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Dear Dr. Michael Wink,

Thank you and the three reviewers for constructive and helpful feedback on our manuscript entitled, "Limited geographic genetic structure detected in a widespread Palearctic corvid, *Nucifraga caryocatactes*" (Reference #2013:10:945:0:0:REVIEW) Please find below our response to the comments provided.

Species Distribution Modeling (SDM)

Reviewers 1 & 2 recommend removal of this from the manuscript and we agree with this feedback. We have removed all sections regarding this analysis from the Materials & Methods and Results, Figure 5 (which documents the results of the SDM), and references to it in the Introduction and Discussion.

Reviewer-specific comments

Reviewer 1

Comments regarding SDM are addressed in general changes above.

Reviewer 2 (Martin Paeckert)

"Figure 5 is debatable because the use of SDM analysis requires a convincing justification" (and subsequent comments).

As per the above changes, we have removed the SDM analysis and thus, Figure 5.

"Table 2 is not relevant because of its low (doubtful) informative value." (and subsequent comments).

We agree with Dr. Paeckert's comment in light of a paper published by R.M. Harding (1997; Institute for Mathematics and Its Applications, Vol. 87, p.15) that suggests F_{ST} values comparing populations with $n < 10$ individuals (of limited polymorphism) are of low informative value. We have removed this table as well as the PCA analysis (based on F_{ST} values) and associated methods, results, and discussion related to these measures. We have chosen to focus on other genetic analyses such as haplotype diversity and the statistical parsimony network.

"Own sequences must be deposited at GenBank - no such statement is given so far in the text nor in the supplemental Table S1."

We will deposit sequences in GenBank upon publication of the manuscript. We have added a line in the results (Lines 49-50) and a column has been added to supplemental Table S1 to reflect this.

"The inclusion of these sequence data was reasonable, but necessarily implied cutting down the sequence alignment and thus again reduces the informativeness of genetic variation when

potential east-west splits shall be analysed. This limitation must be addressed in the discussion.

We have added a note about the number of variable sites within this sequence in the results (Line 85) and mentioned its limitation in the discussion.

"...western (Alps) and eastern (Himalayan) montane refuge areas is widely discussed in l. 176-189."

This section has been removed in response to this comment and Dr. Lopes' comments below.

Reviewer 3 (Ricardo Lopes)

"Please check the best format for scientific names according to the instructions"

We have added "Linnaeus, 1758" to the first reference of *Nucifraga caryocatactes* in the Introduction on Line 31.

"Figure 1 could be integrated into Figure 5..."

Figure 5 has been removed from the manuscript entirely (see above), thus this revision was not made.

"Figure 2 & 3 - ..."

We have revised the colour in these networks to be grayscale (please see figure legend for explanation) for ease of viewing. However, as the other reviewers did not take issue with the block and line design of the network and we feel it is informative, we have left the design as is and not changed it to a pie chart format.

"The sampling locations that can be considered "old" and representative of refugia are few. Therefore, many of the inferences and test of hypothesis regarding the number of refugia and the occurrence of gene flow can't be conclusive."

We agree with this critique and have removed reference to refugial populations from this manuscript.

Sincerely,



Kimberly M. Dohms
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