CONTINUING LEGAL EDUCATION

WINTER 2016

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These Are Additional Materials
They WERE NOT Handed Out at the Live Program

DNA – FST UPDATE

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Sponsored by:
Appellate Division, First Department
Assigned Counsel Plan for the First Department

DNA EXPERT CROSS- WHERE'S MY CASE CONTACT NOTES

Biased nature of OCME LAB- To Testify –ADA makes a call

To get copy of files- Da Asks

OCME will not speak directly expert witness

Routiing Sheet

HST for criminal prosecutions

Development of FST

FST developed by Theresa Caragine and Adele Mitchell

Not used in any other lab

FBI doesn't use it

No Blind Testing- USE of "S" designation for suspect matching?

Touch DNA-

Contact DNA can be added to an item

Direct Contact DNA-

transfer DNA

Conditions in the lab to prevent DNA

No mixing of pieces of evidence

Strict chain of custody must be established

No mixing of evidence samples

Like a shirt and a gun

Sterile ENvironmet

Negative air flow

Double gloving

Instances of contamination in the Lab-

Two lighter circumstances

O'Connor

Ostijic

Property Clerk DNA on item

Contamination in the field

Conditions in the field

Evidence samples handled together

Handling one piece of evidence then another

Pieces of evidence together in a van

Don't know who handled a firearm

Use of special equipment to prevent cross contamination

Chain of custody

Firearm, you don't see weapon, you receive swabs

Both Clothing and Firearm had multiple persons DNA on the items

Robert Gist

Paul Gist DNA Profile run against items?

DNA FROM BUS SEATS SUBMITTED

WHEN DO THE TWO CASES GET LINKED UP FORENSICALLY SPEAKING?

People v Collins

[*1] People v Collins 2015 NY Slip Op 25227 Decided on July 2, 2015 Supreme Court, Kings County Dwyer, J. Published by New York State Law Reporting Bureau pursuant to Judiciary Law § 431. This opinion is uncorrected and subject to revision before publication in the printed Official Reports.

Decided on July 2, 2015
Supreme Court, Kings County

The People of the State of New York, Plaintiff,

against

Jaquan Collins, Defendant.

The People of the State of New York, Plaintiff,- -

against

Andrew Peaks, Defendant.

8077/2010

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In these unrelated cases, defendants Collins and Peaks face violent felony charges. What the cases have in common is that the People applied to introduce DNA evidence at each defendant's trial.

In defendant Collins' case, the People obtained two DNA "mixtures," each apparently from three contributors, from the handlebars of a bicycle ridden by the perpetrator of a shooting. The DNA samples were very small, and so they were tested with "high sensitivity" analysis in the laboratory of New York City's Office of the Chief Medical Examiner ("OCME").After that, a new OCME software program called the Forensic Statistical Tool ("FST") indicated that one DNA mixture was 972,000 times more probable if the sample originated from defendant Collins and two unknown, unrelated people than if it instead originated from three unknown, unrelated individuals. The other mixture was 19.4 times more probable if the sample originated from Collins

and two unknown, unrelated people than if it instead originated from three unknown, unrelated individuals. One might reasonably expect that this evidence would be conclusive on any identity issue at trial.

In defendant Peaks' case, the People obtained a DNA "mixture" from the bra of the victim of a sexual assault. At least one female and two males contributed DNA to the sample. Using standard DNA analysis, not "high sensitivity" analysis, and using the FST software, an analyst determined that the sample was 19.6 times more probable if the sample originated from defendant Peaks, the victim, and an unknown, unrelated person than if it instead originated from the victim and two unknown, unrelated persons. One might reasonably expect that this evidence would be highly persuasive on any identity issue at trial.

Defendant Collins has moved to preclude the DNA evidence in his case on [*2]the theory that neither "high sensitivity" DNA analysis nor the FST is generally accepted in the relevant scientific

community. Defendant Peaks has moved to preclude DNA evidence on the theory that the FST is not generally accepted in the relevant scientific community. This court ordered that a Frye hearing be held, see Frye v. United States, 293 F. 1013 (D.C. Cir. 1923), and the cases were consolidated for the hearing. [FN1]

I. THE UNDERLYING FACTS AND ISSUES

A. Standard DNA Analysis

This court recognizes that judges are, far and away, not the people best qualified to explain science. That observation is doubly applicable when novel scientific techniques are at issue—and that of course is precisely what Frye analysis involves. But courts are bound to do their best.

DNA defines who we are. Who we are depends on the genetic contributions of our natural parents. Each parent contributes half of our genetic coding, in that each provides half of the DNA at each point on our genetic map. That entire map is included in the nuclei of most cells in our bodies. But nature has it that parental contributions vary, even as to most siblings. Apart from identical twins, no one has DNA that is the same as anyone else's.

Law enforcement puts that to use. Under the right circumstances, standard DNA analysis tells whether cells left at a crime scene contain a particular person's DNA. The entirety of the DNA in the cells need not be examined. It is enough to look on the genome at 15 places, chosen for this purpose—each of those places being called a "locus,"

plural "loci"— to determine whether there is a match between a crime scene DNA sample and the DNA of a suspect.[FN2]

At each locus among the select 15, DNA patterns repeat themselves in numbers that differ from person to person. The number of repeats lets us place a distinguishing label on each locus—a number that is the "allele." If the pattern repeats 11 times, the allele at the locus is an 11. At every

locus, we possess an allele from our mother and another from our father. If, at a particular one of the 15 chosen loci, one [*3]parent gave you 11 repeats and the other gave you 15, you will be considered an "11,15" at that locus, and a "heterozygote." If, by chance, each parent gave you 11 repeats, you are at that locus simply an "11" and at that locus you are a "homozygote."

Assume, counter to fact and just to simplify, that there are eight possible repeat numbers at each of the select loci, and thus 64 possible combinations of maternal and paternal numbers at each locus. Likewise assume, counter to fact and just to simplify, that all possibilities, maternally and paternally, are equally likely at every locus. One in 64 people would share the same numbers at a particular locus.

But there are 15 relevant loci. Assume (as the experts agree) that the results at each of the 15 select loci are independent. Then the chances that unrelated people would share the same numbers at two loci would be one in 4096 (64 x 64). Unrelated people would share the same numbers at three loci only one time in 262,144 (64 x 4096). By the time that you find that people have the same numbers at all 15 loci, the odds against the match are well over one trillion to one.

All of that is non-controversial here. As noted above, contested here are two new DNA tools—"high sensitivity" analysis and the FST software.

B. The Facts and Issues as to Defendant Collins

On August 15, 2010, Joshua Hamilton was walking near the Kingsborough Houses in Brooklyn. A man on a bicycle began shooting at Hamilton, jumped off the bicycle, and continued shooting. The assailant then fled, leaving the bicycle behind. Police officers who responded to the scene swabbed the handlebars and sent the two swabs for DNA testing at the OCME laboratory.

Too little DNA was present on either swab to permit standard DNA testing, in which the recovered DNA is copied 28 times before it is analyzed. The OCME lab therefore employed a relatively new procedure, pioneered in Britain, called "high sensitivity" analysis. Under this procedure, recovered DNA is copied in 31 "cycles" instead of 28. The extra three duplications make available to the analyst about eight

times as much material as does the standard procedure.[FN3]

With the three extra cycles come not just more material to examine, but also more "stochastic" effects. The software kits that create DNA profiles vary, but generally were designed to create DNA profiles of the 15 select loci with quantities of DNA that [*4]can be analyzed after the standard 28 copying cycles. But even with standard analysis, the software reveals "stochastic" imperfections—random additions to or subtractions from the material examined.[FN4] Interpretive protocols are adopted by laboratories to filter out these extraneous results. The use of these protocols is not controversial and does not cast doubt

on the scientific validity of standard DNA testing. However, the extra three cycles employed in high sensitivity testing magnify the stochastic effects. New protocols have been created by OCME to compensate. The parties dispute whether the high sensitivity protocols adequately do so. The defense position is that the scientific community has not agreed that high sensitivity analysis yields reliable DNA profiles.

