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## About the Cover...

The cover image shows steps, illustrated by pieces of a puzzle, that DNA analysts must take to identify a unique DNA profile or "genetic print." The pieces illustrate sample collection, DNA amplification, DNA electrophoresis, data generation, data analysis, data-banking and identification. Duplex DNA connects the laboratory phases, emphasizing the importance of DNA manipulation, whereas fiber optic cable links the data through analysis and identification of an individual, genetic print.

Cover illustration by Glenn Fuller. The inset images were supplied by the Forensic Science Service.



# DNA Technology: Where Is It Going?

Forensic and paternity testing laboratories have been using DNA typing methods for a decade. Each year of that decade has witnessed the introduction of improved systems and refinements to DNA typing technology. Analysis has progressed from RFLP (restriction fragment length polymorphism) typing using radioactivity and chemiluminescence detection, to the application of PCR<sup>†</sup> for detecting sequence variation, Amp-FLPs and Short Tandem Repeats (STRs\*). Detection instrumentation has evolved from manual sequencing units to automated fluorescent scanners and capillary electrophoresis systems. It is likely that in the next few years, more rapid and automated methods using DNA chips and mass spectrometry will be available.

Concomitant with this technological development has been the selection of 13 core STR loci to be used in CODIS (Combined DNA Index System), the national database system in the United States. A similar decision to standardize STR loci will be made in Europe later this year. Thus, forensic DNA typing will achieve a degree of standardization worldwide. Forensic DNA typing laboratories are now focused predominantly on one technology and are validating STR typing procedures. Currently, laboratories must perform two PCR amplifications to analyze 13 STR loci. Next year, a new milestone will be reached when a system will be available that enables amplification of more than 13 STR loci in one PCR amplification. The ability to create a unique DNA profile, or "genetic print" using one amplification reaction will save time and money and satisfy the needs of DNA typing laboratories for years to come. Laboratories can then focus on generating DNA typing results instead of validating new DNA technologies.

DNA typing technology has revolutionized the analysis of crime scene evidence and has provided a sensitive means for individual identification. The combination of a highly informative multiplex system, state-of-the-art technology and databasing systems will provide law enforcement agencies around the world the ability to share genetic prints and enhance the effectiveness of this very powerful tool for individual identification.

\*STR loci are the subject of German Pat. No. DE 38 34 636 C2 issued to the Max-Planck-Gesellschaft zur Förderung der Wissenschaften, eV, Germany. Exclusive rights have been assigned to Promega Corporation for uses in human clinical research and diagnostics applications and all forms of human genetic identity. Exclusive rights to human linkage analysis in the research market are assigned to Research Genetics, Inc., Huntsville, Alabama. All other rights are shared by Research Genetics and Promega.

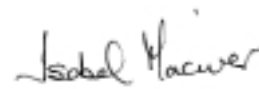
The development and use of STR loci is covered by U.S. Pat. No. 5,364,759 assigned to Baylor College of Medicine, Houston, Texas. Rights have been licensed to Promega Corporation for all applications. Most applications have been licensed on an exclusive basis. U.S. Pat. No. 5,599,666 has been issued to Promega Corporation for allelic ladders for the loci CSF1PO, F13A01, FESFPS, LPL and vWA. U.S. Pat. No. 5,674,686 has been issued to Promega Corporation for allelic ladders for the locus CSF1PO and the combination of allelic ladders for the loci CSF1PO, FESFPS and TH01.

This issue of *Profiles in DNA* includes a feature article from the Forensic Science Service (FSS) in the United Kingdom. In this article the processes and systems used to implement a large DNA database are discussed in detail. The authors also summarize the approach the FSS has used for troubleshooting problems and verifying results. The front cover of this issue also focuses on databases, illustrating the entire process from sample collection to data entry and analysis. Our second feature article is from Charlotte Word of Cellmark Diagnostics and provides a laboratory perspective on the presentation of STR data in court. This issue also contains an article from the National Forensic Science Technology Center that outlines the training and support available through their education program. The "Technical Tips" feature on page 12 provides information on a selection of useful Internet sites that contain information on DNA typing. Upcoming meetings are featured on page 11 and career opportunities and information on the *Ninth International Symposium on Human Identification* are found on page 16.

*Profiles in DNA* is available on the Internet at [www.promega.com/profiles](http://www.promega.com/profiles) and at [www.euro.promega.com/profiles](http://www.euro.promega.com/profiles). Current and past issues may be viewed at this site and comments may be directed to authors or the editor via e-mail. We welcome contributions from readers in the form of articles, letters, comments or suggestions. If you would like to make a contribution in any of these ways, please contact the editor.



Randy Nagy  
Business Manager  
Genetic Identity



Isobel Maciver  
Editor  
*Profiles in DNA*

Use of the *GenePrint™* STR System requires performance of the polymerase chain reaction (PCR), which is the subject of European Pat. Nos. 201,184 and 200,362, and U.S. Pat. Nos. 4,683,195, 4,965,188 and 4,683,202 owned by Hoffmann-La Roche. Purchase of the *GenePrint™* STR System does not include or provide a license with respect to these patents or any other PCR-related patent owned by Hoffmann-La Roche or others. Users of the *GenePrint™* STR System may, therefore, be required to obtain a patent license, depending on the country in which the system is used. For more specific information on obtaining a PCR license, please contact Hoffmann-La Roche.

<sup>†</sup>The PCR process is covered by patents issued and applicable in certain countries. Promega does not encourage or support the unauthorized or unlicensed use of the PCR process.

# Problem Solving: DNA Data Acquisition and Analysis

By Dr. David Werrett<sup>1</sup>, Richard Pinchin<sup>2</sup> and Ros Hale<sup>2</sup>

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In this paper we address some of the issues that arise when setting up and developing a large DNA database. We will also show how the knowledge gained during the process can be captured in an expert system, which we have called STRess.

## MULTIPLE SUPPLIERS OF PROFILES TO A NATIONAL DNA DATABASE

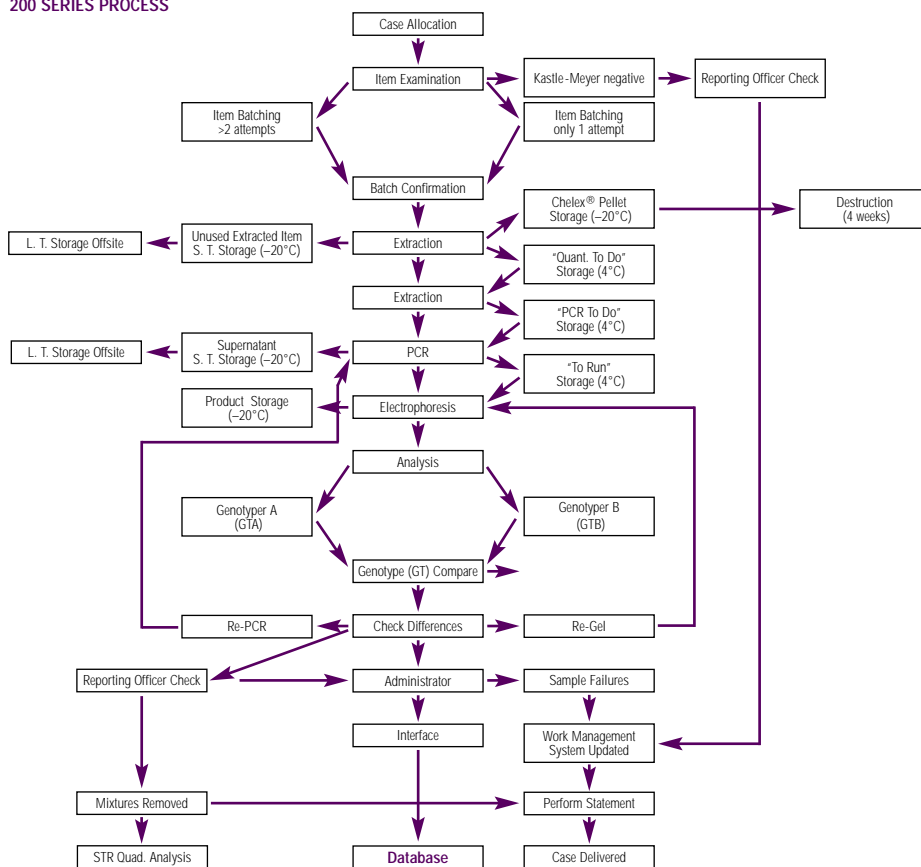
In the UK, the National DNA Database data is owned by the Association of Chief Police Officers (ACPO). They provide the framework for suppliers, such as the Forensic Science Service (FSS), to submit information to the database. In addition to its role as supplier, the FSS acts as custodian for the database by the administration of a proficiency test program. Those supplying profiles to the database must take part in proficiency testing, and potential suppliers must take part in a number of validation tests. The FSS advises the ACPO (on the science used, match criteria, etc.), and the ACPO builds this information into the approval and framework for supply of profiles to the database.

