LR594559.1	8	34.57	0.42
LR594560.2	9	27.80	0.43
LR594562.1	10	23.07	0.44
LR594563.1	11	22.26	0.43
LR594561.1	12	23.32	0.43
LR594564.1	13	20.81	0.45
LR594565.1	14	18.48	0.46
LR594567.2	15	15.32	0.47
LR594569.2	17	11.44	0.48

INSDC accession	Chromosome	Size (Mb)	GC%
LR594570.2	18	12.59	0.47
LR594568.1	19	10.86	0.48
LR594566.1	20	16.38	0.47
LR594571.2	21	7.81	0.49
LR594577.1	22	4.50	0.50
LR594572.1	23	5.94	0.52
LR594573.1	24	5.82	0.48
LR594579.1	25	1.00	0.58
LR594575.2	26	6.47	0.52
LR594576.2	27	6.49	0.50
LR594574.2	28	5.37	0.53
OU015479.1	29	22.41	0.44
LR594580.2	30	0.71	0.52
LR594581.1	32	0.02	0.53
LR594578.1	33	1.28	0.55
LR594555.2	Z	77.54	0.39
OU015480.1	W	8.84	0.43

Table 3. Software tools used.

Software tool	Version	Source
Falcon-unzip	falcon-kit 1.1.1	(Chin <i>et al.</i> , 2016)
purge_haplotigs	1.0.2	(Roach <i>et al.</i> , 2018)
SALSA2	2.2	(Ghurye <i>et al.</i> , 2019)
Bionano Solve	3.3_10252018	https://bionanogenomics.com/support/software-downloads/
scaff10x	3.0	https://github.com/wtsi-hpag/Scaff10X
arrow	2.2.2	https://github.com/PacificBiosciences/GenomicConsensus
longranger align	2.2.2	https://support.10xgenomics.com/genome-exome/software/pipelines/latest/advanced/other-pipelines
freebayes	1.1.0-3-g961e5f3	(Garrison & Marth, 2012)
bcftools consensus	1.9	http://samtools.github.io/bcftools/bcftools.html
HiGlass	1.11.6	(Kerpedjiev <i>et al.</i> , 2018)
PretextView	0.0.4	https://github.com/wtsi-hpag/PretextView
gEVAL	N/A	(Chow <i>et al.</i> , 2016)
BlobToolKit	2.6.1	(Challis <i>et al.</i> , 2020)

Data availability

European Nucleotide Archive: *Streptopelia turtur* (European turtle dove) genome assembly, bStrTur1. Accession number [PRJEB32724](#).

The genome sequence is released openly for reuse. The *S. turtur* genome sequencing initiative is part of the Wellcome Sanger Institute's "25 genomes for 25 years" project. It is also part of the [Vertebrate Genome Project](#) (VGP) ordinal references programme and the [Darwin Tree of Life](#) (DTOL) project.

All raw data and the assembly have been deposited in the ENA. The genome will be annotated and presented through the [Ensembl](#) pipeline at the European Bioinformatics Institute. Raw data and assembly accession identifiers are reported in [Table 1](#).

Acknowledgements

We thank Mike Stratton and Julia Wilson for their continuing support for the 25 genomes for 25 years project.

References

- Burns F, Eaton MA, Balmer DE, *et al.*: **The state of the UK's birds 2020**. The RSPB, BTO, WWF, DAERA, JNCC, NatureScot, NE and NRW, Sandy, Bedfordshire. 2020.
[Reference Source](#)
- Browne SJ, Aebischer NJ: **Habitat Use, Foraging Ecology and Diet of Turtle Doves *Streptopelia turtur* in Britain**. *Ibis*. 2003; **145**(4): 572–82.
[Publisher Full Text](#)
- Browne SJ, Aebischer NJ: **Temporal Changes in the Breeding Ecology of European Turtle Doves *Streptopelia turtur* in Britain, and Implications for Conservation**. *Ibis*. 2004; **146**(1): 125–37.
[Publisher 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](#)
- Chin CS, Peluso P, Sedlazeck FJ, *et al.*: **Phased Diploid Genome Assembly with Single-Molecule Real-Time Sequencing**. *Nat Methods*. 2016; **13**(12): 1050–54.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Chow W, Brugger K, Caccamo M, *et al.*: **gEVAL — a Web-Based Browser for Evaluating Genome Assemblies**. *Bioinformatics*. 2016; **32**(16): 2508–10.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Dunn JC, Stockdale JE, Moorhouse-Gann RJ, *et al.*: **The Decline of the Turtle Dove: Dietary Associations with Body Condition and Competition with Other Columbids Analysed Using High-Throughput Sequencing**. *Mol Ecol*. 2018; **27**(16): 3386–3407.
[PubMed Abstract](#) | [Publisher Full Text](#)
- Garrison E, Marth G: **Haplotype-Based Variant Detection from Short-Read Sequencing**. *arXiv: 1207.3907*. 2012.
[Reference Source](#)
- Ghurye RR, Sundaram K, Smith F, *et al.*: **Novel ADA2 Mutation Presenting with Neutropenia, Lymphopenia and Bone Marrow Failure in Patients with Deficiency in Adenosine Deaminase 2 (DADA2)**. *Br J Haematol*. 2019; **186**(3): e60–64.
[PubMed Abstract](#) | [Publisher Full Text](#)
- Howe K, Chow W, Collins J, *et al.*: **Significantly Improving the Quality of Genome Assemblies through Curation**. *Gigascience*. 2021; **10**(1): gaa153.
[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](#)
- 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](#)
- Rhie A, McCarthy SA, Fedrigo O, *et al.*: **Towards Complete and Error-Free Genome Assemblies of All Vertebrate Species**. *bioRxiv*. 2020; 2020.05.22.110833.
[Publisher Full Text](#)
- Roach MJ, Schmidt SA, Borneman AR: **Purge Haplotigs: Allelic Contig Reassignment for Third-Gen Diploid Genome Assemblies**. *BMC Bioinformatics*. 2018; **19**(1): 460.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Simão FA, Waterhouse RM, Ioannidis P, *et al.*: **BUSCO: Assessing Genome Assembly and Annotation Completeness with Single-Copy Orthologs**. *Bioinformatics*. 2015; **31**(19): 3210–12.
[PubMed Abstract](#) | [Publisher Full Text](#)
- Stockdale JE, Dunn JC, Goodman SJ, *et al.*: **The Protozoan Parasite *Trichomonas Gallinae* Causes Adult and Nestling Mortality in a Declining Population of European Turtle Doves, *Streptopelia turtur***. *Parasitology*. 2015; **142**(3): 490–98.
[PubMed Abstract](#) | [Publisher Full Text](#)

Open Peer Review

Current Peer Review Status:

Version 1

Reviewer Report 21 December 2021

<https://doi.org/10.21956/wellcomeopenres.18842.r47530>

© 2021 White N. 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. The author(s) is/are employees of the US Government and therefore domestic copyright protection in USA does not apply to this work. The work may be protected under the copyright laws of other jurisdictions when used in those jurisdictions.

Noor D. White

Neurobiology Neurodegeneration and Repair Laboratory, National Eye Institute, National Institutes of Health, Bethesda, Maryland, USA

In this article, the authors present a genome assembly of the European turtle dove. The methods are clear and well detailed. The authors use a variety of sequence data types, including several long-read technologies in order to present a solid assembly. The article is clear and straight-forward, and the genome assembly and associated raw data will be of use to the scientific community.

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: Evolutionary genetics, ornithology, comparative genomics, retinal cell biology

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.