In defendant Collins' case, not only the high sensitivity protocols are at issue. The high sensitivity analysis revealed, not a single profile, but a mixture of three people's DNA. The DNA mixtures on the handlebars did not, by themselves, yield highly inculpatory results. When a mixture of DNA from two or more people is analyzed, the quantities of DNA contributed by particular individuals may differ sufficiently to permit the creation of separate DNA profiles of the contributors. In Collins' case, that was not true; the quantities of DNA from the contributors were too nearly equal to permit such differentiation. The high sensitivity results initially indicated only that Collins "could be a contributor" to the DNA sample on one handlebar of the bicycle, because all his DNA alleles were found in the mixture—with many other alleles. As to the other handlebar, not all of defendant's alleles were present, but the absence of the others could be explained. As to that sample, defendant therefore "could not be excluded" as a contributor.

Subsequently, the OCME lab analyzed the mixture results with the new FST software tool. The FST was developed in the hope that more informative statistical information could be reported as to the likelihood that a particular individual contributed DNA to a mixture. The FST was created by OCME through analysis of samples of DNA mixtures made by known contributors. As part of the process, OCME counted the stochastic effects at each of the select 15 loci by comparing the results with the

[*5]contributors' actual profiles. OCME then used the results to calculate the probabilities of additional or missing alleles at each locus. Through mathematical analysis, very importantly factoring in this probability of stochastic effects, the FST software permits an analyst to state a "likelihood ratio": how much more likely, or less likely, a two-person or three-person DNA mixture is if a suspect is a contributor, than it would be if instead the suspect was not a contributor. In defendant Collins' case, the FST yielded a report that the mixture on one handlebar was 972,000 times more likely if it originated from Collins and two unknown, unrelated people than if it came from three unknown, unrelated individuals. The other mixture was 19.4 times more likely if Collins was a contributor.

The validity of the math in the probability analysis underlying the FST software is not at issue. That mathematical analysis is "Bayesian" analysis. Bayes was a mathematician who worked in the 18th century. His methods for calculating probabilities are employed throughout all fields in which probabilities are calculated, including medicine and molecular genetics. Nor does the defense dispute the People's position that the FST software does calculations of Bayesian probabilities like a simple calculator, performing complex mathematical functions with more precision, and certainly with far more speed, than a human could.

Instead, the defense attack on the FST centers on whether the probabilities of stochastic effects, determined in the "known contributor" tests, were produced through methods generally accepted in the relevant scientific community, and whether the methods for testing crime scene samples otherwise allow accurate input to the FST. The defense also complains that the FST wrongly limits analysis to single hypotheticals and unscientifically prevents alternative analyses.

C. The Facts and Issues as to Defendant Peaks

At about 5:00 a.m. on July 13, 2010, an individual who will be referred to here as Victim A was attacked on the sixth floor of a residential building on Stanley Avenue in Brooklyn. Victim A was grabbed around the neck and dragged into a stairwell, where her

attacker touched her breasts and took her purse. When Victim A's brother came to her aid the perpetrator fled, dropping the purse and losing his Yankee cap as he did so.

At about 9:00 a.m. on August 26, 2010, an individual who will be referred to here as Victim B entered the elevator of a residential building on Loring Avenue in Brooklyn. A stranger entered with her and got off with her on the seventh floor. He then put Victim B in a choke-hold and displayed a box cutter. After taking money from Victim B's purse, the attacker ordered her to lift her shirt and bra. When she complied, the attacker put his mouth on her breast. He soon ran from the scene.

In Victim A's case, the purse and the Yankee cap were sent to OCME for DNA analysis. The cap yielded a DNA mixture with a recognizable major contributor and a minor contributor. The major contributor's DNA was subjected to standard analysis, and would be found in only one in over 6.8 trillion people. That profile matches [*6]the profile of defendant Peaks. No issue is presented here as to the testing in Victim A's case.

In Victim B's case, the victim's shirt and bra were sent to OCME for DNA testing. A DNA mixture from at least three contributors was found on the bra. That mixture included both male and female DNA, but—unlike in the case of Victim A—the amounts of DNA left by the contributors were too similar for individual profiles to be identified. A non-standard type of DNA analysis, YSTR testing, was then employed. The YSTR analysis, which examines only alleles contributed by males, indicated that DNA from a major male contributor and DNA from a minor male contributor were in the mixture. Defendant Peaks' YSTR profile matched the profile of the major male contributor, indicating that defendant or a paternal male relative could be the source of the major male contribution to the mixture. This profile would be found in one in a thousand black males. This finding also is not in issue in this motion.

Finally—and very much at issue here—the results of standard DNA testing of the mixture on the bra were analyzed with the new FST software. Defendant's alleles at two loci were not found during the initial testing. Nonetheless, the FST software, taking

stochastic effects into account, concluded that the mixture was 19.6 times more likely if

defendant, Victim B, and an unknown, unrelated individual were the contributors than if the contributors were Victim B and two unknown unrelated individuals.

Defendant Peaks challenges the use of the FST software. Like defendant Collins, he does not dispute Bayesian probability theory, or the use of FST software as a calculator for determinations too complex for ready performance by humans. He instead objects that the scientific community does not concur with the way that FST assesses the probabilities of stochastic effects, and he objects as well that it does not permit assessment of various alternative hypotheses about the contributors of DNA.

II. THE FRYE RULE

This opinion has cited Frye, yet has not explained it. But in New York legal circles, little explication is required. Novel methods of scientific analysis can produce admissible evidence only if the relevant scientific community generally (though not necessarily unanimously) considers those methods to be reliable. Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).

Put another way, a court assessing the admissibility of evidence under Frye is not charged with deciding the validity of novel scientific procedures. It would hardly be sensible to assign that task to the judiciary, most of which is as patently unqualified to perform the task as is this court. Judges should be "counting scientists' votes," and not [*7]"verifying the soundness of a scientific conclusion." Parker v. Mobil Oil Corp., 7 NY3d 434, 446-47 (2006), quoting People v. Wesley, 83 NY2d 417, 439 (1994)(Kaye, C.J., concurring).

One New York trial court has, after a Frye hearing, upheld the use of high sensitivity DNA analysis. People v. Megnath, 27 Misc 3d 405 (Sup. Ct. Queens Co. 2010) (Hanophy, J.). Another has, after a Frye hearing, held that the FST approach to mixture analysis is generally accepted in the DNA community. People v. William Rodriguez (Sup. Ct. NY Co. October 24, 2013) (Carruthers, J.) (unreported). With all respect to the authors of those decisions, this court has counted the scientists' votes differently, and disagrees with their conclusions.

III. HIGH SENSITIVITY ANALYSIS, OFTEN CALLED

LOW COPY NUMBER ANALYSIS

At OCME, standard testing of a DNA sample utilizes what is called PCR-STR analysis to identify the alleles at 15 points on the genome of the individual who supplied the DNA—and it determines the person's sex as well. The laboratory work proceeds in six stages. First, an evidence sample thought to contain DNA is examined with "presumptive" tests to confirm that theory. Second, if the result is positive, chemicals extract DNA from the sample and purify the DNA. Third, the amount of DNA is quantified, and that quantification resolves whether the testing may continue with standard DNA analysis.