The main feature of the validation and proficiency test program is that all suppliers must be accredited by an external organization to ISO9001 and ISO25 international standards, which include the standards of the National Measurement and Accreditation Service, NIS46 and NIS96. Accredited laboratories can then supply samples to the National DNA Database and take part in the ongoing quality assurance program administered by the FSS.

## EMPIRICAL PROCESS FLOWS

The rapid development of the National DNA Database unit within the FSS made us acutely aware of the need for detailed examination of the process flows required to ensure that samples are analyzed correctly, results interpreted and, when necessary, samples re-analyzed. The entire process is illustrated in Figure 1.

### 200 SERIES PROCESS



**Figure 1. Overall process flow.** The entire process, from case allocation to database submission of STR profiles is illustrated in this flow chart.

At the genotyping stage there was some room for subjectivity, and therefore, two analysts (signified by GTA and GTB in Figure 1) genotype the gel independently. These two interpretations are examined by a third individual (signified by GT Compare in Figure 1) who performs a comparison of the genotyping results. Any differences are checked, and decisions are made to either accept the result or re-amplify or rerun the sample. Each part of the process flow was examined in detail, documented and timed. This initiated two projects. The goal of the first of these projects was to automate many

of the manual techniques involved in the process, including extraction, quantitation and PCR. The second project sought to address the considerable time spent analyzing and genotyping gels. These efforts led to the development of a program or "expert system" known as STRess (STR expert system suite). This is a Windows®- and Macintosh®-based program that accepts raw data, generates a file of allele designations and then compares this file to one generated by a human operator. The following pages detail the development of the STRess system, and provide an overview of how the system works.

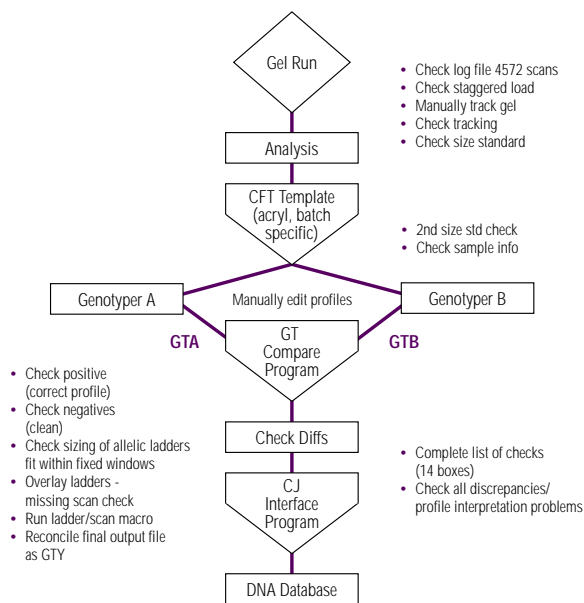


Figure 2. Detail of the genotyping process.

THE STRESS SYSTEM

Having visualized the overall process flow (Figure 1), we were in a position to focus on the particular area or domain that we believed was a potential bottleneck. We decided to concentrate on the part of the process outlined in Figure 2 – the independent analysis of the data by two individuals, genotyper A (GTA) and genotyper B (GTB).

THE OBJECTIVE

The primary objective was to provide a system that would carry out the same analytical processes as a human, to at least the same or higher standard. An additional benefit would be a decrease in processing time, but this would have to be achieved without sacrificing quality. Quality monitoring was an important part of the specification; this required a complete and documented audit trail.

The benefit of the development of this program was the achievement of an increase in throughput by making the most of available human resources and, in turn, providing

value to our customers. In addition, it provided a structured process enabling us to ensure quality and allowing easy problem tracing and subsequent solving. The only remaining issue was how to implement such a system.

THE CHALLENGE

The challenge was to provide a computer program that could be installed on the same Macintosh® computer as the STR analysis software and that was capable and intelligent enough to undertake the role of the second person in the process, genotyper B (GTB). In addition, the same program needed to run in an IBM® PC environment.

It became clear that the best solution was the development of an expert system. These days there is less fear of the term “expert systems”, even though in the late 1980s they were seen as a universal corporate panacea that would allow the replacement of expensive, highly skilled staff with a less skilled and thus less expensive workforce. Fortunately,

this has turned out to be neither practical nor desirable, and today, expert system technology is considered to be a flexible framework for holding all the relevant information about a domain (e.g., data, knowledge, other programs, reference materials, etc.). The best description we have seen to date is that expert systems are regarded as “technological glue”.

Having identified a potential solution, we initiated the STRESS project. After defining the domain of interest, the second stage in the construction of an expert system is the formalization of the relevant knowledge. With around 100,000 samples already processed, we felt we had acquired enough expertise to formulate rules by which our human operators worked.

It should be pointed out at this stage that this process of “knowledge engineering” is a valuable exercise in itself. Many things that are done during laboratory procedures have evolved from simple beginnings into highly complex processes. Taking a critical look at each task and asking the questions, “Why am I doing this?” and “Do I really need to do this?” at each stage often reveals inherited redundancy and, more importantly, can reveal that all-important error waiting to happen.

THE GOAL

It became the primary goal of the STRESS project team to encapsulate the knowledge of the human operator (GTB) and produce a system that could perform that person’s job function to an equal or greater level of competency.

The overriding concern throughout the project was the preservation of data integrity and the maintenance of a zero-error philosophy even at the expense of additional resources. We realized that to accomplish this there would be a price to pay in terms of extra staff time during the initial stages following implementation. In fact, overall processing time did increase initially, but we were confident that this cost would be more than recouped over the long term.

SYSTEM OVERVIEW

The STRESS system accepts data from either of the Applied Biosystems programs, GenoTyper® or GeneScan® Analysis, in the form of a comma separated values (CSV) file. It applies rules and processes derived from the experts to this raw data and produces a number of output files. The file of designated alleles is in the same CSV format as that produced by the human operator so

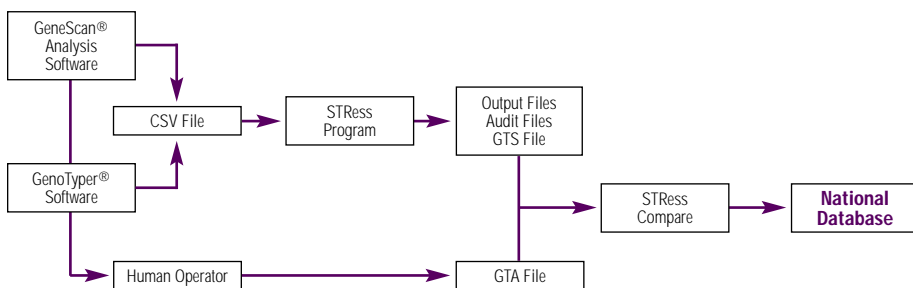


Figure 3. Outline process flow for STRESS.

the “compare” function of the STress program can be used to detect any differences between the two files. This is illustrated in Figure 3.

