Correspondence

Commentary on: Barros de Castro IA, Rinzler CM, Rumjanek FD. Allele frequency distributions for twelve STR loci in a Brazilian population. J forensic Sci 2000;45(4):941.

Sir:

It was with apprehension that we read the communication of Barros de Castro and collaborators published in the *Journal of Forensic Sciences.* The authors have described the absence of the 9.3 allele in the TH01 locus in a population of 307 individuals from Rio de Janeiro, Brazil.

It is well known that this allele, an 1 bp deletion of the 10 allele at the TH01 locus, it is very common in all populations studied so far, including those in Brazil. Moreover, in all those populations, the 9.3 allele is more frequently observed than the 10 allele. Bayoumi and collaborators have stated that "it was difficult at times to distinguish between 9.3 and 10 alleles of the HUMTH01 locus, it was evident that 9.3 was the predominant allele . . ." (Eletrophoresis 18:1637/40, 1997). For instance,our database, which includes several hundreds subjects from Rio de Janeiro and São Paulo, shows that the frequency of the 9.3 allele is 23% while the 10 allele frequency is 2.1%. These frequencies are not different from those described for other populations.

Therefore, taking these facts into consideration, it seems reasonable to recommend that the data from de Castro and collaborators, regarding this specific allele, should be used with caution and carefulness when applied for human genetic identification in the general brazilian population.

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Author's Reply/Response

Sir:

First, the reported data expresses exactly what we have found in the population investigated. Furthermore, the distinction between alleles 10 and 9.3 is not as straightforward when using silver staining of amplified STRs, as pointed out by Drs. Neto-Silva and Bydlowski, who incidentally did not mention whether their own frequencies are based on data obtained using the same methodology. Presumably this group resorted to the same method, and using their own argument, might have themselves introduced a bias towards scoring allele 9.3 rather than 10. The same could be true about the reference quoted in their letter. I also call the attention to data obtained by Promega, in a population of African-Americans, in which the reported frequency for allele 9.3 is 0.090, a value which is significantly different from 23%. It can be predicted that if more populations are compared, a wider spread will certainly be detected. Unfortunately, as is widely known, populations never display an ideal behavior.

Second, the data published by us reveals points that are far more interesting than those pointed by Drs. Neto-Silva-Bydlowski, namely, the atypical allele distribution within certain loci, as revealed by the exact test. That would have been worth discussing, space permitting. Alas, this has been missed by the aforementioned group. Finally, within the context of comparison of population data from different laboratories, the question of "whose data should be used with caution?," could be raised. Which set of data could be considered closer to the truth? Until the alleles have been scored based on data from, say an automatic sequencer, the case for the ambiguity of frequencies remains open.

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