Fourth, standard analysis continues with the "amplification" of the DNA in 28 cycles. In each cycle, the DNA, which resembles a twisted ladder, is sliced in two on its vertical axis. Each half ladder then bonds with chemicals to produce a ladder identical to the original, so that there are twice the number of complete ladders as existed before. After 28 cycles, the result is a sample that is 2 to the 28th power times bigger than the original.

Fifth, the technician employs a capillary electrophoresis machine. That device tracks the passage of DNA through a gel. Alleles with smaller numbers have fewer repeats of their DNA pattern than alleles with larger numbers and, being smaller, can

move through the gel more quickly. For each of the 15 target loci, the machine records the speed of the alleles.

Sixth, computer software analyzes the electrophoresis data about the movement of the alleles. That permits a graph of "peaks" for the loci which identify which alleles are present at each. An analyst then takes over, disregarding stray peaks below a set

threshold and resolving whether the remaining alleles match another DNA profile from a crime [*8] scene sample, a suspect, a victim, or the national DNA database.

Again as noted above, standard DNA analysis is well accepted, and is not at issue. And, with respect to defendant Peaks, it has already been mentioned that standard analysis of the major contributor of DNA on a Yankee cap worn by victim A's attacker was someone with Peaks' DNA profile. One in 6.8 trillion people would share that profile.

But here we deal not with standard analysis, but with high sensitivity analysis of small DNA deposits—or if you prefer, "Low Copy Number" analysis. In the view of OCME, inclusion of more than 100 picograms of DNA in a sample permits standard analysis. About 16 human cells would yield that much DNA. High sensitivity analysis comes into play if the sample is below 100 picograms. One cell will produce about six picograms of DNA, and high sensitivity analysis hopes to provide information where a recovered DNA sample contains between about six, and about 100, picograms. In that range, amplification with 28 cycles does not produce enough DNA to allow electrophoresis analysis.

There are very many cases in which DNA samples smaller than 100 picograms are all that can be obtained. Each case is different, but very often small "touch" samples are obtained—a few cells' worth of DNA were left by someone who touched a gun, a steering wheel, the handle of a drawer, a doorknob, or the handlebar of a bicycle. In other cases, a small DNA sample will be left by someone on a hat or a glove recovered at a crime scene, or by touching the victim of an assault with his mouth. OCME scientists—and many

others—quite understandably wish to develop reliable methods to create DNA profiles from these smaller samples, and thereby increase the odds that the justice system will correctly resolve criminal cases. Of course, reliable DNA evidence can lead either to just convictions, or to proper exonerations.

Defendant Collins asserts, and the People acknowledge, that high sensitivity analysis increases stochastic effects which can impede proper DNA analysis. The People argue that high sensitivity analysis is reliable nonetheless, because OCME's protocols create conservative interpretations of the test data and ensure trustworthy and sound scientific conclusions. This court, after conducting a Frye hearing, will not seek to state whether the People are correct; this court will instead consider the evidence about whether the relevant scientific community generally accepts the OCME protocols.

But some further discussion of those protocols must precede that consideration.

This opinion has already identified the four kinds of stochastic effects that are of general concern in DNA analysis. Drop-out—the failure of any DNA to register at one or more loci in a contributor's sample—is not of great concern in high sensitivity analysis of a crime scene sample left by a guilty person. If no result appears at a locus, the odds behind any inculpatory result are simply reduced to the guilty party's benefit. However, the innocent defendant loses one or, if there is more drop-out, more chances for an exculpatory non-matching allele to appear. Notably, in real-world conditions very small DNA samples are particularly subject to degradation and are thus more prone than larger samples to having alleles simply disappear.

More often problematic is drop-in. Drop-in is, in effect, contamination with extraneous alleles, either at the point of the recovery of a sample or, hopefully less frequently, during the laboratory analysis of the sample. Drop-in is troublesome in any situation, but obviously is of most concern if the contamination should supply an innocent person's alleles to a [*9]sample and increase the perceived chance that he was the contributor.Stutter is in some ways like drop-in, in that it adds an allele that does not belong in the profile. The cause, however, is not contamination. Stutter is a common "echo" effect appearing on the DNA profile—usually one allele before its true allele, or less frequently, just after. Stutter is of little concern in a single contributor's standard DNA analysis, as it is suspect not only for its location, but also because it shows as a peak on the graph that is much shorter than the neighbor allele it "echoes." It is more of a problem with high

sensitivity analysis, as such analysis can involve far less informative peak heights. Stutter may show a peak as high or higher than the true allele, and thus is harder to identify.

And that brings us to peak heights, the fourth stochastic effect relevant here. With standard DNA analysis, the true peaks on a graph of a single contributor's profile are all relatively close in height. Analysts rely on that fact to exclude peaks of extraneous alleles which will (as with stutter) usually have only a fraction of the height of those of the true alleles. But that is not the case with high sensitivity analysis. The small amounts of DNA available for analysis may not yield consistent peak heights for the true alleles and may result in extraneous alleles at some loci that produce higher peaks than do the true alleles.

OCME was of course aware of all this. Accordingly, if the quantification stage of DNA analysis shows

that less than 100 picograms of DNA is present in a sample, different OCME protocols apply. First and foremost, the already small DNA sample is divided into three samples—"aliquots." While it may seem counter-intuitive to divide a small sample, each aliquot is then amplified not 28 times but 31. The analysis proceeds with tweaks intended to enhance its sensitivity. Ultimately, three profiles, one from each aliquot, are created for the analyst. The analyst combines the three profiles into one, but in doing so counts an allele only if it appears in two of the three aliquots. In this way OCME hopes to avoid counting drop-in alleles. And OCME expects the three extra cycles to minimize drop-out. Ultimately the combined profile is treated like a profile produced from standard analysis, and is compared to profiles from crime scenes, suspects, and victims. And at a trial, an OCME analyst will offer the same types of conclusions about the probabilities of a match from a random member of the population that he or she might have offered in any standard analysis case. The defense may of course suggest to the jury that there are flaws in high sensitivity methods, but the expert testimony will be before the jury.

At the Frye hearing, the People produced very impressive witnesses to attest to the reliability of high sensitivity analysis performed under the OCME protocols. The architect of the program, Dr. Theresa Caragine, has her Ph.D. from the Sackler Institute of Biomedical Sciences at the NYU School of Medicine. She also has graduate and post-graduate training in statistics. The doctor began work at OCME in 1991 as a criminalist

performing DNA tests and was eventually named a Deputy Director of the Forensic Biology Laboratory, in charge of, inter alia, supervising the validation and performance of the high sensitivity work there.

Dr. Mitchell Holland received his Ph.D. in biochemistry from the University of Maryland. After extensive DNA work with the Bode Technology Group he moved to the Armed Forces DNA Identification Laboratory, where he became the Director and employed high sensitivity analysis. After then serving as Director of the Bode laboratory, Dr. Holland moved to [*10]the Pennsylvania State University. There he teaches molecular biology and is Director of the Forensic Science Program. At Penn State the doctor in fact teaches classes about high sensitivity DNA analysis. He has also written extensively, and has conducted workshops internationally, on the subject of high sensitivity analysis.

This court finds that both witnesses are extremely skilled professionals who offered honest opinions. [FN5] They believe that high sensitivity analysis is reliable, and that it is not "novel." Dr. Caragine

testified at length about the development of OCME's high sensitivity testing, and in particular about the validation studies performed before such testing was approved for case work.

Those studies produced results that led the DNA Subcommittee of the New York State Forensic Science Commission to give unanimous approval to the use of high sensitivity analysis in case work. The subcommittee was composed of seven highly regarded experts in various aspects of DNA analysis, and the recommendations of this subcommittee are binding on the Commission. The People note as well that over a dozen scientific articles about high sensitivity DNA testing have been published, and that OCME scientists have both published articles on OCME'S techniques, and given over 85 presentations about those techniques at scientific gatherings.

