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RETRACTION

In our article "Two novel prevalent polymorphisms in the hormone-sensitive lipase gene have no effect on insulin sensitivity of lipolysis and glucose disposal" by Stumvoll et al., published in the November 2001 issue of the *Journal of Lipid Research* (Volume **42**, pages 1782–1788), we described two prevalent, previously unknown amino acid polymorphisms in the hormone-sensitive lipase gene. The diagnosis of the point mutations in codons 620 and 681 was based on mutation screening by direct sequencing using the cycle sequencing ready reaction kit and the ABI PRISM® Systems 310 Genetic Analyzer (Applied Biosystems, Foster City, CA). Using the identical method, the mutant bases were reproduced in other subjects on two occasions several months later. We further reported the absence of an association of these two polymorphisms with insulin sensitivity of suppression of lipolysis in healthy humans.

Following the publication of this article, we were contacted by three groups who were unable to detect these polymorphisms in their populations. Therefore, we reanalyzed all the samples, again using the above-mentioned automated sequencing technique, but this time (2 years after the original sequence analysis) we were unable to reproduce the original results. The absence of polymorphisms has been verified by Dr. P. Talmud (London) by PCR plus restriction enzyme digest. Because reinspection of the original sequence chromatograms confirmed the comigration of two bases indicating heterozygosity, we sent these and the raw data to technical staff at Applied Biosystems. Careful assessment by company experts confirmed that the original sequence chromatogram could be interpreted as a heterozygote sequence. However, analysis of the raw data indicates that the original "mutations" are artifacts probably due to overloading of the capillary electrophoresis. This indicates that we had reported a sequencing artifact. Therefore, we retract the published results.

To prevent such errors in the future, Applied Biosystems proposes that interpretation of the sequence analysis can only be carried out if fluorescence intensities are between 1,500 and 4,000 units, a limit that was not recommended at the time of our original analysis. Moreover, since sequencing errors produced by an automated sequencer are possible, DNA sequence variants obtained from direct sequencing must be confirmed by PCR and restriction enzyme digest; this was not done in our reported study.

We deeply regret the error and apologize especially to those who already invested labor and resources based on this publication.