**SYSTEM DETAIL**

Figure 4 shows the processes invoked by the STress program. Process 1 simply accepts data in CSV format. These data are produced from GeneScan® software by exporting a data table or from GenoTyper® software by running a raw data macro. This raw data file defines each peak in terms of position, height and area. Data from GeneScan® software are by color in peak order and data from GenoTyper® software are by locus and sample.

Process 2 is the heart of the system and is responsible for cleaning the raw data ready for allelic designation. The process has been split into five components as follows:

1. Negative control lanes are checked for contamination or primer dimers.
2. Ladders are checked for artifacts and non-allelic peaks; these are removed before proceeding to Step 3.
3. Allelic ladders are compared and any differences are reported. This step will reveal any missing peaks. If there are more than two ladders present, they are compared in the order:



4. Sample lanes are cleaned using the rules contained in the knowledgebase. Examples of the rules used are shown in Figure 5.

The underlying philosophy of the system is to move data from one file to another (rather than remove the data altogether). This allows a clear audit trail that can show the fate of every peak from the input file.

Once the sample data have been cleaned, the remaining peaks have to be designated. Strictly speaking, this needs to be done by reference to the ladder lanes present on the gel. However, this presents a number of problems:

- a) The gel ladder will be shifted from an ideal.
- b) The gel ladder will be incomplete – not all possible alleles will be represented.
- c) There may be missing ladder peaks.

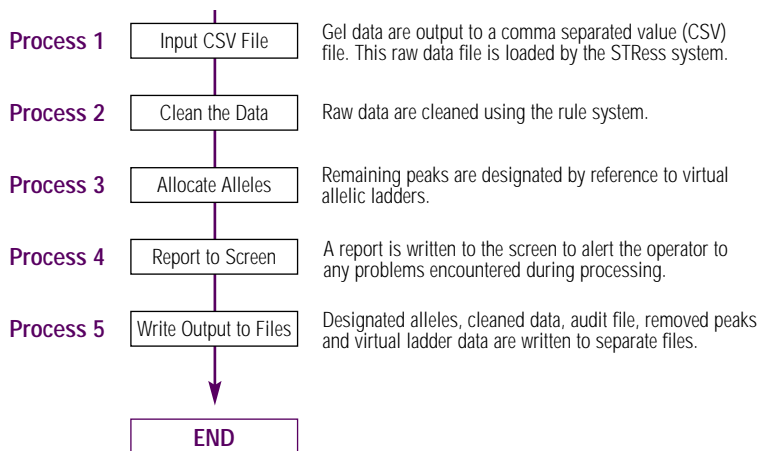


Figure 4. STRESS processes.

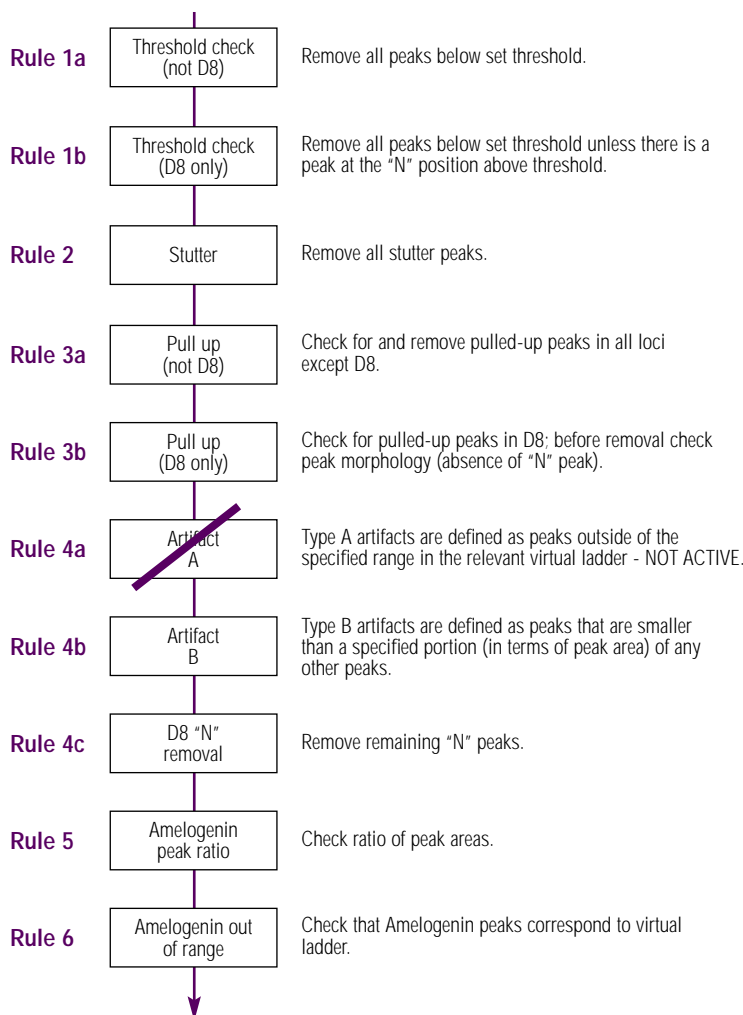


Figure 5. Example knowledgebase.

5. To circumvent these problems, STRESS constructs a “virtual ladder.” This is done by comparing the gel ladder with a known pattern of peaks determined when

the acrylamide gel mix is validated. The shift between ideal ladder and the gel ladder is determined at each peak as shown by  $\delta_1$  in Figure 6, Panel A.

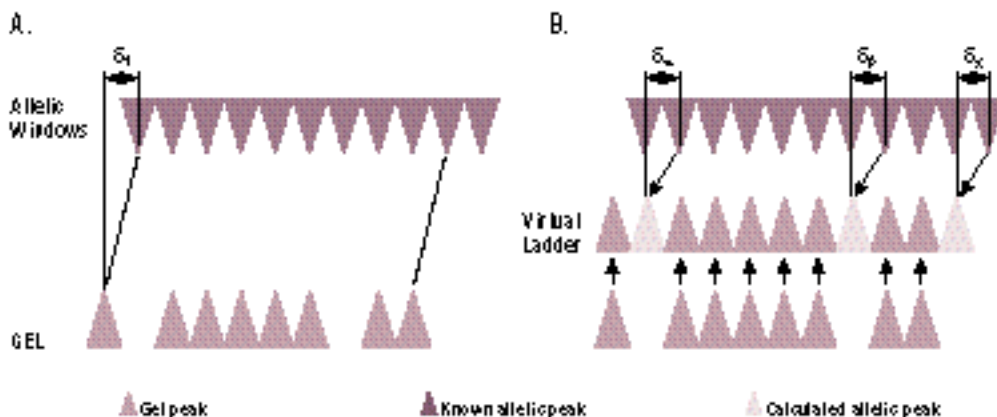


Figure 6. Panel A. Shift of gel peaks from ideal. Panel B. Creation of the virtual ladder.

This shift is then used to compensate for missing peaks. Thus, the virtual ladder is built up from true gel peaks and peaks calculated for the observed shift. This process is carried out for each ladder on the gel and can be visualized as shown in Figure 6, Panel B.

Following the creation of the virtual ladder, the remaining peaks can be designated. This is done by reference to a list of all possible designations. As this list is under the control of the user, labels can be added to indicate such things as rare alleles. Any peak that does not have a corresponding virtual ladder peak can either be ignored or designated by a question mark.

Once the designation phase is complete, customized comments can be added depending on a range of post-designation rules – this process is known as allelic qualification. Figure 7 shows some of the qualifications used by the FSS.

OUTPUT

Once processing is complete, a number of files are generated.

