Corrections to the *LDLR* Gene Polymorphisms Identified in a Taiwanese Population

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Sir,

As the authors of the article “*LDLR* and ApoB are Major Genetic Causes of Autosomal Dominant Hypercholesterolemia in a Taiwanese Population” in the October 2007 issue of the *Journal of the Formosan Medical Association*, we found two numbering errors regarding the novel polymorphisms of the *LDLR* gene we identified in patients with autosomal dominant hypercholesterolemia.

In Table 4, the two novel polymorphisms of the *LDLR* gene were originally numbered as A/p1G1415 in exon 10 and C/p1T2258 in exon 16. However, these numbers are erroneous and they should be relabeled as A→G1374 (exon 10, Arg>Arg) and C→T2358 (exon 16, Ser>Ser), respectively.

The text describing the *LDLR* gene variants in the results section (page 803, lines 17–18 under the *LDLR* gene variants subheading) should also be corrected to “A> G at 1374 and C> T at 2358”).

Both of the polymorphisms were confirmed by screening 50 control DNA samples (100 alleles) and cross-matching in the *LDLR* mutation database.

As the information is important to the understanding of autosomal dominant hypercholesterolemia in Taiwanese people, and as the polymorphisms could also be incorporated into *LDLR* mutation databases, we hereby write in to formally correct our article.

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References


2. Leigh S. *Allelic Variants in the LDLR Database*. Available at: http://www.ucl.ac.uk/ldlr/LOVDv.1.1.0/

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