HEADNOTE:

Ralph Brian Keirsey v. State, No. 1515, September Term, 1994

Evidence - DNA evidence

THERE ARE TWO DISTINCT ISSUES INVOLVED IN THE PRESENTATION OF DNA EVIDENCE: (1) THE RFLP TEST TO DETERMINE WHETHER THERE IS A "MATCH" BETWEEN THE DEFENDANT'S DNA AND THE PERPETRATOR'S DNA, AND (2) THE ESTIMATE OF PROBABILITY THAT A PERSON OTHER THAN THE DEFENDANT ALSO HAS DNA THAT MATCHES THE PERPETRATOR'S DNA. THE FRYE-REED TEST APPLIES TO THE RESULTS OF RFLP TESTING. FRYE-REED IS SATISFIED, HOWEVER, BY CJ 10-915. THE FRYE-REED TEST DOES NOT APPLY TO THE ESTIMATES OF PROBABILITY. THE CRIMINAL DEFENDANT IS THEREFORE NOT ENTITLED TO EXCLUSION OF A PROBABILITY ESTIMATE PRESENTED BY A QUALIFIED EXPERT ON THE GROUNDS THAT THE EXPERT'S OPINION IS BASED ON A THEORY THAT DOES NOT PASS THE FRYE-REED TEST.

REPORTED

IN THE COURT OF SPECIAL APPEALS

OF MARYLAND

No. 1515

September Term, 1994

BRIAN RALPH KEIRSEY

v.

STATE OF MARYLAND

Wilner, C.J.,
Alpert,
Murphy,

Opinion by Murphy, J.

Filed: September 1, 1995

#15373

In the Circuit Court for Worcester County, a jury (Hon. Theodore R. Eschenburg, presiding) convicted Brian Ralph Keirsey, appellant, of burglary, first degree rape, and related offenses. Pursuant to Md. Ann. Code art. 27, § 643B, appellant was sentenced to two consecutive life sentences without the possibility of parole for the burglary and first degree rape convictions. The other convictions merged. His appeal presents seven questions that we have renumbered and rephrased as follows:

I. Did the admission of DNA evidence violate due process of law?

II. Did the trial judge err by denying the defense expert access to relevant information about the State Police DNA laboratory?

III. Did the trial judge err in admitting evidence that DNA testing established a "match" between appellant's DNA and the perpetrator's DNA?

IV. Did the trial judge err by admitting the random match probability computed by the State Police DNA Laboratory using the Multiplication Rule?

V. Are appellant's mandatory life sentences without parole illegal because the State failed to prove the facts necessary for imposition of those sentences?

VI. Was imposition of two mandatory sentences of life without parole illegal?

VII. Must the sentence for burglary be vacated because that crime merges into first degree rape?

FACTUAL BACKGROUND

Appellant was charged with a rape and burglary that occurred in Ocean City on September 15, 1990. The victim was unable to identify her assailant. She made a tentative identification of her assailant's voice from a tape that police played for her. Michael Austin, the person whose voice she identified, was "excluded" on the basis of DNA testing.

The case was investigated by Worcester County Deputy Sheriff Stuart Murray, who learned that appellant had been arrested on unrelated charges shortly after the rape occurred.[1] Murray requested that appellant meet him at the Ocean City Police Headquarters. When they met at that location two days after the rape, appellant professed his innocence. He stated that in the early morning hours of September 15 he had been in the Dutch Bar until it closed, then went to the Kitchen Restaurant with friends, and ended up at the Thunderbird Motel where he was staying.

Appellant's criminal agency was established by expert testimony from Teresa Long, a supervisor in the Maryland State Police Crime Laboratory's biology unit ("MSPCL"). After giving a

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[1] Murray described appellant as a white male, 5'10'' tall, approximately 160 pounds, with sandy blond hair, a moustache, and a gold necklace. The victim described her assailant as a white male, twenty-five to thirty five, approximately 5'8'' to 5'10'' tall, one hundred sixty pounds, sandy-colored hair, with a wiry build, a chain around his neck, hair on his face and wearing a watch. She testified that the man spoke with a "hick country accent," a kind of "twang." She also smelled alcohol on his breath and believed he had just come from a bar because of the odor of cigarettes on his person.

description of the DNA testing process, Long testified that appellant's DNA "matched" the DNA in the sperm recovered from the victim's vaginal swabs. According to Long, (1) the probability that someone selected at random would have appellant's DNA was 1 in 2,200,000; and (2) Michael Austin's DNA did not match the DNA recovered from the victim.

Appellant did not testify. His witnesses challenged the DNA evidence and raised an alibi defense. Dr. William Shields, a DNA expert, disagreed with Long's conclusion and criticized the MSPCL's testing procedure. Shields ultimately opined that, even if the MSPCL's lab results were compatible with the FBI database used to calculate the probability of a random match, the probability of someone selected at random matching appellant's DNA profile was as low as 1 in 1,349. Kimberly Green testified that, on the morning of September 15, she was working at the Dutch Bar and served appellant a Long Island Iced Tea approximately every 15 minutes. She also testified that, after the bar closed, she was at the Kitchen Restaurant with appellant and others until approximately 3:30 a.m. Penny Miles, who dated appellant in the summer of 1990, described him as 6'2", 200 to 220 pounds, with a "roll of fat" around his stomach and tattoos on one arm. She denied that he spoke with a "hick country accent," but did say that he wore a gold chain around his neck and a gold watch.