**GTS file** - As mentioned earlier, this file is equivalent to the human operator output file

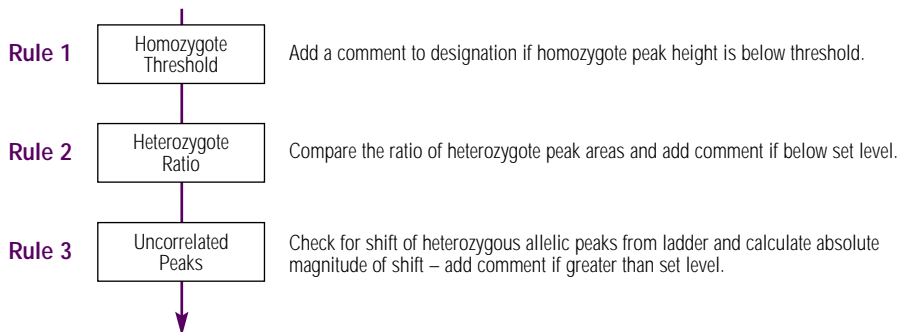


Figure 7. Some qualification rules used by the FSS.

(GTA) with which it is compared using the STress compare function (see next section).

**OUT file** - This contains the cleaned data in the format of the input file (i.e., each peak is defined by its position, height and area).

**REP file** - This reports the fate of each peak discarded.

**AUD file** - The main audit file details all warnings issued during processing together with the operator ID. This file also contains virtual ladder summary statistics.

**VLD file** - This is a full listing of every peak in each of the virtual ladders together with its shift from the ideal ladder.

Each file contains a list of the version numbers of each of the numerous files that comprise the STress environment. In this way version control is strictly monitored.

COMPARE

The final stage is to compare the human output with that from STress. The STress compare function produces a table of differences that allows the “check diffs” (see Figure 2) to investigate the causes of any differences and arbitrate before sending the profile to the National Database.

TROUBLESHOOTING

The processing of large numbers of samples (this year we will process in excess of 200,000 samples, and next year we project up to 300,000 samples) has presented us with several novel problems. We needed a troubleshooting structure that would allow us to address and document problems in each of the three FSS units performing DNA analysis and learn by them. We now have a dedicated troubleshooting procedure whereby problems are identified, documented and brought to the attention of a troubleshooting committee, which has the responsibility for implementing and following up on corrective actions as well as organizing post-implementation reviews.

It is hoped that we can all learn from an exchange of information on problem resolution as databases are implemented throughout Europe and around the world.

SUMMARY

By studying thousands of sample operations of the system and comparing them to the human operator, rules have been refined and the program tuned for maximum efficiency. To date, a saving in time of more than 30% has been achieved by use of the STress program. This is an important saving considering that the FSS has almost 200 people in eight teams at two locations processing about 20,000 samples per month.

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# STR Data Goes to Court: A Laboratory Perspective

*By Charlotte J. Word, Ph.D.  
Cellmark Diagnostics,  
Germantown, MD*

The last ten years have seen the introduction of human DNA identification tests on various biological samples in crime laboratories in the United States and around the world. Laboratories in the United States have acquired vast experience in performing DNA tests and taking the results and conclusions drawn from those tests into the courtroom for presentation to judges and juries. Restriction fragment length polymorphism (RFLP) data have been presented in numerous courts, and there are a significant number of state appellate rulings accepting RFLP data. Similarly, the results from polymerase chain reaction (PCR)-testing have also been presented widely in courts in the United States, resulting in many appellate rulings accepting this technology. Currently, most of the appellate rulings regarding PCR-testing reference data were obtained using the AmpliType® DQ $\alpha$  PCR Forensic DNA Amplification and Typing Kit (DQA1; Perkin-Elmer Corporation). However, there have been several more recent rulings accepting AmpliType® PM PCR Amplification and Typing Kit and D1S80 data. Extensive experience has been accumulated regarding the issues that affect the admissibility and presentation of “new and novel” test results in court. The newest form of DNA testing to become commercially available for forensic DNA analysis is STR (short tandem repeat) analysis. STR testing has been performed on DNA isolated from forensic case samples for a variety of reasons. These include: 1) increasing the chance of excluding a falsely-accused individual, 2) determining whether a sample contains a mixture of DNA from more than one individual, 3) assisting in the interpretation of data from samples containing a mixture of DNA and 4) limiting the number of individuals included as possible donors of the DNA obtained from a sample by providing increased statistical frequencies. As scientists, we can rely on our past experience when testifying to scientific data produced using the newer, commercially available STR systems.

Our role as scientific expert witnesses is to educate the jury and/or judge regarding the type of testing that has been done, the results and conclusions of these tests, and their limitations. It may be helpful to explain the genetic basis for each type of test and the advantages and disadvantages of the systems used. For example, one advantage of PCR-based systems is that they can be used to obtain results from very small samples that do not contain sufficient material for RFLP analysis. There are two major types of variations in nuclear DNA that are used for human identity testing. One type of variation is a single-base change that occurs at a specific location in the DNA (e.g., one person has an “A” and another person has a “G” at the same position). These variations are commonly analyzed using oligonucleotide probes specific for the sequence in amplified PCR products; for example, the dot blot analysis used in the AmpliType® DQ $\alpha$ , PM and PM + DQA1 test kits. The second type of variation arises as a result of differences in the number of blocks of tandemly repeated sequences found at a specific location in the DNA. Variations in the number of these repeats between individuals leads to length differences at specific regions. These are analyzed by electrophoresis of the DNA through a gel matrix, followed by observation of differences in the migration rates of the differently sized DNA fragments.

Blocks of large repeated DNA sequences are referred to as variable number tandem repeats (VNTRs) and are analyzed by RFLP. Variable numbers of shorter repeated DNA sequence blocks that are amplified by PCR are commonly referred to as amplified fragment length polymorphisms (AmpFLPs; e.g., D1S80). Short tandem repeats (STRs) refer to tandemly repeated blocks of very short sequences (generally two, three or four bases), and these, like AmpFLPs, are analyzed after amplification of the DNA using PCR. As STR and VNTR sequences are genetically similar, STR and D1S80 testing use a similar technology to that used for VNTR analysis. STR and D1S80 testing combine the analysis of DNA fragment length variations by gel electrophoresis with the advantage of using PCR amplification to generate multiple copies of the target DNA.

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*Over the last ten years, laboratories in the United States have acquired vast experience in performing DNA tests and taking the results and conclusions drawn from those tests into the courtroom for presentation to judges and juries.*

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*Cellmark analysts have been to court in over 30 cases where the GenePrint™ STR Multiplex System - CSF1PO, TPOX, TH01 (CTT Multiplex) and/or CTT in conjunction with the GenePrint™ Sex Identification System – Amelogenin (CTT-A) data have been presented to the trier of fact.*

These technologies and the use of STR sequences are not “new or novel” to scientists and are widely used in many areas of research and diagnostics outside of the field of forensic human identity testing.

Cellmark analysts have been to court in over 30 cases where the *GenePrint™* STR Multiplex System - CSF1PO, TPOX, TH01 (CTT Multiplex) and/or CTT in conjunction with the *GenePrint™* Sex Identification System – Amelogenin (CTT-A) data have been presented to the trier of fact. Testimony was given in admissibility hearings prior to the trial for some of the cases. As in other admissibility hearings for DQA1, PM, D1S80 and RFLP testing, the testimony presented generally included the following:

- Information regarding the widespread use of PCR and STR testing in other fields.
- The genetic basis for the polymorphisms observed.
- A description of the technology used and types of results obtained.

- Validation studies, including relevant publications.
- Training and experience of the scientist and the laboratory.
- Proficiency testing, controls performed, and safeguards in evidence handling and testing to ensure accurate and reliable results.

Presentations at trial have ranged from a brief description of the technology and a summary of the data to more extensive testimony that includes areas routinely covered in admissibility hearings and test results discussed in detail.

The issues raised in cross-examination have generally been similar to those raised previously for other types of PCR testing and for RFLP testing. These include whether STR testing is “new and novel,” whether multiplexing compromises the assay, whether the sensitivity of PCR testing means that contamination may invalidate the results, and whether small databases are representative of larger populations. These issues can be addressed by the expert witness by citing publications detailing validation studies and databases, by the use of appropriate laboratory standard operating procedures for evidence handling and testing and for performing controls, by proper training of laboratory staff and the use of proficiency tests, and through the application of relevant guidelines such as those from TWGDAM (1) and the DNA Advisory Board.

