Reviewer Report

Title: "A high-coverage draft genome of the mycalesine butterfly Bicyclus anynana"

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Reviewer name: Denis Tagu

Reviewer Comments to Author:

The paper of Nowel et al is a typical well-made genome paper, presenting a good quality genome of a Lepidopteran insect. The sequencing, assembly, annotation and quality assessment are very well performed. The genome data and features are already accessible thought a public dedicated database. I thus have not major issues against its publication in GigaScience.I only have minor interrogations below:When describing the different libraries, I did not understand whether the insert sizes indicated in the tables and text are the expected ones, or the observed data.Concerning the discarding of some reads as putative contaminants, did you check their GC content? More generally, did you scan the reads or contigs for GC content to may be identify "outgroups" that might correspond to putative contaminants? And what could be the nature of these contaminants? May be they correspond to microorganisms associated with B. anynana. Or correspond to mitochondrial genome?The authors clearly show that B. anynana has more predicted genes than other Lepidopteran genomes. The authors suggest a correlation with genome size (which is probably not a good explanation) as well as a consequence of high plasticity. This could be plausible: in the case of Daphnia and aphids, the high number of predicted genes was also discussed in regard to the capacity of these organisms to be plastic (polyphenism). However, those genomes are also characterized by many gene duplications or even expansions that could strengthen the hypothesis of neo-functionalization required for plasticity. Anything in that sense observed for B. anynana?

Level of Interest

Please indicate how interesting you found the manuscript: An article whose findings are important to those with closely related research interests

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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