DISCUSSION

I

Appellant contends that the admission of DNA evidence violated his due process rights because "[a] part of the due process guarantee is that an individual not suffer punitive action as a result of an inaccurate scientific procedure." Higgs v. Wilson, 616 F.Supp. 226, 230 (Ky. 1985). To violate due process, the introduction of the evidence must be "so extremely unfair that its admission violates 'fundamental concepts of justice.'" Dowling v. United States, 493 U.S. 342, 352 (1990) (quoting United States v. Lovasco, 431 U.S. 783, 790 (1977)). No such violation occurred in this case.

Appellant contends that, because DNA evidence is "in a state of flux," whenever such evidence is offered, the accused has a due process right to a Frye-Reed hearing[2] to make sure that the evidence offered is considered to be the "best" (i.e., the most accurate, explicit, probative) at that moment by the relevant scientific community. There is no merit in that contention. The criminal defendant does not have a due process right to a Frye-Reed hearing every time the State offers scientific evidence.

Appellant presents the following challenges to the State's DNA evidence:

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[2] Reed v. State, 283 Md. 347, 381 (1978) and Frye v. United States, 293 F. 1013, 1014 (D.C. Cir. 1923) hold that the results of a scientific test cannot be received into evidence until it is established that the test results are generally accepted as accurate by the particular scientific community that has expertise in the subject matter of the tests.

(1) The State's expert should have been prohibited from opining that appellant's DNA "matched" the perpetrator's DNA because:

(A) The MSPCL used an incorrect "match window."

(B) The MSPCL's internal controls were so inadequate that it was impossible to confirm that the RFLP testing was done properly in this case.

(2) The State's expert should have been prohibited from expressing an opinion about the statistical probability of someone other than appellant having the perpetrator's DNA because:

(A) The State's expert relied on statistical information contained in the FBI database, rather than on a database developed in the MSPCL where the RFLP test was actually performed.

(B) One of the four "probes" used by the State had a "questionable statistical independence" and should not have been included in the "bottom line" conclusion.

(C) The State's probability estimate was based on the "Multiplication Rule" (also known as the "product rule"), a methodology that is no longer generally accepted as reliable by the relevant scientific community.

Each of these challenges is discussed in parts III and IV of this opinion. In light of our disposition of those challenges, we do not reach the issue of whether a criminal defendant has a due process right to obtain the exclusion of unreliable scientific evidence that is admissible by statute.

The proponent of scientific evidence can satisfy the Frye-Reed test in three ways: (1) proving to the trial judge, through testimony and exhibits (including persuasive authority from other jurisdictions), that the relevant scientific community is in agreement that the technique at issue produces an accurate result; (2) asking the trial judge to take judicial notice of a reported opinion in which a Maryland appellate court has held that the technique at issue satisfies the Frye-Reed test; or (3) asking the trial judge to take judicial notice of a statute in the Annotated Code of Maryland that provides for the admissibility of the test results at issue. In this case, the State satisfied Frye-Reed by reliance on the applicable statute, and the defense made no contention that the relevant scientific community is now divided over the issue of whether RFLP testing produces accurate results.

There is a good reason why the defense decided against arguing that the RFLP testing technique cannot satisfy the Frye-Reed test. The reliability of RFLP test results has been established. The relevant scientific community agrees that RFLP testing is capable of determining whether persons' DNA do or do not "match" at a specific location on a particular chromosome. The legislature has expressly recognized RFLP as a reliable method of DNA profiling. So have appellate courts in other jurisdictions.

The only Frye-Reed challenge in this case was addressed to the State's statistical probability calculation. In part IV, we

explain why the Frye-Reed test does not apply to estimates of statistical probability. We therefore affirm the trial judge's refusal to grant appellant's request for a Frye-Reed hearing on the State's DNA evidence.

II

Appellant made two separate motions requesting that his expert gain access to information contained in the MSPCL. The first motion requested that the State, pursuant to Maryland Rule 4-263, "[p]roduce and permit the Defendant to inspect and copy all written reports or statements made in connection with this case by each expert consulted by the State, including the results of any...scientific tests, experiment or comparison...." Appellant never requested a ruling on this motion.

The second motion requested that Dr. Shields be allowed access to the MSPCL for a period of approximately eight hours so he could inspect the lab and assess the work done in this case. That motion was denied as overbroad by Judge Eschenburg who concluded that, "[t]he Md. State Police Lab can not be turned over for inspection in all cases where a Defendant requests it. If this were permitted statewide, the lab would be in total chaos. [The defense] expert literally wants the lab turned over to him for inspection and questioning."

Appellant thereafter made no further request for access to the lab. Moreover, the following dialogue occurred during trial between the Court and appellant's counsel:

> THE COURT: Wait a minute. There was a motion where you wanted to have your expert

go, and he wanted, in effect, the court's order having the lab, in my judgment, turned over to your expert for review and study all these various documents and their equipment and everything else about it, and I denied it.