The first appellate ruling in which STR testing was reviewed and accepted occurred in 1997 [*Commonwealth of Massachusetts v. Adam Rosier*; 425 Mass. 807, 685 N.E. 2d 739 (1997)].

## CONCLUSIONS

STR test results may provide useful information in many cases where DNA testing is possible. Since the genetic analysis of STR sequences has been used widely and has been accepted by molecular biologists in many areas of study for over eight years, the use of STRs is not considered to be a new technique to the scientific community. We as scientists can be confident taking the results of STR testing to court as long as the data are supported by good laboratory practices. Our role as scientific expert witnesses is as follows:

- To be prepared with the appropriate validation studies, training and standard operating procedures, including the use of appropriate controls, proficiency testing, etc., to support the STR data.
- To work closely with attorneys and other relevant individuals to determine which cases can benefit from the use of STR testing.
- To fairly and accurately present STR data to the trier of fact.

## REFERENCE

1. The Technical Working Group of DNA Analysis Methods (1995) Guidelines for a quality assurance program for DNA analysis. *Crime Laboratory Digest* 22, 21.

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AmpliTye is a registered trademark of Roche Molecular Systems, Inc.

# The National Forensic Science Technology Center: Science Serving Justice

*By William J. Tilstone, Ph.D.  
National Forensic Science Technology Center,  
St. Petersburg, FL*

## FROM TECHNOLOGY TO TRAINING – THE HISTORY OF NFSTC

The National Forensic Science Technology Center (NFSTC) is a not-for-profit corporation set up by the American Society of Crime Laboratory Directors (ASCLD) in 1995. The incorporation of NFSTC was triggered by an approach from the Largo, Florida, plant of Lockheed Martin Corporation. The Largo plant was seeking partnership with NFSTC to assist its transition from nuclear weapons technology to the development of peacetime applications. The original goal was a Research and Development facility using the high-technology equipment that existed in the Lockheed plant. It was envisaged that the NFSTC would provide contract research and casework on a commercial basis. However, in October of that same year, Lockheed Martin decided to close the plant, and NFSTC had to review its strategic plan.

Following the withdrawal of Lockheed, the strategic planning direction turned to other areas of need in the forensic sciences. The publicity that surrounded the O. J. Simpson case highlighted the shortage of support in training and quality systems. NFSTC therefore has focused its business activities on accreditation, education and training.

By the time of the October 1995 decision, the University of Central Florida (UCF), the University of South Florida and the Public Safety campus of the St. Petersburg Junior College (SPJC) had all expressed a desire to support the venture. With seed funds from the universities and accommodation at the SPJC, NFSTC opened for business on July 1, 1996.

A strategic plan was developed identifying a mission of “assisting forensic science laboratories achieve the highest standards of operation.” There are three priority areas to achieve this mission: training, education and quality systems support.

The response has vindicated that vision. NFSTC operates on a commercial basis with no soft money grants to underpin it. It has benefited from its customer focus and is on track for a turnover of \$400,000 in its second full year of operations. Since it is a not-for-profit corporation, the margins on that turnover are kept to the minimum needed to meet operating costs. Customers are thus receiving and appreciating a value-for-money service. Customer feedback on our services has been very positive.

## TRAINING AT NFSTC

Training is an essential part of our quality initiative. We have conducted classes at our base in St. Petersburg, Florida, and in California, Colorado, Louisiana, New York, Ohio, Ontario, Oregon and Miami, Florida. Topics covered in the courses range from DNA statistics to fire debris analysis.

More recently, we have adapted workshops for World Wide Web access and have just completed a set of instructional classes for the American Board of Criminalists (ABC) Certification.

## GRADUATE PROGRAM FOR DNA SUPERVISORS

In 1996-1997, NFSTC responded to the DNA Advisory Board's (DAB) proposal that DNA supervisors should have a graduate degree. NFSTC, in conjunction with UCF (one of our academic partners), developed a Master's degree program for those working in crime laboratories.

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*A strategic plan was developed identifying a mission of “assisting forensic science laboratories achieve the highest standards of operation.”*

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*NFSTC, in conjunction with UCF (one of our academic partners), developed a Master's degree program for those working in crime laboratories.*

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### *Crime laboratory accreditation is achieved through the ASCLD/Laboratory Accreditation Board (ASCLD/LAB) program.*

The resulting degree program was launched in January, 1998. It is a 30 semester-hour (shr) Master of Science with 12shr of forensic DNA topics, 12shr of general advanced science and a 6shr (approximately 120 contact hours) research project. Classes are conducted over the Internet, and the first course on bioinformatics and quality assurance is almost completed. Twelve "pioneer" students from Arizona to Virginia are ready to complete these courses and have favorable comments about this program. The consensus opinion is that the program is more challenging than and superior to our original goal.

#### QUALITY SYSTEMS SUPPORT

Accreditation is now an accepted part of operating as a crime laboratory. There has been a particular emphasis in the DNA area, as the DAB has set standards and requires proof of compliance with those standards.

Crime laboratory accreditation is achieved through the ASCLD/Laboratory Accreditation Board (ASCLD/LAB) program. This program is a demanding undertaking, and NFSTC has supported its successful implementation by providing preaccreditation audits to laboratories preparing for accreditation. ASCLD/LAB is a "one-in, all-in" program. That is, a laboratory cannot elect to leave out disciplines covered by the program in its accreditation.

The DAB has set Quality Assurance Standards for Forensic DNA Testing Laboratories. These standards apply to DNA sections of crime laboratories, to private DNA forensic laboratories and to laboratories seeking to perform DNA analysis for databasing (CODIS) work. The standards include a provision that laboratories subcontracting DNA work must ensure that the subcontractor also meets the DAB standards. The ASCLD/LAB Crime Laboratory accreditation program has been accepted by the DAB as sufficient, objective evidence that a laboratory meets its standards.

NFSTC has a Memorandum of Understanding with ASCLD/LAB to audit DNA sections of crime laboratories where the overall facility is not yet ready for accreditation and to grant a certificate of compliance with DAB and ASCLD/LAB standards where warranted. NFSTC provides the same service to private laboratories. The DAB has accepted the validity of this certification.

For a typical DNA laboratory, the process involves a two-day audit of policies, practices and procedures against the DAB standards. All the standards are covered, but particular attention is paid to the following. Documentation of technical standard operating procedures (SOPs) and validation studies are reviewed, as are proficiency tests and calibration, training and education records. Policy and practice on evidence security is scrutinized in detail, as is the way that PCR testing is performed. The assessors are drawn from a pool trained as ASCLD/LAB inspectors and/or successful graduates of the NFSTC laboratory auditing class.

The certificate states that the laboratory has been audited and found to comply with the requirements of the Technical Working Group on DNA Analysis Methods (TWG-DAM), DAB and the relevant provisions of the ASCLD/LAB, or, in the case of a databasing laboratory, that it complies with the requirements of the draft DAB standards for CODIS laboratories. The certification is good for two years and requires an internal audit after the first year. The certification audit itself qualifies as an external audit, as required by the DAB standards.

The certification is recognized by contractors. For example, the Virginia Division of Forensic Science Request for Proposals (RFP) for CODIS work specifically mentions that respondents are required to be accredited by ASCLD/LAB or NFSTC.

It has been our experience that customer laboratories are varied in their wishes for publicity. For this reason, we no longer list certified laboratories publicly but are happy to provide contact points in reference sites to genuine inquirers. NFSTC has audited nine private DNA laboratories for certification of compliance.

#### CONTINUING FORENSIC EDUCATION UNITS

Forensic science has lagged in formal continuing education schemes. Certification has only recently become recognized. Although continuing education is required by the ASCLD/LAB, there is no supporting system for that accreditation board to reference. NFSTC has implemented a plan in which one continuing forensic education unit is equivalent to half of a college class. To obtain credit, the course must show it is of the required academic standard (curriculum, instructors and facilities) and have some form of testing of students to show that they learned from the program. The NFSTC plan is available to any course provider.