But obviously, our trek does not end with the People's presentation. The defense

presented expert testimony as to the high sensitivity protocols as well. First and foremost, the court heard from Dr. Bruce Budowle, currently the Executive Director of the Institute of Applied Genetics at the University of North Texas Health Science Center. In 1979 Dr. Budowle received his Ph.D. in genetics from Virginia Polytechnic Institute and State University. After three post-doctorate years studying genetic risk factors for certain diseases, he moved to the FBI. In sixteen years at the FBI Laboratory, Dr. Budowle performed work that arguably entitles him, as much as anyone, to be considered the father of American DNA analysis. During his long career Dr. Budowle has served as the chair of SWGDAM [FN6] and the chair of the DNA Commission of the International Society of Forensic Genetics. He is also one of the original architects of CODIS, the national DNA database.

Dr Eli Shapiro's Ph.D. in biology is from Yale. After work in a biology laboratory he moved to OCME in 2000. He eventually became the Director of Training at the laboratory, retiring in 2011. As the People note, he does not have the research experience of other hearing witnesses, and he has not published scholarly articles about DNA analysis.

Dr. Angela Van Daal, a molecular geneticist, received her Ph.D. from Macquarie University in New South Wales. She did post-graduate study in the United States and then, for [*11]about 14 years, helped introduce forensic DNA analysis to Australia. In 2005, Dr. Van Daal took a position at Bond University, and she has since been affiliated as well with the University of North Texas.

Dr. Ranajit Chakraborty, a population geneticist, received his Ph.D. from the Indian Statistical Institute in Calcutta in 1971. He moved to the University of North Texas in 1993, and is now a full professor there. He has extensive experience with issues in DNA

analysis. Dr. Chakraborty was a member of the DNA Subcommittee of the New York State Forensic Science Commission when that group approved OCME's high sensitivity analysis, and its FST software as well. He has since changed his mind.

Finally, Dr. Heather Coyle received her Ph.D. in plant biology from the University of New Hampshire in 1994. She is an Associate Professor in the Forensic Science Department at the University of New Haven and founded a consulting company in Connecticut that provides services to the defense bar concerning the analysis of DNA and other biological evidence. Dr. Coyle's academic publications do not include articles about high sensitivity DNA analysis.

The People's witnesses addressed OCME's validation studies of its high sensitivity procedures and otherwise explained why they think OCME's high sensitivity analysis is robust, and not novel. The defense witnesses were not of the same point of view, and some of their objections to OCME's procedures will now be discussed.

We begin with an issue that impacts in particular on high sensitivity analysis of samples containing mixtures of DNA from two or more contributors, which are very common in high sensitivity work. When a graph of DNA alleles in a sample is prepared, alleles are represented on the graph by peaks placed along a base line. The peaks are taller or shorter depending on how much DNA at that locus, and that allele, is present. In standard analysis, each contributor's alleles are likely to produce peaks of roughly the same height; a minor contributor's peaks will be shorter than those of a major contributor.

That can permit an understanding of which alleles are to be assigned to various individual profiles. That advantage is lost with OCME's method of analyzing small DNA samples. The three extra

amplifications, produced by DNA kits not designed for them, create stochastic effects that make peak heights unreliable. Dr. Budowle so concluded.

Dr. Coyle focused on drop-out. It is not disputed that drop-out is more common with high sensitivity analysis, and that drop-out can make a heterozygous locus look like a homozygous one. Or it can make any locus "disappear" with no allele appearing. A person who did contribute to a sample is unlikely to complain. But someone who did not contribute, perhaps an innocent man accused of a crime, may lose the chance to show that someone else's alleles, and not his, were present at relevant loci. The doctor noted that OCME protocols substitute a Z for a number at a locus where an allele may be missing, and that there are many Zs in profiles from high sensitivity analyses of low picogram DNA samples. But the Z might as well be a question mark, and use of the Z hardly substitutes for exculpatory numbers.

Dr. Coyle also addressed "drop-in" contamination of a sample, the appearance of extraneous DNA material that creates reports of false alleles. Drop-in is not a problem with standard analysis. "Negative controls" are run along with case samples. If the negative controls reveal any peaks due to contamination, the run is disallowed. But the extra three cycles used in high sensitivity analysis make contamination a particular problem. The extra amplifications [*12]make drop-in far more likely. Apparently with that in mind, the protocols for high sensitivity analysis permit the analysts to ignore contamination results in negative control tests until ten drop-in peaks appear in at least two of the three aliquots. Dr. Coyle considered that unacceptable. She added that contaminants can appear in high sensitivity samples even if there is no contamination shown in the negative control samples. The possible appearance of peaks due to contamination makes analysis unreliable.

The defense witnesses also addressed stutter. In standard analysis, in the graph depiction a stutter peak is generally extremely small compared to a "true" peak. Dr. Budowle and others have noted that, with high sensitivity analysis, stutter peaks can be magnified dramatically. They thus can appear to be true peaks when they are not. And even if they can be recognized as stutter, their possibly inordinate peak height can mask the appearance of a true allele at the same position—particularly in mixture cases.

The defense witnesses addressed peak heights more generally as well. As noted, alleles are represented at the correct spot on the graph by a sharp peak that, in standard analysis, will be taller

or shorter depending on how much of the contributor's DNA is in the sample. Protocols filter peaks out of the profile if they do not reach a certain percentage of the height of the other peaks. Again as noted, in standard analysis that helps weed out stutter. More broadly, it guards against very low-level contamination. A dozen or three dozen picograms of contaminant DNA will never spoil the graph where the DNA sample is 300 picograms; the low height of the contaminant's peak will give it away. That rather critical advantage disappears in high sensitivity analysis, in which the false report may be based on a higher peak than the report of a "true" allele. Relative peak heights may unreliably indicate which are the true alleles at one or many loci, and result in incorrect profiles.

As a result of issues like these, no public laboratory in the United States, other than the OCME lab, employs high sensitivity analysis to develop profiles for use in criminal cases. Among the labs refusing to use high sensitivity analysis is the FBI laboratory. Moreover, CODIS, which is run by the FBI and contains the national DNA database, will not upload profiles created with high sensitivity analysis. Some laboratories, including Dr. Budowle's lab at the University of North Texas, will use high sensitivity analysis for limited purposes. For example, after a disastrous accident like an airplane crash, high sensitivity analysis of bodily remains can be used to identify the victims of the "closed" population of possible contributors. But that is because the population is limited, and because the remains, for example bones, can be cleaned before the analysis is done. And, unfortunately, a mistaken analysis can be of no consequence to the contributor.

Except for OCME, then, no American laboratory produces high sensitivity conclusions for use as evidence in a criminal case. As Dr. Budowle notes, that does not mean that high sensitivity analysis must be considered totally irrelevant in criminal cases. Such analysis can produce "investigative leads." Critics of high sensitivity analysis agree that if a DNA profile created through high sensitivity analysis suggests that a particular individual is the perpetrator of a crime, that profile can legitimately point investigators at the suspect. In that regard, the results of some other techniques—polygraphs and facial recognition software, for example—likewise can aid an investigation, but are not considered sufficiently reliable to be admissible at a trial.

