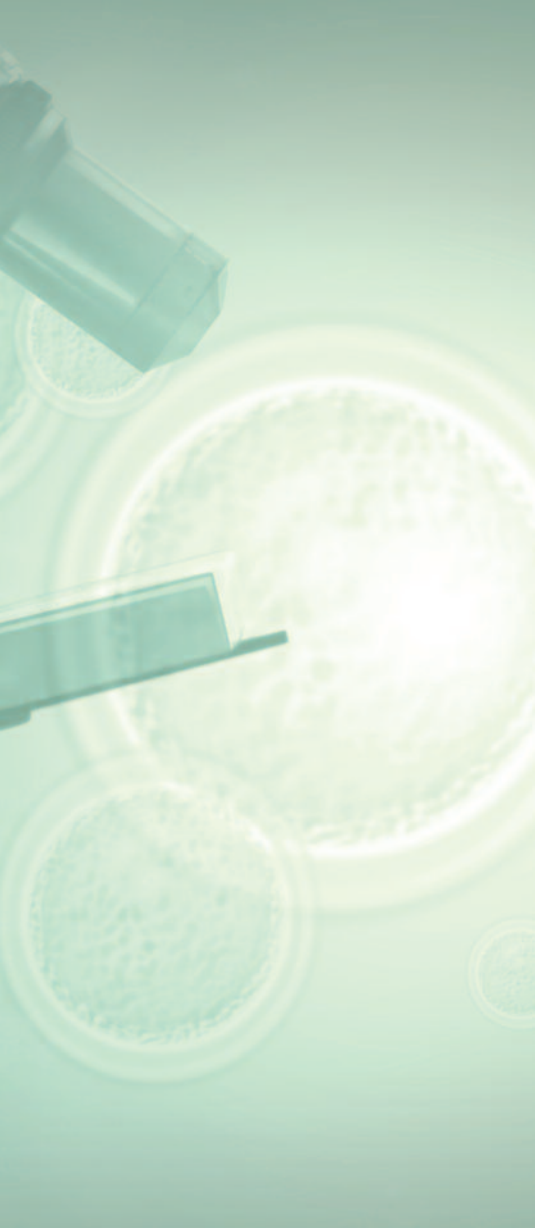
The Continuing Legal Evolution of Forensic DNA

By Karl E. Williams and Michael J. Panella

Lawyers are well aware of the importance of DNA evidence in potentially meeting a lawyer's burden of proof. Whether in a criminal or a civil case, DNA can serve as a key piece of evidence, particularly given the "CSI effect" the media has attached to DNA. However, as with all scientific evidence, there are strengths and limitations of forensic DNA tests, which are important knowledge points for lawyers as they prepare their cases. Furthermore, as with the law, science continues to evolve, which makes it critical for lawyers to be aware of scientific advancements that may support or adversely affect their cases.

Just as with all forensic tests, DNA testing has evolved. Early DNA testing consisted of rudimentary restriction fragment length polymorphism testing, which used restriction enzymes that cut DNA into numerous, variously sized fragments that were then separated via gel electrophoresis into a specific but highly complicated individualized pattern based on this size variation. Such testing was slow and cumbersome and required a large amount of DNA. DNA testing has evolved to the current automated Short Tandem Repeat test that focuses on the variation of several fixed gene foci and uses a Polymerase Chain Reaction, which replicates small amounts of DNA, leading to greater sensitivity. Given the continuing evolution of forensic testing, lawyers must stay current on changes to DNA testing that impact their cases. This article will cover basic forensic DNA science and a recent legal development in Pennsylvania concerning DNA random



match probability calculations of mixed DNA samples that improves the ability to discriminate between individuals.

Before exploring this new development let us briefly examine the various legal issues associated with this evolution of forensic DNA testing. As noted above, DNA testing has its strengths and limitations that the judicial system must recognize in ensuring the appropriate use of DNA at trial. Over the last two decades the courts have struggled with several DNA-related legal issues, such as declaring a match, calculating a random match probability and the appropriate use of laboratory error at trial. For instance, in *People v. Soto*, 21 Cal. 4th 512 (1999), the court noted the effect of different match band criteria used by different forensic laboratories when declaring a match. In addition the issue of statistical calculations in determining random match probability was addressed in *Commonwealth v. Blasioli*, 713 A.2d 1117 (Pa. 1998). There the court had to review the admissibility of the Product Rule, which centers on multiplying the frequencies of each genetic allele detected in a sample when determining the probability of finding this same allelic profile within a population. The *Blasioli* court found the Product Rule admissible in providing the statistical odds of another person sharing the same DNA profile as a defendant. Finally, in *People v. Reeves*, 109 Cal. Rptr. 2d 728 (2001), the court reviewed laboratory error noting that error can be brought up on cross-examination with no formal need actually to factor in such error as part of the random match probability calculation.

