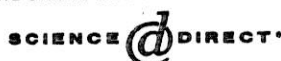




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Editorial

Editorial on the recommendations of the DNA commission of the ISFG on the interpretation of mixtures

The rapid evolution of forensic DNA analysis based on typing results from short tandem repeat (STR) polymorphisms has dramatically increased the significance of biological stains in criminal court proceedings. It has come to the point where DNA evidence alone could be decisive for obtaining a conviction of an accused suspect. Thus the interpretation of the observed DNA profile of a given stain in the context of the case needs to include a reasonable biostatistical evaluation of the weight of the evidence. At the same time, the molecular biological tools available to the forensic geneticist have become more and more sensitive to the point where the genomic DNA from a few dozen cells may be sufficient to obtain a full STR profile from an unknown offender. As a result, the number of DNA mixtures composed from full or partial profiles from two or more contributors (who could be offenders, victims, or individuals not associated with the crime event) has increased significantly. The biostatistical interpretation of such mixed DNA profiles is a very challenging task that sometimes leads to controversial views about correct mathematical approaches for estimating the weight of the evidence. Indeed, diverse practices have already arisen between laboratories, hence there is an urgent need to formulate recommendations.

As the main peer review body of the forensic community dealing with DNA profiling, the International Society of Forensic Genetics (ISFG) has already published numerous recommendations on issues related to nomenclature validation, and interpretation of autosomal, Y-chromosome and mitochondrial DNA typing systems. Typically, the DNA Commission will evaluate an area where sufficient, albeit sometimes uncoordinated scientific evidence, has been established from original research studies. This accumulated experience is used to formulate recommendations to serve as guidelines to standardize the use of new typing systems—a crucial prerequisite in forensic casework. In the recommendations of the ISFG Commission on mixture interpretation (Gill et al., 2006), the Commission has gone beyond this basic task. These recommendations have been written to serve two purposes: to define a generally acceptable mathematical approach for typical mixture scenarios and to address open questions where

practical and generally accepted solutions do not yet exist. This has been done to stimulate the discussion among scientists in this field. The aim is to invite proposals and criticism in the form of comments and letters to the editors of this journal, as well as by opening a discussion forum on the website of the society (<http://www.isfg.org>, available when the manuscript appears in print).

This paper is a 'high level' treatise on the mathematical principles to analyse complex mixtures. We realise that it will not be possible for most laboratories to immediately implement the methods described. Our intention is primarily to specify a consensus approach to act as the foundation stone. Hopefully we will encourage the development of expert systems to take care of the onerous calculations.

However, we also intend to describe pragmatic approaches to interpret mixtures. By comparing results against the mathematical principles described in this paper, the intention is to ensure that pragmatic approaches do not act in a non-conservative way. Often there are limitations to approaches, and our purpose will be to highlight these.

We are hoping to continue the process to allow the DNA Commission to critically revise or extend these recommendations in due time (hopefully at the next ISFG congress in Copenhagen in 2007). We are aware that the DNA Commission has not been able to offer solutions for the entire range of challenging samples that we encounter in our daily casework, but we hope having made a first step in the right direction by publishing the present recommendations.

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