Author’s response to reviews

Title: Associations of BAFF rs2893321 polymorphisms with myasthenia gravis susceptibility

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Author’s response to reviews:

Thank you very much for review our manuscript: Associations of BAFF rs2893321 polymorphisms with myasthenia gravis susceptibility (MGTC-D-19-00278). We have revised our manuscript as requested, the changes made in the revised MS were marked red.

Here are point by point response to the comments.

Mary Anne D. Chiong (Reviewer 1): Very succinct manuscript

1. Abstract - improve paragraphs. do not use the word 'we". In the purpose: you said that BAFF is vital in the progression of MG- please clarify if this has been verified in the literature. maybe you have to restate this

ANSWER: Thank you very much for your comment. First, we have revised all “we” used sentence in the abstract. Second, in our abstract we said “BAFF is vital in the progression of MG”, which can be verified in our introduction part we said “Serum BAFF level also are elevated in MG, and BAFF plays an important role in the pathogenesis of MG”. and this was supported by reference 12 and 13. However, maybe vital is too strong for the role of BAFF, thus we changed the sentence into “BAFF is important in the progression of MG”.(Page 2)

2. In the introduction - in paragraph number 2 you said that serum BAFF are elevated in MG. Could give 1 or 2 sentences that will correlate it with the pathophysiology of MG in terms of ach receptors or
NMJ proteins? Also why did you specifically choose BAFF among the many proteins that can cause autoimmune disease? you need to support this.

ANSWER: Thank you very much for your suggestion. We have added the correlation between BAFF and ach receptor in introduction. As for why we chose BAFF. Besides BAFF can cause autoimmune disease, and specifically can cause MG. The polymorphisms of BAFF has been studied in several autoimmune disease, and rs2893321 was observed to be a susceptible genetic variant in autoimmune disease, however has not been investigated in MG. Thus, we choose to explore BAFF, specifically rs2893321 in the current study. We have added more information of BAFF rs2893321 in the revised MS. (Page 3, line 25-29.)

3. In the study population please elaborate the inclusion criteria. you have to say whether the 4 parameters for Mg diagnosis that you have enumerated should be fulfilled before you got your patients for the study or just a clinical and one diagnostic procedure supporting MG is enough?

ANSWER: Thank you very much for your suggestion. We have revised the methods. Our parameters for MG patients are: age, gender, thymoma or not, ocular or general, AChR status. Besides the basic information, age and gender, ocular or general were also recorded in diagnose. Patients undergo MG diagnosis were all undergo thymoma text and AChR text, they are part of the diagnostic procedure. However, these were not included in the inclusion criteria. (Page 5, line 6-11)

4. In the single nucleotide polymorphism genotyping- can you clarify the statement" we selected 4% samples from Mg and health control groups and the results were consistent with the original SNP genotyping data" What did you mean by original snp data? is that from another literature?

ANSWER: Thank you very much for your comment. To ensure the Genotyping of BAFF rs2893321 were correct, 4% samples from Mg and health control groups were selected to be texted for BAFF rs2893321 genotype again. In order to double check the results and ensure the quality of the first BAFF rs2893321 genotype results.

5. In your discussion there is a contradicting statement on paragraph 2 regarding BAFF and MG. You said in your introduction (2nd par) that BAFF was found to have proliferation in MG and yet in the discussion no study has been investigated yet

ANSWER: Thank you very much for your comment. We have revised our statement. (Page 10, line 14)

6. Apart from hormones, could you make some assumptions based on your findings how this specific polymorphism increased susceptibility to MG based on MG's pathophysiology? This will beef up your discussion

ANSWER: Thank you very much for your suggestion. We have added assumptions based on age in our revised MS. (Page 10, line 29-)

Mainak Sengupta (Reviewer 2): Please include all comments for the authors in this box rather than uploading your report as an attachment. Please only upload as attachments annotated versions of manuscripts, graphs, supporting materials or other aspects of your report which cannot be included in a text format.

Please overwrite this text when adding your comments to the authors.

The authors must state the basis of selection of the single SNP from BAFF gene and sicuss their results in accordance.

ANSWER: Thank you very much for your suggestion, we have added the reason for select rs2893321 in the introduction of revised MS. (Page 3, line 25-28)

The tables' headers have been misarranged in many cases. Please reframe.

ANSWER: Thank you very much, we have double checked our tables' headers, and corrected the mistake.

The risk genotype(s) must be explicitly stated (in the tables and in text) and if there is an association of
the genotype only and not allele, the reason clarified. 

ANSWER: we have added the risk genotype in the results of revised MS. As for why genotype not allele showed significant different. Our study investigated SNP rs2893321, the genotype were AA, AG and GG. The allele were A and G. as we can see in the tables, the frequency of AG genotype was pretty big, thus allele A and G were not so different between groups. we have added this discussion in the revised MS. (Page 10, line 21-25)