

How Not To Give up in Face of DNA Evidence

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Once DNA is brought into a case you should be concerned that all other evidence is diminished to the point that the DNA becomes the sole focus of the case, leading to a conviction.

To not give up in the seductive face of DNA evidence you must simplify it.

DNA is nothing more complex than fingerprints. (It links evidence collected at a scene with a known sample)

You don't have to know everything about DNA. You need an expert for that. However understanding the procedure for DNA can be very helpful. One of the earliest cases where an appellate court outlined the DNA procedure is *United States v. Yee*, 134 F.R.D. 161 (ND Ohio 1991). According to Yee the procedure for DNA is basically:

1. The DNA is removed from the specimen such as blood or semen and "washed" with an organic solvent.
2. The extracted DNA chain is then cut into fragment at specific sites by mixing it with a restriction enzyme.
3. The DNA is then placed on a gel to which an electrical current is applied, causing separation of the fragments into bands according to their length.
4. The DNA bands are then transferred to a nylon membrane while retaining the same positions they previously occupied on the gel. The double-stranded bands are then treated with a chemical that causes them to separate into single strands.
5. Radioactive genetic probes (DNA clones) are applied. They each bind to a specific complementary DNA sequence on membrane. The excess probe is then washed off.
6. The membrane is exposed to an X-ray film and developed so that the DNA banding patterns and length can be seen.
7. The autoradiograph is interpreted by comparing the DNA print to one from another DNA sample to determine if that is a match based on the band lengths.

Where DNA is involved, there are Four things to look at in your pre-trial investigation and preparation:

1. Crime scene integrity
2. Chain of custody
3. Contamination
4. Trial concerns. Incorporating the good or bad into your defense

1. Crime scene integrity:

If the crime scene was not preserved and properly protected, then the DNA evidence may be contaminated.

Any evidence collected must be properly documented. Your responsibility is to check carefully the documentation of the evidence.

DNA evidence is more sensitive than other evidence. Contamination can be caused by the law enforcement officers at the scene: smoking, eating, drinking, littering or moving around. Opening doors, windows, and people moving around can contaminate DNA.

Check the police log for who and how many people were present at scene.

Talk to other people who were at or near the scene to determine if someone else was present at the scene and not listed on the crime scene log.

Check the EMS (rescue squad) to determine what they saw, who they saw present, and etc.

The police should have documented everything about the scene. The documentation (or lack thereof) will give you information regarding the DNA, contamination, and other sources of competing DNA.

Those at the scene should not have touched anything unless it was absolutely necessary. Any touch could lead to contamination.

Possible Crime Scene Location of Sources for DNA

Evidence	Possible location of DNA on evidence	Source of DNA
weapon, bat, hammer, etc.	Handle, End, Impact points	blood, sweat, skin, tissue
hat, bandanna, or mask	Inside, outside	sweat, hair, dandruff
eyeglasses	nose or ear pieces, lens	sweat, skin, hair, dandruff
tissue, cotton swabs	surface areas	mucus, blood, sweat, semen, ear wax
dirty laundry	surface areas	blood, sweat, semen
toothpick	tips	saliva
used cigarettes	cigarette butt	saliva
envelope, stamp	licked area	saliva
rope, ligature, tape	inside/outside surface areas	skin, saliva, sweat, tissue
glass, can, bottles	sides, mouthpiece	saliva, sweat
blanket, pillow, sheet	surface areas	skin, dandruff, mucus, blood, sweat, semen, urine, hair
used condom	inside/outside surface area	semen, vaginal or rectal cells
“passed through” bullet	outside surface	blood, tissue
fingernails, including partials	scrapings	blood, sweat, tissue
bite mark	victim’s skin or clothing	saliva

2. Chain of custody.

Anyone or everyone who takes possession of DNA can possibly contaminate the evidence. Check to insure that everyone who had possession of the evidence from collection thru transportation to lab, to the court hearing is listed. Look for who collected the evidence, where the evidence was found, who package the evidence, was the evidence properly packaged and sealed.

The purpose of chain of custody is to identify the persons having custody of the evidence. However you are look for who had it, how long they had it, and was there any potential for contamination.

3. Contamination. Because DNA evidence can be obtained from such a small source, contamination is easy. Contamination occurs when DNA from another source comes in contact

with the DNA relevant to the case.

PCR (polymerase chain reaction) analysis can identify all DNA in the relevant sample and determine whether it is from the contamination or the DNA found at the scene.

-Law enforcement officers touching the area around the DNA sample will contaminate it.

-Law enforcement officers touching his/her face, nose, hair or mouth and then collecting the DNA will contaminate it.

