Ref: Submission ID fa1020a2-21ec-4977-b8f9-81d75dbf1ac0  
  
Dear Dr Avalos,  
  
Your manuscript entitled "Variation in sexual size dimorphism and fit to Rensch's rule in 45 species of Costa Rican hummingbirds" has now been assessed. If there are any reviewer comments on your manuscript, please find them below.  
  
Regrettably, the above submission, has been rejected for publication in Evolutionary Ecology.  
  
Editor comments  
Two reviewers and the Associate Editor reviewed your manuscript and found it to be insightful and exciting, with the potential to have broad implications for the field, and think it would be a great fit for the journal. However, the reviewers both raised what they consider to be a critical point regarding the need to control for phylogenetic relatedness in the analyses.   We have rejected the manuscript because this change to the analyses is major, essential, and has the potential to alter the main findings. Although the AE is optimistic that the findings will likely be robust to this revision, they agree with the reviewers that this change needs to be made prior to being able to fully evaluate the manuscript.   Again, both reviewers and the AE are excited about this manuscript in principle and we would be happy to consider a new submission of the manuscript that addresses the points raised in the reviews.   If you do opt to resubmit, please include a point-by-point summary of revisions made to address the reviewers' comments. We will endeavour to use the same reviewers for the new version of the manuscript. Also note that reviewer 1 has provided additional comments as a word file. If you are unable to see these, please contact me at [matthew.symonds@deakin.edu.au](mailto:matthew.symonds@deakin.edu.au) and I will forward them to you.  
  
  
Thank you for the opportunity to consider your work. I am sorry that we cannot be more positive on this occasion and hope you will not be deterred from submitting future work to Evolutionary Ecology.  
  
Kind regards,  
  
Matthew Symonds  
Editor  
Evolutionary Ecology  
  
Reviewer Comments:  
  
Reviewer 1  
I have read the MS by Avalos, Triana and Klank carefully. Overall, I find this a good and important paper for evolutionary study of hummingbirds. However, I have two main issues:  
1. Some parts are unnecessarily long, and some sentences were unclear. The authors should re-organize this ms from the intro, methods to the discussion. Specifically,  
a) title: delete “45 species of”  
b) intro, both SSD and Rensch’s rule are correlated, especially about the causes, the authors divided them into two parts, and which means their causes would be divided. I suggested combined them (Lines 59-70, Lines 81-96) together.  
Besides, the authors even did not introduce well the SSD and Rensch rule studies about birds in the intro. As far as I know, there are a lot of birds studies.  
So the format I (just) suggest is: Definition of SSD/Rensch rule — causes/hypotheses of such phenomenon – hummingbirds introduction — aims/predictions.  
c) in the discussion, I suggested that the authors discuss the SSD and Renshch’s rule together. For example, Rensch’s rule, the authors discussed the Male-biased SSD in large-sized taxa. But NOT discuss the female-biased SSD (or less male-biased SSD) for small-sized species. These two parts together result in Pattern follow Rensch’s rule. However, the author referred to reproductive limits, and agility (mostly explain) at lines 321-338.  
d) line 271 Does SSD vary with body size? line 299 Causes of variation in SSD. I think these two parts (and maybe also 319) could be mixed together, Besides, I think the discussion should focus on the causes (line 299) rather than line 271.  
  
2. Analysis: About Rensch rule, although non-phylogenetic method and phylogenetic method have similar results based on a plenty of published paper across many taxa. I think, however, phylogenetic RMA is still necessary for this paper (phytools packages, etc.), because the authors including 45 species. Please added phylogenetic analysis information in the methods and results. I think there are phylogenetic trees about hummingbirds even for the global birds. The authors donot have to build trees by themselves, just use published tree.  
Besides, about RMA, maybe you can also try “smatr” package, I personally think this is good than lmodel package, But the results are same.  
  
Please see attached word file for the details  
  
  
Attachments:  
• <https://reviewer-feedback.nature.com/download/attachment/0b11196c-d668-4658-9314-b88f5ed814b7>  
  
Reviewer 2  
    I was excited to read this manuscript seeking to test how sexual size dimorphism (SSD) varies with body size in hummingbirds, particularly in the context of Rensch’s rule (RR, the prediction that in species with larger males, SSD should increase with body size, whereas in species with larger females SSD should decrease with body size). In particular, if I was able to understand it correctly, the authors predict that, because hummingbirds are near the physiological limits of miniaturization, SSD should be greater in larger than in small species. So I found the premise of the paper to be smart and interesting.  
  
However, the analyses suffer from a crucial flaw that prevents them from answering the questions posed: they don’t control for phylogenetic relatedness. RR is inherently an interspecific pattern. Because species are not statistically independent entities, interspecific analyses that don’t account for phylogeny are invalid. The results of this study will only be meaningful when the authors perform phylogenetic analyses. Non-phylo analyses don’t even need to be presented.  
  
Even for a moment overlooking the issue of phylogenetic correction, I don’t see how the analysis–a simple regression of male size X female size– that the authors purport to be a test of RR does so (Fig. 1, and lines 199-207).This just shows us that size covaries between the sexes, which is a trivial observation. To test RR we need to compare SSD for a set of species with larger male and and a set of species with larger female, expecting it'll be larger for the ones with larger male. I suggest the authors do this with a phylogenetic ANOVA, implemented in the R package phytools. See refs below:  
  
<https://besjournals.onlinelibrary.wiley.com/doi/10.1111/j.2041-210X.2011.00169.x>  
  
<https://academic.oup.com/sysbio/article-abstract/42/3/265/1629506?redirectedFrom=fulltext>  
  
To reiterate, I do think the ideas behind this manuscript have great value, and I congratulate the authors. I will be happy to provide a more detailed review of a revised study with phylogenetic analyses and with more careful goals-methods connections,