

Parabon® Snapshot® Genetic Genealogy Analysis

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What is genetic genealogy?

Genetic genealogy (GG) is a lead generation tool that can be used to identify human remains by tying DNA to a family with a missing person or to point to the likely identity of an individual whose DNA was found at a crime scene. Genealogists accomplish this through the use of comparative DNA analysis, which measures the amount of DNA that is shared between two people (See Figure 1), combined with traditional genealogy research using historical records to infer relationships between individuals.

How is Snapshot GG analysis performed?

Hundreds of thousands of genetic markers are read from a DNA sample using microarray genotyping. Parabon has worked with partner laboratories to create an optimized protocol to ensure high-quality results can be obtained from forensic DNA samples. The resulting genotype data can then be compared to other genotype samples in public GG databases. Using software tools that objectively compare genotype files, it is possible to determine how much, if any, DNA is shared between two individuals and estimate how closely or distantly related they are (see Figure 1 for more details). No raw genetic information is disclosed or exposed by such databases; only the amount and chromosomal location of shared DNA segments can be seen. Highly experienced professional genetic genealogists then cross-reference the DNA results with other data sources used in traditional genealogy, such as census records, vital records, obituaries, and newspaper archives to build family trees. Once candidate shared ancestors are identified, descendency research is employed to try to determine the possible identity of the unknown individual.

What type of DNA testing is used for the comparisons?

Genetic genealogy uses autosomal DNA (atDNA) single-nucleotide polymorphisms (SNPs [pronounced “snips”]) to determine how closely related two individuals are. Unlike other genetic markers, such as mitochondrial DNA or Y chromosome DNA, atDNA is inherited from all ancestral lines and passed on by both males and females and thus can be used to compare any two individuals, regardless of how they are related. However, atDNA SNPs are more difficult to obtain from forensic samples, which is why an optimized laboratory protocol is required to ensure high-quality results are generated even from low quantity, degraded DNA samples.

What information can be obtained from a Snapshot GG analysis?

The amount of information obtained from GG analysis varies widely depending on the distance of the genetic matches and the corresponding genealogical information that is available. In some instances, Parabon has been able to provide an identity for the unknown subject. In other cases, Parabon has been able to identify a specific region from which the family of an unidentified person originated, surnames that will likely appear in his or her family tree, and/or a set of possible identities for the individual. In some cases, the genetic matches are too distant

for the case to be workable within a reasonable amount of time, although such a sample can be monitored for new, closer matches.

Do some genetic genealogy databases allow searches for law enforcement purposes?

Parabon only uses publicly available GG databases, such as GEDmatch, with policies that users must agree to that allow law enforcement usage. Given these policies and the amount of press surrounding the Golden State Killer case and its use of genetic genealogy, Parabon believes that participants are now aware that these databases could be used for law enforcement purposes. It is important to note that such databases do not disclose or expose any raw genetic data; only the amount and chromosomal location of shared DNA segments can be seen.

What is the success rate of using Snapshot GG for law enforcement purposes?

During the pilot phase of the service, Parabon analyzed nearly 100 forensic DNA samples. Around 20% of those appeared to be directly solvable with GG methods alone, and another 40% were deemed to be likely solvable in partnership with law enforcement, which may have access to records and information that is not available to our genealogists. In the first month of offering the service, GG analysis in five unrelated homicide and sexual assault investigations provided detectives with the likely name of the offender in their case.

What does the law enforcement agency do with the information?

GG analysis is a lead generation tool that helps investigators be more efficient by narrowing the pool of suspects to a region, a set of families, or even an individual. It is up to the law enforcement agency to use traditional investigative methods to either confirm the information provided and/or supplement the information. As there will always be DNA available in these cases, hence all positive identifications will be confirmed via traditional DNA matching using STRs prior to arrest.

How long does GG analysis take?

It is not possible to predict how long a case will take to successfully resolve until analysis has begun. Every case is different. For those cases with promising assessment results, Parabon guarantees a written report with analysis results and recommendations within 45 business days or less. Other cases simply do not have sufficient matches to resolve the case at the time of initial analysis. Fortunately, new participants join GG databases every day yielding a greater possibility of finding promising matches, so the status of a case can change rapidly.

How does Snapshot GG differ from familial searches in the CODIS database?

Parabon's Snapshot GG service differs from familial search in three very important ways: (1) only public GG databases that allow such comparisons are searched, not government-owned STR databases, such as CODIS; (2) the SNP profiles generated contain vastly more information than traditional STR profiles, allowing genetic relatedness to be detected at a far greater distance; and (3) genetic genealogy matches can be cross-referenced with traditional genealogy sources, such as newspaper archives, databases of birth, marriage, and death records, and existing family trees to expedite the analysis. This technology and the innovative techniques combine to create a groundbreaking system for forensic human identification.

