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INVITED EDITORIAL

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Coordinating Y-chromosomal STR research for the Courts

Introduction

The growing interest of contemporary biology in the human Y chromosome (Hammer 1995; Jobling and Tyler-Smith 1995) has extended to forensic circles. This trend emerges from a consideration of the increasing number of papers published in forensic science journals concerned in qualifying polymorphisms of human Y chromosomes as tools for molecular identification. Jobling et al. (1997) list a number of forensic issues to which the male-specific profiles could be applied and discuss their appropriateness and suitability. In view of the inherent court application, we wish to discuss some critical aspects of this new class of DNA profiles and issue some guidelines for those researchers who are considering to prepare and submit forensic Y-STR work to the International Journal of Legal Medicine.

A consensus typing scheme for male identification

The perspective that male DNA profiles could become the natural counterpart of mitochondrial polymorphisms and attain the same practical success as the mtDNA control region is endorsed by the broad range of application of haploid profiles. However, many of the currently available Y-profiles have a discrimination power too low for court use because researchers tend to type a small number (< 3) of STRs on a large (> 100) population sample. This strategy seems to be a relic of autosomal typing and is obviously of little forensic value when applied to a non-recombining system such as the Y-chromosome. What is required is extending each individual typing in the sample to as many Y loci as possible, even at the cost of typing smaller sample sizes. Eventually, these haplotype data sets will accumulate into a database large enough for practical use in the courts. Kayser et al. (1997) have already standardised genotyping procedures and proposed a practical "core set" of STRs for further research. We would encourage further publications complying with the proposed standards.

DNA repositories

Significant efforts should be devoted in constructing banks of male genomes accessible to a large circle of researchers for integration into future refinements of male haplotypes. The samples should be drawn from diverse populations, since there is growing evidence that dramatically different frequencies of haplotypes exist in different populations (Forster et al. 1998). It is evident that a publication on a new Y-locus is more informative if it is studied on previously characterised samples than on fresh samples. For example, a research group might have previously published the Kayser et al. (1997) core set of Y-STRs in certain individuals; if they or others then describe a novel locus or novel variants of an existing locus using the published samples, they could quantify the improvement of the new locus on the haplotype resolution and present a useful new publication to the research community (cf. Caglià et al. 1997, 1998).

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