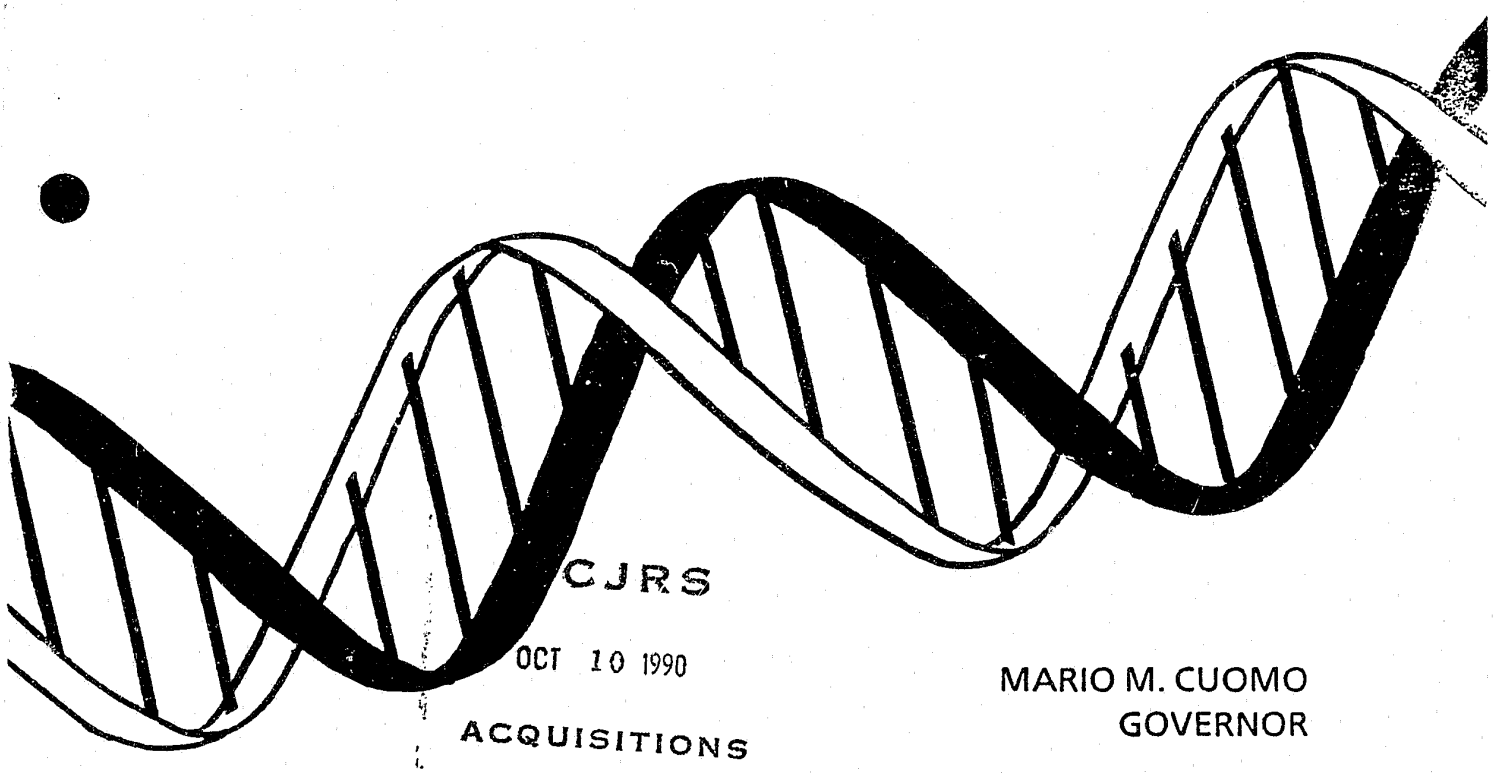
DNA

Report of New York State Forensic DNA Analysis Panel

September 6, 1989



MARIO M. CUOMO
GOVERNOR

JOHN J. POKLEMBA
DIRECTOR OF CRIMINAL JUSTICE
AND COMMISSIONER

EXECUTIVE SUMMARY

Recent advances in molecular biology have revolutionized the potential forensic applications of DNA, the basic genetic material contained in every cell in the human body. Rather than using literal fingerprints to establish identity, DNA can be used to identify a criminal -- or clear an innocent suspect -- based on a few drops of blood or semen, or roots of hair. It is this capacity to individualize, to focus in on one suspect to the exclusion of all others, that makes DNA so important to the criminal justice system.

The forensic utilization of DNA analysis technology requires that biochemical procedures originally developed for genetic research, clinical diagnosis and paternity studies be applied to criminal evidence. The transfer of a technology developed in a research laboratory to a forensic setting can be a complicated and time-consuming process. There are many hurdles that must be overcome, and many questions that must be answered. The power of this technology makes abuse a serious concern.

Rather than urging that New York rush headlong into the use of forensic DNA testing without first considering the possible pitfalls, John J. Poklemba, the State Director of Criminal Justice and Commissioner of the Division of Criminal Justice Services, formed the Forensic DNA Analysis Panel in July 1988. The Panel, which is made up of prosecutors and defense attorneys,

forensic and research scientists, policy makers, legal scholars, and law enforcement experts, was asked to undertake a broad-based study of all of the complex issues associated with forensic DNA testing.

The report examines the scientific, legal and policy considerations inherent in the forensic applications of DNA technology. The scientific issues discussed include the limits of traditional identification techniques, the procedures and assumptions underlying DNA testing, the problems associated with existing technologies and population studies, and the concerns over quality control and subjective assessments. The legal issues section of the report overviews court rulings throughout the country on the admissibility of forensic DNA evidence and discusses the different standards that should be applied when DNA testing results are introduced as evidence for exclusion purposes compared to when they are introduced for inclusion purposes. The discussion in the policy issues section centers on the concerns raised by the testing procedures currently used by the private and public laboratories performing DNA analysis.

At the heart of the Panel's recommendation is a model program for implementing forensic DNA analysis technology in New York State. The Panel recommends the creation of a Statewide DNA network, served ultimately by at least three regional forensic DNA analysis laboratories. The DNA analysis network would

coordinate quality assurance, quality control and safety for the laboratories in the network. An accreditation process would be developed to monitor public and private laboratories providing forensic DNA analysis services throughout the State.

A systematic method is needed to ensure that DNA technology is applied only in appropriate circumstances following established, scientifically-accepted principles. An Advisory Committee, representing the law enforcement, scientific, legal and judicial communities, should oversee the operation of the network. The Advisory Committee would establish uniform standards for determining the types of evidence and documentation appropriate for forensic DNA analysis.

The Panel also recommends the creation of a Scientific Review Board, distinct from the Advisory Committee, to assist courts in evaluating the technologies used in a given case. The Scientific Review Board would examine the scientific standing and accuracy of a test for DNA typing; if asked, its members would act as expert and impartial advisers to the courts. While the Scientific Review Board's conclusions could be challenged, it would nevertheless assist judges faced with the difficulties of determining the scientific validity of a particular DNA test.

The creation of a DNA databank to assist law enforcement officials in solving crimes raises many complex issues. Substantial privacy concerns must be overcome before a DNA databank should be established. The Panel recommends that, if

these privacy concerns are scrupulously satisfied through legislation and regulation, legislation should be enacted mandating that all persons convicted of violent sex crimes or other designated offenses be required to give specimens of their DNA to an authorized agency. To implement the databank, New York State should begin the preliminary developmental work needed to overcome the many technical problems inherent in building a computerized DNA databank.

DNA fingerprinting captures the imagination. It is new science in the making, one with untold potential for criminal justice. Yet, without careful planning its promise may be lost and the technique discredited. The report issued today is designed to assist policy makers and jurists as they chart a course for the future of forensic DNA analysis in New York State.