Is that what would have accomplished that, what you're talking about?

[DEFENSE COUNSEL 1]: No, Your Honor. This could have been accomplished by just simply providing the data.

THE COURT: Well, did you file any such motion? I can't remember. I don't remember that.

[DEFENSE COUNSEL 1]: Yes, your Honor.

THE COURT: So I denied it then, obviously; right?

[DEFENSE COUNSEL 1]: (Nodding head affirmatively).

THE COURT: Is that what you're saying?

[DEFENSE COUNSEL 1]: Well, Your Honor, I'll have Doctor Shields address that.

THE COURT: No. But Doctor Shields has nothing to do with whether or not I denied an order or granted it. Did I grant it or deny it, or did you even file such a motion?

[DEFENSE COUNSEL 1]: Yes, I did file a motion, Your Honor. And as of the date of trial, I never received a ruling.

THE COURT: Well, I asked you before court started if there were any undisposed trial motions, and I was told no.

[DEFENSE COUNSEL 2]: That's correct. And it was probably my fault in miscommunication. You did deny our request for a court order to go in, and that's all we're asking.

THE COURT: And that's that. Okay.

Appellant clearly abandoned the 4-263 motion in favor of the Motion to gain access to the MSPCL. His present complaint, alleging error in the denial of the 4-263 motion, comes much too late.

Appellant also contends that § 10-915 provides for more extensive and specific discovery in a DNA case and that the State failed to provide the necessary information. In the circuit court, however, appellant never alleged that the State failed to comply with its discovery obligation under the statute. The discovery issue has not been preserved for our review.

III

Md. Ann. Code (1989 Repl. Vol.), § 10-915(b) of the Courts and Judicial Proceedings Article ("the statute") provides in part that "[i]n any criminal proceeding, the evidence of a DNA profile is admissible to prove or disprove the identity of any person...." In § 10-915(a)(3) of that statute, a DNA Profile is defined as "an analysis that utilizes the restriction fragment length polymorphism analysis of DNA resulting in the identification of an individual's patterned chemical structure of genetic information."

DNA and the RFLP testing process have been described in a number of opinions, including Cobey v. State, 80 Md. App. 31, at 36-41 (1989). A brief summary, however, is necessary to provide the background for the evidentiary issues presented in this case.

> [Deoxyribonucleic acid (DNA)] contains the...'genetic code' that defines who we are,

> what we look like, and where our talents lie....
>
> Embedded within the nucleus of virtually every cell of each human being's body are forty-six road-shaped chromosomes....Each chromosome has the shape of a twisted ladder or spiral staircase [(a double-stranded helix)]. The 'banisters' of this staircase are made of phosphates and sugars, while the 'steps' or 'rungs' consist of 'base pairs,' or pairs of amino acids bound together. A single DNA molecule -- itself not a very large entity -- contains about *three billion* base pairs.
>
> Located at specific sites, or 'loci,' along each chromosome are large groups of base pairs known as 'alleles,' or 'genes.' Over 99% of these genes are identical among all human beings...The remaining [base pairs, approximately 3 million] -- known as 'polymorphic' genes because they vary in form from person to person -- account for our unique characteristics as individuals. Many polymorphic genes are known to have definite functions: some are responsible for the color of our hair and of our eyes, some for the shape of our body and the type of our blood. Other polymorphic genes, however, appear to have no function whatever. These 'junk DNA' segments...consist of varying lengths of repeating sequences of base pairs....
>
> The remarkable technology which has provided molecular biologists with an entree into the wonders of sub-microscopic exploration has not yet enabled them to compare every base pair in one DNA molecule with every base pair in another to determine conclusively that the two molecules are, in fact, identical. Forensic scientists, seeking to apply the new technology to identify the guilty and to vindicate the innocent, have developed a 'shortcut' for making this determination.

United States v. Porter, 618 A.2d 629, 632 (D.C.App. 1992).

DNA profile evidence involves two distinct procedures. The Restriction Fragment Length Polymorphism (RFLP) analysis determines whether there is a "match" between the DNA of the

defendant and the DNA of the perpetrator. A "match" produced by that process, however, does not prove conclusively that the defendant is the person who committed the crime:

> Even if there is a perfect [visual] match at four or five different loci, there is still a possibility that the two samples came from different people whose DNA patterns at those particular loci are indistinguishable. Thus, the second procedure, calculation of the probability of a random match, generates a ratio which accompanies a match, the purpose of which is to express the statistical likelihood that an unrelated person chosen at random from a particular population could have the same DNA profile as the suspect.

People v. Watson, 629 N.E.2d 634, 637 (Ill. App. 1994).

The RFLP Testing Procedure

There are six steps involved in determining whether there is a "match" between the defendant's DNA and the perpetrator's DNA:

1. Extraction:

The DNA of each relevant person must be chemically extracted from samples of a person's tissue, e.g., blood, semen, hair, bone, or skin.