This court initially wondered why the criticisms of high sensitivity analysis were not matters of weight to be considered by the jury—particularly since even defense witnesses like Dr. Budowle acknowledge that a profile produced by such analysis can be of value. Ultimately, however, that thought is trumped by Frye. The products of polygraph technology and of facial recognition technology similarly can sometimes have value, but evidence produced by those technologies is not generally accepted as reliable by the relevant scientific communities and so cannot be admitted in

trials. The same should be true, at least at this time, for high sensitivity analysis. After all, if the experts in the DNA field cannot agree on the weight to be given to evidence produced by high sensitivity analysis, it would make no sense to throw such evidence before a lay jury and ask the jurors to give the evidence appropriate weight.

The People insist, however, that the relevant scientific community does accept high sensitivity analysis. It is true, as the People note, that OCME's procedures have been described in peer-reviewed articles and in discussions at gatherings of scientists. But this court cannot accept the thesis that publication and discussions equate to general acceptance. Not only the impressive defense witnesses indicate otherwise; so too do the many peer-reviewed articles submitted as defense exhibits which question OCME'S procedures. And, as the defense notes, after all this discussion of high sensitivity analysis, no other laboratory has employed it for use in criminal cases. This court simply cannot conclude that there is a general consensus in favor of high sensitivity analysis, in the face of this contrary evidence.

The People have a more specific argument that decidedly deserves attention. High sensitivity analysis was approved by the DNA Subcommittee of the New York State Forensic Commission. The conclusions of that subcommittee are binding on the Commission, and so the subcommittee numbers are the true decision-makers. And the members of the subcommittee are world-class scientists in various disciplines relevant to

DNA analysis. The subcommittee approved OCME's high sensitivity procedures, and the People suggest that this is very strong evidence of general acceptance in the relevant scientific community.

This court does not agree. It is not just that Dr. Chakraborty, one of the members of the subcommittee, has "defected," and now has testified for the defense. The more important point is that no state subcommittee can be equated with the general membership of the relevant scientific community. Will we next consider the matter closed, because the members of a committee in Idaho or Florida approve of a procedure? This court knows that the members of the DNA subcommittee are indeed experts in their particular fields and that their opinions are valuable. They simply are not determinative.

Nor does the court agree with the People that the OCME validation studies and the audits at the OCME laboratory by outside reviewers are conclusive. Every laboratory validates techniques and procedures before implementing them. But a laboratory's satisfaction with its validation results does not show general acceptance of techniques and procedures, if the validation studies fail to create such general acceptance. And OCME's

validation studies have failed to create general acceptance of high sensitivity analysis. As to audits, they appear to test whether procedures are being implemented in accordance with protocols, not whether the principles underlying the procedures are valid.

IV. THE FORENSIC STATISTICAL TOOL

In standard DNA analysis, and emphatically in high sensitivity DNA analysis, analysts encounter samples that are a mixture of the DNA of two or more contributors. These mixtures frequently present problems. Especially in standard analysis, the peak heights of one contributor may stand out, and thus readily distinguish his alleles from those of the one or more other contributors. But it is often the case, especially with relatively small contributors seen in high sensitivity analysis, that the sample contains a soup from which each individual's alleles cannot be separated out and placed in a profile.

As a result, in the past analysts often could draw only general conclusions from a mixture. For example, a mixture containing three or four alleles at each of the select loci could be called as a two-person mixture. If all of a suspect's alleles were present in that soup, the analyst could say that the suspect could be a contributor to the mixture. If many of the suspect's alleles were missing, he could be pronounced a non-contributor. But if one or a few alleles were not detected, perhaps as a result of degradation or simple drop-out, all that the analyst could say was that the suspect could not be excluded as a possible contributor, or that no conclusion could be drawn. No statistic for the probability of inclusion could be generated.

And so OCME created the FST. The FST is a computer program that calculates a "likelihood ratio" derived from a fraction. The numerator of the fraction represents the chance that the prosecution hypothesis is true—that a particular individual was one of contributors to a mixture. The denominator represents the chance that the defense hypothesis is true—that other random individuals, and not the one of interest to the prosecution, were the contributors. Division of the numerator by the denominator produces the likelihood ratio. That ratio could indicate, for example, that a three-person mixture is 100,000 times more likely as the result of contributions by the targeted individual and two random, unrelated individuals, than as the result of contributions by three random, unrelated

individuals. Or the prosecution hypothesis might be undercut—it might be, for example, that the mixture is only one-third as likely as the result of contributions by the targeted individual and two random, unrelated individuals than as the result of contributions by three random, unrelated individuals. The enormous value of such statistical results, compared to simple statements like "the individual cannot be excluded as a contributor" is obvious—if the statistics are accurate.

To arrive at the likelihood ratio, the FST employs Bayesian mathematics. Asnoted above, Bayesian probability calculations have been made in science for centuries, and no one disputes the mathematical principles involved. The FST simply performs the analysis more swiftly (by far) that a human could. It takes the probabilities of the prosecution hypothesis at each of the select loci and combines them into an overall number. It then does the same for the probabilities of the defense hypothesis at each select locus, and divides the first number by the second to create the result.

The process, to that point, is so non-controversial that many courts have stopped there, finding that there is nothing novel about the FST and thus that there is no basis for a Frye attack upon it. But that does no justice to the actual positions pressed by the defense. The key advance in programs like the FST is that they factor into the Bayesian calculations the likelihood that alleles have appeared or failed to appear as a result of stochastic effects. The defense contends [*13]that the manner in which the drop-in and drop-out rates are assessed at each locus is not generally accepted in the DNA community. The defense further argues that the FST wrongly limits analysis to a numerator and a denominator each reflecting only a single hypothesis, and thus unscientifically prevents alternative analyses.

As to the first complaint, for each locus OCME has specified the probability of drop-in and drop-out in mixtures of different DNA amounts ("quants"). The FST uses the figure at each locus and the particular quant in determining the probability of the prosecution and defense hypotheses. For example, if one of the targeted individual's alleles is not present at a particular locus, the FST program considers the chance, given the quant, that this is the result of drop-out; if the targeted individual's alleles are among those present at a locus, the FST program considers the chance that this is the result of drop-in contamination.

OCME calculated the probability of stochastic effects at most loci the old-fashioned way: they counted. The laboratory analyzed DNA mixtures from known contributors at several quants, and counted how often drop-in and drop-out occurred. But the numbers were modified to a certain extent to resolve divergence from expected patterns in the results. The numbers were also reduced by one

standard deviation in an effort to be "conservative"—to err on the side of producing lower likelihood ratios than the actual counting data would have produced. At two loci, for reasons not relevant here, the probabilities of stochastic effects were calculated, not by counting after actual DNA analysis, but through computer simulations. These procedures create issues for some scientists.

As noted, the FST utilizes different figures for the probability of stochastic effects based on the amount of DNA in a mixture sample. A related complaint about the FST's stochastic calculations concerns that fact. The volume is determined at the quantification step of DNA analysis. The "quant" calculation is not particularly precise; the numbers developed can be as much as 30% greater or lower than the true quant. Such discrepancies are unimportant with samples large enough to be evaluated with standard analysis. They can be far more significant in samples that are less than 100 picograms in weight.

The defense also complains that the FST is a "black box"—that is, that OCME has not published the FST program and is the sole entity able to employ it. As a result, a likelihood ratio can be deduced only for the prosecution hypothesis and the defense hypothesis propounded by the OCME analysts. A defense expert cannot, for example, obtain a likelihood ratio based on a hypothesis that there were a larger or smaller number of contributors to the mixture than OCME supposes, even though the number of contributors is often subject to reasonable dispute. A defense expert cannot determine a likelihood ratio based on a hypothesis that contributors are related. A defense expert cannot determine a likelihood ratio based on a different quant estimate.