TABLE OF CONTENTS

INTRODUCTION

Recent advances in molecular biology have revolutionized the potential forensic applications of DNA, the basic genetic material contained in every cell in the human body. Rather than using literal fingerprints to establish identity, DNA can be used to identify a criminal -- or clear an innocent suspect -- based on a few drops of blood or semen, or roots of hair.

While other forensic techniques can be used to exclude a suspect or indicate the likelihood of a suspect's involvement in a crime, DNA analysis can be used to indicate that a particular suspect was indeed present at a particular crime scene. It is this capacity to individualize, to focus in on one suspect to the exclusion of all others, that makes DNA so important to the criminal justice system.

DNA analysis was originally developed for genetic research, clinical diagnosis and paternity studies. Scientists working in these areas can apply DNA technology under readily controllable conditions to fresh, hygienic, and ample blood samples. Unlike samples used in traditional laboratory research, samples taken from crime scenes are usually of limited quantity and are frequently mixed with foreign substances, such as dirt and other contaminants. The transfer of a technology developed in a research laboratory setting to a forensic setting can be a complicated and time-consuming process, and there are many hurdles that must be overcome.

It is critical that DNA typing techniques used in forensic tests meet appropriate scientific standards. It is also imperative that careful attention be paid to the special legal issues that surround the application of DNA technology to the criminal justice forum, where questions of admissibility of evidence are far more complex than in civil cases where DNA evidence was first introduced.

The New York State Crime Laboratory Advisory Committee and experts from a variety of disciplines have expressed concern that the exciting promise of DNA to positively identify a criminal could be compromised by lack of planning, failure to develop standards and precipitous action. The attention focused on DNA technology by the media, academic, scientific and policy making communities has continued unabated since it was first introduced into evidence in a criminal trial in Florida in 1987. Unless proper safeguards are instituted, this attention, combined with a lack of appreciation for the complexity of the technology, could severely impede full and proper implementation of this scientific advance.

The rapid, increasing involvement of DNA in criminal cases signals that the time has come to ask some hard questions about the appropriate forensic use of the technology.

What are the limits of DNA for the criminal justice system? Should there be a uniform system of minimum statewide or national standards? Should there be mandatory accreditation of public and private laboratories? What are the fiscal implications? The

philosophical questions? What are the legal issues? What about law enforcement training? Should New York State establish a computerized genetic database?

These are the questions that led John J. Poklemba, the New York State Director of Criminal Justice and Commissioner of the Division of Criminal Justice Services, to convene a panel to develop a systematic, broad-based approach to the forensic application of DNA technology. Commissioner Poklemba formed the Forensic DNA Analysis Panel in August 1988 to study these questions and to recommend a model for coordinating the statewide use of the technology.

Because of the broad spectrum of issues involved in the forensic application of DNA technology, Commissioner Poklemba invited experts from a variety of fields to serve on the Panel. The Panel's Chairman is Dr. Howard Harris, the Director of the Monroe County Public Safety Laboratory. Panel members include prosecutors and defense attorneys, forensic and research scientists, policy makers, legal scholars, law enforcement experts and a jurist. The names and professional affiliations of the Panel members are presented in Appendix I of this report.

Although the Panel members have differing perspectives on the criminal justice system, we are unanimous in our underlying recommendation: New York State should begin at once to cautiously implement a model program for forensic DNA analysis testing.

This report begins with a discussion of the major scientific, legal and policy issues surrounding the forensic application of DNA analysis techniques. It concludes by recommending a model program, complete with regional laboratories and statewide standards, for the application of forensic DNA testing procedures. The Panel hopes that its report will be of assistance to policy makers as they seek to chart a course for the future of forensic DNA analysis.

I. SCIENTIFIC CONSIDERATIONS

Limits of Traditional Techniques

The importance of the science of serology, which is the study of biological fluids, in law enforcement has grown significantly in the last few decades. Originally serological techniques were used primarily to distinguish blood stains from other dark-colored stains. As the science developed, forensic serologists were able to classify stains according to the ABO blood typing system,[1] thereby adding a much-needed degree of specificity to the identification process.

The ABO blood typing system has a low differentiating power, however. There are only four different blood types in the ABO system, and over 80 percent of the population is type A or type O. Consequently, a finding that an evidentiary stain is type A, for example, and that the suspect is also type A has limited value for identification purposes since about 40 percent of the population is type A. As a result of the inability to match an evidentiary stain to one specific individual, some courts in New York State have excluded testimony on ABO typing. Nevertheless, while the blood typing system is of limited value for inclusory purposes, its exclusionary value is extraordinarily important.

---

[1] The ABO blood typing system is the basic system of typing antigens of human blood. There are four ABO blood groups - A, B, AB, and O.

By the 1970s, forensic serologists had made great strides in their ability to narrow the potential population from which a sample could have originated. Developments in the application of enzyme analysis[2] allowed blood samples to be classified with greater specificity. Several enzymes occur in the blood in different forms, or isozymes, and testing procedures have been developed to allow scientists to use population data bases to determine the proportion of persons with certain isozymes in their blood. By using both ABO blood typing procedures and enzyme analysis, scientists can reduce the range of persons from whom a blood sample could have been derived. If either the blood type or the form of any enzyme found in the evidentiary stain differ from those found in the blood samples obtained from victims or suspects, there is no match. If the evidentiary stain and the blood sample match in all respects, scientists consult population statistics to determine the probability that the match could arise randomly in the general population.

Enzyme analysis is a major improvement over simple ABO blood typing, yet serious problems exist with the reliability of this technique for forensic purposes. The technique is reliable only with fairly clean, dried blood stains of reasonable size that have been preserved promptly. In the majority of forensic cases, these conditions are not met. Enzymes are fragile and often degrade under crime scene conditions.

---

[2] Enzymes are complex proteins that are produced by living cells and catalyze specific biochemical reactions.

Most of the enzymes used in characterizing blood are not present in sufficient amounts for forensic analysis in semen or other body fluids. In sexual assault cases, obtaining useful enzyme data from semen stains is the exception rather than the rule. Legal controversy about the reliability of widely used methods for enzyme analysis has reduced the utility of the technique in some jurisdictions.

While its ability to discriminate between individuals is vastly superior to the ABO blood typing system, enzyme analysis cannot pinpoint with specificity the source of a blood stain. Rather, where a match is found, the technique can generally demonstrate that the probability of the match occurring by chance is 1 out of 100; in the rare case, it may be possible to demonstrate a 1 out of 50,000 probability of a random match. Such limited degrees of certainty should be insufficient in the criminal justice context.

Another blood typing technique, the HLA white blood typing system[3], is widely used for paternity testing. Unfortunately, this typing system requires fresh liquid blood samples; it is not useful with dried blood stains.

Unlike scientists who analyze fresh blood stains, forensic scientists, who must work with dried evidentiary stains, have long been frustrated by their inability to demonstrate conclusively that an evidentiary stain came from a particular

---

[3] The human leukocyte antigen (HLA) typing system types red-cell enzymes and serum proteins.

individual. Thus, while the potential for forensic serology to aid in the analysis of samples taken from scenes of violent crimes is great, it has often failed to achieve useful results. Crime laboratories have devoted an ever increasing share of scarce resources to forensic serology, and although they have seen improvements, no major breakthrough in their ability to make unambiguous identifications based on dried body fluid was possible until the arrival of forensic DNA analysis techniques.

Emergence of Forensic DNA Analysis Techniques

The era of molecular genetics that led to the development of forensic DNA typing began with a publication in 1953 by Drs. J.D. Watson and F. Crick of a structure for deoxyribonucleic acid (DNA). The identification of this structure - the double helix - immediately led to extraordinarily rapid advances in understanding the genetics of bacteria and viruses.

The application of knowledge derived from molecular genetics to human beings was much slower and had to await the development of recombinant DNA techniques[4] in the early 1970s. The ability to clone human genes resulted in a revolution in human genetics. Forensic DNA typing is a derivative of methods and procedures developed for the analysis of human inherited disorders.

