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DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures

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- Recommendations considered in detail by UK and German working groups

UK DNA working group recommendations

NATIONAL RECOMMENDATIONS OF THE TECHNICAL UK DNA WORKING GROUP ON MIXTURE INTERPRETATION FOR THE NDNAD AND FOR COURT GOING PURPOSES

Peter Gill1, Rosalind M. Brown2†, Martin Fairley3†, Lara Lee3†, Maureen Smyth4, Neil Simpson5, Brian Irwin6, Jim Dunlop7†, Matt Greenhalgh8, Kerry Way9, Emma J. Westacott9, Steven Jon Ferguson10†, Lisa Victoria Ford10†, Tim Clayton11, June Guiness12

(submitted to FSI:Genetics)

Recommendations of the German working group

Allgemeine Empfehlungen der Spurenkommission zur Bewertung von DNA-Mischspuren
[General recommendations of the (German) stain commission on the interpretation of DNA
results from mixed stains]
P.M. Schneider, R. Fimmers, W. Keil, G. Molsberger, D. Patzelt, W. Pflug, T. Rothämel, H.
Schmitter, H. Schneider, B. Brinkmann
Rechtsmedizin 2006, 16 : 401 – 404

- **SWGDAM have now set up a working group led by John Butler**
- **Similar group to be considered in Australia**

- **Rapidly reaching global agreement on the way forward.**
- **Way forward is to convert ISFG recommendations into ‘local’ working guidelines.**

ISFG (2006) Recommendations

- Recommendation 1: **The likelihood ratio is the preferred approach to mixture interpretation.** The RMNE (probability of exclusion) approach is restricted to DNA profiles where the profiles are unambiguous. If the DNA crime stain profile is low level and some minor alleles are the same size as stutters of major alleles, and/or if drop-out is possible, then the RMNE method may not be conservative.

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ISFG (2006) Recommendations

- Recommendation 2: Even if the legal system does not implicitly appear to support the use of the likelihood ratio, it is recommended that the scientist is trained in the methodology and routinely uses it in case notes, advising the court in the preferred method before reporting the evidence in line with the court requirements. The scientific community has a responsibility to support improvement of standards of scientific reasoning in the court-room.

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ISFG (2006) Recommendations

- Recommendation 3: The methods to calculate likelihood ratios of mixtures (not considering peak area) described by Evett *et al.* (*J. Forensic Sci. Soc.* 1991;31:41-47) and Weir *et al.* (*J. Forensic Sci.* 1997;42:213-222) are recommended.

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ISFG (2006) Recommendations

- Recommendation 4: If peak height or area information is used to eliminate various genotypes from the unrestricted combinatorial method, this can be carried out by following a sequence of guidelines based on Clayton *et al.* (*Forensic Sci. Int.* 1998;91:55-70).

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Steps in the interpretation of mixtures

(Clayton *et al.* *Forensic Sci. Int.* 1998; 91:55-70)

Step #1	Identify the Presence of a Mixture
Step #2	Designate Allele Peaks
Step #3	Identify the Number of Potential Contributors
Step #4	Estimate the Relative Ratio of the Individuals Contributing to the Mixture
Step #5	Consider All Possible Genotype Combinations
Step #6	Compare Reference Samples

Figure 7.4, J.M. Butler (2005) *Forensic DNA Typing*, 2nd Edition © 2005 Elsevier Academic Press

ISFG (2006) Recommendations

- Recommendation 5: The probability of the evidence under H_p is the province of the prosecution and the probability of the evidence under H_d is the province of the defense. The prosecution and defense both seek to maximize their respective probabilities of the evidence profile. To do this both H_p and H_d require propositions. There is no reason why multiple pairs of propositions may not be evaluated (Appendix C).

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ISFG (2006) Recommendations

- Recommendation 6: If the crime profile is a major/minor mixture, where minor alleles are the same size (height or area) as stutters of major alleles, then stutters and minor alleles are indistinguishable. Under these circumstances alleles in stutter positions that do not support H_p should be included in the assessment.

- In general, stutter percentage is <15%

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ISFG (2006) Recommendations

- Recommendation 7: If drop-out of an allele is required to explain the evidence under Hp: (S = ab; E = a), then the allele should be small enough (height/area) to justify this. Conversely, if a full crime stain profile is obtained where alleles are well above the background level, and the probability of drop-out approaches Pr(D) ≈ 0, then Hp is not supported.

