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LETTER TO THE EDITOR

Soong Deok Lee

Response by S.D. Lee to the Letter to the Editor by R. Szibor, J. Edelmann, S. Hering: On the article entitled "Polymorphism of nine X chromosomal STR loci in Koreans"

Dear Sir,

First of all I would like to express my thanks for the careful review for my article. Szibor et al. criticise the results of my article in several points. I do not want to discuss it in all points, but I feel there may be some areas of misunderstanding. Here is my explanation for that.

Szibor et al. express the opinion that the wording in my article "No remarkable population differences were found between Koreans and other populations studied" is totally wrong. This may be true but could arise from a misunderstanding due to an incorrect use of words. I did not mean that our data is exactly the same as those for other populations including all the allelic frequencies. I wanted to focus on the general distribution pattern of the X chromosomal STRs. As Szibor et al. point out, there exist population differences, but I feel that all STRs have such a degree of population differences. This is why we report population data on STRs for many different populations.

They have criticised the results on DXS9898 because they cannot find the allele 8.3 in my population study. If you compare the results there exist two repeat number differences between my results and theirs (Hering and Szibor 2000). Instead of 8.3, we reported allele 6.3 and except for this 2 repeat number difference, the general distribution pattern looks very similar, apart from the racial difference. According to their report and this is the same with ours, the repetitive unit of DXS9898 is composed of $(TATC)_2(ATC)$ (TATC)n and the first $(TATC)_2(ATC)$ can be regarded as a non-repeat unit. The (ATC) for allele 6.3 is within the last (TATC)n. If they would have analyzed both data carefully, they would not have insisted that the allele 8.3 is important. I did not mean to ignore the racial difference.

For the mutation rate, I do not want to insist that the rate in my article is exact. I believe that the estimation of the mutation rate must be based on a family study with a sufficient number of samples. I feel the sample number in my article may not be enough to safely estimate the mutation rate. The reason to report the different mutation cases is to find the reason and demonstrate that these are real mutations. My results contribute to this point. The point I want to stress is that I have checked the family relationships and the results for all members of the families.

For the locus DXS6803 I do not want to say that this locus is valuable for practical purposes. The high mutation rate and 1 bp difference must be drawbacks for the practice. I have found unusual results in this locus which others have not reported, and I have thought that my report would assist others who try to establish this locus. I have also added my experience in my article for some loci other than the 9 reported. I still have no answer for the high mutation rate at this locus. It may be highly unstable, and replication or even PCR errors from the unusual structure may be the reason.

Szibor et al. have commented that PAGE and silver staining is an old-fashioned method, and may be the reason for the unusually high mutation rate, but I do not agree with this. As is well known, a 1 bp difference in STR typing is a difficult area technically, so we have paid much attention to check the results. We also amplified the DXS6803 locus only to check the mutation family and have checked the gels several times. They seem to believe that the results in my article are incredible, and this may be the result of the old-fashioned method. Except for the racial differences, the general pattern of the X chromosomal STRs reported looks similar to that found by others (Edelmann et al. 2001). But even with an old-fashioned method, we can get valuable results as our former researchers have had, and I believe that my article has not presented incorrect results.

Soong Deok Lee (✉)
Department of Forensic Medicine,
Seoul National University College of Medicine,
Chongno-gu Yenogon-dong 28, 110–799 Seoul, Korea
Tel.: +82-2-7408353, Fax: +82-2-764-8340,
e-mail: Sdlee@snu.ac.kr

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