STRmix Has Produced DNA Evidence in More Than 530,000 Criminal Cases Worldwide

New Survey Also Indicates STRmix Evidence Has Been Presented in More Than 90 Successful Admissibility Hearings

WASHINGTON, DC, UNITED STATES, January 11, 2024 /EINPresswire.com/ -- STRmix™ forensic software has produced usable, interpretable, and legally admissible DNA evidence in at least 530,000 criminal cases worldwide since its introduction in 2012, according to the results of a new survey (https://strmix.com/news/strmix-has-produced-dna-evidence-in-more-than-530000-criminal-cases-worldwide/).

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>
> *John Buckleton DSc, FRSNZ*

The survey, conducted by New Zealand's Institute of Environmental Science and Research (ESR), also indicates that STRmix™ evidence, which is capable of resolving mixed DNA profiles previously regarded as too complex or degraded to interpret, has been presented in more than 90 successful admissibility hearings.

"STRmix™ has been particularly effective in resolving violent crime and sexual assault cases, as well as cold cases in which evidence originally dismissed as inconclusive was able to be reexamined," notes ESR Principal Scientist and STRmix™ co-developer John Buckleton DSc, FRSNZ.

More than 80 organizations in the U.S., including forensic laboratories operated by the FBI and the Federal Bureau of Alcohol, Tobacco, Firearms and Explosives (ATF), currently use STRmix™ to analyze DNA in criminal investigations. The software is also being used by 27 forensic laboratories internationally, including labs in Canada, the United Kingdom, Europe, Asia, the Middle East, the Caribbean, New Zealand, and Australia.

STRmix™ popularity is due in no small measure "to its ability to interpret DNA results faster than the previous binary interpretation method and use more of the information in a DNA profile," according to Dr. Buckleton. "Combined with DBLR™, STRmix™ is able to match mixed DNA profiles directly against a database – a major advance for cases in which there are no suspects and there is DNA from multiple contributors in one sample."

On the development side, the new ESR survey indicates that there continues to be significant use of Y-STR (male-specific DNA) profile analysis among forensic laboratories currently using STRmix™, with strong interest in a probabilistic genotyping solution for the interpretation of Y-STR profiles.

The survey also shows a notable adoption among STRmix™ users of autosomal Next Generation Sequencing (NGS, also known as Massively Parallel Sequencing) technology, pedigree analysis, and database searching of mixtures.

“We are responding to these trends with an active development program that is designed to address both the current and future needs of all of our users,” says Judi Morawitz, Development and Test Lead at STRmix. This includes the development of variants of STRmix™ capable of interpreting NGS and Y-STR profiles.

“We are very close to releasing a Research and Validation version of STRmix™ NGS which would allow users to research the potential implementation and validation path of Probabilistic Genotyping alongside NGS chemistries and sequencing equipment,” Morawitz explains. “Watch this space for developments with respect to both NGS and Y-STR interpretation.”

The latest version of the groundbreaking software, the recently released STRmix™ v2.11, features enhancements to memory use, general improvements to the models and model maker, and the inclusion of an upper bound to the HPD likelihood ratio (LR). Its most significant change however, is the addition of Amelogenin into the deconvolution and LR.

In addition to STRmix™ v2.11, the STRmix team has developed and previously launched two related software applications:
• DBLR™, an application which when used with STRmix™ allows forensic laboratories to undertake extensive kinship analysis, carry out rapid database searches, visualize the value of their DNA mixture evidence, and carry out mixture-to-mixture matches; and
• FaSTR™ DNA, expert forensic software which seamlessly integrates with STRmix™ (when in use) to rapidly analyze raw DNA data generated by genetic analyzers and standard profiling kits and assigns a number of contributors (NoC) estimate.

In combination with STRmix™, these applications complete the full workflow from analysis to interpretation and database matching. For more information, visit http://www.strmix.com.

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