The primary impetus for forensic DNA applications originated with the success of a major criminal investigation in England in

---

[4] Recombinant DNA techniques use DNA molecules that have been assembled with the use of restriction enzymes; this frequently involves splicing together fragments from different species.

1987 and with the use of DNA typing to identify family members in immigration cases. Since then, there has been an intensive effort by private laboratories and governmental agencies to implement these techniques in the United States.

Forensic applications of the technology are markedly different than the medical applications from which they were derived. In medical genetics, it may be possible to identify the exact mutation in a gene and examine an individual for that precise mutation. The more common medical application, however, is to use DNA markers to follow the inheritance of a mutation within a family. Family members are analyzed, and the results provide internal controls and checks on the performance of the analysis. Unlike the medical setting, in forensics a single evidentiary sample is compared with a single sample from one or more suspects, and there is no opportunity for detecting inconsistencies in the analysis.

DNA typing does not analyze all of the DNA of an individual; rather DNA at a limited number of small sites is analyzed. The information obtained from any one site is limited in terms of unique identification, and the power of DNA typing comes from combining the results from tests of four or five separate DNA regions.

The process of DNA analysis begins when biological material is chemically treated to extract the DNA. The DNA is then cut into small fragments by restriction endonucleases, which are enzymes that recognize and cleave at specific sequences in DNA.

Fragments from different samples are placed in adjacent lanes on an agarose gel and separated on the basis of their size by the process of electrophoresis.[5] The DNA pattern in the gel is then transferred to a membrane using a technique known as Southern Blotting, following which a radioactive DNA probe[6] is applied to detect a specific sequence in a DNA fragment bound to the membrane. Thereafter, X-ray film is used to locate the positions of probe bindings on the membrane; once the X-ray film is developed, it is known as an autoradiograph[7] and a visible pattern of bands is produced. This pattern corresponds to places where the probe binds to the DNA fragments on the membrane. Genetic differences among individuals are reflected in the molecular weights (sizes) of these fragments, and these differences will affect the positions of the bands on the gel.

If a highly polymorphic genetic system[8] is chosen such that most individuals within a population have differently sized

---

[5] Electrophoresis describes the movement of charged molecules or particles through a fluid or gel under the action of an electromotive force applied through electrodes in contact with the gel.

[6] A probe is a small fragment of DNA of known sequence that has been tagged with some tracer substance (a radioactive isotope or specific dye-absorbing compound). It is used to locate and identify the complementary sequence of a DNA fragment on a membrane or region of a chromosome.

[7] Autoradiography is a technique for detecting radioactively labeled molecules in a cell or tissue. An autoradiograph is an image on photographic film.

[8] Polymorphic systems are ones that contain variant forms of a specific gene that occur simultaneously in a population.

bands, then two individuals can easily be distinguished by performing these techniques. If all the bands match precisely using such a system, it can be said with near certainty that the different samples being tested came from the same person, or from identical twins.

It is clear that a revolution in criminal justice is imminent if DNA typing proves acceptable in criminal courts. Personal identifications have always been a major concern of law enforcement, and eyewitness testimony can be unreliable and subject to abuse. With the advent of forensic DNA typing, biological materials found at crime scenes take on unprecedented significance for identification purposes. Individuals erroneously accused of crimes could be cleared of suspicion; alternately, defenses could be rebutted. If DNA testing gains widespread acceptance, it could substantially alter the nature of plea negotiations, with prosecutors less likely to make relatively lenient offers to defendants and defendants less likely to challenge the allegations made against them. Moreover, the number of unsolved crimes might be significantly reduced if a national computerized databank of DNA typing information were created.

Basic Assumptions Underlying DNA Typing

Certain features of the principles and techniques of DNA typing are critical to understanding the task involved in introducing DNA typing into forensic science and the legal system.

The first basic assumption concerns the uniqueness of each individual's DNA. The genetic code carried by the DNA, which is wrapped up in the chromosomes of almost every type of cell in the body, determines, along with environmental influences, everything that makes each of us unique. That is, although we all have DNA molecules, and although these molecules in each of us code for the same proteins, there are subtle differences between everyone's DNA (except that of identical twins). These differences at the DNA level mirror the differences at the protein level that forensic scientists already exploit through enzyme analysis techniques. The uniqueness assumption is fully accepted in the scientific community.

A second basic assumption fully accepted by experts in the fields of population genetics and human molecular genetics concerns the validity of the theories underlying DNA typing. Scientists agree that DNA samples from different individuals can be distinguished from one another by examining polymorphisms at the DNA level, provided that the correct population studies have been performed. As with the first assumption, this is analogous to the examination of protein polymorphisms by forensic scientists, but it is more useful because DNA polymorphisms are more highly variable. The use of DNA polymorphisms has been fully validated in medical genetics, although in that field analyses are done by analyzing DNA samples within families rather than by comparing known and unknown samples, as in forensic applications. Nevertheless, the principles are fully accepted.

The third basic assumption is that the laboratory procedures used to perform the various steps in DNA typing are capable of doing what is required. Thousands of molecular biologists and geneticists throughout the world perform the same types of laboratory procedures as do forensic scientists when they carry out DNA typing; Appendix II describes these procedures, which include restriction enzyme digests, agarose gel electrophoresis, Southern transfers, probe labelling, filter hybridizations and autoradiography. The theoretical reliability of all these techniques is fully accepted; however, their actual implementation in the laboratory is a different matter.

Implementation Problems

Differing Systems and Population Studies

While the scientific principles and practices underlying DNA typing are generally accepted in the scientific community, there are serious questions with forensic DNA testing as it is currently being practiced. An overview of these problems is presented below, and a fuller discussion is included in Appendix II.

Several polymorphic systems have been developed, and laboratories throughout the country use different systems. The assumption that DNA polymorphisms can distinguish among individuals is accepted, but it must be shown that each polymorphic system performs as claimed by its proponents. No consensus exists on which of the available systems is optimal, or even whether all of the systems are reliable for forensic

purposes. Further, it is inevitable that new polymorphism systems will be discovered.

It must be shown that each probe-enzyme combination used in the polymorphic system produces the claimed fragment sizes, and that population studies performed to determine the frequencies of these fragments in the general population are reliable. Approval of any one polymorphic system does not confer automatic approval of other systems; each must be assessed on its own merits.

Without knowledge of the frequencies of certain alleles,[9] as represented by DNA fragment sizes, in a population, it is impossible to calculate the likelihood that a match could arise simply by chance. Such knowledge is critical and depends on the integrity of the laboratory collecting the data. Population studies are time consuming and, in contrast with laboratory procedures, they are unlikely to be replicated. Furthermore, analysis of the basic data is not straight-forward, and no generally accepted procedure exists for carrying out these analyses.

Forensic Samples and Quality Control

The world-wide use of the techniques involved in DNA typing does not guarantee their correct implementation in forensic science. Certain methodological problems are unique to the forensic application of DNA technology. Foremost is the probable poor quality of the forensic DNA as compared with that used in

---

[9] An allele is one of several alternate forms of a gene occupying a given place on the chromosome.

medical genetics laboratories. Forensic samples are often affected by environmental factors such as heat, moisture and the activities of microorganisms contaminating the sample. Consequently, a large number of DNA samples are unusable because of degradation of the DNA. Furthermore, forensic samples of DNA may be too small to analyze, or too small to allow for repetition of the analysis. Forensic laboratories and their users must appreciate that not every test will produce data that can be interpreted reliably.

There are other methodological problems concerning quality control and assurance techniques that are common to all laboratories using DNA typing techniques. These problems are magnified in forensic and medical laboratories where the results of the analyses often have an immediate and pronounced effect on peoples' lives. It is absolutely essential that these problems be resolved and that the most stringent controls be implemented.

