Author's response to reviews

Title: RIDOM: Comprehensive and public sequence database for identification of Mycobacterium species

Authors:

Dr Dag Harmsen (dharmsen@uni-muenster.de)
Stefan Dostal (sdostal@web.de)
Dr Andreas Roth (mikromau@zedat.fu-berlin.de)
Stefan Niemann (sniemann@fz-borstel.de)
Jorg Rothganger (jrothgaenger@ridom.de)
Michael Sammeth (micha@sammeth.net)
Prof Jurgen Albert (mfrosch@hygiene.uni-wuerzburg.de)
Prof Matthias Frosch (mfrosch@hygiene.uni-wuerzburg.de)
Elvira Richter (erichter@fz-borstel.de)

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PDF covering letter
Submission of a revised manuscript for publication in the "BMC Infectious Disease" Journal
(MS: 1092583128214161)

Dear Emma Parkin,

please find enclosed a complete copy of a revised manuscript titled "RIDOM: Comprehensive and public sequence database for identification of Mycobacterium species" by Dag Harmsen, Stefan Dostal, Andreas Roth, Stefan Niemann, Jörg Rothgäenger, Michael Sammeth, Jürgen Albert, Matthias Frosch, and Elvira Richter. All authors of the manuscript agree to its submission to BMC INFECTIOUS DISEASE.

Please find following our point-by-point response to the reviewers comments:

Reviewer Christine Turenne
Discretionary Revisions

1) We state in the text (end of results section) what is meant by “wrong”, i.e. differed excessively from published sequence and phenotypic data. Of course we could give our differentiation results. However, we informed the Culture Collection about our results and in the meantime several of these strains are replaced or withdrawn. Therefore, we believe that stating our results would probably unnecessary confuse the reader (and they can no longer reproduce our results).
Minor Compulsory Revisions
1) Done as suggested.
2) Done as suggested and the paper is now cited.
3) Done as suggested.
4) Done as suggested.

Reviewer Karen Carroll
Minor Compulsory Revisions
1) It is correct that in Table 1 the footnotes are not in chronological order. However, we grouped the footnotes in a logical order and we hope that this is superior to a chronological order (if wished by the Editor we have no problem to change this). The footnotes in the former Table 3 (now Table 2) are in chronological order.
2) Done as suggested.
3) Done as suggested.
4) Done as suggested.
5) This was indeed a mistake of us. Therefore, done as suggested (furthermore changed all other appearances of “legend” throughout the text against “footnote”).
6) Done as suggested.
7) Done as suggested.

Major Compulsory Revisions
1) The paragraph now starts with the second sentence as suggested by the reviewer.
2) Done as suggested.
3) To state the objective of this work more clearly, we added at the end of the Background section the following sentence. The ultimate goal of this study was to come up with an algorithm for genetic differentiation of all mycobacteria, using insertion element and gyrB PCRs in addition to rRNA operon sequencing, when the latter target was not discriminatory enough.
4) Changed as suggested the phrase “previously sequenced” against “previously published”.
5) Done as suggested (the sentence was split into two sentences).
6) To address this reviewers suggestions the following addition was made: Therefore, while the RIDOM database is quite complete, one should not accept it as the sole definitive authority for establishing mycobacterial species.
7) Yes, indeed there was duplicate information in Table 2 and Table 3. We deleted therefore as suggested Table 2 and added the footnotes text to Table 1.
8) It is not our impression that we have overstated the utility of 16S rDNA sequencing in the Conclusion section. We already state there quite cautiously that “… it is possible to differentiate most mycobacterial species by sequence analysis of partial 16S rDNA.” and that “A molecular diagnosis system must involve multiple molecular targets, since not all Mycobacterium species can be differentiated using 5’-16S rDNA sequencing alone.”.

9) Comment added as suggested in Table 2 (former Table 3).

Thank you dear Editor and dear Reviewers very much for your efforts and help!

Yours sincerely,

Dr. Dag Harmsen

Email: dharmsen@uni-muenster.de, Phone: +49-251/8355348, and Fax: +49-251/8355341