Comments On: "ApaI and Fok1 Variants of Vitamin D Receptor Gene Associated with Metabolic Syndrome Among Jordanian Women"

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Dear Editor,

read with interest the study by Atoum titled "ApaI and Fok1 variants of the vitamin D receptor gene associated with metabolic syndrome in Jordanian women", published in the January 2024 issue of your Journal.¹ The author investigated the association of four common genetic polymorphisms (rs7975232, rs1544410, rs2228570, and rs731236) in the vitamin D receptor (VDR, MIM: 601769) with the risk of metabolic syndrome in Jordanian women. It was found that two polymorphisms were significantly associated with the risk of metabolic syndrome. However, I have some comments on the mentioned research.¹

As recommended by the STrengthening the REporting of Genetic Association studies, researchers should compare the observed frequencies of genotypes with the expected frequencies based on Hardy-Weinberg equilibrium in their control groups using the chi-square (χ^2) test and ensure that the observed frequencies are consistent with the expected Hardy-Weinberg equilibrium frequencies. However, many published articles have shown a discrepancy between the expected and observed frequencies.³

I compared the observed genotypic frequencies with the expected ones for four polymorphisms using the information provided in Table 3 of the above article. The results showed that for the rs2228570 polymorphism there was no significant difference between the observed and expected values ($\chi^2 = 0.70$, degrees of freedom (df) = 1; p = 0.401), while

the remaining polymorphisms showed significant differences (for rs7975232: $\chi^2 = 4.68$, df = 1; p = 0.030; for rs1544410: $\chi^2 = 13.57$, df = 1; p < 0.001; and for rs731236: $\chi^2 = 23.93$, df = 1; p < 0.001).

It has been previously reported a significant difference between the observed and expected values can be seen in the presence of sampling bias or genotyping error.^{2,4} It can be concluded that sampling bias or genotyping error occurred in the present study. I should also add that the STrengthening the REporting of Genetic Association statement recommends that when multiple genetic polymorphisms of a given gene are studied, haplotype analysis should also be performed, and linkage disequilibrium parameters should be reported. Unfortunately, this was not done. In light of the above discussion, the results reported in this paper need to be interpreted cautiously.

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