There are no widely accepted criteria for quality control or proficiency testing for forensic laboratories at a state or national level. Concern is mounting in the scientific community that the forensic laboratories performing DNA typing are not following all of the necessary and appropriate practices. If proper quality control procedures are not used, the reliability of the data produced is questionable. These concerns are discussed in greater detail in the section of this report on private and public laboratories.

Subjective Assessments

Despite the remarkable statistics that have been quoted in court cases, and the very impressive nature of DNA data as evidence, all stages of DNA analysis require some form of subjective assessments. Judgements must be made about whether a DNA sample is of adequate quality for testing; whether a restriction enzyme reaction is satisfactory; whether an autoradiograph is of sufficient quality to read and interpret; whether the most appropriate method is being used to compare samples. It is important that the legal and policy making communities resist being overwhelmed by the technicalities of DNA typing and remember that complexity does not guarantee infallibility.

II. LEGAL CONSIDERATIONS

Admitting DNA Evidence in Court

Under our legal system, juries have the inherent responsibility of deciding questions of fact. To assist juries in carrying out their duties, the criminal law permits opinion testimony from qualified experts as long as a proper foundation for the experts' testimony has been laid. Our adversarial system of justice gives the opposing parties equal opportunities to present expert testimony. Opponents are free to cross-examine and impeach proponents' experts, as well as to adduce different opinions through their own experts.

Opinion testimony from an expert is admissible where the conclusions to be drawn from the facts depend upon professional or scientific knowledge or skill not within the range of lay persons' experience or training. Judges preview the evidence to ensure its reliability before deciding whether it should be submitted to the jury.

When the facts from which the expert's conclusion is drawn are themselves the product of a scientific technique, the judge must first rule upon the reliability of the technique. The standard for admissibility, known as the Frye test,[Frye v. U.S., 293 F. 1013 (D.C.Cir. 1923)], has been applied in the courts of New York whenever the prosecution or defense seeks to introduce the results of a new scientific test.

In Frye, the Court of Appeals of the District of Columbia stated at page 1014: "Just when a scientific principle or

discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere, in the twilight zone the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs."

At a pre-trial Frye hearing, the court must determine whether the underlying scientific principles, technique and results are generally accepted as reliable within the appropriate scientific community.[10] Applying this standard to the admissibility of forensic DNA typing, the judge must decide whether the prosecution has met its burden of demonstrating that the laboratory technique, including protocols and scientific controls, for declaring a match and the methods used to calculate population probabilities are generally accepted as reliable by the relevant scientific communities. Even if these Frye requirements are met, before the judge can let the evidence go to the jury, the court must be satisfied that the testing laboratory actually used and properly followed the generally accepted methods in the particular case.

Courts in twenty-four states have admitted forensic DNA evidence at least once in criminal cases, with Florida leading

---

[10] People v. Hughes, 59 NY 2nd 523, 537 (Ct. of Appeals, 1983).

the other states, having admitted DNA forensic analysis evidence at least fifteen times to date.[11] At least thirty Frye hearings on the admissability of DNA evidence have been completed nationwide. With one exception, the trial courts have uniformly found that forensic DNA typing passes the Frye test.

There have been at least thirty Frye hearings conducted across the country. The first, and until recently the only, Frye hearing[12] to exclude DNA evidence was decided in California and involved the admissibility of a polymerase chain reaction DNA test,[13] the results of which excluded the defendant. Just three months earlier, the same test performed by the same laboratory passed Frye in a Texas court in which the evidence was a match and thus offered by the prosecution.

Three Frye hearings have thus far been conducted in New York. The first, a consolidated evidentiary hearing in two unrelated cases, People v. Wesley and People v. Bailey, 533 N.Y.S. 2d 643 (1988), upheld the prosecutor's motion to extract blood from defendant Bailey for the purpose of comparing his DNA

---

[11] The other states to admit DNA evidence are New York, Maryland, Virginia, Texas, Washington, Michigan, Oklahoma, South Carolina, Kansas, Ohio, Indiana, Alabama, Colorado, West Virginia, Mississippi, Wisconsin, North Carolina, Hawaii, Idaho, Georgia, Iowa, Missouri and Tennessee.

[12] People v. Martinez, Sup. Ct. No. A 709321 (L.A. Sup Ct. 1989).

[13] The Polymerase Chain Reaction test, known as PCR, is a technique for amplifying a selected portion of DNA. The test requires considerably less biological material than other DNA tests, and therefore may be useful on samples too small to produce an interpretable result by other techniques.

with DNA from an aborted fetus, and from defendant Wesley for the purpose of matching his DNA with DNA from his bloodstained clothes. Although this hearing was extensive, the Court did not have the benefit of reviewing autoradiographs to compare the underlying theories of the technology with actual test results.

In the second Frye hearing, People v. Lopez, (Sup. Ct. Queens Co. 1988), a case involving allegations of multiple rapes, the trial court allowed the introduction of DNA evidence. While the Lopez court had the benefit of the forensic autoradiographs, the hearing was limited in that the defense called no witnesses in opposition to the introduction of the DNA evidence.

On August 14, 1989, a ruling was issued in the third and by far the most thorough and informative New York State Frye hearing, People v. Castro, (Bronx Co. Ind. 1508/87). The court found that the genetic tests linking the murder suspect to the victim were flawed and, along with the calculation of allele frequencies, scientifically unreliable. The decision, which will likely be viewed as the first serious challenge to forensic DNA testing, was based on a 12-week pretrial hearing filled with extensive testimony by molecular biologists and genetic experts. Although the Castro court found most of the results unreliable in the instant case, it did not question the theories underlying DNA testing, nor did it dispute the ability of the technique to produce reliable results if proper procedures are followed.

Even before the court issued its ruling in Castro, the prosecution admitted that the DNA evidence in the case was not

sufficiently reliable to permit its introduction at trial as evidence of a match. This admission followed a statement by two prosecution experts who joined with defense experts in calling for a study by the National Academy of Sciences "to reach general scientific agreement about appropriate standards for the practice of forensic DNA typing." Further, the validity for forensic application of the key peer review article relied upon by the prosecution in the Wesley and Lopez decisions was seriously challenged when the article's peer reviewer testified in the Castro case. The peer reviewer testified, based on the evidence first revealed at the hearing, that had he known the actual method being used for declaring matches was contrary to the method asserted in the article and had he known that unsubmitted raw data did not support the authors' claims about population genetics, he would not have allowed those representations to remain in the article.

The courts that have applied the Frye standard have generally limited their inquiry to the general acceptance of DNA typing techniques without seriously considering the methodological differences between traditional DNA diagnostics and the forensic application of DNA typing. Most of the Frye hearings have not been vigorously contested by the defense. In many, the defense failed to call a single witness in opposition. This may be due to a perceived lack of scientific resources available in the judicial arena as well as an inability on the

part of many defense attorneys to adequately rise to the challenge of highly technical scientific evidence.

The first appellate decision on the admissibility of forensic DNA typing was Andrews v. Florida, 533 So.2d 841 (1988). Affirming the trial court's decision to admit the DNA evidence, the Florida intermediate appellate court relied on a different legal standard than Frye. In Andrews, as in Lopez, the defense called no witnesses in opposition. Only a few other appellate courts, none of which are in New York, have considered the issue.

Expert testimony is often given considerable weight by juries. When that testimony involves the results of DNA testing, the influence on the jury may be even more substantial than expert testimony on other scientific techniques. It is thus critical that courts have access to the best scientific thinking about forensic DNA techniques and their application in any given situation.

There are several forensic DNA methods currently being used by the few laboratories nationwide that offer forensic DNA analysis services. Although the competing methodologies have elements in common, substantial and significant differences exist in laboratory methods, scientific controls, and techniques for calculating population frequencies. Scientists disagree over the criteria for determining whether or not two samples match; the types and number of probes that should be examined; the control experiments required in forensic testing, where there is frequently no opportunity to repeat the experiment; the

population studies required; and the appropriate formulas for calculating probabilities. Thus, given the lack of consensus within the scientific community, it is likely that in deciding whether to admit DNA evidence, judges will be exposed to a host of differing views from expert witnesses.

