

STATE OF WASHINGTON, Respondent,
v.
AARON ROBERT BANDER, Appellant.
No. 61125-9-I
Court of Appeals of Washington, Division One.
Filed: June 8, 2009

Appeal from Snohomish Superior Court. Docket No: 07-1-00271-0. Judgment or order under review. Date filed: 12/17/2007. Judge signing: Honorable Richard J Thorpe.

Counsel for Appellant/Cross-Respondent, Nielsen Broman Koch PLLC, Attorney at Law, 1908 E Madison St, Seattle, WA, 98122.

Christopher Gibson, Nielsen Broman & Koch PLLC, 1908 E Madison St, Seattle, WA, 98122-2842.

Counsel for Respondent/Cross-Appellant, Mary Kathleen Webber, Snohomish County Prosecutors Office, Msc 504, 3000 Rockefeller Ave, Everett, WA, 98201-4061.

Dwyer, A.C.J. —

Aaron Bander appeals from the judgment entered on a jury's verdict finding him guilty of murder in the first degree. Bander contends that proper application of the Frye¹ standard, which requires that certain expert testimony be based on generally accepted scientific principles, would have barred testimony from two of the State's witnesses. He also contends that the trial court erred by not applying several evidentiary rules to limit the testimony of these witnesses. Finally, he claims to have received ineffective assistance of counsel. Finding no error, we affirm.

I

On November 5, 2006, Everett police officers discovered the dead body of Terilynn Gardner in the trunk of a stolen car. The body was wrapped in a plastic shower curtain, a comforter, a t-shirt, and plastic trash bags. A gag made of assorted materials was twisted around Gardner's throat. Her limbs were bound with electrical and phone cords, strips of webbing, and plastic tape. The entire cocoon was tied together with additional tape and cords. Police officers also found an unsmoked cigarette in the car. Police officers and the medical examiner secured these items for forensic analysis at the state crime lab. After performing an autopsy, the medical examiner determined that the cause of Gardner's death was blunt force trauma to her head and an incise wound to her neck.

A tipster later told police that Suzie Le had confessed that Le, Aaron Bander, and a third person had imprisoned Gardner in an apartment, tied her to a chair, and tortured her for several days before clubbing her on the head and cutting her throat. Although not legal tenants of the apartment described, both Bander and Le lived there in the months leading up to Gardner's murder. Police arrested Bander in late December 2006, and Le

surrendered herself a week later. Inside the apartment, detectives found blood stains on the carpet, a chair with tape on the arms similar to the tape found on Gardner's body, wadded tape in trash cans, several electrical and phone cords, and various knives.

At the state crime lab, DNA samples were extracted from several items recovered from the car and the apartment. Crime lab forensic DNA analyst Greg Frank prepared the samples using a process known as polymerase chain reaction for short tandem repeats (PCR-STR) and tested them with commercial kits known as Profiler Plus and COfiler, manufactured by Applied Biosystems. He then used an ABI Prism 310 genetic analyzer to type the DNA profiles from these samples. The State also hired ReliaGene Technologies, Inc., a private DNA testing lab located in New Orleans, to test some samples specifically for the Y chromosome. Gina Pineda oversaw ReliaGene's testing process, which used the PCR-YSTR method and the ABI Prism 3100, a later-model genetic analyzer similar to the one used by Frank. Analysts in both the state crime lab and at ReliaGene also profiled Bander's DNA for comparison with the profiles of the DNA on the crime scene evidence.

Only the cigarette found in the car contained DNA from a single source. This DNA profile matched Bander's in every way tested. Frank calculated the probability that a random person would exhibit the same profile at 1 in 470 billion.

The other DNA samples extracted from items collected from the car and the apartment contained DNA from multiple sources, some with as many as four contributors. For some of these items, Frank concluded that Bander was a possible contributor based on profile similarities. However, unlike the match probability estimate for the sample from the cigarette, Frank calculated much higher odds that random members of the population might share these same profiles.² When Bander's DNA profile directly conflicted with the samples' profiles, Frank categorically excluded him as a possible contributor to those samples. Some test results, however, were inconclusive. Bander's profile did not directly conflict with the profiles for some samples and thus did not warrant categorical exclusion, but neither were the similarities strong enough for Frank to characterize Bander as a possible contributor. ReliaGene's analysis also indicated that Bander and his paternal relatives, who are the focus of YSTR testing, could not be excluded as possible contributors to the samples that it tested.

Bander retained Donald E. Riley, Ph. D., a research professor in the Department of Urology at the University of Washington, to observe Frank's testing. Dr. Riley prepared a report criticizing the methods and findings of the State's forensic experts.

Prior to trial, Bander requested a Frye hearing to determine whether the State's forensic experts utilized methods to interpret the DNA test results for mixed-source samples that were generally accepted within the scientific community. He also moved to exclude the test results and related expert testimony as being inadmissible under ER 402,³ 403,⁴ and 702.⁵ The trial court denied Bander's request for a Frye hearing, ruling that courts had already recognized the methods utilized by the State's experts as being generally accepted. It also denied his motion in limine, finding relevant that some DNA

evidence did not categorically exclude Bander from the crime scene. The court further concluded that Bander's objections concerning the forensic experts' interpretation of the DNA test results went to the weight of the experts' conclusions, rather than to the admissibility of their opinions.

At trial, Frank and Pineda described the DNA testing they performed and interpreted the test results. Frank testified about what it meant to exclude Bander as a possible contributor, to classify him as a possible or potential contributor, and to interpret some results as inconclusive or as not excluding Bander as a possible contributor. With regard to the samples yielding inconclusive test results, Frank testified that he did not include calculations of the probability of random matches for each of these profiles in his report because the probability of random matches for these samples was relatively high compared to the other calculations. However, when asked what the probability of a random match for these samples would be, Frank testified that it would range from "one in ten to everybody." He opined that these statistics "were not very significant" and that what these test results indicated was that Bander could not be categorically excluded as a contributor.