The People produced impressive expert testimony in support of the design and the testing methods underlying the FST. The principle architects were Dr. Caragine and Dr. Adele Mitchell. Dr. Mitchell owns a Master's Degree in statistical genetics and a Ph.D. in human genetics and molecular biology from Johns Hopkins School of Medicine; her doctoral thesis focused on the effects of drop-in and drop-out on the statistical analysis of alleles. She has taught in her field both at Mt. Sinai School of Medicine and the NYU School of Medicine. She and Dr. Caragine received the Frederick O'Reilly Hayes Prize, an annual award for outstanding New York City employees, for their work on the FST.

Also testifying for the People was Dr. Hilda Haned of the Netherlands Forensic Institute in The Hague. Her Ph.D. studies at the University of Lyon were in statistical methods for analyzing DNA mixtures. Dr. Haned worked with Dr. Peter Gill, the DNA pioneer in Britain, to develop a likelihood ratio program modeling drop-out, and she developed a likelihood ratio program for her own laboratory as well. Dr. Haned had studied the FST and considered it a reliable method for

determining a likelihood ratio. She was particularly impressed with OCME's use of quant to calculate which drop-in and drop-out probability statistics to employ. Dr. Haned hoped to implement the quant method in her own laboratory.

But the defense presented experts as well. Dr. Shapiro disagreed with an FST protocol, intended to be "conservative," that might underestimate the number of contributors to a mixture and with another that could lead to a false understanding of the drop-out rate. He criticized the fact that OCME's validation studies included quant estimates with a "plus or minus" range of even more than 30%. The doctor also contested other aspects of the FST programming such as its failure to consider relatedness and its methods for determining the likelihood of alleles in members of various races.

Dr. Rori Rohlfs, who received her Ph.D. from the University of Washington, is a post-doctoral fellow at the University of California at Berkeley, and is a population geneticist. Dr. Rohl's testimony focused on the FST's false positive tests.

Dr. Noah Rosenberg's Ph.D. in biology is from Stanford University, and he is now a population geneticist and statistician there. His post-doctoral studies at the University of Southern California were in molecular and computational biology. Dr. Rosenberg's testimony also was centered on the false positive testing of the FST.

In addition, Drs. Coyle, Van Daal, Budowle, and Chakraborty offered criticisms of the FST. These defense witnesses had many issues with the program. Dr. Budowle agreed that the FST is "novel," and indeed unique, in how it determines which drop-in and drop-out rates to use. He also believed that this was a problem. OCME never formally tested the theory that quant could reliably determine drop-in and drop-out rates and Dr. Mitchell's "exploratory" tests on that front were not documented. Perhaps more importantly, in Dr. Budowle's view, the validation studies based their drop-in and drop-out percentages on the stochastic effects appearing in studies of "pristine" DNA samples created in the laboratory. That was no indicator of what the results would be in the real world, in which DNA samples, especially small samples, degrade over time and to a degree that is based on the circumstances of the case. Notably, different alleles in a sample may well degrade at different rates and as result a uniform overall quant estimate may, even apart from the problem that is just an estimate, mask the fact that some alleles may be far more subject to stochastic effects than others.

Next, the defense challenged the assumption by the FST architects that drop-out rates at various quant levels would increase in a linear fashion as the quant rates decreased. When the counting of drop-out was done, the assumption proved not necessarily to be the case. Nonetheless, the OCME numbers were changed from the "counted" results, to reflect the expected "linear" results. This court does not suggest for a moment that these changes were anything but the result of objective scientific judgment. But Dr. Budowle and other scientists noted by the defense do not agree that the OCME assumptions are necessarily valid.

Next, Dr. Budowle and others differ with OCME as to the use of the same drop-in [*14]and drop-out rates in the numerator and denominator to create the fraction which becomes the likelihood ratio. For example, Dr. Gill and prosecution witness Dr. Haned have published an article opining that the denominator, the "defense hypothesis," should reflect the views of the defense. This is particularly important given Dr. Mitchell's testimony that, with very small DNA samples, drop-out can be extremely high.

Further, the fact that FST software is not open to the public, or to defense counsel, is the basis of a more general objection. This court understands the city's desire to control access to computer programming that was developed at great cost. But the FST is, as a result, truly a "black box"— a program that cannot be used by defense experts with theories of the case different from the prosecution's. The prosecution will present a likelihood ratio based on assumptions — for example, that other possible contributors to a mixture are unrelated to a suspect. There is no information for the jury about whether the suspect is more or less likely than his brother to have been a contributor— even in a case in which the identity of the rider of a bicycle is in dispute.

Similarly, the FST gives numbers that are based on a conclusion about how many people contributed to a DNA mixture. But a mixture, and especially a mixture that will be classified as one requiring high sensitivity analysis, will present a challenge to one trying to determine how many people contributed to it. The fact that, for example, there are at most four alleles at each locus does not mean, necessarily, that a third person's alleles are not in the mixture. Likewise, that there are anywhere from three to six alleles at each locus does not mean that four individuals' DNA is not present. But the "black

box" nature of the FST prevents any defense attorney from informing the jury of the likelihood ratio, should the prosecution estimate of the number of contributors be incorrect. The jury will hear only

one number: the one that is produced by "the program" as it assesses the prosecution hypothesis, and a dictated so-called defense hypothesis.

Some experts would add to this "black box" criticism. OCME's laboratory, like others, sets threshold levels for peak heights below which an allele will not be recognized. Acknowledged experts like Dr. David Balding and Dr. Mark Perrin were not witnesses at the hearing, but have opined that possible alleles should be considered even if below a set threshold, and that conclusion is especially weighty where high sensitivity analysis, and questionable peak heights, are involved.

The prosecution answer to this and other criticisms seems to be that the FST formula is "conservative" and automatically reduces the likelihood ratio sufficiently to compensate. But, as noted, there are no studies which show that the FST consistently under-estimates the proper ratio, especially when an innocent suspect is thought to be a contributor. It may even be assumed that a true contributor's likelihood ratio is dropped by, for example, lowering the results by one standard deviation. But it would not follow, in the absence of pertinent testing, that the same would apply to a non-contributor, who might well benefit by not having the results reduced. There is no data, either way.

Dr. Budowle had more general doubts on this "conservative" issue as well. He testified that "there is a certain sweet point...". Depending on the circumstances of the case, if the drop-out rate is high it will give a conservative result, but at a certain point "it will go in the opposite direction" (Testimony of 12/9/13 at 829-30).

A possible response to these "black box" criticisms is that the defense can call its [*15]own experts, and can cross-examine the People's witnesses about the fact that alternative analyses are not considered. This court does not agree with the response. An OCME expert may come to court and say that, based on his analysis, a mixture is 1,000,000 times more probable if a defendant is a contributor than if he is not. It is little comfort to the defense that the defense attorney can ask, "well, what if there were three contributors, not two," and have the expert respond that there were only two, and that the results if there were three are unknown.

There is much more that can be discussed. For example, defense witnesses challenged OCME's

racial population statistics. Heavy objections were made to OCME's statistics on false positive tests. But this court need not go beyond the issues already addressed. The evidence on the other matters is in the record, and can be reviewed in future litigation. This court concludes, based on that record, that the FST is not generally accepted in the DNA scientific community.

. REARGUMENT

The parties rested in December, 2013, and prepared briefs for the court. This court announced its decision orally on November 7, 2014, before its written opinion was completed. The People almost immediately moved to re-open the hearing and to reargue. The People relied on what they considered to be new information that was not available when the parties rested. The defense has responded and the People have replied to the response. This section of the opinion will address the parties' positions as to the reargument application.

