Reviewer's report

Title: Cholinergic receptor nicotinic alpha 5 subunit polymorphisms are associated with smoking cessation success in women

Version: 0 Date: 05 Jan 2017

Reviewer: Kevin Jensen

Reviewer's report:

Many of my initial concerns have not been addressed adequately, and I have some responses to the revised manuscript. My responses are included below the authors' responses and numbered as 1a, 2a, 3a, etc.

Answers to Reviewer 1:

Methods/Results

1. Additive genetic effects should be tested for each SNP. Most of the literature indicates that the genetic effects at these nicotine receptor genes are additive.

We tested the additive model for each SNP; but for these SNPs, the dominant model is more reported in the literature and our findings were consistent.

1a. It's understandable that the dominant model was tested and the authors may consider discussing their finding in relation to other studies that used a similar approach. For example, how do the dominant model results compare to the results reported by Tyndale et al. (PLoS One. 2015 May 26;10(5):e0128109) and others. However, the additive model results should also be reported in the manuscript because several studies have tested additive effects, including some of the largest genetic studies on smoking behavior (n > 100,000; Nat Genet. 2010 May;42(5):441-7) and cessation (n = 29,072; J Natl Cancer Inst. 2015 Apr 14;107(5)).

2. What are the non-white races?

Non-white races are blacks, intermediates, Asians and Amerindians.

2a. The number of white, blacks, intermediates, Asians and Amerindian participants should be described in the paper. The non-white participants are a large fraction (~35%) of the sample, so this group needs to be described more precisely.
3. Results for an analysis of each race should be presented separately.

We were not able to conduct a stratified analysis for each race because the sample size is very small. However, the same result is observed in the White and Non-White groups.

3a. Results for the analysis of each racial group should be presented separately somewhere in the manuscript.

4. Were males and females analyzed together with a genotype by sex interaction term included in the model? Was this interaction significant?

Yes, but the interaction analyses was not significant.

4a. This is an important result that should be reported in the text if the model was analyzed as described above.

5. Was genotype associated with treatment course, for example did genotypes differ by NRT vs bupropion vs varenicline treatments?

No, the same frequency of genotypes were observed in the drug groups.

5a. This should be mentioned somewhere in the manuscript.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

No

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Yes

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes
Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

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