The State also presented testimony from two of Bander's acquaintances, David Gonzalez and Meagan Bevans. Gonzalez testified that, at Le's request, he had helped steal the car used to conceal Gardner's body and that Le and Bander had both confessed to him that they had murdered Gardner. Bevans, a former girlfriend of Bander's, also testified that Bander had admitted to her that he had killed Gardner. The jury convicted Bander of murder in the first degree, and the trial court subsequently sentenced him to serve 333 months in prison.

II

We review de novo a trial court's decision not to hold a Frye hearing based on a finding that the evidence at issue is generally accepted in the relevant scientific community. State v. Gregory, 158 Wn.2d 759, 830, 147 P.3d 1201 (2006). The core concern under Frye is whether the expert testimony or other evidence being offered is "based on an established scientific methodology." State v. Russell, 125 Wn.2d 24, 41, 882 P.2d 747 (1994). We consider "(1) whether the scientific theory upon which the evidence is based is generally accepted in the relevant scientific community, and (2) whether the technique used to implement that theory is also generally accepted by that scientific community." State v. Gentry, 125 Wn.2d 570, 585, 888 P.2d 1105 (1995) (citing State v. Cauthron, 120 Wn.2d 879, 888-89, 846 P.2d 502 (1993)). Unanimity is not required. State v. Gore, 143 Wn.2d 288, 302, 21 P.3d 262 (2001) (citing State v. Copeland, 130 Wn.2d 244, 270, 922 P.2d 1304 (1996)), overruled on other grounds by State v. Hughes, 154 Wn.2d 118, 131 n.2, 110 P.3d 192 (2005). A dispute over "whether a generally accepted technique was performed correctly on a given occasion . . . go[es] to weight, not to admissibility." Gentry, 125 Wn.2d at 586 (citing Cauthron, 120 Wn.2d at 889; State v. Kalakosky, 121 Wn.2d 525, 541, 852 P.2d 1064 (1993)). In determining whether a theory or technique is generally accepted, we may consider evidence not in the record, including scientific and law review articles, and decisions from other

jurisdictions. Cauthron, 120 Wn.2d at 888. Bander contends that the State's forensic experts' interpretive methods are not generally accepted within the relevant scientific community. Although Bander does not challenge the underlying scientific theory of DNA typing or the particular testing methods used here, we review these aspects of the forensic DNA evidence introduced against him to illuminate his arguments about the State's forensic experts' interpretation of the DNA samples in this case.

III

The PCR-STR typing process used by Frank allows forensic scientists to isolate and analyze DNA segments that vary from person to person. These genetic variants are known as alleles. Scientists have identified certain polymorphic loci or markers along DNA strands where there appear alleles that can be used for human identification. At each locus, an individual has a pair of alleles, one inherited from each biological parent. The alleles at a given locus may be different or may be the same. Furthermore, although many people might have alleles in common at a particular locus, the overall combination of alleles — one's DNA profile — is sufficiently different from person to person that it is widely accepted that no two people, except for identical twins, have the same DNA profile. See Committee on DNA Forensic Science: An Update, National Research Council, *The Evaluation of Forensic DNA Evidence* 60-63, 69-70 (1996) (hereinafter NRC II).

In PCR-STR processing, DNA segments at specific loci are amplified or copied millions of times over so that the forensic analyst can determine which alleles are present. The PCR-STR method is particularly useful for testing degraded DNA samples or samples with low levels of DNA. During the amplification process, a Taq polymerase enzyme and a dye are injected into the sample. The Taq polymerase enzyme facilitates amplification. The dye enables an analyst to identify specific alleles. See NRC II at 69-73; John M. Butler, *Forensic DNA Typing* 63 (2d ed. 2005).

ReliaGene used a PCR-based process known as YSTR testing to type the DNA samples it tested. YSTR amplification is essentially the same as the PCR-STR process that Frank used, except that it permits the analysis of only male DNA in a mixed-source sample that also contains DNA from a female contributor. The DNA segments that are the focus of YSTR testing are inherited as a block through an individual's paternal lineage. This block is known as a haplotype — "a set of closely linked genetic markers present on one chromosome which tend to be inherited together." National Forensic Science Technology Center, President's DNA Initiative: DNA Analyst Training Glossary, <http://www.nfstc.org/pdi/glossary.htm#H> (last visited May. 12, 2009). All men in the same paternal lineage have the same DNA profile at these markers on their Y chromosomes. Based on PCR-YSTR typing, a forensic analyst may determine whether a known source and all of his paternal relatives can be excluded as possible contributors to an unknown DNA sample. See Butler at 201-02, 204.

After amplification, all of the samples underwent capillary electrophoresis in semi-automated DNA sequencers. During this process, alleles are separated according to their

size, and a laser illuminates them. Depending on the type of allele, the dye marker added during the amplification process causes alleles to fluoresce differently as they are illuminated. An internal camera records these colors and transmits the information to a computer that analyzes the data and generates an electropherogram — a graph that visually represents a DNA profile and serves as the basis for profile comparison in forensic DNA analysis. See Butler at 318-20, 325-30, 345-61.

When an allele is detected at a particular locus, it is represented as a peak plotted at a point along the electropherogram's X-axis that corresponds to a particular locus. The intensity at which alleles fluoresce is reflected in the peak heights along the Y-axis of the electropherogram. Fluorescent intensity is measured in relative fluorescent units (RFUs). Testing laboratories determine the threshold RFU value that must be exceeded in order to report the presence of a specific allele and to declare that two profiles have matching alleles at particular loci. See Butler at 325-30. The reporting threshold value that Frank used was 150 RFUs. ReliaGene set its minimum reporting threshold value at 75 RFUs. Testing laboratories may also designate a lower analytic threshold value to be used for exclusion purposes. Frank testified that when the electropherogram depicted an allele that was detected during electrophoresis but which fell below the reporting threshold on the graph, he would rely on the below-threshold peak in considering whether the testing results could be used to exclude someone as a possible contributor. But he would not include it in calculating the profile's statistical significance.