As a preliminary matter, the defendants argue that the court should, for various reasons, simply deny reargument. Certain of defendants' arguments may have technical merit, but this court agrees with the People that it would be unwise for this court to ignore their new submissions. These Frye proceedings have lasted for over two years. It would make no sense for this court to say that the People's new evidence and arguments cannot

be considered until another court expends the resources to duplicate what has been done here. However, defendants can take some consolation from the conclusion which the court reaches on reargument: defendants' motions will still be granted.

A. The DNA Subcommittee

As noted above, in 2005 the DNA Subcommittee of the New York State Forensic Science Commission approved the use of high sensitivity DNA analysis under the protocols promulgated and validated by OCME. This court did not find this dispositive of the issues. The People now report that, in 2014, the current members of the DNA Subcommittee addressed questions more recently posed

by the Forensic Science Commission. The subcommittee advised the Commission in September, 2014, that there have been no material procedural changes in OCME's high sensitivity procedures since 2005.

The People consider this to be a new endorsement of high sensitivity analysis. The court disagrees, concluding from the 2014 report only that the current members have found OCME's practices to be materially unchanged since 2005. There was no new consideration of the reliability of high sensitivity analysis. This court's initial conclusion was that the endorsement of high sensitivity analysis by the subcommittee could not be conclusive on what [*16]the scientific community as a whole believes. That conclusion remains unchanged.

B. Other Programs Assess Mixtures

The People assert that there now exist at least eight software packages which, like the FST, state likelihood ratios between the probability that a defendant is a contributor to a DNA mixture and that the defendant is not a contributor.

The People misunderstand the nature of the court's ruling as to the FST. By no means did this court suggest that there is anything wrong with using likelihood ratios or that no method for calculating likelihood ratios can be created that will gain general approval in the scientific community. What is at issue is whether OCME's FST program in particular, developed as it was, has general approval. That other programs are on the market has nothing much to say about that.

In that regard, it is important to remember the ways in which the FST is different from most, if not all, of the other programs. For example, it is very significant that the FST gives one ratio—OCME's ratio. The defense cannot "tweak" the program with alternative hypotheses that may be reasonable, to see if different results emerge. Other programs now identified by the People are more flexible.

Moreover, as noted above, OCME utilized a number of procedures to produce the FST program that differ from those used to create other programs. For example, at two loci, OCME departed from its

own general "counting" techniques. Moreover, the FST uses "quant," rather than peak heights, to determine which drop-in and drop-out rates to utilize. That practice is controversial, and it seems to remain correct that no other program for assessing mixtures utilizes "quant." And, as noted above, OCME's particular and unique methods for assessing drop-in and drop-out rates are in dispute.

The People assert that a prominent DNA expert, Dr. John Buckleton, has opined that the FST is as sound as other mixture programs. Dr. Buckleton's view is plainly relevant, but does not by itself change the calculus concerning "general" acceptance. And, for the reasons noted by the defense, the doctor's views do not appear to be based on a solid familiarity with the FST.

It is considerations such as these that cause respected scientists to withhold approval of the FST. That other, different programs are on the market does not change that. Nor is the court impressed with the argument that the FST "quant" approach to choosing drop-in and drop-out rates, and the alternative "peak heights" approach, both involve estimates. That one method of making an estimate is generally considered reliable does not show that an alternative method is acceptable as well. And the court's difficulty with the "fixed parameters" of the FST drop-in and drop-out rates is fundamentally not only that they are "fixed" but with the method through which they were set.

C. The Practice of Defense Counsel

The People note that defense advocates are happy to rely on high sensitivity and FST testing results when those results do or might exculpate their clients. The People assert, for example, that the Innocence Project "routinely" asks OCME to perform high sensitivity DNA testing for convicted defendants, and that four exonerations had resulted by the time of the People's reargument motion. The court finds the argument of little moment. First, the advocate [*17]for a convicted defendant has little to lose by requesting DNA analysis even under a procedure that is not generally accepted as reliable, if there is a chance that testing will produce exculpatory results.

Second, the court has by no means concluded that high sensitivity analysis cannot show that a suspect is excluded as the contributor of a DNA sample. Nor is the court even saying that high sensitivity analysis will never correctly identify a contributor; defendant Peaks, for example, is inculpated by high sensitivity results that are seemingly confirmed by a standard DNA sample. And a

lie detector may sometimes detect a lie. The court's conclusion is simply that high sensitivity results in general are not generally accepted as reliable in the relevant community.

Nor does the court find it troublesome that Legal Aid Society attorneys seek to introduce high sensitivity and FST evidence in other cases in which the testing favors the defense. That defense advocates would make inconsistent legal arguments in an unsettled area, on behalf of clients whose legal interests differ, comes as no shock to the court. It would hardly surprise the court to learn, for example, that in one case an attorney would seek to admit exculpatory polygraph or bite mark evidence, while opposing the admission of such evidence in a case in which it is inculpatory. This court's views would require the exclusion of the types of DNA evidence contested here in any case in which either side objected to it.

D. The FBI and SWGDAM

CODIS and the FBI do not permit high sensitivity DNA profiles to be compared to profiles in the CODIS databank. Since the parties rested, SWGDAM has issued guidelines for the potential validation of, and for quality assurances of, high sensitivity DNA analysis. The People in effect argue that it is only a matter of time before high sensitivity profiles can be uploaded for CODIS searches, and that this is further proof that OCME's high sensitivity analysis is now generally accepted.

The court first makes what it supposes is the most obvious response: the time has not yet come, and there is no way to know whether OCME's procedures will ultimately be accepted. Indeed, the SWGDAM position expressly is that it has not offered an opinion on "the viability of " high sensitivity testing. The possibility of a future SWGDAM/CODIS endorsement does no harm to the People's position. At the same time, a simple possibility adds little to it.

The People add that the FBI occasionally contracts with OCME to have high sensitivity analysis performed. At least one local federal judge has found that OCME high sensitivity results are admissible, see United States v. Morgan, 53 F. Supp.3d 732

(SDNY 2014)—albeit under the Daubert admissibility test, which is less rigorous than the Frye test. But the FBI laboratory still does not perform high sensitivity testing. That FBI personnel devoted to making cases are content to accept DNA procedures tells this court little, when those procedures are not accepted by the scientists in the FBI laboratory.The People note as well that CODIS search protocols are difficult to apply with OCME's high sensitivity results and that this practical difficulty, not scientific issues, is responsible for the CODIS refusal to look for matches with high sensitivity samples. When OCME high sensitivity analysis identifies only one allele at a locus, OCME assigns a "wild card"—a"Z"—as the second allele, because of the real possibility that the second allele has dropped out. It could be that, at [*18]this locus, the contributor is instead simply a homozygote, with the second allele being the same as the first. Or it could be that any other possible allele was present, but dropped out. CODIS searches therefore return "hits" for all contributors in the database with the first allele and any other possible allele. The result is often a very large number of possible profile matches at the allele in question. Because high sensitivity samples produce drop-out at so many alleles, the court is told, this aspect of CODIS searches is problematic.

If high sensitivity test results, with their relatively high drop-out possibilities, are too problematic for the CODIS computers, that hardly speaks in favor of high sensitivity analysis. But this court cannot conclude that the Z factor would prevent the CODIS experts from trying to match high sensitivity samples if in fact OCME's methods were considered reliable. A search could be done only on those loci in a sample where two alleles were found. Such "partial" searches are common where two alleles are found at ten or more loci, and can yield strong evidence for or against a suspect.

VI. THE PRIOR CASE LAW

This opinion will close with a discussion of five prior court opinions. None is controlling. Our slate is not entirely clean, but no New York appellate decision on the relevant issues has yet been written. Three cases deal with high sensitivity analysis, and two with the FST.

A.