In assessing the general acceptance and reliability of the methods used for declaring a DNA match and for calculating the probabilities of a random match, courts could consider the opinions of experts from several scientific fields. With respect to laboratory methods, the fields of molecular biology and genetics are most relevant. Due to the specific problems inherent in evidentiary stains as opposed to fresh blood, the opinions of criminalists and forensic experts could also be considered. On the issue of probabilities and population frequencies, experts in the fields of population genetics, mathematics and statistics can offer useful insights into the techniques that are, as well as those that are not, generally accepted as reliable.

There are many concerns with applying the technology in criminal cases. Forensic DNA typing techniques are new, with the DNA test entering the judicial arena in just the last two years. The history of science demonstrates that a lapse of several years may occur before the scientific community perceives methodological errors in any new scientific technique. The scientific methodologies involved in the forensic application of DNA analysis are evolving; techniques will no doubt change in the

future. It is thus critically important that the judiciary be provided with the most current and informed views on the subject.

Exclusion Versus Inclusion

DNA analysis offers great benefits to prosecutors: A declaration of a match between an evidentiary sample and the suspect's blood can solidify the State's case against the suspect. The benefits to the defense are equally strong: A declaration of a non-match can play a powerful role in exonerating a suspect.

The methodological problems with the currently marketed DNA techniques are particularly germane should they lead to a false inclusion, that is, a finding of a match when in fact no match exists. Many of the methodological problems that arise in determining an inclusion are not present, however, when the test results exclude a suspect. The finding that two samples do not match is considerably more conclusive than the finding of a match.

Concerns about the underlying population data used to calculate the probability of a match do not apply in exclusion. Testing procedures that are conclusive with respect to excluding a suspect are frequently inconclusive with respect to including or identifying a suspect. While inadequate population studies may make it impossible to distinguish one person's DNA from that of all other people, distinctions between a smaller number of people are possible, as has long been the case in simple ABO blood testing and other established identification techniques.

Put differently, a test used to establish identity (inclusion) must distinguish between everyone, whereas a test that yields a different response between two samples (exclusion) must simply be capable of distinguishing between two people.

The justification for treating exclusions and inclusions differently is inherent in our system of justice. Even where test results that exclude a suspect are susceptible to similar methodological concerns as test results that identify or include a suspect, the standard for determining the admissibility of exculpatory evidence is not necessarily the same as that for judging the admissibility of evidence generally. The adversary system is built on the premise that the prosecution bears a heavier burden than the defense.

III. POLICY CONSIDERATIONS

Private Laboratories

Three private companies dominate the market in the sale of forensic DNA typing services: Lifecodes Corporation, Cellmark Diagnostics and Forensic Science Associates. Together, these companies have analyzed samples and provided testimony in dozens of cases across the country.

In theory, there is nothing wrong with private laboratories providing forensic DNA services. Indeed, it can be argued that the pace of development in this area would have been too slow if public funding had been relied upon exclusively, especially since forensic criminal laboratories have never been well-funded, nor do they generally function as centers of research.

While it may be theoretically appropriate to use private laboratories, in practice doing so raises several serious concerns. Questions about the quality of the work being done by the private laboratories have not been satisfactorily answered, and the laboratories' adherence to accepted scientific procedures has not been demonstrated.

Without a careful examination of the quality controls that lie at the heart of private laboratories' DNA typing procedures, it remains unknown whether proper controls are in place for determining if there is sufficient DNA to perform a test, protecting against contamination of probes, deciding if observed patterns come from bacteria as opposed to human DNA, and determining how matches are established.

Private laboratories make sweeping claims of accuracy, stating that the probability of error is one in a million, or in some cases one in a billion. These claims are suspect. While one of the private laboratories recently published an article describing their methods for calculating such probabilities, the basic population data used by laboratories have been seriously questioned by the scientific community. Until the population data are available for thorough review, either by publication or by independent experts, the laboratories' probability claims are subject to criticism.

Private laboratories are reluctant to share information about their procedures, and they have generally adopted a proprietary stance and treated their protocols as trade secrets. At one laboratory, scientists who take the technology transfer training course and the litigants who oppose the admission of DNA typing evidence have been required to sign agreements not to disclose the methods and procedures used by the private laboratory. Yet, the laboratories' scientists claim, as they must under Frye and most of its progeny, that their techniques are generally accepted as reliable in the scientific community. It is difficult to reconcile the practice of cloaking a methodology in secrecy with the claim that the methodology is widely accepted. Until private laboratories allow their procedures to be reviewed by the general scientific community, it will remain impossible to evaluate their merits.

The adversary system does not always respond rapidly to new scientific techniques. Courts have occasionally embraced new scientific techniques only to find out later that incorrect identifications (false positives) were possible, despite claims that the technique would either be foolproof or yield no result. This was the fate, for example, of the paraffin test and certain techniques used to determine the presence of narcotics in hair samples.

In regulating private drug companies, the Food and Drug Administration uses a system of blind trial testing. State agencies and professional organizations have laboratory standards and systems for blind trial testing of AIDS testing facilities, blood banks, and laboratories that do other forms of testing for medical treatments. DNA typing for forensic purposes is so new that no such standards or testing procedures have been developed, and few serious proficiency or blind trial tests have been conducted. One test that was conducted, however, produced disturbing results.

In a proficiency study conducted in California by the Orange County Sheriff's Department crime laboratory,[14] two of the three private laboratories made an error in analyzing samples. One company was wrong in one of the forty-four matches it identified, another was wrong in one of fifty matches, and only the third company was correct in all of its matches. These results fall

---

[14] As reported by Mark Thompson in the April 3, 1989 issue of The New Republic.

far short of the private laboratories' claims of absolute certainty of forensic DNA testing. Furthermore, the laboratories made the mistakes knowing that their results would be scrutinized carefully.

It is important that law enforcement officials, jurists and policy makers examine critically the position generally advanced by the private laboratories that DNA typing procedures for forensics have already been perfected; that current typing procedures generate probabilities of error of less than one in a billion; and that they are foolproof -- you either get the right result, or no result, but never a false positive.

Public Laboratories

Like the private laboratories, public laboratories should follow scientifically accepted principles and procedures when conducting forensic DNA analysis.

Most forensic analysis in New York State is conducted in the fourteen forensic laboratories operated by federal, state, county and local governments: the Federal Drug Enforcement Administration Laboratory in New York City; the four laboratories operated by the New York State Police, located in Albany, Newburgh, Binghamton and Olean; the laboratories operated by the counties of Erie, Monroe, Nassau, Niagara, Suffolk and Westchester; and the laboratories operated by the cities of New York, Syracuse and Yonkers. Twelve of these laboratories conduct serological examinations on physical evidence; serological tests are not conducted by the Drug Enforcement Administration, whose

efforts are devoted exclusively to drugs, and the City of Yonkers, which forwards evidence of this type to the Westchester County Laboratory. Larger counties and the major metropolitan areas of the State also analyze forensic evidence in their medical examiner's laboratories.

The application of DNA to criminal investigations is at various stages of development in New York State's public laboratories. For example, the Nassau County Police Department has trained analysts, purchased equipment and recently begun testing forensic samples; the Nassau County Medical Examiner's Office has also begun training staff for DNA analysis. Suffolk County has received equipment funding and is sending its scientists to the Federal Bureau of Investigation's (FBI) training program. Erie County and Niagara County are working together to apply the technology to physical evidence within their region. Except for the laboratory in Monroe County, the rest of the laboratories in New York State, as well as the New York City Medical Examiner's Office, are planning on implementing forensic DNA analysis in the future.