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ISFG (2006) Recommendations

- Recommendation 8: If the alleles of certain loci in the DNA profile are at a level that is dominated by background noise, then a biostatistical interpretation for these alleles should not be attempted.

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ISFG (2006) Recommendations

- Recommendation 9: In relation to low copy number, stochastic effects limit the usefulness of heterozygous balance and mixture proportion estimates. In addition, allelic drop-out and allelic drop-in (contamination) should be taken into consideration of any assessment.

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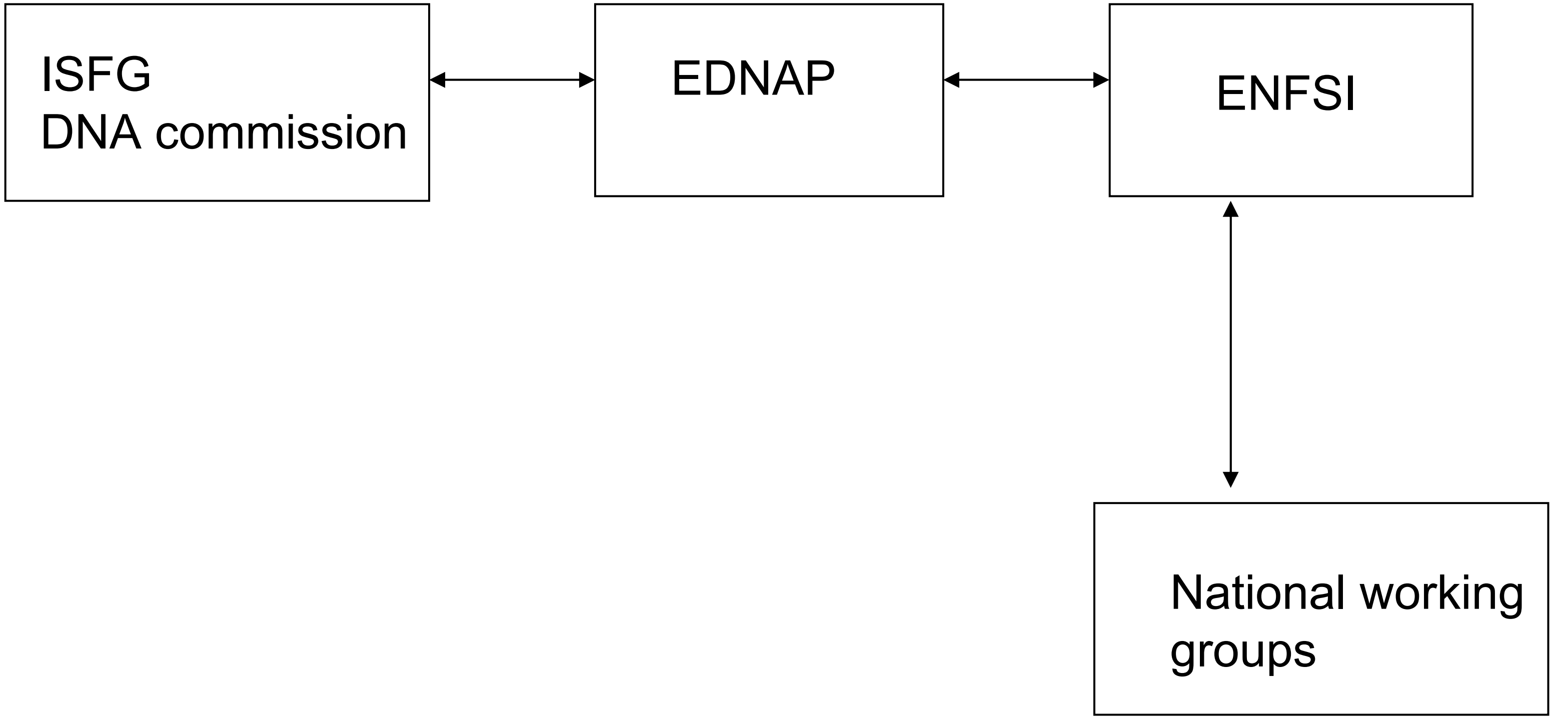
Bringing the commission to a conclusion

- How to demonstrate a consensus?

Peer review process



ISFG
DNA commission

EDNAP

ENFSI

National working groups

ENFSI Statement:

The general principles described by ISFG DNA commission recommendations on mixture interpretation are accepted by the ENFSI group