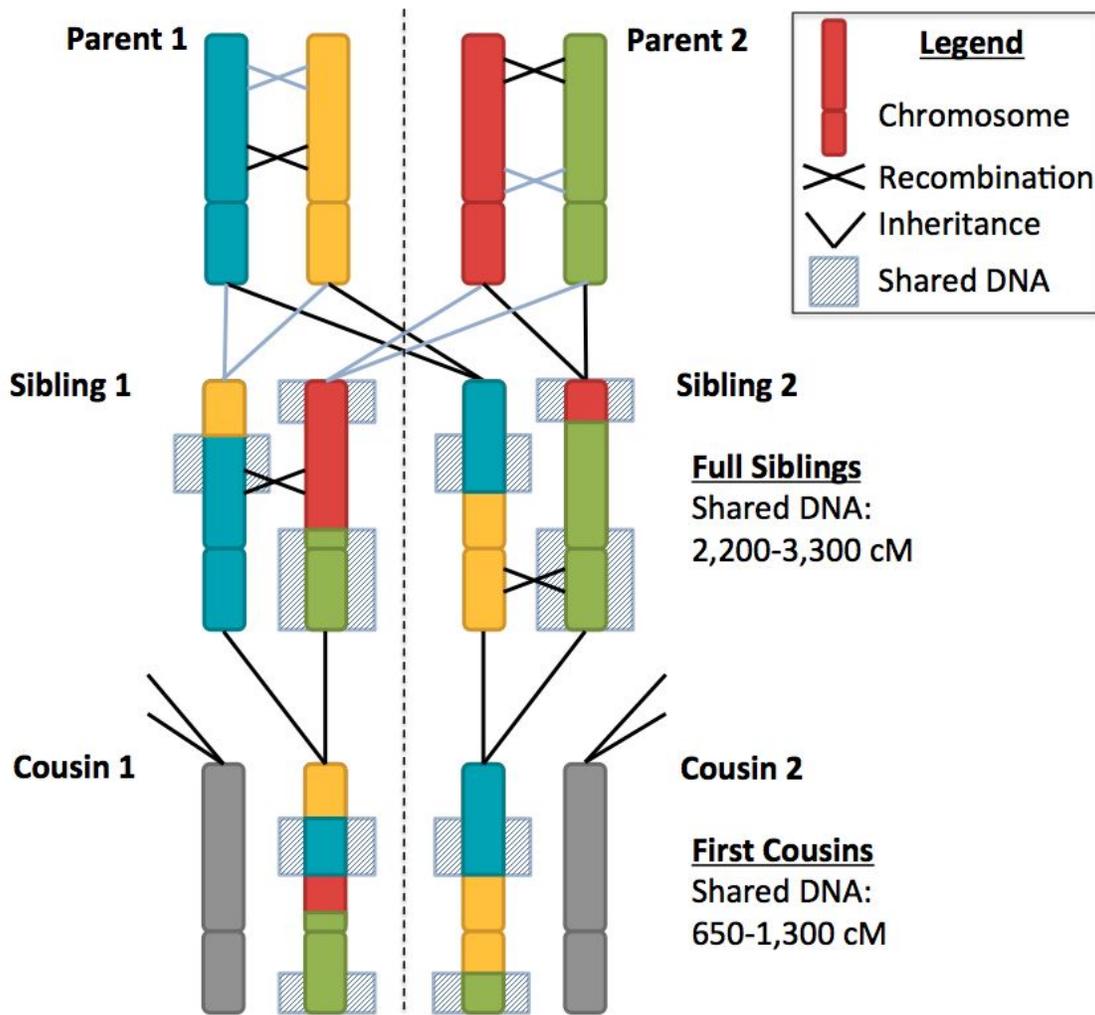


Figure 1: The process of genetic inheritance that results in closer relatives sharing larger amounts of DNA, which is measured in a unit of genetic distance called centimorgans (cM). The Parent level shows two parents' chromosomes, which undergo random recombination to create new chromosomes that are passed on to their children, Siblings 1 and 2. Much of the DNA inherited by the two Siblings is shared between them (shaded boxes), which translates to a large cM value for shared DNA. The chromosomes then recombine again, and Cousins 1 and 2 inherit smaller segments of shared DNA, along with non-shared DNA from their other parents (gray chromosomes), which translates to a smaller cM value.