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Letter to the Editor: Genetic Contributions to Childhood Obesity: Association of Candidate Gene Polymorphisms and Overweight/Obesity in Korean Preschool Children

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▸ See the article "Genetic Contributions to Childhood Obesity: Association of Candidate Gene Polymorphisms and Overweight/Obesity in Korean Preschool Children" in volume 32 on page 1997.

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Dear editor:

I have read with interest the study by Yoo et al.,[1] on the "Genetic Contributions to Childhood Obesity: Association of Candidate Gene Polymorphisms and Overweight/Obesity in Korean Preschool Children." The authors reported that their data suggest that overweight children exhibited a higher frequency of the A allele in the AT2 C3123A polymorphism compared to the controls (odds ratio [OR], 1.72; 95% confidence interval [CI], 1.03–2.88; $P = 0.038$), and the frequency of C allele in the transforming growth factor beta-1 (TGF-β1, OMIM: 190180) T869C polymorphism (OR, 1.93; 95% CI, 1.15–3.21; $P = 0.010$) was also higher in obese or overweight children than in control subjects.[1]

However, I have three comments on this study. First, the authors used AT2 for gene symbol, while the symbol of angiotensin II type 2 receptor (OMIM: 300034) is *AGTR2*. Second, the *AGTR2* gene has been mapped to the human X chromosome band q22–23.[2,3] We know that females have two X chromosomes and males have only one X chromosome. Therefore, there were quite different patterns for genotypes of genes located on X chromosome. In females, we can observed three genotypes (AA, AC, and CC) and in males we can determine subjects carrying the A or C alleles (AY and CY). Therefore, for such polymorphisms, investigators should report the genotypes in each gender group separately. Unfortunately, the authors report the genotypes in the pooled samples.

I mentioned in my previous letters that unfortunately, in some genetic association studies, the observed genotypic frequencies showed significant deviations from the expected values based on the Hardy-Weinberg equilibrium (HWE).[3-8] It is strongly recommended by STrengthening the REporting of Genetic Association studies (STREGA) that authors should investigate the HWE in their samples.[9] Using data presented in the above mentioned article, we can find that the observed genotypic frequencies of the TGF-β1 T869C ($\chi^2 = 4.21$; df = 1; $P = 0.040$) polymorphisms showed statistical significant deviation from the expected frequencies based on the HWE. The significant difference between the observed and expected frequencies of the study genotypes may be interpreted by occurring errors in genotyping

determination and/or by occurring errors during selection of the participants. Therefore, the results presented by Yoo et al.[1] should interpret with caution.

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