VEROGEN

From DNA to Identification

Multi-application sequencing solutions from Verogen

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Applications for Every Case

Generate data that lead to a human identification

When human identification matters, Verogen offers the technology that generates powerful investigative intelligence from a DNA sample. Forensic genetic genealogy (FGG), mitochondrial DNA (mtDNA), short tandem repeats (STRs), and single nucleotide polymorphisms (SNPs) can work together to solve cold cases, identify missing persons, or exonerate and convict—a portfolio of capabilities exclusive to the Verogen MiSeq FGx® Sequencing System.

To provide a unique, turnkey solution, Verogen is integrating the MiSeq FGx Sequencing System, the only next-generation sequencing (NGS) instrument specifically designed and validated for forensic applications, with an expanding range of application-specific, single-workflow library prep kits, matched software tools, and now, a genealogical database. Backed by validation and implementation services, leveraging these tools is straightforward for any laboratory with access to a MiSeq FGx System. Maximize your ability to deliver the data that lead to a human identification.

Forensic Genetic Genealogy

Expand your network of information

FGG combines genetic and genealogy methods to identify people through relatives. The results provide investigative intelligence that exonerates the innocent, matches adoptees, and creates leads for cold cases. FGG is particularly useful when traditional methods are inconclusive, or all other options are exhausted.

A recent Verogen acquisition, the genealogical database GEDmatch aggregates DNA data files from known, voluntary contributors. Uploading a DNA data file yields a simple measurement of relatedness to help estimate kinship. This type of result makes GEDmatch a valuable tool that can create leads or eliminate suspects.

FGG and the GEDmatch database are gaining traction in real-world scenarios, providing meaningful investigative breakthroughs and resolving cases like the following.

- The charging of Joseph DeAngelo with 13 cases of murder and 13 cases of kidnapping. After decades of dead ends, GEDmatch assisted with the identification of DeAngelo as the alleged Golden State Killer.
- The conviction of William Earl Talbot II of a 1987 double homicide was the first conviction to apply FGG. Data from DNA collected at the crime scene over 30 years ago were uploaded to GEDmatch and ultimately led investigators to Talbot.
- The exoneration of Christopher Tapp for the 1996 homicide of Angie Dodge and the charging of Brian Leigh Dripps marked the first genealogy-based exoneration. A DNA sample from the crime scene was processed and compared in GEDmatch, narrowing the focus to Dripps. A DNA sample from Dripps then confirmed him as the source of the crime scene material.

Leveraging the MiSeq FGx System and working in concert with the forensic community, Verogen is developing FGG as an end-to-end, fully integrated solution. As the only portfolio to include this capability, Verogen is uniquely able to bring the next era of genealogy into your laboratory.

Mitochondrial DNA

Extract more answers from challenging samples

When nuclear DNA is compromised, mtDNA can be a plentiful and robust source of additional intelligence. In some cases, sequencing mtDNA might be the only way to obtain an association from degraded or limited samples. Rootless hairs, teeth, and other challenging sources are hallmarks of missing persons and disaster victim identification (DVI). By targeting mtDNA, these samples can still aid investigations.

In Vietnam, for example, analysts used mtDNA to successfully link two brothers. Working with bone fragments recovered from a mass grave, they sequenced DNA extracted from both a bone sample and the blood sample of a possible brother. The sequences revealed a matrilineal connection, establishing kinship—and ultimately identity—for the previously anonymous remains.*

mtDNA has the potential to become a standard forensic tool. Quality and scaling issues have confined mtDNA to a limited role in the hands of a few specialists. The ForenSeq™ mtDNA portfolio opens up mtDNA to a broader range of applications and laboratories. A simple, efficient workflow underpins all Verogen chemistry, minimizing training and implementation hurdles and facilitating the transition from traditional methods—especially for laboratories already using ForenSeq kits. The ForenSeq mtDNA portfolio features highly curated, extended primer sets that generate the lowest mean amplicon size of any commercial workflow to maximize outcomes on degraded and unknown samples. Integrated Verogen software reduces complex bioinformatics to data that are easy to review and interpret.

The Verogen mtDNA workflow centers on the MiSeq FGx System. Laboratories already processing ForenSeq libraries can leverage the same instrument, protocols, and infrastructure to quickly and easily insource mtDNA capability. For those new to the MiSeq FGx System, ForenSeq mtDNA offers a straightforward access point to mtDNA and NGS capabilities.

STRs and SNPs

Translate samples into phenotypical traits

STRs are the bedrock of current DNA profiles. Sequencing STRs grants an additional level of resolution for determining differences between individuals, including the ability to see intra-STR SNPs. Instead of relying on fragment length alone, the MiSeq FGx System generates the sequence of each fragment in a precise, base-by-base result, revealing variations within STR amplicons and providing identity-informative data beyond length variation. These data are important for kinship analysis and mixture deconvolution, particularly when DNA contributors share alleles of the same length.

In a recent Dutch case, Peter de Knijff and his staff at Leiden University Medical Center (LUMC) analyzed a mixed sample and generated discriminating data that proved decisive in a sexual assault conviction. Because the capillary electrophoresis (CE) profile contained alleles in stutter positions of alleles belonging to the survivor, the LUMC team could not determine whether the suspect contributed DNA to the mixture. Subsequent NGS results were much clearer: the team saw minor alleles that implicated the suspect. The verdict stated that the NGS evidence, combined with likelihood ratio statistics, led to the conviction.†

When DNA is too degraded for STRs to yield conclusive results, identity-specific SNPs can provide additional means of identification. Ancestry-informative SNPs (aiSNPs) and phenotype-informative SNPs (piSNPs), which estimate traits such as hair and eye color, help sketch a physical description and generate leads. For example, if phenotypic piSNPs indicate blue eyes, an investigation can reduce the scope of the suspect pool.

Verogen offers the first and only kit that interrogates all of these markers—including a range of SNP types and autosomal, X-, and Y-STRs—in one test to recover more useful genomic data from low-quality DNA and mixtures. This approach preserves precious sample while maximizing the impact the data has on forensic investigations.

* For details, see *A Comprehensive Massively Parallel Sequencing Workflow for Severely Degraded Nuclear DNA (Document # 20180216.2003).*

† For details, see *How Next Generation Sequencing Resolved a Difficult Case, Leading to the First Criminal Conviction of Its Kind (Document # VD2019024).*

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MiSeq FGx System

Start the complete solution

The MiSeq FGx System is the first fully validated, NGS system designed for forensic laboratories. Dedicated library prep kits, reagent kits, and software generate the data that can lead to a human identification.

Combining proven data quality and ease of use, the MiSeq FGx System is the key to a unique, single-platform solution built on gold-standard sequencing technology. Prepare libraries, sequence libraries, and analyze data in a single workflow that's built to scale. With the system in place, a laboratory is ready to realize the full power of NGS for a variety of applications, including FGG, mtDNA, STRs, and SNPs.

This multi-application solution starts with the MiSeq FGx System:

- Set up a sequencing run through an intuitive touch-screen interface.
- Minimize hands-on time with load and go reagents packaged in a pre-filled cartridge.
- Interrogate hundreds of STRs and SNPs in one run, with higher resolution results.
- Target DNA for forensic applications in Forensic Genomics mode or use Research Use Only (RUO) mode for greater flexibility.

Ready to learn more about NGS solutions and human identification?

Discover more at www.verogen.com

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