Reviewer’s report

Title: Prevalence of CCR5delta32 in Northeastern Iran

Version: 1 Date: 30 Sep 2019

Reviewer: Daniela Zanetti

Reviewer's report:

The authors did not address the majority of my previous comments, specifically the followings:

Major comments:

1. The authors assessed that the frequency of CCR5Δ32 allele in the general population of North East of Iran has not been investigated, and that the low prevalence of CCR5Δ32 CCR5Δ32 allele in the Iranian population may result in the increased susceptibility to HIV-1.

Has the prevalence of HIV-1 in Iran been investigated before? Is the prevalence of HIV-1 in Iran higher than in Europe and in East Asia? The authors should analyze the allele frequency of the CCR5 locus in relation to the HIV-1 prevalence in Iran and in other countries.

The authors added a table in the new version of the manuscript of CCR5Δ32 allele distribution in Iran, but my question was focused on the link between HIV-1 and CCR5Δ32 frequency.

3. The Δ32 mutation at the CCR5 locus is a well-studied example of natural selection acting in humans. It would be interesting for the manuscript to perform some type of selection analyses (spatial ancestry analysis or maybe a geographical distribution of the minor allele frequency of the CCR5 locus) using the Iranian population together with the 1000 Genome Populations, if no other populations are available.

In addition to this, it would be interesting to compare the geographical allele frequency distribution of the CCR5 locus with the prevalence of HIV-1 in different countries. The two maps (allele frequency of CCR5 and prevalence of HIV-1) will be useful to discuss about the origin of CCR5 in Iran compared to other countries.

The authors added a table in the new version of the manuscript of CCR5Δ32 allele distribution in Iran, but my question was about natural selection and/or about adding a plot comparing the geographical allele frequency distribution of the CCR5 locus with the prevalence of HIV-1 in different countries.

The points 1 and 3 would be helpful to support their conclusion about the low prevalence of CCR5Δ32 allele in the Iranian population and the increased susceptibility to HIV-1. Since the
authors did not perform any functional study or observational association between the CCR5Δ32 allele and HIV-1, their conclusions are not supported by their data right now.

4. Page 7: Some studies have shown the relation between CCR5Δ32 allele and MS disease. Can the authors discuss the possible links between CCR5Δ32, MS and HIV-1?

5. Can the authors explain this sentence?

An application of this research can be identified the most appropriate individuals to work with HIV-1 in the laboratories, in which we could enroll personnel having this mutation to reduce the risk of HIV-1 infection in the laboratories.

What does it mean "to work with HIV-1 in the laboratories"? Is there perhaps an high risk of HIV-1 infection in the laboratories? Could the authors contextualize this affirmation?

The authors did not explain their previous affirmations, but they simply removed their previous sentences indicating a very poor effort in increasing the value of the manuscript.

Minor comments:

1. What does the term Caucasian mean in this context? Europeans? The reference 17 did not use the term Caucasian.

The authors did not explain the reason why they are using the term Caucasian. The term European would be more appropriate.

8. Availability of data and materials

Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

What about the 400 samples genotyped? I think that the authors generated and analyzed new data in the current study.

The authors added a description of their data for the Reviewers, without changing any section in the manuscript and without giving any reference in the Availability of data and materials section.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.
Yes

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

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I am able to assess the statistics

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