2. Fragmentation:

The DNA is then cut by *restriction enzymes*. Often described as "molecular scissors," these enzymes are designed to cut the DNA strand into fragments. The cuts are made at places on the DNA strand that the enzyme recognizes as being "nonvariable", i.e., the same in everyone. If everyone's DNA were the same, the enzymes would produce fragments of the same length. The

fragments cut by the restriction enzyme are not the same length, however, because in each fragment there are repetitive sequences of base pairs unique to each individual. These sequences are known as "VNTRs" ("variable number of tandem repeats"). The VNTRs are called "*polymorphic*" because they differ from person to person.

3. Gel Electrophoresis:

This process sorts the fragments according to length. The fragments are placed on a slab of gel, and an electric current is applied to move the fragments toward the positive end of the gel. The distance that the fragments travel will depend on their length. Smaller fragments will travel further than larger fragments.

4. Southern Blotting:

To facilitate the interpretation of the DNA fragments, they are then transferred to a nylon membrane. In a procedure called *southern blotting*, the fragments are blotted onto the membrane.

5. Hybridization:

DNA is a double stranded fragment. At this point it is chemically treated to "unzip" it, turning it into a single strand. The VNTRs on this strand are located with the use of *radioactive probes*. A probe is a single stranded fragment of cloned DNA. Probes are predeveloped in laboratories around the world and are designed to identify strands of VNTRs at a

particular "address" (section) on a specific chromosome.[3] As the State's expert explained it,

> ... a probe looks at a specific point or a locus on a chromosome or a location on a chromosome. The D stands for DNA; the number following that stands for which chromosome it's found on; S stands for region; and the number following that stands for which region on that chromosome.

The probe is placed on the membrane. When a probe recognizes a complementary strand of DNA, it will act like a magnet and "bind" itself to the fragment at that sequence. This will "light up" the entire fragment, including the polymorphic portions, i.e., the portions that vary in length from individual to individual depending on the number of VNTRs contained within them. The probe thus allows the technician to measure the length of each person's variable DNA at a particular locus (location) on a specific chromosome.

The State's expert explained the hybridization process as follows:

> Basically,...the probe flows up the membrane. When it finds its compl[e]mentary match for every time there's an "A" on the DNA fragment of the nylon membrane and "T" in the probe, and everything matches all along the line, it will zip back up in a double strand of DNA fragment.
>
> And what's so special about this probe is that we've made it radioactive so we can detect it later on...

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[3] Probes are named for the exact location to be examined; i.e., D2S44, D17S79, D1S7. The number following the D represents the particular chromosome and the number following the S represents the specific "address" (location) on the chromosome. Therefore, D2S44 means the 44th section on chromosome number two.

> Now, when I mention "probe," what a probe does is looks for one area of the DNA that is specific to one chromosome.

6. Autoradiograph:

Once the probes have attached, the nylon membrane is exposed on x-ray film. Black bands appear where the probes have attached to the fragments. The result is an *autoradiograph* or *autorad*. A visual comparison is made of the autorads containing the victim's sample, the suspect's sample and the perpetrator's sample. The lab technician is looking for bands that (1) have identical lengths, and (2) occupy the same position on the autorad. The RFLP test does not allow the technician to determine the specific sequence of bases in the DNA fragment.

The State's expert showed the jury the autorads produced in this case,[4] and testified as follows:

> I...received a...blood sample...from Brian Ralph Keirsey. Again, the DNA profile were generated for the genetic loci D2S44; D17S79; D1S7; S(sic)10; and (sic) S28. They were developed from the blood samples of the victim, blood sample of the suspect Brian Keirsey, and the victim's vaginal swabs....The DNA profile obtained from the vaginal swabs...matches the DNA profile that came from the blood sample of Brian Keirsey.

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[4] Although the autorads are part of the record in this case, we are unable to determine what the witness was showing the jury when she described locations as "here and here" or "here and there." "...[I]t is impossible for an appellate Court to ascertain with accuracy what a witness means when he [or she] is testifying from a drawing on a blackboard and he [or she] uses such expressions as 'from here to here'..." Gatling v. Sampson, 242 Md. 173, 175 (1965). Despite the somewhat confusing testimony, the defense agreed that there was a visual "match" in this case. Dr. Shields testified, "[w]ell, let me first begin by stating that I personally agree with the description of a visual match...There is a visual match, in my opinion."

> The first autoradiograph for the probe is D2S44. Again, you can see our molecular ladders across the gel and the sides of the bands. You can see in the second lane here is our real control line or cell line. You don't produce a more suitable pattern. That's been pre-determined, and you gauge yourself to the proper places.
>
> The next lane is the victim's band pattern. It has a band here and here. And S-1 is the first suspect...and here and there. (Indicating) and Q1 is the male fraction of the vaginal swabs. That's generated the entire length here. (Indicating) And you can see visually that this band pattern from the male fraction vaginal swabs does not match [the first suspect].
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> When we received the blood of Brian Keirsey -- it's hard to see these on your overhead. You see this band pattern here is the male fraction vaginal swabs. Right here is the blood of Brian Keirsey: This band here and that band there. Again, that's a visual match, and we would go on the size of that.
>
> (Emphasis added)

A margin of error is built into RFLP testing because it is impossible to measure the sample fragments precisely. Watson, *supra*, 629 N.E.2d at 639. This margin of error is called the match window. The MSPCL uses the FBI laboratory's match window of +/- 2.5 percent. Thus, the process produces a "match" if -- at a particular section of a specific chromosome -- the length of the suspect's polymorphic DNA strand is no more than (1) 2.5% longer, or (2) 2.5% shorter than the length of the perpetrator's polymorphic DNA strand.