After two years of study, the FBI opened a forensic DNA laboratory in October 1988. Thus far, the laboratory has analyzed samples from approximately three hundred cases, of which several were submitted from New York State. The FBI is also providing training in DNA analysis techniques for state and local laboratory personnel.

State and local jurisdictions across the country have undertaken extensive efforts to implement DNA technology. California, Virginia, North Carolina, Maryland and Florida have either begun DNA testing or are planning to do so shortly; many other states have requested funding to implement a forensic DNA system. Internationally, several European countries are developing the technology.

While the number of New York cases thus far submitted for analysis is relatively small, it is anticipated that the need for such services will grow rapidly in the coming years. As the demand for service increases, and as localities respond by creating their own DNA analysis capabilities or sending more and more cases to private laboratories, the urgency of developing Statewide guidelines and standards is manifest. Without such uniform standards, the reliability of the forensic techniques will remain suspect, and the full potential of this promising criminal justice tool will not be realized.

Computerizing and Standardizing Genetic Information

Population Studies

As mentioned earlier in this report, the population studies that are currently used to calculate the likelihood that a DNA match could arise by chance, that is, occur at random in the population, are based on relatively small samplings. Larger numbers of observations on well-defined populations are needed. The Panel recommends that all data generated by the DNA analysis network, which is described later in this report, be kept in a

format that will allow the generation of local population statistics.

Since allele distribution can vary considerably among racial and ethnic populations and sub-populations, as well as by geographical region, it is important that population statistics used in New York reflect this State's population structure. The population data would be collected for the sole purpose of validating population statistics. The data would not contain information traceable to an individual.

With the exception of the FBI, which has begun to develop its own population statistics, the existing allele frequency data for probes of forensic identification purposes are largely held by private companies, which maintain a proprietary interest in that information. Moreover, allele frequency data are valid only for the probe/enzyme combinations used to generate that data. The information is not transferable to other probe/enzyme combinations. Since the field of forensic DNA analysis is changing rapidly, New York may choose to use technology different from that used currently by the private laboratories. Population statistics consistent with New York's selected probe/enzyme combinations would then have to be acquired. The Panel thus recommends that New York create its own population statistics. To assist in this effort to broaden and better validate population statistics, New York should use compatible data generated by others where possible.

DNA Databanking

The creation of computerized files containing investigative support data to assist law enforcement officials in solving crimes raises issues that are far more controversial than those raised by the collection of population statistical data. There are many serious privacy concerns that must be overcome before a DNA databank of coded DNA prints from designated offenders should be established. If these privacy concerns are scrupulously satisfied through legislation and regulation, the Panel recommends that legislation be enacted mandating that all persons convicted of violent sex crimes or other designated offenses be required to give specimens of their DNA to an authorized agency. To implement this databank, the Panel further recommends that New York State begin the preliminary developmental work needed to overcome the technical problems inherent in building such a databank.

Proponents argue that databanking is an appropriate law enforcement tool that would be especially helpful in solving serial crimes and other crimes where there is a high rate of recidivism. Opponents, on the other hand, fear an abusive intrusion into one of the most fundamental privacy concerns - a citizen's genetic makeup. Genetic information, if not scrupulously secured, could conceivably be used to read an enormous array of information from a person's genes, information that people have a right to believe will remain confidential. For instance, employers, insurers and other non-law enforcement

personnel could use information on familial relationships, genetic predispositions to certain diseases, or genetic deficiencies that perhaps indicate a propensity toward violent or antisocial behavior.

These critical privacy concerns are far from abstract. The eugenics movement in this country, which resulted in thousands of involuntary sterilizations, the suggested screening of violent men for an extra Y chromosome, the sickle cell screening tests employed to prohibit marriages, and the current privacy concerns over HIV screening, underlie the Panel's following recommendation: Use of a databank for other than law enforcement suspect identification purposes should be expressly prohibited and subject the abuser to criminal penalties.

The theory underlying a criminal investigation databank is straightforward: By preserving a DNA code in a computer, society will improve its ability to identify suspects in certain types of crime - particularly rape and other sexual assaults. Much like the way in which computerized fingerprint systems are used to examine latent fingerprints found at crime scenes, DNA extracted from an evidentiary sample could be matched against DNA coded information stored in a database.

The first step in building a DNA databank is the collection of DNA samples taken from designated offenders. These samples would then be coded on a computer. The DNA "print" itself would not be computerized, only the identification data obtained from the coding of that print would be maintained in the computer

file. The process would begin when a sample of DNA collected from a crime scene was analyzed at a DNA laboratory; the laboratory would then develop a code for the DNA found at the crime scene; thereafter, the code would be entered into the database and searched against all of the codes contained in the database; if a matching code was found in the database, the existence of the match could be used to identify a possible suspect.

The technological issues inherent in creating a DNA databank may be substantial. Once these issues are resolved, the identification information generated from the samples taken from convicted violent sex offenders or other designated offenders would be computerized along with pertinent demographic information, such as name, address, date of birth and criminal history. The potential for abuse of this type of information is minimal.

To avoid the improper use of the underlying DNA sample, the Panel recommends that the actual DNA sample itself not be saved. The only information that would be retained is the computerized coding of the identification and demographic data contained in the databank. This will ensure that the information never be used to identify genetic predispositions. Furthermore, in the event that a conviction for a particular enumerated crime that gave rise to the taking of the DNA sample is reversed or otherwise terminated in favor of the subject as defined by Criminal Procedure Law, Section 160.50 (2), the computer's soft

copy as well as any hard copies in circulation should be destroyed.

The Panel recommends stringent rules governing the use of a computerized match. If the computer makes a DNA match, the information would be transmitted to the investigating authorities who could use it, along with other investigative tools, to determine if reasonable cause exists to further pursue the identified suspect. While it is ultimately for the courts to decide whether an arrest can be made based solely on information contained in the databank, the Panel recommends that, because of the infancy of the technology and all of the problems enumerated in this report, that the DNA match should not be the sole basis for making an arrest. We recommend that a computer generated DNA match be used only to provide the legal justification for questioning a suspect or securing a court ordered line-up, search warrant, fingerprint, or extraction of samples of physical evidence from the suspect. Additionally, if a search of the DNA databank reveals a "hit" on an evidentiary sample taken from a crime scene, a court order could be obtained to take a fresh DNA sample from the suspect. Making a second, new DNA comparison could cure many of the technical and scientific challenges to the accuracy and reliability of the older DNA code lodged in the computer.

Standardization

Although with the appropriate privacy safeguards in place we recommend the collection of DNA samples from the targeted

population, there are numerous technical obstacles that need to be overcome before computerization commences. As noted above in relation to computerizing population statistics, computer codes used to create databanks for DNA information on designated offenders are not transferable from one probe/enzyme system to another system.

Currently, two major private forensic DNA laboratories and the FBI employ three different and hence non-transferable probe/enzyme systems. The differences are exacerbated by the use of different equipment to size DNA fragments (e.g., digitizing bit pad vs. video camera image processing), different electrophoresis gels, and various sizing standards. Furthermore, testing technologies are under rapid development, with new probes and new methods for analysis becoming available regularly. Thus to be cost effective, flexibility will have to be built into any computer system developed by the State. Since dissimilar information cannot be compared, serious consideration should be given to establishing national standards for all testing procedures, analysis, interpretation, and coding of data, including the standardization of sizing techniques. The creation of national standards would enable one state to search the databases of every other jurisdiction. Further, by establishing national standards against which to measure laboratories performances, the important goal of ensuring that appropriate quality controls are observed by laboratories would be furthered.

In recommending that databanking be conducted in the manner outlined above, the Panel believes that, with appropriate legislative safeguards, the compelling privacy concerns can be addressed. The Panel believes that its recommendations strike an appropriate balance between competing privacy and legitimate law enforcement interests.