In these judicial decisions the courts assessed the admissibility of DNA forensic evidence through the analysis of general acceptance of such scientific methodology within the forensic community. In Pennsylvania such DNA admissibility review centers on application of the general acceptance *Frye* test when using potential novel DNA techniques. Under *Grady v. Frito-Lay, Inc.*, 839 A.2d 1038 (Pa. 2003), the court noted that the *Frye* test, with its use of general acceptance, serves the purpose of assessing whether the proposed new scientific evidence is reliable and thereby admissible. Consequently, in reviewing the use of novel DNA technique at trial a Pennsylvania court must determine if there is a genuine dispute within the forensic community regarding the reliability of an expert's conclusion concerning the DNA results. Such admissibility review of a potentially novel DNA technique recently occurred in *Commonwealth v. Foley*, 2012 PA Super 31 (Pa. Super. Ct. 2012). In that case the court was confronted with the use of computer analysis for mixed DNA samples. Before we discuss *Foley*, let us first examine basic DNA science and the problem of mixed DNA samples and how this new computer analysis may rectify this problem.

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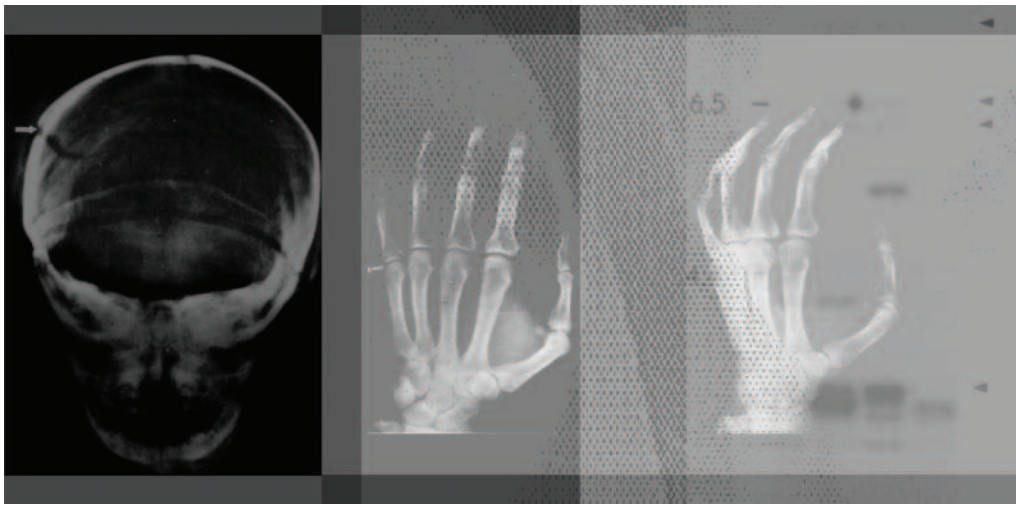
The modern age of genetics began in 1954 when Watson and Crick established the structure of DNA. DNA is a double helix of cross-linked strands of complementary sequences of four simple amino acids. The cross-linking of each matched amino acid pair in the chain is known as a *base pair* and is the fundamental unit of measure along the DNA molecule. The longest human chromosome (Chromosome 1) has 247 million base pairs.

Fundamental to the knowledge of patterns of inheritance and the associated forensic significance is the concept of an *allele*. An allele is a sequence of base pairs found at a specific location on a chromosome. An individual receives two alleles at each location on the 23 paired chromosomes, one from each parent. An allele may "code" for a specific substance, for example, the abnormal hemoglobin that causes sickle cell disease; however, most sequences seem to have no obvious purpose at all and are therefore called "junk DNA." This junk DNA comprises 98 percent of the human total chromosomal DNA — the *genome* — and is where forensic DNA is found.

There are two basic types of forensic DNA. Variable Number Tandem Repeats (VNTR) or "mini-satellites" are larger sequences of 10 to 60 or more base pairs. Standard Tandem Repeats (STR) or



"micro-satellites" are shorter sequences of four to six base pairs. As the "R" in the names imply, the specific sequences of base pairs repeat themselves a variable number of times at any one allelic location. For example, an individual may inherit 15 repeats of a four-base-pair sequence in an allele from one parent and 18 repeats of the same four-base-pair sequence in an allele from the second parent, both at one specific location on the paired chromosomes. More than 157,000 VNTRs have been identified in the human genome. About 10,000 STRs have been identified. Thirteen of these STR loci are employed internationally as the basis for establishing identity.

Forensic identification is a two-step process. Forensic material is examined for comparison of specific patterns of repeat DNA sequences (VNTR or STR) in known (reference) and unknown (evidence) specimens. The frequency of these individual patterns is statistically known in the general population. The frequency of two different pairs occurring together is determined by multiplying the separate frequencies of the individual pairs, which is the basis of the Product Rule discussed above. If specific patterns of paired STR alleles are found in an unknown piece of evidence and the incidence of those allele pairs is rare in the general population, then the likelihood that the evidence comes from a random individual is extremely rare. If similar patterns of alleles are found in both evidence from a crime scene and an accused individual, it becomes highly probably (the Likelihood Ratio) that the two specimens are associated.

