Author's response to reviews

Title: Analysis of EIF4G1 in ethnic Chinese

Authors:

Kai Li (liskai@126.com)
Bei-sha Tang (bstang7398@yahoo.com.cn)
Ji-feng Guo (guojifeng2003@yahoo.com.cn)
Ming-xing Lou (loumx1988@163.com)
Zhan-yun Lv (gdximng@163.com)
Zhen-hua Liu (liuzhenhua2503@163.com)
Yun Tian (tianyun294@163.com)
Cheng-yuan Song (dcschengyuan@163.com)
Kun Xia (xiakun@sklmg.edu.cn)
Xin-xiang Yan (xxyan1268@yahoo.com.cn)

Version: 3 Date: 20 December 2012

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The Biomed Central Editorial Team


Thank you for consideration of our manuscript for publication in your journal. We have reviewed the above manuscript according to your reviewer’s comments.

Reviewer  （Carles Vilarino-Guell）

Reviewer's report:

amongst many others. Please do NOT add GYGIF2 to the list of genes implicated in PD in your introduction. This was a really poor comment by the editor, and I hope in the future she considers up to date literature before making this kind of comments. Similarly, Omi/Htra2 is conclusively not a gene implicated in PD biology. Although several inconclusive but suggestive papers have been published since the initial report, and reviews still continue to mention them, over the last few years an enormous amount of data has been generated proving that Omi/Htra2 is not implicated in PD, and it is time to stop promoting the erroneous data. Even the author of the original identification of Omi in PD is now confirming that this gene is not implicated in disease (http://www.ncbi.nlm.nih.gov/pubmed/20036034). Moreover, the originally described as pathogenic mutation (p.G399S) has been identified in cases and controls at similar frequencies (1%) (http://www.ncbi.nlm.nih.gov/pubmed/18790661). There are many other reports like those, and the conclusion is that Omi/Htra2 is not a PD gene and should never again be considered or mentioned as a PD gene. The mention of GYGIF2 and Omi are the kind of quotes that keep misleading the field and wasting people’s time doing functional research which is irrelevant to the disease.

• Thank for your comments. We have deleted GYGIF2 and Omi/Htra2 from list of genes implicated in PD in our introduction in our revised
manuscript.

2. Regarding the manuscript, the authors have addressed most of the concerns and it is much improved. In reference to the analysis with one or two degrees of freedom, the authors should understand that the three genotypes are not independent values, as they are dependent on allele frequencies; in a way the first genotype is $p$-squared, the second is $2pq$ and the third is $q$-squared; therefore only two variables $p$ and $q$ are present, and hence only one degree of freedom is the appropriate analysis. Please correct the values on the table to represent a one degree of freedom analysis.

- Thank for your comments. We have changed our p-value from 0.413 to 0.184 in table2 by using one degree of freedom analysis.

- Minor Essential Revisions –

1. In several instances, the authors refer to previously reported pathogenic mutations as “mutations”, this is not very clear and doesn’t read right. These should be corrected probably to “previously reported pathogenic mutations” or “reported mutations” or something similar, and these are found in page 2 line 11; page 5 line 2 from the bottom and page 6 line 5 from the bottom.

- Thank you for your comment. We have changed “mutations” to “reported mutations” in our revised manuscript.

2. In page 4 the authors write “The translation initiation complex is a
large family, including eukaryotic translation initiation factor 4E, eukaryotic translation initiation factor 3e (eIF3e) and so on.” I believe this sentence would read better as “The translation initiation complex is a large family, including eukaryotic translation initiation factor 4E and eukaryotic translation initiation factor 3e (eIF3e)”.

• Done.

3. The authors state in two places that “the eight intronic variants are in introns” this is rhetoric and unnecessary, and should be removed. Also in page 6 line 3; it would be better to describe the “two exonic variants” as “two nonsynonymous variants”.

• We have rewritten the sentences in the paper as “The synonymous coding variant rs2230571 in exon 27 and the eight intronic variants were not used for further sequencing, but the specific mutation c.3614G>A (p.R1205H) and the two nonsynonymous variants (rs13319149 and rs2178403) were chosen for further analysis in a case-control study.”

4. In several instances the authors report exon numbers without a space from the exon (ie exon27); a space should be added between the exon and the number. A few similar errors with spacing can be found throughout the manuscript.

• Done.

5. The new title is not grammatically correct… it read as if EIF4G1 has Parkinson’s disease… I would suggest “Analysis of EIF4G1 in ethnic
Chinese Parkinson’s disease patients” or “Analysis of EIF4G1 in ethnic Chinese”. Although the grammar has been significantly improved, a final double checked would be welcomed.

- We have changed the title to “Analysis of EIF4G1 in ethnic Chinese”. Also, we have the language in our manuscript edited by a native-English speaker with scientific expertise in Edanz.