Author’s response to reviews

Title: The susceptibility of FSHB -211G>T and FSHR G-29A, 919A>G, 2039A>G polymorphisms to men infertility: an association study and meta-analysis

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Author’s response to reviews:

Dear Editor,

We now send the revised manuscript entitled “The susceptibility of FSHB -211G>T and FSHR G-29A, 919A>G, 2039A>G polymorphisms to men infertility: an association study and meta-analysis”. We thank you for your high enthusiasms and comprehensive analyses of our manuscript. Regarding for the comments you proposed, We have fully addressed your comments and already tried my best to make the correction. If you have any question, please do not hesitate to contact me. I hope that this manuscript can be fit your satisfaction and published in BMC Medical Genetics. I assure that the paper is not under consideration by another journal or publication source, and it has not been submitted elsewhere. The manuscript has been read and approved by all the authors. The research adhered to the tenets of The Declaration of Helsinki.
The Ethics Committee of Jinling Hospital approved the protocol. The patient gave written informed consent. No financial or other conflict of interests has been involved in this article. Thank you for your attention.

Best wishes,

Sincerely yours,

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For your convenience, we now provide our point-by-point responses to all the concerns as detailed below.

Answers to Editor:

Comments 1. Remove all results (table, text, mention of subgroup analysis) and mention of subgroup analysis based on HWE p < 0.05 and p > 0.05. Just present results for studies with HWE p > 0.05 (in methods state that removed studies with SNPs with HWE p < 0.05 from meta-analysis).

Responses 1: According to your request, we have already removed it.

Comments 2. Rename the "other" group as Brazilian or remove from paper (only 1 study) and report only CAU and AA results.

Responses 2: In our meta-analysis, we have already used "Brazilian population" instead of "other group".

Comments 3. Regarding the RR vs WW comparison: This might be done by others in reported research but does not mean this is correct. This is not a standard genetic model and seem more like "fishing" to find a significant association. Please add a note in paper that you did adjust for
multiple testing if key this results in or only present results for a single genetic model (dominant, co-dominant or additive).

Responses 3: At first, thank you for your comprehensive analyses of our manuscript. Then regarding for the RR vs. WW comparison, we have searched Theory & Practice of Systematic Review/Meta-analysis (Luo J, Leng WD, et al. Beijing: Military Medical Science Press, 2013. 511-512), which indicated that there were 3 genetic models, including co-dominant model [the rare allele homozygote (RR) vs. wild-type homozygote (WW), the heterozygous (WR) vs. WW], dominant model (RR+WR vs. WW), recessive model (RR vs. WW+WR). At the same time, this were confirmed by some literatures, as follows:


In our this study, significant differences were observed for the model RR vs. WW in SNPs rs6165 and rs6166 (Table 5). Therefore, we think it is necessary to save it. And this three genetic models were recognized by the theory and practices. In my opinion, it might be not necessary to add a note in paper.