-Sneezing or coughing near the DNA will contaminate it.

-Evidence must be placed in new paper bags, not plastic bags.

-Direct sunlight and warm conditions can degrade DNA

-Storing evidence in the hot trunk of a police vehicle will contaminate it.

-If DNA came off an accuser, then check the conditions of the accuser while being transported. E.g. If she was covered with a blanket, sheet, then contamination could come from that.

-Review the law enforcement policies and procedures for collection of evidence to insure the law enforcement officers followed their own policy.

4. Trial concerns. Own the Good, The Bad and The Ugly of your case, including the DNA. Incorporate the good and the bad into your case theme, including jury voir dire.

A. For jury voir dire:

Obtain commitment from jurors not to give greater weight to scientific evidence than any other evidence.

Obtain commitment from jurors to hold "experts" to meaningful and intelligent opinions to which jurors can relate.

Examples: The state may call experts in one or more areas, including DNA.

What do you think [know] about DNA evidence?

What have you heard about DNA evidence?

I want to be the first one to tell you that the State is going to introduce many complicated details regarding the presence of DNA evidence in this case. Why do you think the State intends to introduce this DNA evidence?

I have this fear that if the DNA evidence is complicated and confusing that you will want to convict [client] because the details are so complicated and confusing. What do you think about my concerns?

As the district attorney mentioned, you as a Juror are free to accept any of the DNA expert's testimony. You may accept all of such evidence. . . . some of such evidence. . . . or none of such evidence. This is the law of North Carolina. What

do you think about this concept as it relates to DNA evidence.

[Client]'s freedom is very important. Can you hold the DNA expert to provide you with meaningful and intelligent opinion which is understandable to you as a juror?

B. Cross Examination: Consider the "So what" cross. Consider no cross. Remember Professor's Irvin's Ten Commandments: 1) Be Brief. 2) Short plain questions. 3) Only leading questions. 4) Don't ask a question to which you do not already know the answer. 5) Listen to the answer. 6) Do not quarrel. 7) Do not permit explanation. 8) Do not ask witness to repeat direct testimony. 9) Do not ask one question too many. 10) Save you explanation for closing argument.

Checklist for Cross:

1. Know your subject matter. (Consider having your expert help you with preparing your cross)
2. Know the language of the DNA tests.
3. Review (with your expert) the lab note, bench notes and protocol of the State's expert.
4. Reduce the cross examination testimony to layperson's talk before the jury.
5. Remember the basics: "Treat the DNA expert as you would any other witness."
6. Reduce the logic of the DNA expert the same as you would any other witness.
7. Let the jury know the DNA expert is being paid by the State.

Cross examine on: 1) Crime scene integrity; 2) Chain of custody issues; 3) Contamination issues; 4) What should have been done; 5) What was done; and 6) especially what was done improperly.

Example: Michael E. Tigar's I love America Cross:

You believe in America don't you?

I understand what you have testified to here today, but you agree that the jury has to decide this case?

Because that is the American way?

And you don't mind me asking you all these questions?

Because the jury needs to know all the facts that both sides bring out?

And you, I, and the DA will not be deciding this case?

In America that is the jury's job?

To give both sides an equal, fair chance?

Then go into some case specific cross such as below:

Generic Examples: You can't testify as to when the DNA was left at the scene?

If many people were at the scene, then they each could have left DNA evidence?

The mere fact that DNA was recovered does not mean that a crime occurred?

If many people handled this piece of evidence, then each may have left DNA evidence?

1. Forensic Application of DNA Technology

A. DNA Technology

Attached to this report is a copy of a description, taken from a recent Report of the Congressional Office of Technology Assessment (Exh. 73), of basic DNA structure in the human cell and how the characteristics of that structure are employed for forensic purposes to enable comparisons between a known sample of DNA (typically from a suspect) and an unknown sample (usually collected at a crime scene). The technical steps by which the F.B.I. undertakes to compare DNA samples are also depicted in the attachment.

The human genome is composed of twenty-three pairs of chromosomes containing approximately six billion individual nucleotide bases comprising approximately three billion nucleotide base pairs. Each chromosome consists of two long chains of deoxyribonucleic acid (DNA) linked together by hydrogen bonding between complementary pairs of nucleotide bases. The overall physical structure of the DNA molecule, otherwise called a double helix formation, has been likened to a ladder the sides of which are twisted or coiled along its longitudinal axis.

