Reviewer’s report

Title: EFFECTS OF FACTOR V LEIDEN POLYMORPHISM ON THE PATHOGENESIS AND OUTCOMES OF PREECLAMPSIA

Version: 2 Date: 10 Aug 2019

Reviewer: Mariza de Andrade

Reviewer's report:

The revised paper by Abadio GK et al. discuss the effects of FV Leiden polymorphism on the pathogenesis and outcomes of preeclampsia.

My first issue in the paper is regarding the race admixture in GHANA subjects. FV Leiden is a caucasian mutation identified in Leiden, Neederlands and it is rare. The authors should explain the percent of caucasians these women inherited and from which countries. I am surprised based on the results in Table 1 that cases (BP and PE) has higher allele frequency for the G allele than the A allele which is opposite in the control group. The paper will be much better if the authors provided the different races involved in these females that can be easily done using principal components using PLINK or using STRUCTURE.

The second issue is the lack of explanation in Table 2. The authors should explain that the table described the 3 genotypes: AA, AG, GG for the three groups of women (CTRL, BP, PE) and the clinical data available. There are missing values of GG in the controls groups since these group is neither pregnant but healthy. The authors should discuss why probably because they are health and not pregnant. The FV mutation was asseses with HW equilibrium using Chi-Square test.

The description of the recruitment and material collections are explained well as well as the exclusion criteria. The statistical analysis is simplistic either they used Student's t test or ANOVA. Since they have 3 groups, they did not correct the p-value for 3 groups.

From 96 subjects only 81 were enrolled. The analyses used FVL exons 8 and 10 with allele frequency in exon 10 of 0.67 and 0.34 for G and A respectively. The authors observed an increased in FVL mutations in PE and hypertensive subjects. But the HWE are not in agreement with the frequencies in PE and hypertensive due to the loss of heterozygosity, which is an interesting observation.

As mentioned above the authors should focus in the admixed populations in GHANA subjects to better understand the founder effects or genetic drifts.

I agree with the authors when they attributed the absence of FVL mutation in exon 8 identified mutant homozygous in FVL exon 10.
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.

No

Are the conclusions drawn adequately supported by the data shown?
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No

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I am able to assess the statistics

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