The Promega STR Workshops are in the leading group to be approved under the scheme.

For more information, visit our web site at [www.nfstc.org](http://www.nfstc.org) or contact us at:

**NFSTC**  
3200 34th Street South  
St. Petersburg, FL 33711  
Telephone: (813) 341 4497  
Fax: (813) 341 4547

**NFSTC**  
Science Serving Justice

# Hitachi FMBIO® Users Group Meeting: Hilton Head Island, South Carolina, January 1998

*By Jeffrey Ban  
Virginia Division of Forensic Science,  
Richmond, VA*

A two day FMBIO® Users Group meeting entitled “Advanced Fluorescent-STR MegaPlex Technology Workshop” was held at the Palmetto Dunes Resort on Hilton Head Island, South Carolina, from January 11-13, 1998. This meeting was sponsored by Promega Corporation, the Bode Technology Group, Inc., and Hitachi Software Engineering America, Ltd., and was supported by the Virginia Division of Forensic Science and Palm Beach County Sheriff’s Office. The purpose of this workshop was to enhance the skills of the forensic scientist on the use of the FMBIO® Fluorescent Scanner and to address related STR (Short Tandem Repeat) issues for casework analyses. Representatives from nine laboratories attended, including Indiana State Police Department Crime Laboratory, Alabama Department of Forensic Science, Palm Beach County Crime Laboratory, Bode Technology Group, North Carolina Bureau of Investigation, Maryland State Police Crime Laboratory, South Carolina Law Enforcement Division, Arkansas State Police Department and the Virginia Division of Forensic Science.

A dinner reception for the 58 attendees was held at the Palmetto Plantation Country Club on Sunday evening, January 11, 1998, with welcoming remarks by Tom Bode from the Bode Technology Group, Tom Mozer from Promega Corporation and Paul Ferrara from the Virginia Division of Forensic Science. Presentations were given on Monday and Tuesday, January 11 and 12. The presenters were James Schumm (Promega Corporation) on molecular biology of eukaryotes, Robert Bever (the Bode Technology Group) on forensic sample preparation and troubleshooting techniques, Cecelia Crouse (Palm Beach County Crime Laboratory) on polyacrylamide gel electrophoresis of megaplex systems, Sonja Klein and Deborah Smead (Hitachi Software Engineering Co.) on the recent updates to the FMBIO® Analysis and StarCall™ Software and the FMBIO® Fluorescent Scanner Technology, and George Li and Jeffrey Ban (Virginia Division of Forensic Science) on case approach, STR databasing and CODIS software applications. An informative and interactive question and answer session was held at the conclusion of each presentation. Each attendee also received four CPE credits from the National Forensic Science Technology Center for the two-day workshop.

FMBIO is a registered trademark of and StarCall is a trademark of Hitachi Software Engineering Company, Ltd.

## *Upcoming Meetings*

### **SOUTHWESTERN WORKING GROUP ON DNA ANALYSIS METHODS (SWGDM)**

May 27-29, 1998

Austin, Texas

Contact: John Krebsbach  
(505) 768 2230

### **SOUTHERN ASSOCIATION OF FORENSIC SCIENCES**

September 3-7, 1998

Port Canaveral, Florida

Contact: Michelle Shepherd  
(404) 244 2827

### **MIDWESTERN ASSOCIATION OF FORENSIC SCIENTISTS**

October 5-9, 1998

Ann Arbor, Michigan

Contact: Dorothy Martus  
(248) 380 1000

### **9th INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION**

Symposium  
October 7-10, 1998

Workshops

October 5

“Basics of PCR and DNA Typing”

October 6

“Expert Witness Testimony”

Orlando, Florida

Contact: Carol Zabit  
(608) 277 2670

# STR Information on the Internet

By Kimberly A. Huston  
e-mail [genetics@promega.com](mailto:genetics@promega.com)

With the advent of the Internet, many useful sites are available at the touch of a button. This medium contains a wealth of information that may be updated regularly, so that accurate, current data may be accessed at any point in time. In this article, I will highlight some Internet sites that may be of interest to the DNA typing community.

**Q: What is on the Promega Internet site?**

**A:** The Promega Internet site is a helpful tool that may be used to access various resources that provide valuable information to those involved in DNA typing. The address for the Promega Home Page is [www.promega.com](http://www.promega.com) (Figure 1). From this page, many different areas of the web site may be accessed. The Genetic Identity page

can be reached from a link on the Promega Home Page, or directly at the following address: [www.promega.com/geneticidentity/](http://www.promega.com/geneticidentity/). On the Genetic Identity page are listings of new products; Meetings, Tradeshows and Workshops; Customized *GenePrint*<sup>™</sup> System Protocols; current and past issues of *Profiles in DNA*; *GenePrint*<sup>™</sup> Product Information; Symposia Proceedings; and contact information.

To view the new product information, simply click on the hypertext link. This link will open a page containing product description and catalog information.

The Meetings, Tradeshows and Workshops section provides links to information on upcoming events in the DNA typing community. Currently, information on the Second European Symposium on Human Identification is available. This link contains

information on registration as well as a schedule and speaker update.

Customized *GenePrint*<sup>™</sup> System Protocols also may be accessed from the Genetic Identity page. Customized *GenePrint*<sup>™</sup> Protocols are designed for each user's specific needs, based on their choice of *GenePrint*<sup>™</sup> System and detection method. See page 14 of this issue for further information on the Customized Protocols. These protocols may also be accessed via the Technical Resource Center button, found at the top of each screen.

Issues of *Profiles in DNA* are accessed easily through the link on the Genetic Identity page or directly from [www.promega.com/profiles/](http://www.promega.com/profiles/). On the *Profiles in DNA* page, any article from a past issue may be retrieved. A subscription to the postal mailing of *Profiles in DNA* may also be requested at this site.

Product descriptions for all of the *GenePrint*<sup>™</sup> DNA typing products are available by selecting *GenePrint*<sup>™</sup> Product Information. To send an e-mail message directly to the Genetic Identity team, select the "Talk to Genetic Identity" link on the Genetic Identity page.

The Technical Resource Center of the Promega Internet Site contains a number of valuable links to Promega publications, technical literature and product bibliographies, as well as general technical information. The address for this page is [www.promega.com/techserv/](http://www.promega.com/techserv/). All of the *GenePrint*<sup>™</sup> Customized Protocols, *Profiles in DNA* issues and Technical Manuals are accessible from this site as well as from the Genetic Identity site. In addition, a list of interesting Internet sites can be found under the BioLink hypertext in the upper right hand portion of the page. The address for the BioLink page is [www.promega.com/biolink/](http://www.promega.com/biolink/).



Figure 1. The Promega Home Page.

The BioLink Resources for the Life Scientist are comprised of seven areas. These are Life Science Databases, Suppliers of Reagents and Equipment, Molecular Biology Servers, Information Resources, Organism-Specific Information, Societies, Institutions, and Government Agencies, and Journals. The Life Science Databases section contains several links including those to the GenBank® sequence database under the NCBI site, and the MEDLINE® database under the Entrez™ Site.

**Q: Are there any sites that will tell me the chromosomal location of short tandem repeat (STR) regions?**

A: There are many useful sites for determining chromosomal location of STR regions. The first is the Cooperative Human Linkage Center (CHLC), located at [www.chlc.org](http://www.chlc.org) and linked from the BioLink Resources page of the Promega site. This site is a useful source for genetic maps of PCR-formatted microsatellite markers. Genetic maps of each chromosome are listed with the positions of these markers. Searching for information about specific microsatellite markers using the CHLC Marker Maps prompt is quite easy. Information retrieved on specific markers includes other names that have been used for that marker, and the chromosomal location in recombination fractions and Kosambi centimorgans (cM).