The RFLP test is an essential component of the expert's opinion that the defendant's DNA does or does not "match" the perpetrator's DNA. That test is based on a precise scientific

technique "controlled by inexorable, physical laws." State v. Allewalt, 308 Md. 89, 98 (1986). If, as in this case, such a scientific technique is an essential component of an expert's opinion, that technique must satisfy the Frye-Reed test. Keene Corp. v. Hall, 96 Md. App. 644, 660 (1993), cert. granted, 332 Md. 741 (1993). As we stated in Part I, however, compliance with Frye-Reed was fully satisfied.

Section 10-915 does not require the admission of unreliable evidence. As is the case with any scientific evidence, a proper foundation is required before RFLP test results can be admitted.[5] The State's foundational evidence must establish that (1) the equipment necessary for performing each phase of the test was in proper working order, and (2) the persons operating the equipment at every stage in the process were qualified to do so. See 5 Lynn McLain, Maryland Evidence, § 401.4(d) (1987). In this case, the State's foundational evidence was more than sufficient to establish that a correct "match window" was used and that the MSPCL's internal controls were adequate.

IV

Statistical Probability Analysis

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[5] No statute could require the admission of scientific evidence gathered in an unreliable fashion or tested by an incompetent technician. Appellant had a right to, and did, challenge the evidence gathering and MSCL procedures employed in this case. The Frye-Reed test, however, is not applicable to the issues of whether the evidence was gathered correctly, or tested properly, in a particular case.

The statistical probability analysis attempts to answer the question, "What is the likelihood that a person other than the defendant has the same DNA as the perpetrator?" The RFLP process does not determine with precision either the exact number of base pairs or the exact order of the VNTR sequence for any DNA fragment at issue. The process only makes it possible for the technician to measure the overall length of a polymorphic DNA fragment that is located at a particular locus on a specific chromosome.

"A match is virtually meaningless without a statistical probability expressing the frequency with which a match could occur." State v. Vandebogart, 616 A.2d 483, 494 (N.H. 1992). That is why it is misleading to suggest that the RFLP test produces a "fingerprint." That is also why a statistical probability analysis is necessary to determine the chance that some other person chosen at random from the general population has DNA that matches the defendant's DNA.

Scientists agree that if they could test every strand of DNA in the human body there would be no need for a statistical probability analysis. It is impossible under current technology to test every strand of DNA. For that reason, a statistical probability analysis is the final step in the DNA identification procedure. Different probability analyses produce different expert opinions. Dr. Shields offered the following explanation of the statistical analysis issue:

> What you're trying to do is, after you've decided that somebody can't be

excluded, you want to decide what's the likelihood that somebody else might have left [the sample at the crime scene]...So what you end up having to do is find out, if you can, what's the likely frequency of this particular profile that resulted in a particular case in the general population or in the appropriate population.

* * *

[The statistical method employed by the State] is reliable. Now, the formula itself is nothing more than a representation of the basic principle or probability. What ends up happening is that you can make different sets of assumptions about when you can use that formula or how you use that formula. And the formula, in the absence of knowing anything about the other assumptions, will produce a number. Whether that number is reliable is a different question of whether the formula is reliable.

* * *

It is the basic principles of probability and statistics. And the way to do that is to think about it in the context of how I asked the question of what's the likelihood of an event; what's the likelihood of drawing an ace from a deck of cards. If people understand a deck of cards...they're going to say there are four aces; there are fifty-two cards; and the probability of drawing an ace is one in thirteen....

So if you're going to draw one card from a deck of cards and that card you want to know is likely to be an ace, you're going to say one in thirteen. But only if it's a regular deck of cards. If it's a pinochle deck of cards, the number changes; and that's where the argument starts coming from. It's whether it's an appropriate database; whether this database can actually represent the case in question, can that produce the same number.

Well, if I had an urn up here and I told you there were black and white balls in it, and I asked you what's the probability of drawing a white ball, nobody could answer. So the way most people would attempt to

answer is if they dumped the urn and count the number of balls. And then you find out there are five white; five black - a total of ten...Half the time you expect to draw a white ball. Now you know something. That's because you know the frequency of what white and black is in your urn. That's too easy a system in one sense of the word. It's not the system we work with most of the time in the real world.

The real world, what we're talking about with DNA is, we got a urn out in the middle of the room that has billions of balls in it. And those billions of balls come in a hundred and fifty or two hundred, three hundred colors. They range from yellow to light yellow to the lighter yellow to the lightest yellow to dark yellow and all the oranges and all the in-between. That's what we're talking about with VNTR, because they can range from one thousand base pairs to eleven thousand base pairs continuously.

