We thank the reviewers for providing thoughtful comments that have helped us to improve this manuscript. We have incorporated changes that address the reviewer’s concerns, and we believe have significantly improved the clarity of the manuscript. We hope that you find the revised manuscript suitable for publication. Below we have included each of the reviewer's comments in blue and our responses in black.

**Reviewer 1**

A main issue is that the authors praise their current study to go deeper than a former study that looked at the impact of holocentricity at the level of orders (line 75) and indeed the authors use several genera per order. However, the results amalgamate the inferences again to an order level (same in the abstract - line 26). It would be important to assess and discuss the variation within each order also because such variation may provide hints about the underlying processes. This has been shown for Lepidoptera in De Vos et al. (2020 Philosophical Transactions of the Royal Society B) where the authors compared rates of speciation in relation to chromosomal variation.

XXX

Another potential issue I see is that chromosome numbers per genus can be very variable. The authors tried to get around with this by sampling from the distribution (lines 238/239), but how robust is this and how does such variation relate to the variation in R?

XXX

Line 27: Here and throughout the manuscript it would be important to state in which orders polyploidy is common. It is for example highly debated if polyploidisation occurred in Lepidoptera – the authors only highlight that there were ancient whole genome duplications (line 186-188) but even that has been debated (ref 41 in the manuscript). See also Lukhtanov et al (2015, Proceedings of the Royal Society B).

XXX

Line 48 onwards: It is important to note that these processes described here, e.g. Robertsonian translocations, are based on monocentric chromosomes. I would suggest to expand this section to also indicate processes involved for holocentric chromosomes (reviewed in ref 21 in the manuscript).

XXX

Line 63: However, many species are often not variable at all in terms of chromosome numbers, such as Lepidoptera where most known species show a karyotype close to the putative ancestral state (ref 36 in the manuscript and De Vos et al. 2020).

XXX

Line 70 onwards: This argument makes only sense if holocentricity would result in fission events, yet fusion is also possible.

XXX

Line 101: Perhaps remind the reader what rate you are looking at.

XXX

Line 106: Clarify that you refer to the tree of Misof et al.

XXX

**Reviewer 2**

First, the title conclusion is too broad given the scope of the paper. The title should be changed to:  
  
Chromosome number evolves at equal rates in holocentric and monocentric insects.

XXX

Second, the machinery for rate estimation is too opaque. In particular, the authors should provide a simplified version of the core likelihood equation that is being used.

XXX

Some clarification should be provided on how the polyploidization rate is estimated. In particular, would a polyploidization even be inferred when there is a doubling of chromosome number inferred in an ancestor? Presumably there is no other karyotypic signal identified. What signal in the phylogeny provides the support for these estimates? Some brief discussion would be helpful.

XXX

Finally, since the machinery for estimating fusion, fission and polyploidization rates is novel, it would be worth running some simulations on the tree that is being used, with fixed rates on subclades, followed by rate estimation on the simulated tip values for chromosome number. The degree to which the machinery used is good at estimating rates from simulated data is important to know.

XXX