STRBase, a web site sponsored by the National Institute of Standards and Technology (NIST), also contains a list of chromosomal locations for STR loci. The address for this site is [ibm4.carb.nist.gov:8800/dna/home.htm](http://ibm4.carb.nist.gov:8800/dna/home.htm) (see next question).

All of the above sites give GenBank® accession numbers, which allow GenBank® records to be retrieved from the Internet. The address for the GenBank® site is [www2.ncbi.nlm.nih.gov/cgi-bin/genbank](http://www2.ncbi.nlm.nih.gov/cgi-bin/genbank).

**Q: Are there any web sites that are specifically devoted to Short Tandem Repeats (STRs)?**

A: STRBase is a very useful database that contains sequence information on commonly used STR systems, population data, PCR primers and conditions and a technology review for STR analysis. This site can be accessed at [ibm4.carb.nist.gov:8800/dna/home.htm](http://ibm4.carb.nist.gov:8800/dna/home.htm) or from Promega's BioLink page. This site also contains background information on STR loci and a list of references supporting each locus. More information on this site can be found in reference 1.

**Q: Are there any journals that have sites on the Internet?**

A: Many journals have Internet sites. The *American Journal of Human Genetics* site, which can be found at [www.faseb.org/genetics/ashg/jou-ashg.htm](http://www.faseb.org/genetics/ashg/jou-ashg.htm), contains recent full text issues that are searchable. *BioTechniques* is available at [www.biotechniques.com](http://www.biotechniques.com). Although this site does not contain a current issue to peruse, articles may be found using a keyword search. The Internet site for the *Proceedings of the National Academy of Sciences* allows access to full text articles for current subscribers. The address for that site is [www.pnas.org](http://www.pnas.org). Abstracts and Tables of Contents are available for *Human Molecular Genetics* and *Nucleic Acids Research*. Full text articles for these journals are offered only to those individuals who have a current subscription to the journal. The address for *Human Molecular Genetics* is [www.oup.co.uk/hmg/](http://www.oup.co.uk/hmg/), and the address for *Nucleic Acids Research* is [www.oup.co.uk/nar/](http://www.oup.co.uk/nar/). *Nature Genetics*, located at [www.genetics.nature.com](http://www.genetics.nature.com), only contains abstracts for current articles.

**Q: What are the web addresses of some other organizations that are involved with DNA typing?**

A: The Internet addresses for the American Academy of Forensic Sciences and the American Association of Blood Banking are [www.aafs.org](http://www.aafs.org) and [www.aabb.org](http://www.aabb.org), respectively. The European DNA Profiling Group (EDNAP) has an Internet site at [www.uni-mainz.de/FB/Medizin/Rechtsmedizin/ednap/ednap.htm](http://www.uni-mainz.de/FB/Medizin/Rechtsmedizin/ednap/ednap.htm). The Federal Bureau of Investigation site can be found at [www.fbi.gov](http://www.fbi.gov), and the Forensic Science Service Internet site is [www.fss.org.uk](http://www.fss.org.uk). The Internet address of the Perkin-Elmer Genetic Analysis site is [www2.perkin-elmer.com/ga/index.htm](http://www2.perkin-elmer.com/ga/index.htm).

**Q: What other general resource sites are available?**

A: Carpenter's Forensic Science Resources site, located at [www.tncrimlaw.com/forensic/](http://www.tncrimlaw.com/forensic/), is an interesting source of information on forensic science-related issues. Under Forensic DNA Analysis, a basic discussion of DNA is listed, along with links to forensic and general DNA-related sites.

A vast amount of information is available on the Internet; this is only a sample listing of the Internet sites that may be useful to the DNA typing community. The Internet is readily accessible and is a valuable tool for staying informed of current developments in and related to the field of forensic DNA typing.

REFERENCE

1. Butler, J.M. and Reeder, D.J. (1997) STRBase: a short tandem repeat DNA database. *Profiles in DNA* 1(2), 8.

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Entrez is a trademark of and MEDLINE is a registered trademark of the National Library of Medicine. GenBank is a registered trademark of the U.S. Department of Health and Human Services.

# GenePrint™ Custom Protocols

By Isobel Maciver, James Lloyd,  
Julie Pederson, Ann Lins and Kimberly A. Huston  
Promega Corporation  
e-mail [genetics@promega.com](mailto:genetics@promega.com)

## INTRODUCTION

The "Technical Tips" article in this issue of *Profiles in DNA* focuses on using the Internet to obtain information on various topics pertinent to genetic identity testing. One of the sites featured is the Promega website ([www.promega.com](http://www.promega.com) or [www.euro.promega.com](http://www.euro.promega.com)), where up-to-date information on GenePrint™ products, meetings, training and symposium proceedings are available. Recent additions to this site include Custom Protocols for the use of GenePrint™ STR Systems.

These protocols are provided in a format that allows the user to key in information such as the STR system, detection instrument, enzyme and thermal cycler used. The program then generates a specific protocol for each system based on the chosen parameters.

The GenePrint™ Systems have been developed in multiple formats, allowing the user to choose a system that will perform well with their preferred detection method and instrumentation. Currently available GenePrint™ STR Systems can be classified into three groups based on the complexity of the system and the method used for detection of amplified fragments. Selected examples from each of these groups are shown in Figure 1.

The first group comprises the GenePrint™ PowerPlex™ System (Figure 1, Panel A). This system contains eight loci that can be amplified in a single reaction. Four of the loci (D16S539, D7S820, D13S317 and D5S818) are labeled with fluorescein and the other four (CSF1PO, TPOX, TH01 and vWA) are labeled with carboxy-tetramethylrhodamine (TMR). The PowerPlex™ 1.1 System may be detected using the Hitachi FMBIO® Fluorescent Scanner.

The second group comprises the GenePrint™ Fluorescent STR Systems. These quadriplex systems each contain four loci that are labeled with fluorescein. The three currently available quadriplex systems are the CTTv Multiplex (CSF1PO, TPOX, TH01 and vWA), the GammaSTR™ Multiplex (D16S539, D7S820, D13S317 and D5S818) (Figure 1, Panel B) and the FFFL Multiplex (F13A01, FESFPS, F13B and LPL). The amplification products of these systems can be detected using the Hitachi FMBIO® Fluorescent Scanner, the ABI PRISM™ 310 Genetic Analyzer, the ABI PRISM™ 377 and ABI 373 DNA Sequencers and the Molecular Dynamics FluorImager™ Fluorescent Scanner.

The third group, the GenePrint™ STR Systems, are designed for silver stain detection. These are the CTT Multiplex (CSF1PO, TPOX and TH01) (Figure 1, Panel C), the FFv Multiplex (F13A01, FESFPS and vWA) and the SilverSTR™ III Multiplex (D16S539, D7S820 and D13S317). The nine loci available in the silver multiplex detection format offer significant discriminating power to laboratories with lower cost, lower throughput needs.

The development of both silver stain and fluorescent detection methods for the same set of loci allows each user the flexibility to choose the detection method best suited to his/her throughput needs and budget. Each GenePrint™ System contains the appropriate 10X Primer Pairs, STR 10X Buffer, loading solution, the appropriate allelic ladders, K562 DNA (positive control) and a detailed Technical Manual.

