

Forensic identification of an individual in complex DNA mixtures (Yissum) code: 6-2010-2361 <u>Ariel Darvasi</u>, HUJI, Faculty of Science, The Alexander Silberman Institute for Life Sciences

Efficient forensic identification method

Categories	Forensic sciences, DNA forensic
Development Stage	Algorithm and method completed; working on technology implementation for proof of concept
Patent Status	Provisional application filed
Highlights	

- New method to establish the presence or absence of an individual's DNA in a mixture of DNA (such as found at the scene of a crime) comprising up to ten individuals
- There is no current efficient method for identifying individuals in DNA mixtures containing more than two contributors.
- The new method is highly accurate under a wide range of actual forensic conditions, meeting court admissible standards.

Specific advantages:

- Efficiently allows the exclusion of relatives, preventing from the defence to claim that the suspect's relative is represented in the mixture.
- Does not requires accurate allele frequency data for an appropriate reference population, which might not be available.
- Does not require accurate estimates of allele frequencies in the DNA mixture, only a robust estimation about the presence or absence of each allele.

Our Innovation

Genotyping a specially designed panel of 1,000-10,000 single nucleotide polymorphisms (SNPs), each with a relatively low (