**Rebuttal Letter – for version REVISED-2**

**Additional comments: new territory, new co-author**

In this version, we are adding an author and an additional territory.

Jean-Yves Meyer, a scientist in Tahiti, was already in contact with us. He very recently found in his archives dated photographs taken in Wallis and Futuna (a French territory in the centre of the Pacific Ocean, biogeographically and administratively distinct from French Polynesia). The specimens on the photographs could be identified by us as *Platydemus manokwari*.

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| Editor's comments The reviewers and I all feel that only minor revisions are necessary (mostly rewording), but please pay particular attention to the detailed comments from Reviewer 3, who gives you a helpful guide for obtaining the correct results. I will send the manuscript back to this reviewer once you have resubmitted it, so please respond in full to all recommendations. Please also thank your reviewers in the acknowledgements section.  The editor has attached an annotated manuscript to their decision.  **Answer:** Thank you for these comments. All minor suggestions in the annotated PDF have been taken into account. Reviewer CommentsReviewer 1 (Anonymous)Basic reporting This new version has a more complete introduction. No Comments. Experimental design I accepted your explanation about the analysis. No Comments. Validity of the findings No Comments. Comments for the author I consider this new version is better than the first. The manuscript is well written, is clear and concise, and provides novel and useful information. It is very important to quickly communicate the presence of species considered invasive in order to accelerate control measures. I recommend its publication.  **Answer:** Thank you for these comments. Reviewer 2 (Lisandro Negrete)Basic reporting No comments. Experimental design In "Material and methods", the section "anatomical analysis" seems to be a bit short. Indeed, the second paragraph of results (in "morphological identification", lines 148-157) belong to the section M & M.  **Answer:** According to this suggestion, a short part of the text has been moved. Validity of the findings No comments. Comments for the author The section "results" starts with the analysis of molecular data. Perhaps, it could start with the morphological identification, to follow a logic sequence with "material and methods" and "discussion".  **Answer:** The Results begin with the mention of the existence of two molecular haplotypes, and then the morphological section is about a search for differentiating these two haplotypes with morphology. Hence the order in the text, which seems logical to us.  In results, it would be interesting to add a figure with histological sections of the copulatory apparatus of two specimens of different haplotype. This would be helpful in order to compare with futures findings of this species in other regions, since this is highly expected.  **Answer:** Details have been added in the text.  In discussion, the last paragraph of the section "Morphological identification of specimens" (lines 235-247) would fit better in a separate section, like "analysis of molecular data", since is not dedicated to morphological aspects.  **Answer:** Following this suggestion, we changed the title of the section to “Morphological and molecular identification of specimens”  The last part of the discussion (Significance of these new records – a threat to biodiversity) sounds a bit long and repetitive with section "Time of invasion and other remarks". Perhaps it could be shortened.  **Answer:** in a previous version, certain reviewers estimated that the text was too short… We believe that this section cannot be shortened because it will be important for the public and decision makers – especially in the US.  Minor corrections along the manuscript are included in the pdf version. Annotated manuscript The reviewer has provided feedback as annotations on the manuscript PDF.  **Answer:** All minor suggestions taken into account. Reviewer 3 (Anonymous)Basic reporting This is a second revision, the general impressions is that the ms is better than the first version but there are still some problems with the methodologies used. The authors have incurred in some mistakes that I feel is compulsory that they solve before the ms is published in a journal that is going to be read by many people and that can be used by some as example of how a certain analysis has to be done. Experimental design It is compulsory that the authors do changes on the phylogenetic inference section. It is true that a NJ tree is more than enough for what they want to show and also that MEGA6 is an adequate program to run such an analysis. However one has to be careful because user-friendly programs may allow doing things that are not correct, and the authors in this case have done some mistakes in applying the methodology.  In the first place to run a phylogeny on distances, as is the case of NJ, one has to calculate a distance and better if also applies a correction (as a Kimura-2 parameters, the more general used). But they have used the number of differences method (an absolute number of differences), as they explain in the material and methods section and can be seen in the tree figures where the scale shows a 5 and a 20 respectively. This is wrong. Although the general aspect of their tree is not going to change much, it is important that any analysis published in a good journal is accurate since anyone can copy the methodology and in others cases this can make a big difference, and as I stated it is wrong, neighbour-joining as all distance methods are prepared to work on genetic (or whatever) distances not absolute numbers of changes. So, it is necessary that the authors redo this analysis (which will take them 10 minutes: in the phylogeny inference select NJ and then select for example Kimura-2p distance to infer the tree; redoing the tree as a nice picture will take some more time, but it will be no more than a pair of hours).  Also it is better that they deselect the box indicating “non coding” sites in that window. Since they are working only with a coding region they are only dealing with 1st, 2nd and 3rd codon sites, so there are no “non coding” sites. However, again a user-friendly program is prepared to use those types of sites, and so it offers the possibility. If the authors do not deselect it then it appears on the figure legends the program prepares automatically and it does not make any sense. As for the sentences included in the figure legend given automatically by MEGA6, that now the authors have used as the material and methods, there is a terrible and difficult to follow sentence stating: “The trees were drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the number of differences method (… ) and are in the units of the number of base differences per sequence”  This sentence is constructed by the program as the sentences of GPS navigators, by putting together sentences already prepared and adding some information: the first sentence is exactly the same in all cases only stating that the branch lengths are in the units of the evolutionary distance used, and then comes the sentence that the program adds in each case, stating which evolutionary distance has been used in each case (which in the case of this ms was not an evolutionary distance but the number of substitutions), and then comes another automatic sentence “and are in the units of” and then again the specific case. This is terribly difficult to read. If the authors now use the kimura-2p as I propose in the material and methods they simply need to state: “The program MEGA6 was used to estimate genetic distances (p-distance and also Kimura-2 p) and the evolutionary history was inferred from the kimura-2p distances using the N-J method (ref) all codon positions were used.”   To give the information on the tree branch lengths they only have to state in the tree figure legend that “the scale bar indicates the number of substitutions per site” (if they use a genetic distance the value over the scale bar will be below 1).  In the material and methods they also state that “all ambiguous positions were removed from each sequence pair”. Again here MEGA gives a not totally clear information. It offers the possibility of removing from all the alignment (complete deletion) or for each sequence pair (pairwise deletion) the gaps and missing data. If you select the first the caption automatically written will say: “all positions containing gaps and missing data were eliminated”; But if you select the second it says “all ambiguous positions were removed from each sequence pair”. The term ambiguous here is certainly equivocal, it is better that the authors write “all positions containing gaps and missing data were removed from each sequence pair” or simply "the pairwise deletion option was selected". Ambiguous can be used to refer to polymorphic sites but also to those regions in an alignment for which the alignment is not sure, so in the case of MEGA it is better to specify that they refer to gaps and missing data (N’s) only. Validity of the findings The findings are valid  **Answer:** We followed all suggestions from the reviewer. The section “Trees and distances” in the Material and Methods is now shorter. All analyses have been redone with MEGA6 with settings as indicated. Figures 5 and 6 have been redone.  As expected, the topology has not changed and the new trees are identical. |