Reviewer’s report

Title: Association of common variants identified by recent genome-wide association studies with obesity in Chinese children: a case control study

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Reviewer: Annique Claringbould

Reviewer’s report:

Wang and colleagues describe an association study of 40 SNPs previously found associated with obesity. The association of 32/40 SNPs is checked in a sample of 2030 Chinese children, of which 718 are overweight, and 705 obese. The authors use logistic regression to test for association with overweight or obesity, and linear regression to test the effect of each SNP on the BMI standard deviation score. The study is executed well and shows some interesting associations. However, low power of the study (as indicated by appropriate power calculations) results in the detection of only two associations after p-value correction for multiple testing.

Minor Essential Revisions

The correction for multiple testing could be avoided, given the prior hypothesis of the common origin of the variants leading to obesity in major ethnic groups, therefore the expected transferability between ethnicities (several T2D and obesity papers could be cited). Therefore, any variant associated at 0.05 significance could be referred to as associated in this relatively small sample.

It would be good to expand on the comment on different effect sizes between ethnicities for one locus. The differences found at rs543874 of SEC16B and rs2241423 of MAP2K5 are interesting, but a statistical evaluation along the lines of “Transethnic meta-analysis of genomewide association studies,” Morris, A.P. (DOI: 10.1002/gepi.20630) would provide more insight into this effect. It could be worthwhile to look into other loci with less pronounced evidence of heterogeneity as well to find more potentially interesting differences in effect sizes between populations.

Discretionary Revisions

Mention the participants’ average age in the text on p.7, and refer to table 1 with characteristics of participants here, rather than in the results section.

Could the authors state what value the BMI in the 95th percentile is (p.7) ? Maybe a graph of the BMI distribution or a table of what BMI constitutes obesity and overweight at different ages could be added.

On p.9, line 8: could you also select proxy SNPs based on the CHB HapMap sample, rather than CEU? It does not seem logical to use CEU with the Chinese
participants.

Use the term GWA studies, rather than GWAS. The authors often write ‘GWAS studies’, which translates to ‘genome-wide association studies studies’.

The abbreviation BMI is introduced twice (p. 5 in background and p. 7 in subjects)
In table 2, indicate the proxy SNPs.

**Level of interest:** An article of importance in its field

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

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