By comparing DNA profiles, forensic analysts may determine whether a known individual possibly contributed to a DNA sample of unknown human origin. If the reported alleles in the samples from the known and unknown sources do not match — i.e., if there is any direct inconsistency between them — then the known source can be categorically excluded as a possible contributor. Two profiles are consistent when the genotypes are identical at the same tested loci. When such a "match" occurs, the known source can be treated as a possible contributor. The discriminating power of DNA evidence is directly proportional to the number of loci where there are identical genotypes between two samples. In some situations, however, DNA testing may prove inconclusive, often because it may be unclear whether a particular allele is present. Such results are inconclusive in that an analyst cannot definitively exclude someone as a possible contributor. See 4 David L. Faigman, et al., *Modern Scientific Evidence: The Law and Science of Expert Testimony* § 32:41 (2005-06 ed.).

These interpretive principles apply to profiles for both single-source DNA samples and mixed-source DNA samples. A single-source sample is DNA that came from only one person (e.g., hair or blood from an unidentified victim or saliva from a suspect). A mixed-source DNA sample is one to which two or more persons have contributed. The appearance of three or more allelic peaks at a particular locus indicates a mixed-source sample. Since a profile for a single source would exhibit at most only two allelic peaks per locus, any number of peaks in excess of two indicates more than one source of DNA. See Faigman, et al., § 32:41.

The application of these interpretive principles to single-source DNA samples is fairly straightforward. Two single-source profiles can be compared similar to the way two Social Security numbers might be compared for consistency. Just as any variation in the nine-digit numerical sequence would indicate Social Security numbers for different people, if any discrete alleles between two DNA samples differ, then the samples originated from different sources.

The interpretation of mixed-source DNA profiles, however, can be more complicated.⁶ One significant problem that analysts face is potential difficulty in distinguishing between the profiles of major and minor contributors to a sample. If some alleles are consistently reported across tested loci at high RFU levels relative to other alleles, it may be possible to treat such higher-peaked alleles as a single profile from the "major" contributor. In contrast, the lower-peaked alleles can be designated as making up the profiles for "minor" contributors. But when the profile is ambiguous, i.e., when peak heights are not sufficiently variegated, it may not be possible to determine which alleles make up which profiles. See Butler at 154-64. In 2000, the United States DNA Advisory Board⁷ explained these interpretive challenges posed by DNA mixtures as follows:

In some situations, elucidation of a contributor profile is straightforward. An example would be the analysis of DNA from an intimate swab revealing a mixture consistent with the composition of the perpetrator and the victim. When intensity differences are sufficient to identify the major contributor in the mixed profile, it can be treated statistically as a single source sample. At times, when alleles are not masked, a minor contributor to the mixed profile may be elucidated. Almost always in a mixture interpretation, certain possible genotypes can be excluded. It may be difficult to be confident regarding the number of contributors in some complex mixtures of more than two individuals; however, the number of contributors often can be inferred by reviewing the data at all loci in a profile.

Interpretation of genotypes is complicated when the contributions of the donors is [sic] approximately equal (i.e., when a major contributor cannot be determined unequivocally) or when alleles overlap. DNA Advisory Board, Statistical and Population Genetics Issues Affecting the Evaluation of the Frequency of Occurrence of DNA Profiles Calculated from Pertinent Population Database(s), 2 Forensic Sci. Comm. No. 3, ¶¶ 17-18 (2000), <http://www.fbi.gov/hq/lab/fsc/backissu/july2000/dnastat.htm>.

Frank and Pineda each sought to identify major contributors to the samples they tested. Although Frank was able to distinguish between major and minor contributors for some samples, he was unable to identify Bander as the major contributor to any one sample. Pineda, on the other hand, identified Bander as the major contributor to one of the three mixtures that ReliaGene tested. She could not, however, identify a single major contributor to the other two samples that ReliaGene tested.

Two other related phenomena that can complicate the interpretation of DNA mixtures are stutter and allelic dropout. A stutter is an allelic artifact resulting from slippage of the Taq polymerase enzyme during electrophoresis. It appears on the

electropherogram as a smaller peak immediately preceding the peak representing the detected allele. Although scientists have settled on criteria that make identification of stutters straightforward in single-source samples, in a mixed sample, a stutter peak might be confused for a minor allele. See Butler at 154-64; P. Gill, et al., DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures, 160 *Forensic Sci. Int'l* 90, 95, 101 (2006) (hereinafter Gill, et al. (2006)).

Allelic dropout occurs when an allele is not detected above the reporting threshold. See Butler at 132. Sample degradation, very low levels of DNA, and problems during the amplification process can result in dim fluorescence during electrophoresis so that an allele's RFU measurement falls below the reporting threshold or, in some instances, even below the detection threshold. See Butler at 133. In mixed-source samples, it may be difficult to distinguish minor alleles from stutters and dropouts. As the DNA Advisory Board observed, "stochastic fluctuation during polymerase chain reaction (PCR) arising from low quantity of DNA template can make typing of a minor contributor complicated." DNA Advisory Board at ¶ 18. Short peaks at one locus might be identified as stutters, whereas at another, they might appear to be minor alleles. Likewise, a set of minor alleles that might consistently appear above the reporting threshold at some loci might include peaks that fall below the threshold at other markers.