The complementary bases bond only with each other. That is, among the four bases which comprise the DNA double helix, the base adenine (A) will bind only with thymine (T), and the base guanine (G) will bind only with cytosine (C). Thus where the order of bases on one strand of the DNA molecule is GGACAATGTCAT the order of bases on the corresponding portion of the other strand, i.e. the complement to this string of nucleotide bases, will be CCTGTTACAGTA.

The long strands of DNA, the biomolecular basis of the chromosome, carry the functional unit of heredity, the gene. The genetic information encoded in the human genome contains the essential instructional material for the assemblage and maintenance of biological life. The genetic information contained in the chromosomes is ultimately responsible for the biosynthesis of the thousands of proteins and enzymes which regulate all the minute biochemical functions of the body.

The nucleus of virtually every cell in the body contains a complete copy of a person's genetic material. Some biological material, e.g. red blood cells, urine, and feces, contains little or no DNA. White blood cells do contain nucleic DNA, thus allowing blood samples to be used in DNA typing.

Most of the DNA belonging to a species is identical. In humans 99% of the genes are the same for all persons, thereby accounting for the abundant shared characteristics of all human beings. Some DNA is, however, different from person to person, population to population, race to race. These differences, which account for our unique characteristics as individuals, as well as the differences between ethnic groups and races, are the result of variation in the base sequences of the genes that encode for these individualizing characteristics. The portions of the genetic material which differ are called polymorphic to indicate that the base sequences that comprise these regions of the genome occur in varying forms.

Just as polymorphic regions of the genome produce physical characteristics in the organism which individualize that organism, so too is the DNA chain itself distinct from person to person. It is this individualized character of the polymorphic regions of the DNA polymer that is the basis upon which the several DNA based genetic identification technologies have evolved.

The technique utilized by the F.B.I. to perform DNA identification testing is referred to as Restriction Fragment Length Polymorphism analysis, or RFLP analysis. The F.B.I. employs the RFLP technology to ***170** isolate and analyze regions of the human genome known as Variable Number Tandem Repeats, or VNTRs.

VNTRs are regions of the human genome for which, at least to date, no biological function has been discovered. The physicochemical structure of a VNTR is implied in its name.

VNTRs are regions of the DNA molecule that are composed of segments of nucleotide bases that repeat in tandem many, many times. A base pair sequence that forms one of the many segments of a VNTR that are repeated over and over again is composed of an arrangement of nucleotide bases (for example, AGTTAAGCCGGCAGAGCCT). This sequence of base pairs is bonded to its corresponding complementary segment.

A single segment of a VNTR may be composed of just a few or as many as several dozen nucleotide bases. This sequence of bases (i.e. the segment) constitutes a unit of a VNTR and repeats itself over and over again. The repeated segments or units are positioned one after the other in tandem, like boxcars of a long train where each boxcar represents a single unit of the VNTR and all the boxcars are identical (i.e. composed of the same arrangement of base pairs).

The number of repeated, tandem sequences comprising a VNTR can vary among persons. VNTRs are polymorphic in that not all individuals possess the same number of repeat sequences for a VNTR at a given gene locus. Thus, for example, in a given individual, a VNTR may be composed of only sixty repeat sequences while for another individual that same VNTR may be composed of two hundred repeat sequences. This example is intended for illustrative purposes only in that VNTRs usually occur in two forms in a person's genome.

RFLP technology, described below, when applied to VNTRs, permits the isolation and identification of the different VNTRs that form part of an individual's genome by a method that represents and distinguishes the VNTRs by length. Thus individuals can be differentiated from each other using this technology because the RFLP technique enables the molecular geneticist to identify the different forms, i.e. lengths, of VNTRs as they occur in different persons. VNTR based RFLP technology may be used to compare genetic material derived from known and unknown samples to determine whether those samples may have come from an identical source.

i. Determining a Match

As depicted in the attached materials from the OTA Report, the following steps are undertaken in a forensic laboratory to determine whether one sample of DNA matches with another.

1) DNA is extracted from a sample of biological material like blood or semen. The specimen is dissolved in a solution that breaks down unwanted chemical contents and allows the DNA to be separated from the remaining biological materials. The DNA is precipitated out of solution.

2) The resultant DNA is then digested by an enzyme called a restriction endonuclease. The enzyme reacts with specific sequences of nucleotide bases. The effect of this enzyme on the DNA is to cut it at specific sites, producing numerous DNA fragments of varying lengths. Different enzymes will cut the DNA at different locations depending on the sequence of bases the enzyme reacts with. The resultant DNA fragments vary in length from a few base pairs up to several thousand base pairs.