How do we determine what the frequency of a particular band is going to be? We don't. We have to sample them. And sampling is something that's part of statistics from day one. You go out and you say, "Okay. I can't know the exact number, because it would take forever to count. So I'm going to take a thousand individuals and count up the number of balls. Just take a thousand out of that urn. And if there are a hundred red ones, I'm going to hope that the hundred red divided by the thousand in the sample give me ten percent, and that ten percent was a good estimate of the number of red balls in the giant urn where there's billions of them. That's the way statistics enters into population genetics, and it's used in DNA typing.

So the notion is that you have to go out and sample, okay. The same is true with decks of cards....I'm going to hand you a deck and ask you what's the probability of drawing an ace. If you go out with a true fifty-two of them and you know all decks of cards are the same, it's an easy answer. Now, you can do four over fifty-two. But if you only did twenty-five, you might come up with the wrong number. You might come up with the first four aces and you decide that's the databases. You can do the same

> thing with spades and clubs. And if the deck was not shuffled, you might decide that everything is a spade because the top of a new deck of cards is all spades.

In order to determine the statistical probability that someone other than the defendant is the source of the perpetrator's DNA sample, the FBI has developed a method known as the *fixed bin analysis*.[6] The State applied that analysis in this case.

Scientists have compiled databases that identify and categorize samples of DNA taken from a number of persons in the population. The probes described above are used to obtain a sample from the same "locus" on the same chromosome of each individual, and the samples are categorized by size. A database has been compiled for each probe.

The fragments are arbitrarily sorted into "bins" depending on their length. The length measurement is described as a number of base pairs.[7] The FBI has prepared a table for each probe that shows how many samples are contained in each bin. Those tables, published in the Crime Laboratory Digest (Vol. 18, No. 1, January 1991, pp. 12-26), were received into evidence without objection.

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[6] For a more detailed explanation, see Budowle, Giusti, Wayne, Baechtel, Fourney, Adams, Presley, Deadman & Monson, Fixed Bin Analysis for Statistical Evaluation of Continuous Distributions of Allelic Data From VNTR Loci, For Use in Forensic Comparisons, 48 Am. J. Hum. Genetics 841 (1991).

[7] The RFLP analysis measures the length of the polymorphic section of a DNA fragment. It neither counts nor "sequences" the actual number of base pairs on that fragment. Nonetheless, in the fixed bin analysis, the overall measurement of each VNTR fragment is described in terms of base pairs.

The State's expert used those tables to calculate the chance of a random match in this case.

For example, the FBI table shows that on D2S44 (the second chromosome, at section 44) bin 1 has a range of 0 to 871 base pairs, bin 2 has a range of 872 to 963 pairs and so on. Each VNTR fragment in the database that measures from 0 to 871 base pairs at that locus is assigned to bin 1. Each fragment that measures 872 to 963 base pairs at that locus is assigned to bin 2, etc. How the bins are chosen depends on the number of samples in the database. Each bin that does not contain at least five samples is "merged" with an adjacent bin to establish an acceptable minimum number of samples. To estimate the chance that some other person has a VNTR fragment that "matches" the fragment identified by a particular probe, the number of samples in each bin is divided by the total number of samples in the database for that probe. There must be a sufficient number of fragments in each bin to make the data "statistically significant." Too large a bin, however, will cause the comparison to be statistically insignificant.

The chance of a "random" match, i.e., another person having the suspect's DNA, is estimated by determining the frequency with which the defendant's fragment appears in the particular database. To compensate for the measurement imprecision associated with RFLP testing, the defendant's fragment is assigned to the bin in the match window of +/-2.5% that contains the highest frequency (the greatest number of samples). As an

example, for D2S44 there are 1584 samples in the FBI database and 8 samples in bin 1. Eight divided by 1584 yields a fraction of .005. Under the fixed bin approach, therefore, if probe D2S44 measures the suspect's VNTR fragment to be of a length that falls into bin 1, there is a .005 percent probability that someone chosen at random from the general population would "match" the suspect's DNA.

Dr. Shields testified that each laboratory needs to develop its own match window because conditions differ from laboratory to laboratory. Other laboratories that use the FBI database have developed their own match windows. The State's DNA expert, a former employee of the FBI lab who participated in the development of the FBI match windows, testified that she performed the correct validation studies to determine whether the FBI's match window was transferable to the State Police laboratory. That foundational testimony was sufficient to permit the State's expert to use the FBI database.

The State's DNA expert gave the following explanation of the fixed bin approach:

> In order to calculate the statistics of the match once we determine it is a match, you want to put some weight on that match. We use what's called the fixed bin approach...
>
> So basically what we do is, we take a random sample of the population and run a DNA test, and we just count how many times do we see a ladder between this bin; how many times do we see a band between these bins right here. We develop frequencies for those bands - how often do we see them.
>
> In order to be conservative--because we're not sampling the whole world, we're

taking a random sample of a population--we only have one, two, three, or four occurrences or four times where we see a band in that bin, and determine that that's not enough. So we'll combine that bin with the bin next to it in order to give a higher frequency that will be more conservative in our estimate.

Well, what we'll also do is what's called a higher bin frequency measurement. If a band should happen to occur here in a bin boundary, there could actually be with a measurement here; it could fall in this bin or fall in that bin down here. You can see that there are frequency numbers point one two for bin 2 and point-0-three for bin 3. So actually, this bin is more common in the population.