The main evidentiary concern about a mixed-sample DNA profile is that ambiguities in allelic peak appearance may diminish the profile's exclusionary value. Further, there is concern that an ambiguous profile may incorrectly lead to the inclusion of a known source as a possible contributor because two profiles might partially match at fewer than all loci tested but not exhibit direct inconsistency at remaining loci that would allow for categorical exclusion. Although the same exclusionary principle of profile inconsistency that operates in comparisons of single-source profiles applies equally to evaluations of mixed-source samples, the increase in possible allelic pair combinations complicates the isolation of individual profiles. Alleles reported at roughly equal RFU levels can be hard to separate into discrete pairs. If an allele at a particular locus in a mixed sample has dropped out, it can be difficult to identify the specific alleles present at that locus.

Consider, for example, a situation in which a known source's genotype appears at most loci in an unknown mixture, along with other allelic pairs. At one locus, however, only one of the known source's two alleles appears above the reporting threshold, while another peak, that might be an allele, appears below the reporting threshold. This unreported peak might actually be an allele that is inconsistent with the known source's genotype and could therefore have exclusionary value. But because this peak is not clearly detected, it remains unclear whether the two profiles are inconsistent with one another for exclusion purposes.

Once crime-scene and known-source DNA samples have been typed and compared and the forensic analyst has determined that the samples are sufficiently similar such that they could have originated from the same source, the analyst must then determine the statistical significance of the profiles. There are two widely recognized statistical calculations that can be performed to convey the probative value of a DNA profile typed

according to the PCR-STR process that Frank used. DNA Advisory Board at ¶ 18. The first type of calculation estimates the probability of exclusion (PE) or probability of a random match, which expresses the probability that a random person has the same DNA profile as the evidence profile or, in other words, the probability that a random person is not excluded by the evidence.⁸ Given that the forensic analyst has concluded that a suspect or known source is a possible contributor to the unknown sample in light of the consistency between profiles, PE can be "regarded as an estimate of the answer to the question: What is the probability that a person other than the suspect, randomly selected from the population, will have this profile?" NRC II at 127.

The PE calculation is based on the product rule. Using this rule, the analyst will multiply the frequencies at which particular alleles appear at specific loci by each other to determine the frequency with which the overall genotype of the tested sample could be expected to appear in the population. The factors used in PE calculations are derived from population databases that document the frequency with which particular alleles appear across a number of loci. Our Supreme Court illustrated the use of the product rule in a PE calculation:

For instance, allele A may be found in 1 of every 10 people; allele B found in 1 of 20; and allele C found in 1 of 5. Under the product rule, if there is a match for each allele, the expert can multiply $(1/10 \times 1/20 \times 1/5)$ to achieve the result that only 1 person in 1,000 will match all three sites. Cauthron, 120 Wn.2d at 901. PE is typically expressed as 1 in X number of people that could have been the source of the unknown sample.

The discriminating power of a PE calculation increases according to the number of loci at which matching alleles are reported. The greater the number of matching loci, the greater the number of frequencies that can be multiplied, resulting in a smaller overall probability. "The smaller that probability, the greater the likelihood that the two DNA samples came from the same person." NRC II at 127. Thus, a very small probability strongly suggests "that either the two samples came from the same person or a very unlikely coincidence has occurred." NRC II at 127.

The product rule can be used in a PE calculation for an ambiguous mixed-source sample, i.e., one whose contributors are not easily distinguishable as either major or minor. But doing so involves an extra step that is not included in the application of the product rule to a single-source sample or a sample where major and minor contributors can be distinguished. The National Research Council explained in 1992 that "[i]f a suspect's pattern is found within the mixed pattern, the appropriate frequency to assign such a 'match' is the sum of the frequencies of all genotypes that are contained within (i.e., that are a subject of) the mixed pattern." Committee on DNA Technology in Forensic Science, National Research Council, DNA Technology in Forensic Science 59 (1992). The addition of multiple allelic frequencies at a specific locus captures the probability that any one person could have contributed DNA to a sample with multi-allelic markers. The combination of multiple frequencies results in a frequency sum that is greater than that of the frequency for a single allelic pair. Because the resulting greater factor will be used in the ensuing multiplication, the final product will also be greater

than if all of the frequencies had been individually multiplied by each other. The end result is that the probability of a random match will correspondingly be greater for a mixed-source sample than for a single-source sample. In other words, it will be more likely that a random member of the population could have contributed his or her DNA to the unknown evidence sample.

The second statistical calculation that a forensic analyst may perform is an estimation of the likelihood ratio (LR). An LR calculation measures the strength of evidence under alternative hypotheses about the source(s) of the DNA in the unknown sample. For instance, an LR calculation estimates how much more likely it is that the suspect is the source of the evidence than it is that the evidence originated from a randomly selected member of the population unrelated to the suspect. NRC II at 127-28. Essentially, this calculation involves dividing the probability of one origin hypothesis (e.g., that the suspect's DNA is in the sample) by another origin hypothesis (e.g., that DNA in the sample came from someone else). "The greater the likelihood ratio, the stronger is the evidence in favor of the hypothesis corresponding to the numerator, that the source of the evidence-sample DNA and the suspect are the same person." NRC II at 128. Thus, "in the usual case, the likelihood ratio is the reciprocal of the probability of a random match." NRC II at 128.

Here, Frank calculated only the probability of exclusion for the samples that he typed. For the single-source sample extracted from the cigarette, which matched Bander's profile at every tested allele, Frank calculated that the probability of a random match was quite low at 1 in 470 billion. Regarding the mixed-source samples to which Bander possibly contributed, Frank's PE calculations were much higher, ranging from 1 in 14 to 1 in 86 persons. Concerning the several samples with test results that were inconclusive or that weakly indicated Bander as a possible contributor, Frank testified that the probability for random matches ranged anywhere from 1 in 10 persons to 1 in 1 or "everybody."

