

Review of: "High-Quality Genome Assembly of the Endemic, Threatened White-Bellied Sholakili *Sholicola albiventris* (Muscicapidae: Blanford, 1868) From the Shola Sky Islands, India"

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Potential competing interests: No potential competing interests to declare.

I was really impressed with the manuscript "High-Quality Genome Assembly of the Endemic, Threatened White-Bellied Sholakili *Sholicola albiventris* (Muscicapidae: Blanford, 1868) From the Shola Sky Islands, India". It describes the assembly and annotation of the genome of *Sholicola albiventris*, an endemic and threatened passerine bird from the Shola Sky Islands in the Western Ghats of India. The authors used a combination of long-read (Nanopore) and short-read (Illumina) sequencing to produce a high-quality assembly, which will serve as a valuable resource for future studies on landscape connectivity, subpopulation genetics, local adaptation, and conservation genetics of this species.

The authors obtained a high-quality genome assembly, with an N50 of 68.64 Mbp and an L50 of 6. The completeness of the genome is corroborated by the high percentage of BUSCOs (99.9%) and UCEs (96.9%) recovered. The combined use of long and short reads made it possible to obtain a more complete and accurate assembly, overcoming the limitations of each individual technology.

The authors also carried out a comprehensive annotation of the genome, including the identification of genes, repetitive elements, and the complete mitochondrial genome. Comparison with the genomes of *Taeniopygia guttata* and *Gallus gallus* provided valuable information on the chromosomal evolution and organization of the *S. albiventris* genome.

My assessment is that the reference genome of *S. albiventris* will be a crucial tool for conservation studies, allowing the assessment of population structure, landscape connectivity, and local adaptation. The authors have made the raw data, genome assembly, and annotations available in public databases, ensuring the reproducibility of the research and access to the data by the scientific community.

Points for improvement:

Discussion of results - The results and discussion section could be expanded to include a more in-depth analysis of the findings, exploring the implications for the biology and evolution of *S. albiventris*.

Comparison with other genomes - In addition to the comparison with *G. gallus* and *T. guttata*, a more detailed comparison with other bird genomes, particularly those of closely related species, could provide additional insights into the evolution of the genome and the evolutionary history of *S. albiventris*.

Analysis of song production - The authors mention complex song production as a topic of interest but do not explore this trait in detail. A more in-depth analysis of the genes and genomic regions potentially involved in song production could be included.

Suggestions:

Although the work is well-structured, I suggest including a more detailed analysis of the demographic history of *S. albiventris*, using genomic data to infer past events of population expansion and contraction, and how these may have affected the genetic diversity of the species.

Investigate the presence of genes or genetic variants potentially associated with local adaptation, exploring genomic differences between subpopulations of *S. albiventris* on different islands or geographical areas.

Carry out a comparative analysis of song production between *S. albiventris* and other bird species, seeking to identify the genetic and evolutionary bases of song complexity in this species.

Explore the potential of the reference genome for developing genetic markers for population monitoring studies and evaluating the effectiveness of conservation measures.

Articles that could help improve this work:

-García, Natalia C., et al. "Comparative genomics of two Empidonax flycatchers reveal candidate genes for bird song production." *Evolution* 77.8 (2023): 1818-1828.

-Aamodt, Caitlin M., Madza Farias-Virgens, and Stephanie A. White. "Birdsong as a window into language origins and evolutionary neuroscience." *Philosophical Transactions of the Royal Society B* 375.1789 (2020): 20190060.

-Zimmerman, Shawna J., Cameron L. Aldridge, and Sara J. Oyler-McCance. "An empirical comparison of population genetic analyses using microsatellite and SNP data for a species of conservation concern." *BMC genomics* 21 (2020): 1-16.

This manuscript presents a significant contribution to the knowledge of bird genetics and genomics, providing a valuable resource for future studies on *S. albiventris* and other species. The high-quality genome assembly and comprehensive annotation represent an important advance for research into bird genetics, with implications for the conservation and understanding of the evolution of this group.

I therefore recommend that it be published after evaluating its relevance and incorporating suggestions for improvement. The necessary minor revisions will further strengthen the work and increase its impact on the scientific community.