Reviewer’s report

Title: Genetic diversity of Leishmania donovani that causes cutaneous leishmaniasis in Sri Lanka: a cross sectional study with regional comparisons

Version: 2 Date: 14 Nov 2017

Reviewer: Sanjay Mehta

Reviewer's report:

Overall the manuscript is much improved and is doing a better job at highlighting the unique findings of this work.

Minor comments

Abstract

- Background S3 change "widely known" to "widely shown"
- "sub clusters" should be written as sub-clusters
- Conclusion - revise as follows to clarify

This study reveals high levels of haplotype diversity of L. donovani in Sri Lanka with a distinct genetic association with clinically relevant phenotypic characteristics. The use of genetic tools to identify clinically relevant features of parasites has important therapeutic implications for leishmaniasis.

Background

- line 47 change to "to the standard antimonial drugs routinely used in clinical practice."
- Change line 54 to " A2 protein production [18, 20, 21], lipophosphoglycan (LPG) activity [22-24], gP63 gene expression [25, 26], acid phosphatase activity [18, 27] and variation in the mini-exon genes of chromosome 36 [17] are known factors that influence the virulence of…"
- line 59 - change to "of differences in virulence and pathogenicity."
- line 61 change "usage" to analysis.
- line 67 modify to "containing a conserved region nearly 200 bp in length and a ~600 bp variable region."

- line 68 clarify by removing extra information to "Minicircle sequence differences allow for accurate discrimination between species [32-34]."

- line 72 similarly clarify by modifying "Previous studies using minicircle kDNA footprint assay based on PCR have enabled rapid identification of previously known or unknown species with a high level of sensitivity[35]."

- line 75 - change "depends" to "depend"

- line 78 - to clarify "The aim of this study was to use the kDNA footprint assay to study L. donovani strain specific sequence diversity and determine the associations between sequence variations and distinct clinical characteristics in individuals with leishmaniasis in Sri Lanka."

Materials and Methods

- Clarification line 91… change to "A patient was considered a 'poor responder', if the lesion size (ulceration area in case of ulcers or the induration area in case of non-ulcerative lesions) did not decrease at least by 50% from the pre-treatment size, as judged by the collaborating dermatologists, following a minimum of 10 IL-SSG injections given at weekly intervals, similar to previously used criteria.

- Please clarify S1 under Laboratory and confirmation of Leishmaniasis

- Line 128 - recombinants may be the wrong term here… don't you mean transformed colonies?

- Line 138 - Simplify the first sentence of the paragraph… break it up, as it is, it is too hard to follow.

- Line 173 add space after "in"

- Line 174 Reference the Maximum composite likelihood method

Please clarify what sequences were used for the multiple sequence alignment. The sequence shown in the supplementary material is only about 25 nucleotides long… as opposed to the 120bp listed in the methods.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Unable to assess

Are the conclusions drawn adequately supported by the data shown?
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Yes

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