On the samples that underwent YSTR testing in ReliaGene's lab, Pineda performed an entirely different statistical calculation, known as the counting method. The PE and LR approaches are not used as part of YSTR testing because the tested alleles in the Y chromosome are linked and inherited together as a haplotype. The United States Scientific Working Group on DNA Analysis Methods (SWGDM) has recognized that "[t]he basis for the haplotype frequency estimation is the counting method." See SWGDAM, Y-chromosome Short Tandem Repeat (Y-STR) Interpretation Guidelines, 11 Forensic Sci. Comm. No. 1, ¶5.3 (2009), http://www.fbi.gov/hq/lab/fsc/current/standards/2009_01_standards01.htm. Using the counting method and the population database for YSTR markers maintained by Applied Biosystems, Pineda concluded that 99.9 percent of the population could be excluded as possible contributors to the sample extracted from the electrical cords recovered from Gardner's body and to which she identified Bander as the major contributor. Pineda testified that because she could not identify a major contributor to the other samples that ReliaGene tested, she did not perform a statistical analysis of these other samples.

IV

Bander first contends that the identification of alleles in DNA mixtures involving more than two contributors involves novel scientific techniques requiring a Frye hearing. He further contends that the State's forensic experts did not follow a generally accepted method for identifying the presence of specific alleles in ambiguous profiles. The trial court correctly ruled otherwise.

In support of his arguments, Bander principally relies on the sworn declaration of Dr. Riley.⁹ Dr. Riley criticized Frank's conclusions that Bander could not be excluded as a possible contributor to several samples in which Bander's DNA was not detected at all of the genetic markers tested. He pointed out that "[f]or several of these samples, the defendant has multiple alleles that are absent from the evidence," and declared that

[t]he majority of other laboratories would call these either exclusions or inconclusive results. The phrase, [sic] "not excluded" is normally used when the sample shows a clear, single donor profile consistent with a known sample.

To see the same phrase used here in the context of mixed samples that do not show defendant's alleles is incorrect both logically and scientifically. This usage is profoundly troubling. If the laboratory is willing to ignore the fact that the defendant's known alleles are absent from the evidence, this approach could be used to imply inclusion of anyone.

After reviewing Mr. Frank's interview by defense counsel, I understand that the phraseology, "not excluded . . . but if he is" is something he may be bound to by protocol and that he himself is calling those results, inconclusive. If so, I agree. Such results could be called inconclusive or even, exclusions.

Dr. Riley further observed that, in some of the samples from which Frank did not categorically exclude Bander as a contributor, multiple alleles of Bander's were "not seen in the evidence," and that it was "clear from the results . . . that many of the mixtures have alleles and loci dropping out." He also opined that there is "little agreement for interpreting mixtures" among DNA laboratories and that the typing accuracy of current testing technology is bound to diminish as mixtures become more complex and the incidence of allelic dropout increases. Dr. Riley ultimately declared that the State Crime Lab "erroneously included [Bander] in multiple samples where his genetic markers were absent. That practice may have been due to an erroneous protocol. Interpretation of profiles when alleles are below threshold or missing represents a decline in standards from previous forensic DNA practices . . . [and] cannot be considered generally accepted nor [sic] reliable."

Bander also relies on an unpublished research paper presented by Mark W. Perlin, M.D./Ph. D., at an annual forensic sciences convention. See Mark W. Perlin, Scientific Validation of Mixture Interpretation Methods (Dec. 5, 2006) (unpublished manuscript, on file in Clerk's Papers at 161-94). Dr. Perlin is the C.E.O. of Cybergenetics, a private DNA testing laboratory and research firm. Perlin touted the ability of Cybergenetics' patented

software, the TrueAllele Casework System, to validate the interpretation of mixed-source DNA profiles. He argued that there is no way to validate a particular forensic analyst's or laboratory's interpretation of a mixed-source DNA sample because different analysts and labs, even when following the same protocols, can interpret the same data differently. Unlike single-source DNA samples, which Perlin claimed can produce only one correct profile and are therefore susceptible to concordance studies, mixed-source DNA samples, even when the contributors are known, can yield ambiguous profiles that can be interpreted differently. Perlin at 4. In other words, what might appear as stutter to one analyst might appear as an independent allelic peak to another, yet with no way to determine conclusively which interpretation is correct. Concordance studies, which assess the degree to which different tests or analysts identify the same alleles in the same samples, are not possible for mixture interpretations since different analysts interpreting the same mixtures can infer discordant but equally valid profiles. Perlin at 4. Perlin argued that because mixture profiles can be interpreted differently, any one interpretation may not be reproducible, rendering mixture interpretation inherently unreliable. Perlin at 4. Perlin then devoted the remainder of his paper to demonstrating how his firm's software serves as a validation mechanism by reporting the likelihood that a certain allele would appear at a particular locus based on population frequencies. Perlin at 6-13.

Bander essentially argues that there was no way for the State's experts to correctly infer the presence of alleles in the tested DNA mixtures. But he is wrong. As the DNA Advisory Board explained, interpretation of test results from DNA mixtures, although potentially difficult, involves the same principles used to interpret test results from single-source DNA samples. In actuality, Bander's argument challenges whether the experts correctly identified the presence of peaks, not whether the testifying experts used an accepted analytical method to interpret the results. Our Supreme Court has repeatedly held that challenges to DNA evidence of this nature do not concern admissibility under Frye but, rather, concern admissibility under ER 702 and the weight that the trier of fact may accord to the evidence. See, e.g., *Gregory*, 158 Wn.2d at 831 (incidence of improper interpretation and alteration of laboratory test); *State v. Jones*, 130 Wn.2d 302, 307, 922 P.2d 806 (1996) (use of appropriate match windows); *Copeland*, 130 Wn.2d at 270 (prevalence of lab error and error rates); *Russell*, 125 Wn.2d at 51-53 (allelic dropout). Bander's argument regarding whether the State's experts used accepted methods to identify the presence of alleles is analogous to the issues addressed in those cases. Frank's and Pineda's explanations in their testimony of the meaning of the terms "exclusion," "possible or potential contributor," and "inconclusive" that they used to describe test results were consistent with the manner in which those terms are used in forensic DNA literature. Whether Frank or Pineda mistakenly identified alleles in test results are questions of whether they correctly administered the PCR amplification and electrophoresis processes, and whether they properly read the resulting electropherogram in light of the selected RFU thresholds. Notably, Bander does not contend that the State's experts erroneously inferred the presence of alleles as being consistent with his profile or that they employed deficient testing procedures.