IV. A MODEL DNA ANALYSIS SYSTEM

Regional Laboratory System

The Panel recommends the creation of a Statewide DNA laboratory network, with forensic DNA analysis services provided by region. At least three regional locations should be established. Region one would cover New York City and Long Island; region two would extend from New York City through the Hudson Valley and central and northern New York; and region three would cover Western New York. These regions could be further subdivided later if workloads dictate.

The Panel recommends that DNA testing be equally available to defense and prosecution. Justice demands that any technique with the power to include or exclude a suspect with a high degree of certainty be made available to all parties.

Costs associated with the regional system should be apportioned by some mechanism other than on a per-case basis. Decisions on whether DNA analysis will be applied in a given case should be made on the merits of the case, not on whether there is sufficient money in the budget to pay for the analysis. By spreading costs over a wide population base, no jurisdiction would be denied access to this potentially critical evidence purely on economic grounds.

In the absence of national standards, the Statewide DNA laboratory network would coordinate quality assurance and quality control for all laboratories in the network. The importance of these functions cannot be overestimated, and everyday caseload

pressures should not be permitted to compromise quality control procedures or system-wide quality assurance safeguards. Further, the scientists in the network should keep abreast of current developments in this rapidly changing area; this critical function would require several full-time staff and a part-time commitment from others.

The Panel recommends the accreditation of DNA laboratories (see page 46). Among other requirements, to be accredited each local public or private laboratory that performs forensic serology and intends to perform DNA testing must maintain at least one analyst certified by the DNA Analysis Network as qualified to examine, purify and isolate genetic material from forensic case materials. This person should also be trained to perform initial screening tests on isolated DNA to establish suitability, that is, sufficient quality and quantity, of genetic material for further DNA testing.

Training

The regional DNA laboratories should provide training for local law enforcement personnel, other forensic medical and laboratory personnel, prosecutors, defense attorneys and judges. Although the training for each group would focus on different issues, the underlying aim of the training would be to improve the collection and preservation of evidence and to instruct users on how to interpret, evaluate and present the DNA results. The training would be coordinated on a statewide basis to ensure consistency and high standards.

Further training should be conducted by integrating issues related to DNA analysis into on-going training programs, such as the training program for law enforcement officials conducted by the Bureau of Municipal Police at the Division of Criminal Justice Services. DNA techniques do not require a change in the way crime scene evidence is handled, although the preciseness and importance of the technique magnifies the impact of improperly handled evidence. Control of all crime scenes should be strict and access should be severely limited. By adhering to established crime scene guidelines, a high level of integrity of the physical evidence will be maintained.

Role of Local Laboratories

All evidence should be examined initially by a local crime laboratory using traditional forensic techniques before being sent for DNA analysis. Not all biological samples are appropriate for DNA testing, and this new method should not be viewed as an automatic substitute for the forensic methods now used in crime laboratories.

DNA testing procedures often consume the sample, and it cannot thereafter be used for traditional forensic testing. By requiring that all case materials with potential for DNA analysis be submitted in the first instance to a local crime laboratory for preliminary evaluation before submission to the regional DNA laboratory, it is less likely that other valuable forensic evidence will be overlooked. This is essential because the

practical difficulties with the tests ensure that a proportion of DNA typing tests will be inconclusive.

In considering whether to submit a sample for DNA analysis, the local laboratory should consider the probative value and the size and condition of the evidence. This initial evaluation will often reveal that traditional forensic testing is sufficient, and that there is no need for DNA testing in a particular case.

Requiring that local laboratories continue to conduct the classic serological tests will also ensure that funds allocated to DNA typing are used for that purpose exclusively. If they are assured that the local crime laboratory personnel performed the appropriate tests before shipping the sample, scientists working in DNA laboratories can concentrate their energies on DNA testing without concern for other procedures.

Advisory Committee

DNA technology is expensive, and its very power makes abuse a serious concern. Therefore, there should be a systematic method to ensure that DNA technology is applied only in appropriate circumstances following established scientific guidelines. The Panel recommends the establishment of an Advisory Committee, which would establish such guidelines.

The guidelines developed by the Advisory Committee would include general standards and appropriate documented procedures to be followed in all cases. The guidelines would not be case specific or in any way designed to tell either side how to proceed with their criminal case.

The Advisory Committee would be made of representatives from law enforcement, forensic science, prosecution and defense, and the judiciary.

Scientific Review Board

The admissibility of DNA analysis procedures for forensic applications is being evaluated in courts throughout the state. Each time a case is presented that involves this technology, a new Frye hearing is being conducted. Courts' ability to efficiently and fairly evaluate the technique would be vastly improved if an impartial scientific board existed to screen all of the available technologies and methodologies.

The Panel recommends the establishment of a Scientific Review Board, distinct from the Advisory Committee, that would set essential minimum scientific controls and examine the scientific standing of a test for DNA typing. Approval of the Review Board would be necessary before the test system could be used in New York State for forensic purposes. If new scientific information indicates that a previously approved procedure should be upgraded, the Board could reassess its prior approval.

A major criteria in determining whether a new form of scientific evidence should be admitted in court is whether the principles underlying the new test and techniques have gained general acceptance in the relevant scientific community. In making this determination, courts generally consider whether the technique in question has been published in peer review journals. In the case of DNA analytical techniques used in forensic work,

peer review journals may be an inappropriate and unrealistic measure for two basic reasons.

First, acceptance by a peer review journal in human genetics might not constitute an appropriate review. While such a review should be competent to judge the quality of the molecular biology and the population studies, there are other considerations that may determine if the new development is suitable for application in the forensic laboratory. These considerations might include the ease with which the different sized DNA fragments can be distinguished, or whether the new development involves significant changes in procedure that require a higher level of laboratory skill.

Second, a publication, peer review standard would often be difficult to enforce as most journals would not be interested in publishing information about new probes and enzymes, or about the results of the population studies. These issues, while germane to forensic DNA analysis, are not generally considered new and innovative enough to warrant publication in peer review journals. While it may be possible to find a journal that will publish the results of such work, the quality of the peer review of that journal may be unsatisfactory.

The Panel recommends that the Scientific Review Board assume some of the functions traditionally performed by publications and peer reviews. The Board would act as an expert and impartial adviser to the courts. While the Board's conclusions could, of course, be challenged by the prosecution or the defense, their

expert views should nevertheless help judges faced with the difficult task of determining the scientific validity of a DNA test being introduced into court.

The Scientific Review Board would assess the scientific accuracy and the potential forensic use of each DNA typing test being proposed for introduction in court. The Board would review all published materials on the submitted test, and the laboratory submitting the test would be expected to supply to the Board any relevant unpublished data or documentary evidence. The laboratory would be required to submit a written description of critical aspects of its tests, including information on the probes used in the analysis and the polymorphisms detected by the probes in combination with restriction enzymes. The data used to derive the allele frequencies for these polymorphisms in different populations must be available, and the calculations used to estimate allele frequencies must be justified.

The laboratory would be required to justify and validate any changes in procedure or any unusual features of the proposed analysis. Prior to granting its approval, the Board could require a practical demonstration by an independent laboratory of the utility of the proposed analysis.

The Scientific Review Board should be composed of not more than five members, selected as follows: two population geneticists competent to assess such matters as the validity of the population studies used to determine allele frequency and the calculations derived from these frequencies; a molecular

biologist with experience in using similar techniques in a medical DNA diagnostics laboratory; a forensic scientist with experience in using similar techniques in a forensic science laboratory; and a chairperson with practical experience in molecular genetics who is aware of the broader implications of the use of these techniques in forensic science.

Accreditation

Basic Operating Standards

As part of the model DNA network, a state accreditation process should be developed to monitor public and private laboratories providing forensic DNA analysis services in New York State. At a minimum, to be accredited, laboratories would adhere to the following operating standards.

