Reviewer Report

Title: De novo assembly of the Indian Blue Peacock (Pavo cristatus) genome using Oxford Nanopore Technology and Illumina sequencing

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Reviewer Comments to Author:

The manuscript entitled "De novo assembly of Indian Blue Peacock (Pavo cristatus), from Oxford Nanopore and Illumina sequencing reads" details the results from sequencing and assembling the peacock genome. This manuscript, as a data note, is appropriate. However, there are several ways it can be improved.
1) The focus of the manuscript should be on how different sequencing platforms improved the assembly of the peacock genome. However, the benefits (or downside) to using Nanopore technology are not at all addressed. This should be the main point of the manuscript. Perhaps, they can compare an assembly using only Illumina data to that with which they present in the manuscript using both Nanopore and Illumina sequencing data.
2) The authors detail the genome assembly but only supply the SRA data for the public. I know it is not standard for many genome studies, but I think the actual assembled genome should be made public.
3) Generally, the manuscript would benefit from an English speaker going through it thoroughly and correcting the grammar and awkward sentences.
4) The citations are not numbered in the manuscript.
5) I don't know why they reconstructed the mitochondrial phylogeny. It seems out of focus for a data note type manuscript.
6) The conclusion sections of the Abstract and main manuscript are inappropriate and generally should be condensed.
The abstract's "Conclusions" section needs to be completely rewritten. I don't think they addressed any of it in the manuscript except vaguely in the main manuscript conclusions (see below).
The main manuscript Conclusions should be condensed. The first and last paragraphs are the only paragraphs that could be retained. The other paragraphs are more of a discussion nature. Furthermore, they do not discuss the benefits or downside of Nanopore sequencing combined with Illumina sequencing for genome assembly.

Level of Interest

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