Further, we find no merit in Bander's implicit argument that there is no generally accepted method for the identification of alleles in ambiguous mixtures and therefore no

way to attack the inference that a particular allele is present at a specific locus. As Perlin's assertions are unpublished, we have no way to credit his view that any interpretation of DNA mixtures is inherently unreliable without the use of his firm's software. Cf. Copeland, 130 Wn.2d at 268 (noting significance of whether scientific literature has been published in peer-reviewed journal). Both Frank and Pineda testified as to the RFU levels to which their automated sequencers were calibrated and, further, that they adhered to their respective lab's DNA testing and interpretation protocols, which included peer review by other forensic analysts. Bander does not argue that either lab's protocols are not generally accepted among forensic scientists. In the absence of any showing that there is a significant dispute among scientists over the acceptability of the labs' protocols for profile interpretation, a Frye hearing on the issues of allele identification and conclusions about whether to exclude or include Bander as a possible contributor was unnecessary. The trial court correctly so ruled.

V

Bander also contends that the trial court erred by not holding a Frye hearing on the admissibility of the statistical calculations that Frank performed on DNA mixture profiles using the PE method. Again, we disagree.

Bander maintains that the scientific community does not generally accept the PE calculations that Frank performed. In support of this proposition, he again relies on Dr. Riley's declaration. Dr. Riley generally asserts that presentation of a statistical probability for a mixture involving three or more persons' DNA is "unusual and not well supported by the recent forensic literature nor by proficiency test data involving hundreds of laboratories." Dr. Riley opines that "[t]he use of a combined probability (those ranging from 1 in 14 to 1 in 86) to describe several of the mixtures is controversial and misleading Seemingly hard scientific numbers are given when there is no scientific justification nor support." Dr. Riley also criticizes Frank's calculations because "[a]llele and locus dropout was not taken into account for the statistical probabilities," and he asserts that "[i]f they had been taken into account, it is doubtful any probative value would be left for any of the three or four person mixtures."

Dr. Riley himself relies heavily on the 2006 recommendation of the DNA Commission of the International Society of Forensic Genetics (ISFG)¹⁰ that the LR calculation should be recognized as "the preferred approach to mixture interpretation." See Gill, et al. (2006) at 92. The DNA Commission concluded that the LR framework is preferable to the PE method for interpreting a complex mixture because it allows for "stutter and dropout [to] be assessed probabilistically." Gill, et al. (2006) at 91. It further characterized the LR approach as "the only way to provide a meaningful calculation based on the probability of the evidence under" alternative hypotheses about the origin of DNA in the tested sample. Gill, et al. (2006) at 91. With respect to the PE approach, the DNA Commission critiqued it as entailing "an unrealistically simple model of DNA evidence" and criticized it for not making "full use of the evidence." Gill, et al. (2006) at 91. On those grounds, the Commission recommended that use of the PE approach be

restricted to "unambiguous" profiles (i.e., mixture profiles in which major and minor contributors can be clearly distinguished). Gill, et al. (2006) at 92.

Significantly, however, the ISFG DNA Commission did not conclude that a PE calculation for an ambiguous mixture profile is invalid per se. Instead, the Commission recognized that, "conceptually, [the PE and LR approaches] are equivalent." Gill, et al. (2006) at 91. Further, it acknowledged that the PE "result is still correct, given the model," just not "optimal," because it "does not make efficient use of the available information." Gill, et al. (2006) at 91.

A review of the literature on DNA mixture interpretation reveals that even though some members of the scientific community recognize that the LR method has certain advantages over the PE approach, namely its fuller use of profile information, the PE calculation remains generally accepted as a valid interpretive method among forensic scientists. Starting with the NRC II report, we find it noteworthy that although the Committee advocated use of the LR approach, it did not conclude that the PE method is invalid for the interpretation of DNA mixtures. To be sure, it criticized the PE approach for "not mak[ing] use of some of the information available" and generally described the LR approach as the "correct procedure." NRC II at 130. But it did not formally recommend that forensic analysts interpret DNA mixtures exclusively with the LR method, or not at all.

More significantly, the United States DNA Advisory Board in 2000, with full recognition of the NRC II report published in 1996, affirmed both the PE approach and the LR method as acceptable means for interpreting mixture profiles. The DNA Advisory Board recognized that "the PE [method] does not make use of all of the available genetic data." DNA Advisory Board at ¶ 19. Nevertheless, it concluded that "[t]he probabilities derived [from the PE method] are valid and for all practical purposes are conservative." DNA Advisory Board at ¶ 19. It found "one or both PE or LR calculations acceptable." DNA Advisory Board at ¶ 21. In so doing, it lauded the PE method as "particularly useful in complex mixtures, because it requires no assumptions about the identity or number of contributors to a mixture." DNA Advisory Board at ¶ 19.

