Author’s response to reviews

Title: Association analysis between the tag single nucleotide polymorphisms of DENND1A and the risk of polycystic ovary syndrome in Chinese Han women

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Author’s response to reviews:

Dear Editor,

Re: MGTC-D-19-00211R4 (Research Article) Zhu et al "Association analysis between the tag single nucleotide polymorphisms of DENND1A and the risk of polycystic ovary syndrome in Chinese Han women".

We would like to thank the editor for their final requests. Editor’s requests are responded as follows. We hereby resubmit our revised manuscript to BMC Medical Genetics. Regarding the data deposition, we are trying our best to do as the requirements of the editor. But it seems to take a long time, we cannot finish it before 16 Dec 2019. I hope you'll give us more time and some instructions.

1. Availability of data and materials

Please note that all data must be made public prior to publication and we cannot proceed to publish your manuscript if your data is not deposited and made publicly available.
Data availability statements should include information on where data supporting the results reported in the article can be found including, where applicable, hyperlinks to publicly archived datasets analysed or generated during the study. By data we mean the minimal dataset that would be necessary to interpret, replicate and build upon the findings reported in the article.

We are an open access journal and submission of a manuscript to a BMC journal implies that materials described in the manuscript, including all relevant raw data, will be freely available to any scientist wishing to use them for non-commercial purposes. As your data falls under the list of data types which must be deposited (listed below), we ask that you please provide the relevant accession numbers, and the name of the database in which your data is stored, if your data has been deposited into a database or the appropriate web links if the data has been uploaded into a repository. If the data has not yet been deposited, please do so and provide the relevant information needed to access it in the ‘Availability of data and materials’ section in your manuscript. Please ensure all data is already released and that any accession numbers/web links are in the ‘Availability of Data and Materials’ in their final form, and that all links and accessions allow access to public data.

**Please note that BMC mandates data deposition for the following:**

- Protein sequences
- DNA and RNA sequences
- DNA and RNA sequencing data
- Genetic polymorphisms
- Linked genotype and phenotype data
- Macromolecular structure
- Microarray data (must be MIAME compliant)
- Crystallographic data for small molecules

Response:
The editor required us to deposit the data and make it publicly. We can understand that is the requirement of BMC. Unfortunately, this is the first time we've been asked to do this. So we're not familiar with this process. We are trying our best to finish it as quickly as we can.

We have two questions about the process.
Firstly, we want to know if we have to deposit the data. Although our study is about SNPs, it doesn't involve datasets like GWAS. Our study is a lab experiment of Tagman PCR. All the data of the study were put in the public paper. Does the data still need to be deposited? We don't know what database will accept this type of data? In the other hand, our research is still in progress. We are collecting more samples for further research. We may not be able to make all the data public now.

Secondly, which database should we choose? We downloaded several papers from BMC Medical Genetics. Not so many papers have deposited the data. According to the guideline about “Availability of data and materials” and a published article [Jitian Wang et al. Novel gene mutation in von Hippel-
Lindau disease- a report of two cases. BMC Medical Genetics (2019) 20:194 Page 5 (https://doi.org/10.1186/s12881-019-0930-8)], we have registered on NCBI and website of clinvar. We got the email from clinvar staff, since this is the first time to register we can only submit after receiving the approval email from the organization. It needs 1-3 working days. Today and yesterday were weekends. At present, we have obtained the submit number (Figure). So we cannot finish it before 16 Dec 2019.

We have carefully read "how to submit" of clinvar. We find that the process is very complicated and difficult for us. We will try our best. Maybe it need a long time. I would like to consult the editor whether this database is appropriate. Would you please give us some suggestions? Thank you very much.

The letter from ClinVar staff:

"Dear yong wang,

Thank you for registering your organization with ClinVar:

Submission ID: SUB6690601
Organization name: Nanjing University, Medical School

Our staff will confirm the information provided for your organization. You should hear from us within one to three business days, either to confirm that your organization is approved or to ask clarifying questions about the organization. Once your organization is approved, you will be able to upload submissions in the ClinVar Submission Portal.

If you have questions about your registration, please contact us at clinvar@ncbi.nlm.nih.gov and mention any of the identifiers above.

Thank you for registering with ClinVar.

Regards,
ClinVar staff
clinvar@ncbi.nlm.nih.gov"

2. At this stage, please upload your manuscript as a single, final, clean version that does not contain any tracked changes, comments, highlights, strikethroughs or text in different colours. All relevant tables/figures/additional files should also be clean versions. Should you wish to respond to these revision requests, please put your responses to the reviewers'/editors’ comments in the Response to Reviewers box in Editorial Manager. Please do not upload a separate letter.

Response:
We've gone through the manuscript as required. Now the manuscript is a single, final, clean version that does not contain any tracked changes, comments, highlights, strikethroughs or text in different colours. If there is any dirty or something else, please let us know. Thank you very much.
Yours sincerely,

On behalf of my coauthors
Yong Wang Ph.D.