3) The residual mixture of DNA fragments is then subjected to a process of separation by size by a procedure known as gel electrophoresis. During electrophoresis, a solution of DNA fragments is placed at one end of a thin slab of a gelatinous semi-solid like agarose, and an electrical current is applied. DNA fragments are negatively charged molecules. When the current is activated the DNA fragments move across the gel toward the positively charged end. The distance these fragments travel, while subject to influence from other factors, is primarily a function of the fragment's size, mass, and electrical charge. The larger and heavier fragments *171 move more slowly, and thus, a shorter distance than the smaller, lighter fragments. The end result of electrophoresis is that DNA fragments are arrayed across the gel according to fragment size. The longer are located closer to the top of the gel, the shorter fragments toward the bottom.

After the electrophoretic separation process is completed the DNA is denatured and neutralized. Denaturation of DNA occurs when the original double helix structure is "unzipped" and the two complementary strands of DNA are separated.

4) Because the gel on which the process of DNA fragment separation has been achieved is relatively

unstable and is not a convenient medium for permanent storage, the array of DNA fragments are transferred to a more stable matrix. This process is known as Southern transfer or Southern blotting. The arrayed DNA fragments are caused to move by capillary action from the gel onto a more stable nylon membrane. A buffered electrolyte solution is placed beneath the gel, and an absorbent material is placed over the nylon membrane which is sandwiched between the gel and the absorbent material. As the solution is absorbed upwards the DNA fragments are carried onto the nylon membrane.

5) The DNA is then hybridized to a radioactive probe. Hybridization is a process in which the single strands of DNA bind to complementary sequences to reform the double helix structure. Hybridization in effect "zips" the DNA molecule back into its original double helix form. The probe hybridizes to only those DNA fragments which contain base sequences complementary to the base sequences of which the probe is composed. The DNA probe is a segment of DNA cloned by recombinant DNA technology to produce thousands of identical sequents. Probes are radioactively labeled with an isotope of phosphorous. Probes differ according to their size and the composition of the repeating base sequences. Several different types of probes are available. The F.B.I. employs single locus probes. Such probes isolate and hybridize to polymorphic regions of the human genome that occur at only one locus of the genome. After hybridization, the nylon membrane is washed to remove excess, unbound probes.

6) The probe hybridized membrane is then exposed to a piece of X-ray film in a process known as autoradiography. The radioactive phosphorous in the probe will react with the film, serving to locate the DNA fragments to which the probe had hybridized. The X-ray film will not react where there is no radioactive probe, therefore the location of fragments that have not been hybridized by the probe will not be indicated on the film.

7) The final step in the process is interpretation. Interpretation is done visually or with the assistance of a computer imaging and measuring system. The primary function of interpretation, whether visual or computer assisted, is to assess the quality of the final product and, most importantly, to compare DNA band patterns from known and unknown samples to determine if they are in alignment. Ultimately, the interpreter declares that it is likely that a known sample and an unknown sample come from an identical source, do not come from an identical source, or that the results of the tests are inconclusive.

ii. Probability Estimate

The F.B.I. uses the following method to estimate the probability that a person picked randomly from the population would have a DNA profile identical to the DNA profile generated from the forensic sample.

First, the Bureau developed a table of allele frequencies. The frequencies of the alleles corresponding to the DNA sample that is being tested are then determined by reference to this table. Finally, the frequencies of the individual alleles from the DNA samples are multiplied together according to the method of calculation developed by the F.B.I. to compute an aggregate probability estimate of the probability that the combination of alleles found in the sample DNA would be encountered in the Caucasian population.

The F.B.I. uses what it has called the fixed bin method to construct its table of allele frequencies. The F.B.I. ran DNA profiles for approximately 225 randomly *172 chosen agents. Each agent was profiled for the five or six probes the F.B.I. uses, or had intended to use, in its casework. Relative to each probe, the allele or alleles resulting from the profile run on each agent were assigned to a predetermined bin.

The bins, as they are called by the F.B.I., were established with reference to the size markers that were run with each test. The size markers, or sizing ladders as they are also called (which are also, according to F.B.I. protocol, run with all casework tests) are commercially available solutions composed of DNA fragments of known, predetermined fragment lengths. The size markers appear on the final autorad as an array of bands relatively evenly distributed along the length of the gel. Because the fragments of the size markers are of known lengths, the size of an individual's DNA bands can be determined by comparison to the band of known length on the sizing ladder that is nearest in location to the sample band of unknown length.