As with the DNA Advisory Board, other forensic standards organizations have recognized that the PE approach is an acceptable method for interpreting mixture profiles. For instance, the Technical UK DNA Working Group, which includes one of the authors of the ISFG DNA Commission's report, stressed that the PE approach "is a recognized and advocated interpretation method." P. Gill, et al., National recommendations of the Technical UK DNA working group on mixture interpretation for the NDNAD and for court going purposes, 2 *Forensic Sci. Int'l: Genetics* 76, 77 (2008). More recently, the Biology Specialist Advisory Group (BSAG) of the Australian and New Zealand forensic science community weighed in on the ISFG DNA Commission's recommendations. It clarified that although the LR approach is commonly used to interpret mixtures, the PE approach "is considered an acceptable alternative approach to DNA interpretation." Petra Stringer, et al., Interpretation of DNA Mixtures — Australian and New Zealand consensus on principles, 3 *Forensic Sci. Int'l: Genetics* 144 (2009). In

addition, the German Stain Commission has recognized that "[i]f a major DNA profile cannot be identified based on unambiguous DNA profiles, or if the number of contributors cannot be determined, calculations of the probability of exclusion . . . or the probability of inclusion . . . for randomly selected persons is appropriate." P.M. Schneider, et al., *The German Stain Commission: recommendations for the interpretation of mixed stains*, 123 *Int'l J. Legal Med.* 1, 4 (2009). Further, one of the co-authors of the ISFG DNA Commission's report, John Buckleton, found "little force to . . . the argument that [the PE method] is illogical." John Buckleton & James Curran, *A discussion of the merits of random man not excluded and likelihood ratios*, 2 *Forensic Sci. Int'l: Genetics* 343, 347 (2008); see also Carll Ladd, et al., *Interpretation of Complex Forensic DNA Mixtures*, 42 *Croat. Med. J.* 244, 245 (2001) (discussing merits of both LR and PE approaches).

Significantly, courts in several other jurisdictions have approved of the use of the PE approach to interpret mixed-source DNA profiles.¹¹ Although a scientific method's acceptance within the relevant scientific community is that which matters for purposes of a Frye analysis, these judicial decisions themselves reflect the scientific community's widespread acceptance of the PE method. The decision Roberts v. United States, 916 A.2d 922 (D.C. 2007), is particularly instructive. Echoing the DNA Advisory Board's observations, the court in Roberts explained that the PE method is especially useful for interpreting a mixed sample because it "does not require identification of individual contributors and thus produces a ratio much more conservative than if the frequency of alleles were determined for a single-source profile." 916 A.2d at 927-28.

In light of these scientific articles and the decisions of courts in other jurisdictions, we conclude that use of the PE calculation is a generally accepted method for interpreting the profiles of DNA mixtures among forensic scientists. In so holding, we emphasize that our "role is not to evaluate the merits of [a particular] theory" but rather to determine whether "a genuine and important controversy exists." Cauthron, 120 Wn.2d at 902. That some forensic scientists may prefer the LR approach to a PE calculation is of no moment. Frye does not require unanimity. Just because the PE method may sit lower on some scientists' preference hierarchy does not mean that it is not generally accepted as a valid interpretive technique. Any concern that Frank cloaked the true probative value of the mixture profiles from which Bander could not be excluded as a possible contributor goes to the weight of the evidence, not its admissibility under Frye.

VI

With respect to Pineda's use of the counting method to interpret the mixed-source samples that underwent YSTR testing in ReliaGene's lab, Bander does not cite to any authority indicating that this statistical calculation lacks general acceptance. Indeed, he does not even specifically challenge Pineda's use of the counting method. Regardless, we note that both SWGDAM and the ISFG DNA Commission recognize the counting method as acceptable for interpreting YSTR test results. See SWGDAM at ¶5.3; P. Gill, et al., *DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs*, 124 *Forensic Sci. Int'l*

5, 8 (2001). In the absence of any argument or authority to the contrary, we conclude that a Frye hearing on ReliaGene's use of the counting method was likewise unnecessary.

VII

Bander separately argues that both Frank's testimony and Pineda's testimony about inconclusive DNA test results without attendant statistical calculations for specific samples were inadmissible under ER 402, 403, and 702. We review a trial court's admission of evidence for abuse of discretion. State v. Magers, 164 Wn.2d 174, 181, 189 P.3d 126 (2008). Upon such review, we conclude that the trial court did not abuse its discretion by admitting evidence of inconclusive test results.

Bander first contends that evidence of inconclusive test results without accompanying statistical calculations is irrelevant and therefore inadmissible. This contention is without merit.

Pursuant to ER 402, only relevant evidence is admissible. Relevant evidence is that which has "any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence." ER 401. Frank's and Pineda's challenged opinion testimony were each relevant within the meaning of ER 401. If DNA analysis indicates that Bander could have handled any of the items from which DNA samples were extracted, then the State's theory that Bander participated in Gardner's murder tends to be made more plausible. By the same token, exclusionary test results would tend to raise doubt about Bander's involvement. Results indicating that a relatively large proportion of the population could have contributed to the DNA samples go to the weight to be accorded to those test results, not to their relevance.

Nor is there merit to Bander's second argument: that inconclusive test results were unaccompanied by statistical calculations and were therefore meaningless and misleading, in contravention of both ER 403 and ER 702. For this proposition he relies on *Cauthron*, in which the court ruled inadmissible expert testimony that *Cauthron's* DNA profile undoubtedly matched profiles from crime-scene DNA samples because that testimony was unaccompanied by any statistical calculations. 120 Wn.2d at 906-08. Of particular concern to the court was the experts' failure to develop their opinions in the context of an adequate population database.

