Reviewer’s report

Title: HNF1A gene p.I27L is associated with early-onset, maturity-onset diabetes of the younglike diabetes in Turkey

Version: 1 Date: 06 Mar 2019

Reviewer: Monika Dmitrzak-Weglarz

Reviewer's report:

The text still needs language correction. The lack of the use of correct articles, the lack of an appropriate form of singular or plural and typos are often repeated errors.

It is moving away from the use of MODY with the number; it is necessary to complete the correct names with gene mutations.

The scheme of including patients in the study is incomprehensible. Of the 567 patients with suspected MODY, 76 patients were excluded who had mutations in one of 4 genes, including HNF1A. Subsequently, variants in the HNF1A gene were again examined in the remaining patients and controls. Please complete the information on which variants were examined in the first part of the study.

Over 30 genes contribute to an increased risk of developing type 2 diabetes. The most important risk factor is the TCF7L2 allele, which increases the risk of developing diabetes 1.5 times and has not been included in the study. It is necessary to provide a more detailed justification for the selection of polymorphisms studied only in one gene, without the others having a more significant impact.

Adoption of an arbitrary age of 45 as an early and late age cut-off point is not a right approach, mainly since the average age of onset of the subjects was 28.17 +/- 12.66. Determine the cut-off point individually for the study group by determining the median age of diagnosis +/- 2SD. It may turn out that there will be a completely different distribution of patients and the frequency of polymorphisms.

At work, it should be supplemented how many patients meet the criteria for early and late onset of type 2 diabetes. The results should also be supplemented with a comparison between these two groups.

When using the Bonferroni correction, it is not possible to consider a statistically significant value of p <0.05. Please complete the calculation.

After completing the results, the text, in particular, the conclusions should be modified.
In the conclusions, the authors should put information on the usefulness of the obtained results and the recommendation on the presence or absence of diagnostic/practical value of the studied polymorphisms.

Literature needs updating, no citation from 2017-2019.

**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.

No

**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

**Quality of written English**
Please indicate the quality of language in the manuscript:

Needs some language corrections before being published

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