In order to be more conservative with the frequency we have here, this band right here, with this measurement error, could fall in either this bin or that bin, but we're always in the same the bin with the higher frequency, in other words, in order to be more conservative.

* * *

Simply what you do is, you look at your DNA profile or band pattern, you see where that band has occurred and which bin did it fall in, and you look in a table and see what the frequency is for that bin.

You generate a frequency for the total profile for the two bands that are found. You do that for each and every probe. You develop a frequency at that profile. Then you take and you multiply the frequency for one loci from the frequency of another loci times the frequency of that other loci, times the frequency of another loci. And that will give you the combined frequency of finding a similar pattern across those four areas in a population.

The probability analysis in this case was based on VNTR measurements at four loci, including D10S28. Dr. Shields opined that the results of this probe should be excluded from the calculation because the relevant scientific community is not in

general agreement that the VNTR fragments on section 28 of chromosome 10 are "independent" of fragments on other sections. The State's expert disagreed. When Dr. Shields removed D10S28 from his calculations, he calculated the probability of a random match to be 1 in 1349 persons.

The Multiplication (or Product) Rule was used to calculate the ultimate probability testified to by the State's expert. That rule involves multiplying together the probability fraction obtained for each locus in order to determine the overall probability of a random match. When § 10-915 was enacted, the Multiplication Rule was the standard method used to determine statistical probability. This method of calculation favors the prosecution. In the Porter case,[8] Dr. Harold Deadman, a DNA expert, offered the following explanation of the Multiplication Rule:

> If I were to take a die and throw it a hundred or, let's say ten times, each of those are independent of each other. The result that you get the second time you throw it is not going to be dependent on what you obtain the first time. The result that you get the third time is not going to be dependent. Each throw is completely separate. And we're arguing that the same thing applies here.
>
> Let's take a pair of dice. Each one, assuming they're honest dice or die, is independent of the other. You throw one, you have one chance in six of getting [a number]. [T]hrow both of them together, you have one chance in 36 of getting two numbers, the same numbers, two sixes or two ones or whatever, because those are independent events. You

[8] United States v. Porter, Case No. F06277-89, Superior Court of the District of Columbia, (Transcript I at 128-130).

> multiply the frequency or the probability of one die becoming a six and the other die becoming a six and you generate a number one in 36.

People are not dice. The Multiplication Rule is based on two assumptions: (1) that groups in the database (caucasians, blacks, hispanics) mate at random, i.e. without regard to religion, ethnicity and geography; and (2) the DNA fragments that have been identified on one locus are independent of fragments on other loci, i.e., the size of a person's VNTR fragment at one locus provides no indication of the size of his or her VNTR fragments at other loci. The first of these assumptions is not true and the second has not been proven to be true. Respectable members of the relevant scientific community have nonetheless concluded that the Multiplication Rule does produce an accurate estimate. Others disagree.

Some members of the scientific community have advocated a more conservative method of calculating the statistical probability of a random match. The Ceiling Frequency Principle is a more conservative method of statistical analysis. Under this principle, for each bin in which the probability of a random match is less than 10%, the probability is increased to 10% before the Multiplication Rule is employed. This method of computation obviously favors the suspect.

According to appellant, the Multiplication Rule should not have been used in this case because the Ceiling Frequency Principle ("CFP") has now been accepted by the relevant scientific community as a more accurate testing procedure than

the Multiplication Rule.[9] In addition, appellant contends that the State's random match calculation was further "tainted" by the use of probe D10S28 because the relevant scientific community has yet to resolve the issue of whether that probe is statistically independent from the other probes used.

We agree with appellant that "[a] procedure's acceptance or lack of acceptance among experts is not necessarily permanent." The Frye-Reed test, however, is applicable to expert testimony only when an essential component of the expert's opinion is a scientific test result "controlled by inexorable, physical laws." Allewalt, *supra*, 308 Md. at 98; Meyers v. Celotex, 88 Md. App. 442, 460 (1991). As is obvious from Dr. Shields' explanation of how the statistical probability analysis is calculated, that process does not involve a scientific technique controlled by inexorable, physical laws.

The Multiplication Rule is nothing more than a theory that produces an estimate. The Ceiling Frequency Principle is nothing more than a policy that produces an estimate. The databases for the various probes are used to arrive at an estimate. We are persuaded that the Reed-Frye test does not apply to any of those methodologies.

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[9] That assertion is based on a 1992 report by the National Research Council of the National Academy of Sciences recommending that CFP be used as an alternate testing procedure. Appellant's Motion To Exclude DNA Evidence, however, cited cases holding that there is no general agreement as to the precise method to be used.