In the fixed bin procedure, the size markers define the boundaries of the bins. The frequencies associated

with the bins were established by assigning the bands generated from the profiles of the F.B.I. agents to the bins into which the bands fell. After all the profiles of the agents were completed, and the bins into which their bands fell were determined, the total number of bands located in each bin were counted. As to each probe, the frequency for each bin was calculated by the simple procedure of dividing the total number of bands located in a bin by the total number of bands resulting from the profiling of all the agents tested for that probe.

The F.B.I. applied a standard statistical safety measure used in data collection studies of this sort by "collapsing" into each other, bins that contained fewer than five occurrences. That is, if a particular bin displayed fewer than five bands it would be merged into the adjacent bin and this process was continued until there was a total of at least five bands. The resultant bin would be larger in size. The frequency associated with this bin would be calculated in the same manner described above.

Once the bin frequencies are established for the probes used in casework, these numbers, which are referred to as the "Caucasian database," can be applied to determine the estimate of the probability that a person picked randomly from the population would have a DNA profile identical to the DNA profile generated from the forensic sample. The first step in this process involves identifying the bins in which are located the various bands that comprise the sample's DNA profile. This "binning" process involves a visual and computer assisted assessment of the location of the band on the autorad.

When a casework band is located between two adjacent size marker bands, that casework band is said to lie in the bin defined by those two adjacent size marker bands. The frequency assigned to the casework band is the frequency that had previously been determined for that bin through the frequency study described above.

If a casework band is found to lie on the border of two bins, the F.B.I. deems that band to belong to the bin that has the highest frequency, i.e. the more common bin. This, according to the F.B.I., is a conservative measure that favors the defendant because the subsequent calculations will use a number that is of a greater magnitude, thereby raising the final frequency and diminishing the degree of rareness associated with the occurrence of that DNA profile in the population.

Because the F.B.I. has ascribed a size range to a band (i.e. +/- 2.5%), a casework band is said to fall on the border of a bin where any portion of the possible range of sizes for the band that are within the plus or minus two and one-half percent window fall on a bin border. In that case also the frequency assigned to that band would be the higher of the frequencies of the two bins in which that casework band lay.

After the frequencies for the various bands are determined, the overall frequency for the DNA profile is calculated. In *173 performing this calculation frequencies must be calculated one probe at a time. Thus, the frequency of the band or bands identified by the first probe are determined, and the overall frequency associated with that probe is determined. Then the frequency of the band or bands for the second probe is ascertained, and the overall frequency associated with the second probe is calculated, and so on. The frequencies of all the different bands comprising the sample's DNA profile are not, however, all individually multiplied together.

When done correctly the DNA profile at a single probe will display either one or two bands. Those profiles that display only one band are called homozygotes (which simply means that the polymorphic form of the VNTR identified by the probe was the same in both parents of the person from whom the sample was obtained). Those profiles that display two bands are called heterozygotes (which means that the polymorphic forms of the VNTR identified by the probe were different in the two parents of the person from whom the sample was obtained).

For probings that display a heterozygotic, i.e. two banded, pattern the F.B.I. calculates the frequency of occurrence for that particular band pattern at that probe using a formula derived from classical Mendelian genetics, $2PQ$, where "P" is the bin frequency associated with one of the bands and "Q" is the bin frequency associated with the other band.

For probings that display a homozygotic, i.e. single banded, pattern the F.B.I. calculates the frequency of occurrence for that band pattern at that probe using a formula modified from the one normally associated with determining the frequency of homozygotes in classical genetics. Traditional genetics would calculate the frequency for a homozygote with the formula of $P \times P$, i.e. P squared. Because of a variety of considerations, related to issues involving whether single banded patterns are true homozygotes, issues too complex to address in the present context, the F.B.I. decided to apply a formula to calculate the frequency of single banded patterns that would compensate for these various problems and would protect the defendant.

Based on these considerations, the F.B.I. chose to use the $2P$ formula when calculating the frequency of occurrence of a single banded pattern, where " P " is the bin frequency associated with that band.

Finally, after the frequencies of occurrence for the profiles of the different probings are calculated, the aggregate frequency for the overall DNA profile can be computed by simply multiplying together the frequencies determined for the several probings. The reason that these frequencies associated with the different loci (as the area of the gene identified by a probe is called) can be multiplied together is that the occurrence of the genetic events at any one loci are considered to be independent of the occurrence of the genetic events at any other loci. Given this assumption, one of the most rudimentary principles of probability theory then follows: that the frequency of occurrence of independently occurring events may be multiplied by one another to determine the frequency of occurrence of the aggregate of those events.

With this final calculation, the frequency of the sample's DNA profile has been determined, and an estimate of the probability that a person picked randomly from the population would have a DNA profile identical to the DNA profile generated from the forensic sample can be made.

