Centre Universitaire Romand
Médecine Légale

Unité de génétique forensique

Centre hospitalier universitaire vaudois
Hôpitaux Universitaires Genève

VALUE OF THE COMPARISON BETWEEN DNA MIXTURE PROFILES OF MORE THAN TWO CONTRIBUTORS IN SWITZERLAND

Patrick Basset (Patrick.Basset@chuv.ch),
Louanne Toulemont, Christian Gehrig, Tacha Hicks and Vincent Castella
Unit of Forensic Genetics, Chemin de la Vulliette 4, CH - 1000 Lausanne 25, Switzerland

Introduction

For a DNA profile to be submitted to the Swiss national DNA database, it is required that the DNA comes from no more than two persons. This means that about 10% of the DNA mixtures recovered in criminal cases cannot be searched for potential candidates nationwide, nor can the traces be compared to one another to provide investigation leads. Police services can request comparisons with DNA profiles of known persons; however, this happens in only a small proportion of the cases. In addition, the DNA profiles are rarely compared to each other; thus, it is not possible to highlight potential series with DNA in those cases. With the advent of probabilistic genotyping software and its associated tools, it is now possible to carry out this type of comparison, based on likelihood ratios (LR).

Method

In this study, we compared a total of 235 mixture DNA profiles pairwise using the mixture-to-mixture tool of the software STRmix v2.7 [1] with the aim of contributing to identify potential common contributors. These DNA profiles originated from traces collected by six different police services from western Switzerland between 2021 and 2022. The investigators selected traces based on information that supported that these were serial cases. Only pairs of profiles with LR values (H1: the two profiles share one common contributor *vs.* H2: all contributors of both profiles are unrelated) larger than 1'000 were explored further. The potential associations that were highlighted between profiles were then compared by the police to expected investigative associations to define the value of this approach in the Swiss context.

Results

- Among the 27'495 comparisons of profiles, 88 pairs (0.3%) showed at least one potential common contributor (Table 1):

  - 80 of these were DNA profiles from the same police service (1.6% of the intra police service comparisons);

  - 8 were DNA profiles from different police services (0.03% of the inter service comparisons).

Table 1. Number of pairs of DNA profiles with LR > 1'000 intra (orange) and inter (green) police services (FR, Fribourg; Ge, Geneva; JU, Jura; NE, Neuchatel, VS, Valais and VD, Vaud). N = number of profiles submitted by each service.

	FR (N = 30)	GE (N = 47)	JU (N = 32)	NE (N = 48)	VS (N= 20)	VD (N = 58)
FR	15	-	-	-	-	2
GE		18	1	-	2	-
JU			8	2	-	-
NE				6	-	1
VS					2	-
VD						31

- Most of the associations were qualified by the police services as "expected" (60/88) or "possible" (22/88). 6/88 associations were qualified as "unexpected" (Figure 1). Five possible case associations expected by the police were not detected by our analysis.

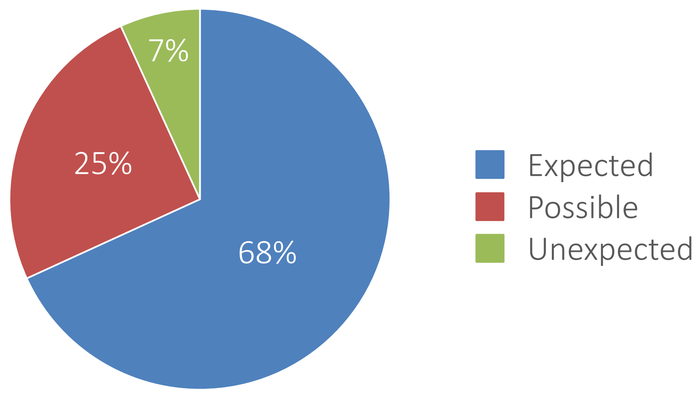

Figure 1. Proportion of associations qualified as expected, possible and unexpected by the police services.

- All Log10(LR) of unexpected associations were ≤ 5 but several expected or possible associations also showed relatively low Log10(LR)(Figure 2).

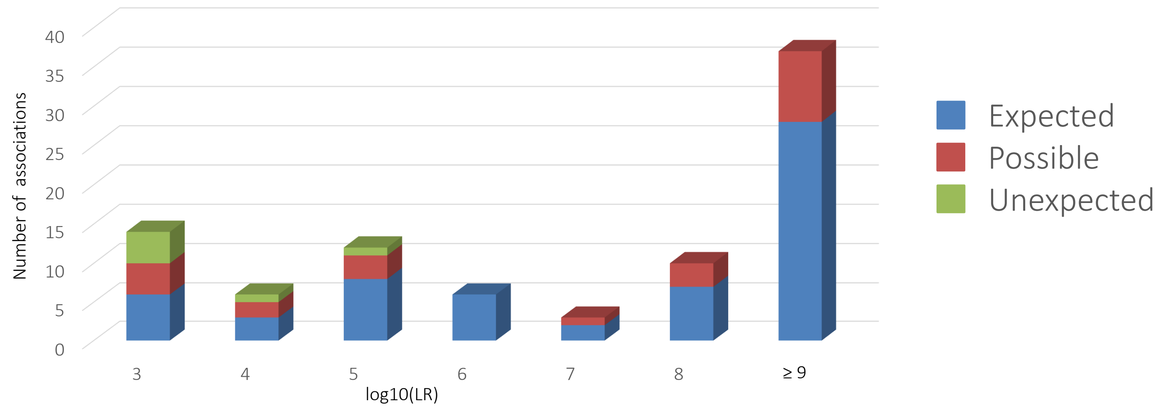

Figure 2. Number of expected, possible and unexpected associations and their log10(LR).

Discussion and Conclusions

- Multiple possible associations were underlined by our analysis illustrating **the potential to highlight series using DNA mixtures profiles**.
- Most possible associations were compatible with police investigative leads. This is especially true when the LRs were large.
- Such analyses are time consuming (especially STRmix deconvolutions). A cost-benefit analysis taking into account the type of cases (e.g., same police service, severity of crime) and resources available could be performed before comparisons.
- Potential associations need to be evaluated in the context of the case. Note that this approach has to comply with local regulations.

Reference: [1] Slooten K. 2017 Identifying common donors in DNA mixtures, with applications to database searches, Forensic Sci. Int. Genet. 26 (2017) 40–47.