Reviewer's report

Title: Association of ADAM33 gene polymorphisms with COPD in a northeastern Chinese population

Version: 1 Date: 21 May 2009

Reviewer: Mayumi Tamari

Reviewer's report:

Major Compulsory Revisions

Wang and colleagues reported an association study of ADAM33 gene variants with COPD in a northeastern Chinese population. It is important to determine whether the finding is replicable in other independent populations.

I have following comments.

The authors firstly selected eight Tag SNPs for genotyping. The author mentioned that they selected SNPs from published ADAM33 SNPs associated with excess decline in FEV1 and/or presence of COPD. References should be added after the sentence.

Linkage disequilibrium among the selected eight SNPs should be explained with actual D’ and r2 values and allele frequencies. It would be better to explain about differences of linkage disequilibrium between northeastern Chinese and Caucasian populations.

How many SNPs with minor allele frequency >5% will be captured with the finally genotyped eight SNPs in human ADAM33 genes?

In European children, M+1 SNP was associated with lower FEV1 [24]. Why the authors did not include the SNP in this study?

The present study showed that the T1, T2, S2, and Q-1 were significantly associated with COPD. The authors should also discuss about the direction of allelic association in previous studies and this study.

The authors reported association studies of ADAM33 polymorphisms in adult allergic asthma and rhinitis in a Chinese Han population [30]. The similarities and differences of the results among the studies should be discussed in detail.

Level of interest: An article of limited interest

Quality of written English: Not suitable for publication unless extensively edited

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

Declaration of competing interests:
I declare that I have no competing interests' below.