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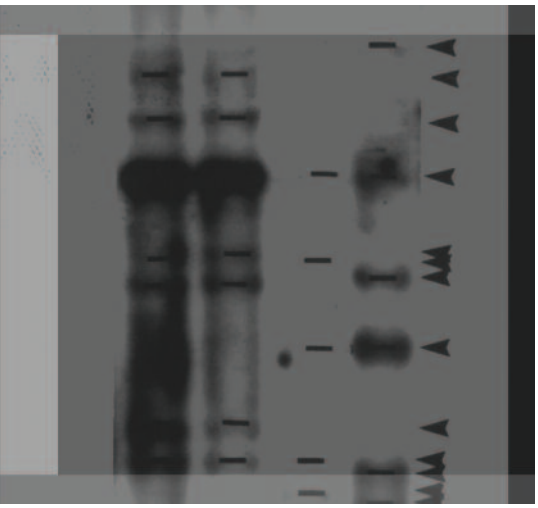
The *Blasioli* case stands at the crossroads of science and the law and contains an abundance of useful analytic information with references about DNA analysis and the Product Rule. The rape that was the occasion for this case occurred in 1993 when the standard laboratory process was an evaluation of VNTR by a now-outdated laboratory technology known as slab gel electrophoresis. By the time the decision was handed down in 1998 a transition had been made to a more rigorous, refined and reproducible technique for the measurement of STR by capillary gel electrophoresis. The measurement of STR by capillary gel electrophoresis is the basis for the 5 million convicted offender and arrestee profiles maintained by the FBI in the Combined DNA Index System.

It is the use of an automated, computer-based analysis (True Allele©) of such STR profiles in detecting real data from artifact in DNA testing that is central to the recent *Frye* hearing and decision in *Foley*. In *Foley* the court had to assess the admis-



sibility of this computer-assisted STR analysis for mixed DNA samples where two or more individuals contributed to the sample. Such mixtures may cause a diminution of STR peaks for an allele and make it difficult to declare the presence of a suspect's STR within a sample. The issue in such cases is whether a low STR peak in a mixed sample is legitimate or a nonspecific background finding that must not be used in the Product Rule when determining the random match probability. In the Court of Common Pleas of Indiana County Criminal Division at No(s): CP-32-CR-0001170-2007 the *Foley* trial court had admitted the testimony of a DNA expert, who for the first time in Pennsylvania used this computer analysis, which increased the ability to discriminate between a true STR peak and nonspecific background noise. This use of the computer analysis markedly decreased the odds of a random match probability between the defendant and a sample retrieved from under the victim's fingernail from one in 13,000 to one in 189 billion. The trial court admitted the expert's use of the computer analysis believing that its use was a refined application of the Product Rule and that the methodology of the analysis was generally accepted.

Based on the increased discriminating nature of the computer analysis, the importance of this analytic technique in DNA mixture cases for lawyers is obvious. However, before this new technique could be used successfully in Pennsylvania courts, the computer analysis faced a general acceptance *Frye* admissibility challenge. The *Foley* appellate court had to assess whether there was a legitimate dispute in the reliability of the DNA expert's use of the computer analysis when calculating the random match probability for mixed samples. The court found that the computer analysis was "not novel," which met the *Frye* admissibility standard, and upheld the admission of the forensic DNA expert's application of the computer analysis in calculating the random match probability. The court's ruling centered on three factors. First, the reliability of the computer analysis had undergone testing and was validated in peer-reviewed studies. Second, the computer analysis was "not novel" given that it was used in other settings, including the New York State forensic DNA data bank, United Kingdom forensic science service, World Trade Center 9/11 victim identification and Allegheny County crime lab in Pittsburgh. Finally, the court noted that the general acceptance of the technique's reliability centers on the scientific community and not whether the computer analysis has ever been used by the courts. As noted above, the computer analysis had met this general acceptance standard within the forensic scientific community.

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The *Foley* decision has opened the way for the application of this computer analysis in potentially complicated DNA mixture cases. Besides the implications of admitting the computer analysis in Pennsylvania courts, the case emphasizes the importance of lawyers carefully assessing the strengths and limitations of forensic tests with review of new developments

within the appropriate scientific discipline. If such new scientific developments exist the lawyer must be prepared to argue the general acceptance of the reliability of these new developments within the scientific community. Finally, as exemplified by the use of the computer analysis in DNA mixture samples, DNA technology continues to evolve, with lawyers needing to recognize such new developments in maximizing their effective use of DNA evidence at trial. ✦

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