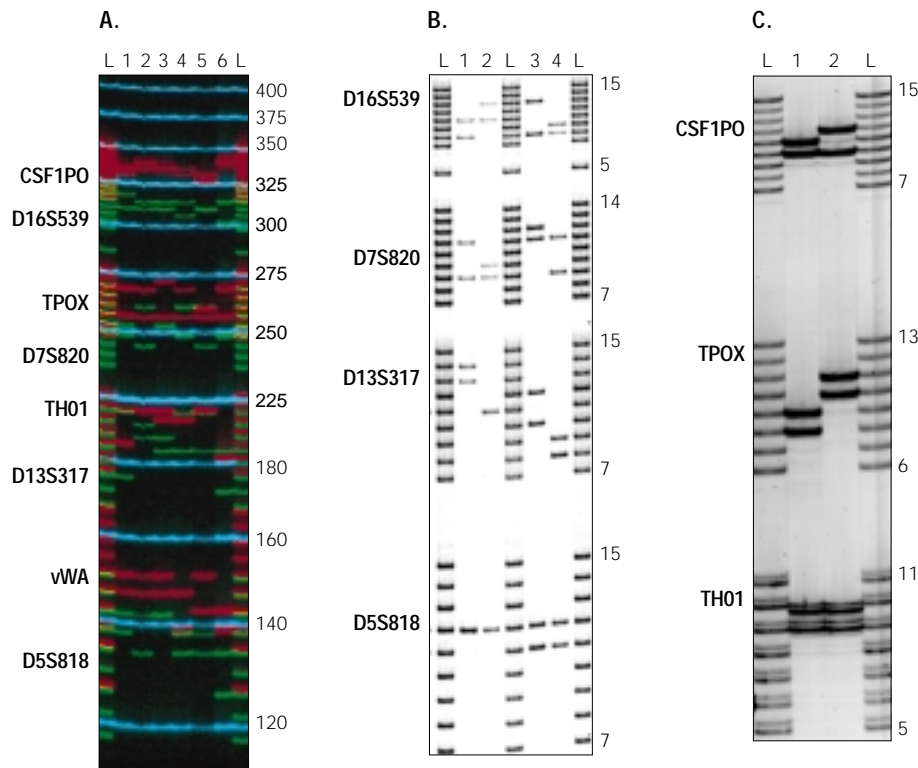
## TECHNICAL MANUALS

Extensive instructions for use of the GenePrint™ Systems are given in the Technical Manuals provided with each product. These are the GenePrint™ STR Systems (*Silver Stain Detection*) Technical Manual #TMD004, the GenePrint™ Fluorescent STR Systems Technical Manual #TMD006, and the GenePrint™ PowerPlex™ 1.1 System Technical Manual #TMD008. These

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*On the Internet a dynamic protocol  
that is designed to be specific to a  
single user's need is created.*

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**Figure 1. Representative GenePrint™ STR Systems.** **Panel A:** STR analyses performed using the GenePrint™ PowerPlex™ 1.1 System. The amplified products of the four fluorescein-labeled loci (D16S539, D7S820, D13S317 and D5S818) are shown in green, while the four TMR-labeled loci (CSF1PO, TPOX, TH01 and vWA) are shown in red. The products of six amplification reactions (lanes 1-6) were separated on a 4% polyacrylamide denaturing gel and detected using the Hitachi FMBIO® II Fluorescent Scanner. An additional size marker, the Fluorescent Ladder (CXR) is shown in blue. Allelic ladders for the corresponding loci are shown in the lanes labeled L. **Panel B:** STR analyses performed using the GammaSTR™ Fluorescent Multiplex System (D16S539, D7S820, D13S317 and D5S818). Four DNA samples (lanes 1-4) were amplified, separated on a 4% polyacrylamide denaturing gel and detected using the Hitachi FMBIO® II Fluorescent Scanner. Allelic ladders for the corresponding loci are shown in the lanes labeled L. **Panel C:** STR analyses performed using the GenePrint™ STR System-CTT (CSF1PO, TPOX, TH01). Two DNA samples (lanes 1-2) were amplified, separated on a 4% polyacrylamide denaturing gel and detected by silver staining. Allelic ladders for the corresponding loci are shown in the lanes labeled L. In Panels B and C, the number of repeats for the largest and smallest alleles are noted to the right of the gels.

manuals are also available on the Internet at [www.promega.com/tbs/](http://www.promega.com/tbs/). Each technical manual contains extensive information on the STRs used in each system, detailed DNA extraction methods, protocols for DNA amplification and detection, representative data, extensive reference listings, and population data for all of the alleles in each system.

**CUSTOM PROTOCOLS**

The custom protocols available on the Internet are designed as a supplement to the Technical Manuals, and are not intended as a substitute for them. For background information, information on DNA extraction, references, population data and detailed explanation of terms, please refer to the manual specific for the system used. Each manual provides information on the use of several different GenePrint™ Systems and provides a number of options for DNA amplification and detection for each system. These protocol options vary depending on the user's choice of system, enzyme, thermal cycler and detection instrumentation. On the Internet a dynamic protocol that is designed to be specific to a single user's need is created. These custom protocols ask a series of questions of the user, then gather the corresponding usage

information relevant to these requirements from the larger Technical Manual and distill it into a protocol that is tailored specifically to the needs of a single user.

Custom protocols are provided for the PowerPlex™ 1.1 System, for all of the GenePrint™ Fluorescent STR Systems and for the GenePrint™ STR Systems for silver stain detection. The user selects their choice of enzyme (AmpliQa® or AmpliQa Gold™ DNA polymerase), thermal cycler (Perkin-Elmer 480 or the GeneAmp® PCR System 9600), GenePrint™ System and detection method. Protocols also offer the option of including or excluding BSA from the amplification reaction and including the Fluorescent Ladder (CXR) as a size marker with the fluorescent systems.

After the user selects choices from a series of pull-down menus, the program generates a unique set of usage instructions based on these parameters. These instructions include a list of the loci in the system of choice, a complete protocol for setting up amplification reactions and a thermal cycler program. They also include the appropriate protocols for electrophoresis and detection on the instrument of choice.

We hope that users will find the speed and convenience of obtaining custom-designed protocols through this website to be of value. Historically, GenePrint™ products have always been provided as systems customized for multiple instrument platforms and detection formats. We are now expanding this approach and are beginning to use the Internet as a means to provide protocol information in a way that is tailored to meet the needs of each individual user. The custom protocols are a pilot project in this area. Please visit the web site at [www.promega.com/geneticidentity/](http://www.promega.com/geneticidentity/) and let us know what you think.

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*Career Opportunity*

**Promega Corporation** has a position available for a **Senior Scientist** on our Genetic Identity team. We seek an experienced scientist to assist with program development as well as product research and development in the areas of nucleic acid purification, amplification, fluorescent detection and automation of these processes.

Requirements include: a Ph.D. in Molecular Biology, Molecular Genetics, or a related area, and at least three years of industrial, clinical or forensic research and development experience with demonstrated success in leading projects; experience with nucleic acid analysis (i.e., purification, amplification, detection, automated formats); a demonstrated record of collaboration; ability to design and interpret scientific experiments and to work independently or as part of a team; expertise with computer-based analyses; and excellent oral presentation and writing skills in English.

*Career Opportunity*

**Promega Corporation** has two positions available on our Genetic Identity team: **European and United States Regional Technical Specialists.**

The successful applicants will help Promega achieve sales goals for the Genetic Identity product line within the designated regions by developing and maintaining relationships with Genetic Identity market leaders and implementing the sales and marketing plan for the region.

The successful applicants will maintain relationships with key contacts within the industry, including forensic and paternity laboratories, implement sales and marketing strategies, work with Promega's European branches and distributors to provide technical assistance to customers and represent Promega at various technical and sales functions, including tradeshows and symposia.

Qualifications include a broad-based technical background in molecular biology techniques, and DNA typing laboratory experience. A scientific degree in molecular biology, forensic science or equivalent required; advanced scientific degrees preferred. Extensive experience performing DNA typing protocols is required. English language skills (fluency), both written and spoken, required; multiple languages preferred. Regular travel is required up to 50% of the time.

**For confidential consideration**, please submit your CV electronically to [hr@promega.com](mailto:hr@promega.com) or to 2800 Woods Hollow Rd., Madison, WI 53711. Please indicate the position and the territory in which you are interested. For more information on other opportunities at Promega, please visit our website at [www.promega.com/hr](http://www.promega.com/hr).

**Equal Opportunity Employer**

## Workshop

**October 5**

"Basics of PCR and DNA Typing"

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# 9<sup>th</sup> International Symposium on Human Identification

Coronado Springs Resort, Orlando, Florida  
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## Workshop

**October 6**

"Expert Witness  
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