The concerns that animated the court's decision in *Cauthron* are not present here. Frank and Pineda did not testify that Bander's DNA profile matched the mixed samples at issue. They testified only that Bander could not be excluded as a possible contributor to those samples or that the results were inconclusive. They testified about this evidence in conjunction with evidence concerning the cigarette, to which Bander was very likely the sole contributor, and samples where the profile comparisons were sufficiently similar to identify Bander as a possible contributor. The witnesses explained the differences in meaning between their conclusions that Bander was a possible contributor to some samples and their conclusions that he could not be excluded as contributor to other

samples. Frank's explanation of the different interpretive terms that he employed made clear that "inconclusive" or "not excluded" did not mean that Bander's DNA profile unequivocally matched a crime-scene sample. Further, the State's experts did offer statistical calculations for inconclusive test results. Frank testified that the probability of exclusion for the inconclusive results was anywhere from 1 in 10 persons to everybody. Pineda explained that 99.9 percent of the population could be excluded as possible contributors based on her calculations using the counting method. Accordingly, we find no error in the trial court's admission of this expert testimony.

VIII

Finally, Bander contends that his trial counsel rendered ineffective assistance by failing to impeach the credibility of Gonzalez and Bevans on cross-examination. Specifically, he takes issue with his attorney's alleged failure to question both witnesses about their past drug use, past and pending criminal charges, motivations for testifying, and inconsistent statements. Once again, we find no merit in Bander's claim.

To prevail on a claim of ineffective assistance of counsel, a defendant must show both deficient performance on the part of his or her counsel and resulting prejudice that deprived him or her of a fair trial. Strickland v. Washington, 466 U.S. 668, 687, 104 S. Ct. 2052, 80 L. Ed. 2d 674 (1984). Scrutiny of counsel's trial tactics is deferential, and if they can be characterized as legitimate, then such tactics cannot serve as the basis for an ineffective assistance claim. State v. Thomas, 109 Wn.2d 222, 226, 743 P.2d 816 (1987); State v. Adams, 91 Wn.2d 86, 90, 586 P.2d 1168 (1978).

The trial transcripts reveal that the prosecutor elicited testimony from Bevans and Gonzalez on the very credibility issues that Bander raises on appeal. Once this information was before the jury, Bander's trial counsel could have reasonably concluded that she either had no basis to address it further on cross-examination or that doing so would undermine her strategy for defending Bander. Bander does not explain what other information his counsel might have elicited or how further questioning would have undermined these two witness's credibility. Accordingly, Bander's claim of ineffective assistance of counsel is unavailing.

Affirmed.

Grosse and Becker, JJ., concur.

Notes:

1. Frye v. United States, 293 F. 1013, 54 App. D.C. 46 (D.C. Cir. 1923).
2. Frank calculated the following random match probabilities for four mixed samples:

Item	Probability of Random Match among U.S. Population
T-Shirt from body wrapping	1 in 86 people
Binding tape from body wrapping	1 in 14 people
Tape from left arm of chair	1 in 79 people
Tape from apartment trash can	1 in 24 people

3. Pursuant to ER 402, "[a]ll relevant evidence is admissible, except as limited by constitutional requirements or as otherwise provided by statute, by these rules, or by other rules or regulations applicable in the courts of this state. Evidence which is not relevant is not admissible."

4. ER 403 provides that "[a]lthough relevant, evidence may be excluded if its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by considerations of undue delay, waste of time, or needless presentation of cumulative evidence."

5. ER 702 governs the admission of expert testimony: "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise."

6. As noted, all but one of the tested samples were mixed-source samples or DNA mixtures.

7. Congress created the DNA Advisory Board to "develop, and if appropriate, periodically revise, recommended standards for quality assurance" in DNA analysis, including "proficiency tests to be applied to the various types of DNA analyses used by forensic laboratories." 42 U.S.C. §§ 14131(a)(1)(C), 14131(a)(3).

8. This calculation is also variously referred to as the profile probability or "random man not excluded" (RMNE) approach. See, e.g., Gill, et al. (2006) at 91, 101; NRC II at 127.

9. Dr. Riley's research interests include PCR-STR DNA amplification techniques, and he has authored dozens of published academic articles on DNA and molecular and cell biology. He has testified as a defense expert witness in numerous criminal cases in which the defendants have challenged the admissibility of DNA evidence, but several courts have rejected his opinions. See, e.g., United States v. Shea, 957 F. Supp. 331, 339 (D.N.H. 1997) (rejecting his opinion that lab testing protocols could result in typing errors in part because he offered no scientific support for his opinion); People v. Smith, 107 Cal. App. 4th 646, 664, 671-72, 132 Cal. Rptr. 2d 230 (2003) (affirming trial court's rejection of his opinion that the Profiler and COfiler testing kits and the Prism 310 genetic analyzer were not generally accepted testing devices in the scientific community); State v. Faulkner, 103 S.W.3d 346, 357-59 (Mo. Ct. App. 2003) (rejecting his opinion that STR testing was not generally accepted in the scientific community).

10. The ISFG describes its work and that of its DNA Commission as follows:

Since 1989, the DNA Commission of the ISFG has published numerous recommendations addressing important topics to help establishing scientific standards in particular for new typing methods and genetic marker systems. Thus the society has adopted a pivotal role to take up the generally accepted scientific knowledge in the field of forensic genetics and condense it into specific guidelines with the overall aim to harmonize the important work derived from the studies of genetic markers in humans for the judicial system.

International Society of Forensic Genetics, <http://www.isfg.org/About/History> (last visited May. 12, 2009).

11. See, e.g., United States v. Trala, 162 F. Supp. 2d 336, 349 (D. Del. 2001) (applying Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993)), aff'd, 386 F.3d 536 (3d Cir. 2004), vacated on other grounds, 546 U.S. 1086, 126 S. Ct. 1078, 163 L. E. 2d 849 (2006); Roberts v. United States, 916 A.2d 922, 932, 934-35 (D.C. 2007) (applying Frye); People v. Coy, 258 Mich. App. 1, 10-11, 669 N.W.2d 831 (2003) (applying Frye); State v. Whittey, 149 N.H. 463, 821 A.2d 1086, 1096 (2003) (applying Frye).