Reviewer Report

Title: **Divergent evolution in the genomes of closely-related lacertids, Lacerta viridis and L. bilineata and implications for speciation**

Version: **Original Submission** **Date:** 6/20/2018

Reviewer name: **Ben Wielstra**

Reviewer Comments to Author:

Kolora and colleagues assemble the genomes of two sister species of green lizards to determine the basis of the genomic incompatibility between them. The study is quite explorative and descriptive, testing a whole bunch of stuff that turned out to be of interest in other taxa. The MS is generally well-written but there are some textual issues listed below.

In general I find this study lacking a clear focus. In lines 116-120 a clear aim of this study is missing. You do a whole bunch of analyses and the MS is quite long-winded, but the common thread is missing or at least obscured. The elements are all there though, so I would like to ask you to make this a bit tighter and to the point. The green lizard hybrid zone is a great system so leverage that in your advantage.

Lines 55-61: I find this section confusing. Your point ii simply seems a restatement of what you want to argue. From point iii it does not follow why this should prevent species merger, because could this not actually drive interspecific introgression?

Lines 71-76: For example, this is all very general and what is lacking is a clear reasoning why you are doing this analysis for the green lizards in particular.

Line 338-344: Your argument here is not clear (to me). The Ne of Lbil is larger than Lvir because of more structure in Lbil but then you appear to be talking about a subpopulation of Lvir (eastern clade) so that suggests Lvir has plenty of substructure?

Textual:

Line 46: The "non-essential" is a bit misleading of course, it depends on what perspective (something similar in abstract too).

Line 105: The "Furthermore" does not follow, it is a disadvantage of the mtDNA/nuDNA sequence study over allozymes that you highlight here. Your aim is to show that there are still uncertainties.

Line 109 and 111: Two times "This" is confusing. I don't see how it follows here that genomic re-arrangements are likely.

Line 333-334: "which are 95% identical", these words are unnecessary and make for a confusing sentence (identical to what exactly?).

Line 362: word "is" missing

Line 398: word "with" redundant

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

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