We recognize that some jurisdictions have held that any statistical probability estimate presented to the jury must use the most "conservative" estimate, i.e., an "estimate resolving all uncertanties in favor of the defendant." Vandebogart, *supra*, 616 A.2d at 495; Porter, *supra*, 618 A.2d at 642. We hold, however, that the Multiplication Rule, the Ceiling Frequency Principle, and the database for probe D10S28 are all admissible to support the estimate of an otherwise qualified expert.[10]

V & VI

Upon conviction, the State filed a Notice of Mandatory Penalty pursuant to Md. Ann. Code art. 27, § 643B alleging that appellant had committed, been convicted of, and sentenced to four prior crimes of violence.[11] Appellant contends that the life sentences without parole imposed in this case were illegal and should have been vacated. The State agrees with that contention. So do we. While it is true that appellant was convicted of and

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[10] Appellant's trial counsel also argued that the State's DNA expert was not qualified to express a statistical probability opinion. That argument has not been presented to us. We have been asked to hold that the State's statistical probability calculations flunked the Reed-Frye test. We have not been asked to reverse appellant's conviction because the State's DNA expert was neither offered nor accepted as an expert in the field of population genetics or statistics.

[11] Md. Code (1957, 1992 Repl. Vol.), Art. 27 § 643B(b) provides for a mandatory life sentence for "[a]ny person who has served three separate terms of confinement in a correctional institution as a result of three separate convictions of any crime of violence shall be sentenced, on being convicted to a fourth time of a crime of violence, to life imprisonment without the possibility of parole." Burglary is one of the crimes enumerated in the statute.

served time for four prior burglaries, none of those burglaries constitutes a "crime of violence" under § 643B.

Appellant has four prior convictions for burglary, two in Florida and two in California. "Whether a criminal act constitutes a 'crime of violence' must be measured against the Maryland statute, and it matters not whether the particular crime may be a violent act in the foreign state." Mitchell v. State, 56 Md. App. 162, 183 (1983). At the time of sentencing in this case, burglary in Maryland required both a "breaking" and entering. The mere entering of a dwelling house is insufficient to constitute a "crime of violence." Brown v. State, 311 Md. 426, 441 (1988). The Florida and California burglary statutes do not require a "breaking."

VII

Appellant urges that his sentences should have been merged under the Rule of Lenity or out of fundamental fairness. Those principles are used when the legislative intent is unclear as to whether separate punishments are appropriate. In this case, however, appellant was convicted of two clearly distinct crimes, burglary and first degree rape.

> We thus have two separate criminal acts for which the Legislature has provided distinct punishments. Appellant presents us with no case law or legislative history suggesting that the Legislature did not intend to punish both of these criminal acts, nor can it be seriously argued that an ambiguity exists when the statutes are applied in tandem. It makes sense that, because the two crimes and penalties address

> different criminal behavior, separate sentences be imposed.

Wooten-Bey v. State, 76 Md. App. 603, 629 (1988).

"In Maryland, trial court judges are vested with broad discretion in the exercise of the 'awesome responsibility of imposing sentence' on criminal defendants." Jones v. State, 336 Md. 255, 265 (1994) (quoting Johnson v. State, 274 Md. 536, 538 (1975)). When appellant is resentenced, the trial judge will be entitled to exercise that broad discretion.

CONVICTIONS AFFIRMED; SENTENCES VACATED; CASE REMANDED TO THE CIRCUIT COURT FOR WORCESTER COUNTY FOR A NEW SENTENCING PROCEEDING; COSTS TO BE EQUALLY DIVIDED BETWEEN APPELLANT AND WORCESTER COUNTY.

UNREPORTED

IN THE COURT OF SPECIAL APPEALS

OF MARYLAND

No. 1515

September Term, 1994

ON REMAND

BRIAN RALPH KEIRSEY

v.

STATE OF MARYLAND

Wilner, C.J.,
Murphy,
Alpert, Paul E.
(Retired, Specially
Assigned)
JJ.

PER CURIAM

Filed: July 2, 1996

#15373

In Keirsey v. State, 106 Md. App. 551 (1995), we held that the State's DNA evidence was admissible, affirmed appellant's convictions, and remanded for a new sentencing proceeding. On April 8, 1996, the Court of Appeals vacated our decision and ordered that we reconsider our conclusions "in light of Armstead v. State, 342 Md. 38 (1996)." Keirsey v. State, 342 Md. 120 (1996). We have little to reconsider. The holding of Armstead requires that appellant's convictions be affirmed.

In Armstead, the Court of Appeals concluded that the Reed-Frye test applies to the scientific process that determines whether there is a "match" between the DNA of the defendant and the DNA of the perpetrator. We had reached that very conclusion in this case. The Armstead court then concluded that the Reed-Frye test applies to the estimate of likelihood that the DNA of someone other than the defendant also matches the perpetrator. We had held that the Reed-Frye test should not be applied to such estimates of statistical probability.

In Armstead, however, the Court of Appeals also held that the very same kind of probability estimates presented against appellant actually satisfied the Reed-Frye test. In light of that holding, therefore, the "bottom line" simply cannot change: whether the Reed-Frye test was inapplicable to the probability estimate (as we held in Keirsey), or whether that estimate satisfied the Reed-Frye test (as the Court of Appeals held in

Armstead), the DNA evidence was correctly admitted in this case. Appellant is not entitled to a new trial.

CONVICTIONS AFFIRMED; SENTENCES VACATED; CASE REMANDED TO THE CIRCUIT COURT FOR WORCESTER COUNTY FOR A NEW SENTENCING PROCEEDING; COSTS TO BE PAID BY APPELLANT.