Reviewer's report

**Title:** Association of Vitamin D Receptor Apal polymorphism with asthma among the Chinese Han population: a case-control study

**Version:** 1  **Date:** 23 April 2009

**Reviewer:** Giovanni Malerba

Reviewer's report:

Saadi and colleagues reported the association between rs7975232 marker (VDR gene) and asthma in Chinese Han population (567 asthmatics and 523 controls). Five markers of the VDR gene were investigated by single marker analyses and haplotype analysis. Haplotype analysis confirms the association observed for the rs7975232 marker.

Results are interesting, however manuscript is a little bit confused resulting uncleared in several sections.

Comments

**Major**

1) Structure of the manuscript
The Methods, Results and Discussion sections should be rearranged by moving several sentences from one section to the other according to the content of the sentence (for example in the Results-Genotyed SNPs subsection, authors describe locations and the selection method for each SNP: this should be moved into Methods section).

2) Phenotypes
Authors indicate that clinical characteristics have been described in previous papers. However I think that a brief description of the sample would help the reader in understanding the association results. I would suggest to include a brief description of the sample set (asthmatic individuals are atopic? what is the definition of atopy? etc).

3) SNP selection
It is not clear how the SNPs have been selected. They are candidate SNPs from previous published results, or they are tagSNP for haplotype of Chinese population, or other? Authors should describe the method used (to be described in the Methods section and not in the Results section).

4) Statistics
Bonferroni
Authors write (Methods - Statistical analysis) they used Bonferroni correction to adjust for multiple tests but this correction was not applied throughout the
manuscript. Authors should fix the point by adjusting the results or explaining why they did not correct for multiple tests.

5) Graphic analysis
In the Results section the authors mention the Graphical analysis software. This should be described in more detail and moved to the Method section. Authors should explain the meaning of the Z statistics to make the results of table 3 interpretable.

6) Linkage Disequilibrium
In figure 1, author report that D'>0.6 corresponds to high LD. I don't agree (a D' > 0.9 is generally thought to indicate high LD), however I understand that this is a questionable point. Authors should explained why they consider a D'>0.6 as a high LD value.

7) Block B
Authors mention block "B" in the 'Results-Genotyped SNPs' and 'Discussion' sections but block "B" is defined nowhere. Definition of block "B" should be included or any reference to block “B” should be removed.

Minor
8) Methods- SNPs selection
I would suggest to remove all the sentences (or summarize them) describing the PCR and tools used to detected the mutations, since they are commonly used standard methods . Authors should report primers and restriction enzymes only.

9) SNP nomenclature
I suggest to use the rs# name to identify each SNP instead of the name of the less clear name of the restriction endonuclease used.

10) Haplotypes
Authors state that " ... a haplotype transmission analysis was later conducted ...". I think that the word transmission is wrong since all the individual are unrelated one with the other. The word "association" would be preferable. Authors should adjust the sentence or explained the meaning of "transmission".

Level of interest: An article of limited interest

Quality of written English: Needs some language corrections before being published

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:
declare that I have no competing interests