Reviewer Report

Title: The unique composition of Indian gut microbiome, gene catalogue and associated faecal metabolome deciphered using multi-omics approaches

Version: Revision 1 Date: 11/21/2018

Reviewer name: Cédric Laczny

Reviewer Comments to Author:

The authors have reasonably addressed the comments I raised in the original submission.

Only one general comment and a few minor comments remain, which should all be readily addressable by the authors.

General comments:

L286-291: It would be good to test whether the location and diet are correlated and to which extent. In fact, given the information from the authors, I would expect them to be correlated. Hence, the observed results (Fig. S12) are to be expected and this should be qualified. If no such test is performed, I would recommend to at least reemphasize the (strong) influence of location on the diet of the studied Indian populations. This is also important with respect to the results in L333-335.

Minor comments:

Throughout: Frequently, "the"/"a" is missing, e.g., L158 "analysis of microbiome", L159 "reads from other three datasets", L163 "This shows that the addition of subset".

L149-150 - "and unique to IGC": This reads as if the 943,395 genes are unique to the IGC, but aren't his unique to the newly constructed Indian microbial gene catalogue?

L161 - "did not show a significant (P< 0.01)": Not sure if the significance level (alpha = 0.01) is meant here or if the p-value was "< 0.01". In the latter case, it would be considered significant at alpha = 0.01. Please clarify and verify throughout.

L212-214: Species names should be italicized.

L270: "be" is missing -> "needs to be collected".

L275: The text suggests a "significance", yet the p-value is listed as 0.6841. Please clarify.

Supplements: Fig S11 still contains a reference to "enterotypes" which, as suggested by Reviewer 1 (and I agree) should be generally avoided, unless in combination with the non-Indian populations. Please check this throughout.

L304-305: This is not a necessity for the revision, but rather a question out of curiosity: Was an association with age tested here, in addition to BMI?

L317 + L319: What do "19 MGS/CAG" and "67 MGS/CAG" refer to here? Are these the numbers of MGSs/CAGs that were annotated to likely be P. copri populations, i.e., multiple strains/sub-species of P. copri were identified? Please clarify this.

L339: Did Cluster-2 show *no* association with location, i.e, was a mixture of samples from LOC1 and LOC2?

Legend Fig.S17: "OPLD-DA" -> "OPLS-DA"

Fig. S18: Panel A is rather small and the fonts are hard to read. Please increase the size of the panel.

L409-411: I welcome the qualification of the sequencing depth here. Nevertheless, the argument of 2x150bp sequencing is misleading here. Read-length clearly plays a role, so does the overall sequencing depth. While 2x150bp is commonly used currently, and hence the current study is up-to-date, I would suggest the authors to rephrase this slightly. My suggestion would be: "... deviation), the inclusion of 110 individuals from two distinct geographic locations as well as the identification of Indian gut microbiome-specific genes provide a first insight into the Indian gut microbiome and are thus considered important additions to the field."

L411-413: This sentence reads contradictory in itself. If there is a high diversity, how can (only) two locations be considered representative? I would suggest to rephrase this.

L431: It is not readily clear what "Its" refers to here. I assume it is "Prevotella", yet this should be clarified.

L439: Please consider removing "driver" unless you can show a causation rather than the association which was presented in the results.

L442: "bacteria" -> "bacterium"

L470-471: The "statistically sound" is not readily clear here. Please consider removing this as I do not find it relevant in this context.

L500: "Firmicute" -> "Firmicutes"

L515: Please remove "populations", it does not fit in here.

L578: Please check correct capitalization.

L582: Please be consistent in the numbers: "mean = 1.36 Gb" vs. "1.5" (L408).

L585: Consider removing "bacterial" unless there was some enrichment step for bacterial DNA.

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