The leading New York decision on high sensitivity analysis, and apparently the lead decision in the country given OCME's unique position in that field, is a decision by Justice Hanophy. See People v.

Megnath, 27 Misc 3d 405 (Sup. Ct. Queens Co. 2010). The holding is that OCME's high sensitivity procedures are generally accepted in the relevant scientific community. This court, as noted, disagrees.

Megnath pointedly refuses even to acknowledge that high sensitivity analysis involves "novel" scientific procedures that would require Frye review. In light of the evidence produced for this court by very diligent attorneys on both sides, that conclusion seems impossible to defend. None of the witnesses at the hearing in this case, and none of the articles introduced as exhibits, suggest that the issue in this case is a "gimme." Even the People's experts were quick to acknowledge that moving from standard DNA analysis to high sensitivity analysis means crossing a border to a different world.

In particular, the Megnath opinion is dismissive as to the increase in stochastic effects that is the natural result of employing 31 cycles with software designed for 28 cycles. That, as the opinion notes, there can be stochastic effects in any DNA analysis hardly suggests that the substantial increase in such effects in high sensitivity analysis is irrelevant. And of course it does not suggest that the expert opinions explaining why these effects are not adequately dealt with by OCME's protocols can be ignored.

To similar effect is United States v. McCluskey, 954 F. Supp.2d 1224 (D. C. N. Mex. 2013). The McCluskey court excluded a primitive high sensitivity analysis—though, concededly, on facts enormously different from those of this case. In McCluskey, a laboratory did analysis of DNA samples with fewer DNA picograms than usual, with no changes in their usual procedure. When the court analyzed the OCME procedures described in Megnath, it noted that in several ways they were more sensible than those used in New Mexico. But the opinion ended by criticizing Megnath for suggesting that high sensitivity analysis does not involve new science. And the court also disagreed with the apparent and illogical Megnath view that the increased stochastic effects in high sensitivity analysis are, basically, no matter of concern, because there are stochastic effects even with standard analysis.

This court rejects both of those thoughts from Megnath. So do, it seems, all the experts who gave relevant evidence for either side.

B.

The leading New York decision on the FST is Justice Carruthers' opinion, not officially reported, in People v. William Rodriguez, NY Co. Ind. No. 5471/2009 (Sup. Ct.

NY Co. October 24, 2013). Rodriguez concludes that the FST is generally accepted in the relevant scientific community. But the opinion is focused on matters not in controversy, such as the general acceptance of PCR-STR analysis; of the use of likelihood ratios in the evaluation of DNA mixtures; and of taking account of drop-in and drop-out rates in calculating likelihood ratios. Moreover, the court deprecated the "counting" of scientists' "votes" on disputed points, giving extreme deference to the view of New York's DNA Subcommittee and of its chair, Dr. Ballantyne. This court has already noted its view that the subcommittee's conclusions are by no means binding.

Further, the Rodriguez opinion pays no attention to what, at least at this court's hearing, was a major focus of scientific contention: the manner in which the likelihood of stochastic effects at the relevant loci was computed for the FST. Similarly touched on only lightly was the pronounced controversy over the FST's use of "quant", rather than peak heights, to determine which figures to employ in assessing the likelihood of drop-in and drop-out. In its brief remarks on the subject, the court in fact simply and inappropriately decided the scientific issue in the People's favor. Finally, the opinion concluded that it is a positive asset to the FST that it remains a "black box," and that it can examine only the prosecution's hypothesis; this court has already mentioned its view to the contrary.

This court ends with a word about another opinion upholding use of the FST—People v. Wendell Belle, 2015 NY Misc Lexis 1503 (Sup. Ct. Bronx Co. April 29, 2015). The Belle court first notes, as so many other courts discussing Frye and the FST have done, that Bayesian analysis is universally accepted and that the FST simply performs Bayesian calculations faster and more reliably than a human can. But the Belle court, to its credit, does not stop there, recognizing that other aspects of the FST are also in issue.

Still, the court then jumps over those aspects without discussion because the defense in that case performed its own FST-like calculations and arrived at a likelihood ratio very different from OCME's—though still highly inculpatory. The court's

conclusion is that the FST methodology is no longer at issue in the case, and that a jury should hear

the experts and decide which highly inculpatory likelihood ratio is correct.

But the conclusion does not follow. Of course, the defense can maintain its legal

challenge to the FST, and upon losing still take the fall-back position that the less damaging ratio should be considered.[FN7]

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The preceding analysis was complete, but not yet in full opinion form, on November 7, 2014, when the court orally announced its views. The People almost immediately asked to present additional evidence of developments since the People's case concluded. The defense objects to this court considering the People's new submissions, but the court believes that under the circumstances of this case the People's reargument application should be granted. This court accepts the additional information, and will simply add that the People's additional considerations do not change the result.This court concluded that evidence derived both from high sensitivity analysis and from the FST are not yet proved to be admissible under the Frye test. The court is not happy with that result. This court has heard for years about the high sensitivity initiative, with all of the incumbent expense. And this court understands as well the sincere effort that Dr. Caragine, Dr. Mitchell, and many others have put into the development of the FST. They must continue, if they are to persuade.

E N T E R:

_____Mark Dwyer

Justice of the Supreme Court

Dated: July 2, 2015

Footnotes

Footnote 1:After the court announced its ruling, defendant Collins pleaded guilty to Assault in the Second Degree in return for a prison sentence of six years. The charges against defendant Peaks are scheduled for trial on July 6, 2015.

Footnote 2:Another point in the genetic map is also examined to determine the sex of the person who contributed the DNA. At this locus women have two X chromosomes. Men have but one X chromosome, paired with a famously "broken" Y.

Footnote 3:"High sensitivity" analysis is also referred to as "low copy number" analysis, "LCN" analysis, and "low template" analysis. The routine 28 cycle procedure is sometimes referred to as "high template" analysis. Use of the " high" and "low" terms can be most confusing. In this opinion, the new 31 cycle procedure will be termed "high sensitivity" analysis, and the standard 28 cycle procedure will be called "standard" DNA analysis. It should also be noted that while OCME "high sensitivity" analysis employs 31 cycles, other laboratories may employ more.

Footnote 4:The hearing evidence focused on four stochastic effects that may complicate DNA analysis under any procedure, including standard DNA analysis. "Drop-in" is the contamination of a sample by an allele or alleles at one or more loci, from a source unconnected to the person or persons who actually supplied the DNA sample. "Stutter" is a frequently-occurring echo phenomenon in which a report of an allele at a particular locus leaks back to the previous locus—or, less commonly, forward to the next locus—to give a false result at that previous or subsequent locus. "Drop-out" is the failure of an allele at a particular locus to register at all in the test results. "Peak imbalance" is much the same: an allele fails to register fully at its locus, relative to the strength with which other alleles register. As a result, the allele might be considered contamination rather than a true allele.

Footnote 5:After she testified, Dr. Caragine was obliged to leave OCME because she resolved a dispute over analysis in a DNA case in a manner inconsistent with OCME protocols for how analyst disagreements should be handled. This court does not consider that to be remotely relevant to her assessments of high sensitivity analysis.

Footnote 6:The Scientific Working Group on DNA Analysis Methods is a group of scientists from federal, state and local DNA laboratories in the United States and Canada. SWGDAM has created national standards for federal and state forensic DNA testing.

Footnote 7:The Belle court also was distracted by what this court considers to be two irrelevancies. First, the court was troubled by the fact that defense attorneys in other cases seek to have the jury hear exculpatory FST evidence; this court, as noted, finds that unremarkable. Second, the Belle court emphasized the strength of the People's other evidence in the case. This court thinks that the other proof in the particular case has nothing to do with the FST's status under Frye.