To be accredited, public and private laboratories providing DNA analysis for civil or criminal cases in New York State should fully document their methods and maintain careful quality assurance records. New methods should be fully evaluated and tested before introduction. Validation should meet rigorous scientific standards and be verifiable by qualified outside experts. All methods should have been validated on forensic samples, and such studies should be available for examination.

The laboratory should be thoroughly equipped for molecular biology techniques. Each DNA laboratory should be a secure facility with examination areas closed to unauthorized personnel. Confidentiality of all records should be maintained. Each

laboratory should also have secure long term cold storage capability.

As part of the accreditation process, laboratories would be required to demonstrate their proficiency in genetic profiling by participating in state or national proficiency testing programs that include both known and blind tests. The regional DNA laboratories would subscribe to the same quality assurance programs and frequently exchange materials to ensure the uniform quality of service throughout the State.

Accreditation would require that the technical supervisor of each DNA laboratory be a doctoral-level scientist experienced in molecular biology, or that a person with such a background was available to the supervisor on a consultant basis. In addition to technical control of the facility, the supervisor would decide the suitability of any case submitted for forensic DNA analysis. Technical personnel should be trained in molecular genetic techniques and should have at least a year's experience before being allowed to handle case materials without direct supervision.

Validation Procedures

Several different technologies and methodologies are currently being used in forensic DNA analysis. The validation of one procedure does not necessarily imply that others are equally valid. Each technique contains an inherent potential for error, as do the population studies that are the basis for calculating the significance of a finding that a suspect's DNA matches

evidence recovered from a crime scene. Thus, each technique should be screened through a validation procedure.

Validation procedures are commonly used in the health profession to screen new clinical tests for use in medicine. For example, the Federal Drug Administration commonly reviews new diagnostic procedures, such as new kits and devices to test for viral or bacterial infections. Since a faulty forensic DNA analysis system can have equally dire consequences as a faulty clinical test, the same sort of assurances that are used in the health profession should be used with DNA technology.

Probes must have been fully described in the scientific literature or approved by the Scientific Review Board. Information on the allelic frequencies in different populations must be fully documented. Data on alleles must be sufficient to calculate the statistical significance of a match given the underlying population.

Information on the influence of the forensic environment on the typing method and the allelic polymorphisms for each probe system must have been published in the scientific literature or approved by the Scientific Review Board.

Scientific test procedures are valid only when conducted in a properly controlled fashion by experienced technicians and scientists. DNA analysis techniques used to identify potential criminals should be no exception. The Panel recommends an extremely strong commitment to quality assurance for forensic DNA analysis.

Admissibility in Court

To support admissibility in court the following factors must be present:

1. The public or private laboratory must be accredited and its technology approved by the Scientific Review Board.
2. All necessary documentation to establish the quality of the DNA sample and the validity of the testing procedure must be available for examination.
3. All notes, charts, exhibits, etc., necessary to support and document the conclusions reached must be open to examination.

Financing the Model System

The Forensic DNA Analysis Panel is aware of the State's current shortfall in revenues. Consequently, a variety of options for funding the DNA network should be considered.

The cost of the new system could be funded entirely by the State or by local governments; federal funds could also be pursued. It would be preferable, however, if the costs were shared by the State and the localities, with the funding formula based on population, level of criminal activity, or other relevant measures.

The regional laboratory system should be developed in stages. During the initial stage, the Advisory Committee and the Scientific Review Board would be established and their policies formulated. Thereafter, an initial regional laboratory would be created. The lessons learned in establishing the first

laboratory would be valuable in developing the other regional laboratories.

First-phase funding requirements for the network will be less than $50,000. The initial costs will be limited primarily to financing the work of the Advisory Committee and the Scientific Review Board's meetings and training sessions. Second-phase costs will be limited to the cost of a single laboratory, with the remaining two laboratories to be established in subsequent years as necessary to meet the demand for this service.

Additional expenses will be incurred in establishing a DNA databank. In anticipation of the resolution of the privacy concerns discussed in the databanking section of this report, one or more persons with technical expertise should be hired to begin addressing the many technical issues involved in creating such a computerized capability.

A more detailed description of cost estimates is presented in Appendix III of this report.

APPENDIX I: FORENSIC DNA ANALYSIS PANEL MEMBERS

Howard Harris, Ph.D., Chairperson
Director, Monroe County Public Safety Laboratory
Rochester, New York

Michael Baden, M.D.
Director of Forensic Sciences
New York State Police
Albany, New York

Rhonnie Broder, J.D.
Deputy Bureau Chief of Sex Crimes Special Victims Bureau
Kings Co. District Attorney's Office
Brooklyn, New York

Lorraine Flaherty, Ph.D.
Chief of the Laboratory of Immunology
Wadsworth Center for Laboratories and Research
Albany, New York

Pamala L. Griset, Ph.D.
Deputy Commissioner, Office of Funding and Program Assistance
NYS Division of Criminal Justice Services
Albany, New York

Robert W. Horn
Director of State Police Laboratory System
New York State Police
Albany, New York

Leigh F. Hunt
Chief of Police, Syracuse Police Department
Syracuse, New York

Robert Kaye, J.D.
Assistant Coordinator of Operations
Office of Coordinator of Criminal Justice
New York, New York

Peter Kehoe, J.D.
Executive Director & Counsel, NYS Sheriff's Association
Troy, New York

Mark Mahoney, J.D.
Attorney-at-Law
Bermingham, Cook & Mahoney
Buffalo, New York

Judge Joseph P. McCarthy
Erie County Court
Buffalo, New York

Peter Neufeld, J.D.
Attorney-at-Law
New York, New York

Peter Preiser
Professor of Law
Albany Law School
Albany, New York

Barry C. Scheck
Professor of Law
Benjamin N. Cardozo School of Law
New York, New York

Jan A. Witkowski, Ph.D.
Director, Banbury Center, Cold Spring Harbor Laboratory
Cold Spring Harbor, New York

Appendix II - TECHNICAL APPENDIX

DNA

An appreciation of the structure and behavior of the DNA molecule is important in understanding DNA typing. The essentials of the DNA structure are:

- The DNA molecule is composed of two chains, made up of small molecules called nuclectides. Each nucleotide comprises a base, a sugar molecule and a phosphate group. The nucleotides are linked together through their phosphate groups with chemical bonds called phosphodiester bridges.
- There are four bases - adenine, guanine, thymine and cytosine.
- The two chains are held together by interactions between the nucleotides on the opposite chains, and the chains are twisted to form a double helix.
- The interactions between bases are such that the adenine of one chain is always paired with a thymidine in the other chain, and a guanidine is always paired with a cytosine.
- It is the order of the bases along the chain that constitutes the genetic code, and the cell has a very complex machinery for translating this code and using it to synthesize proteins.

The essential feature of the DNA double helix that underlies all manipulations of DNA is the complementary base pairing

between the chains. The two chains of the helix can be separated by a variety of means, and under appropriate conditions the two separated chains will come together (hybridize) and reconstitute exactly the same molecule. Similarly, a small segment of DNA will find its complementary sequence. Such small segments are called probes, and the accuracy of the hybridization process is such that a DNA probe only nineteen nucleotides long will find its exact complement in the whole of the human genome of 3×10^9 nucleotides.

Restriction Fragment Length Polymorphisms (RFLPs)

The type of DNA variation between individuals that is exploited for DNA typing is called restriction fragment length polymorphism (RFLP). Restriction endonucleases are bacterial enzymes that cut DNA molecules. DNA is not cut at random; rather each enzyme cuts the DNA strand at a particular sequence of base pairs - its recognition site - unique for each enzyme. If a single base pair in the recognition site is changed, the enzyme fails to cut. Changes of this nature are very common in the human genome; they differ between individuals and are inherited just like genes.

When DNA from a person is treated with a restriction endonuclease ("digested" in the jargon of the molecular geneticist), many millions of fragments are produced. If a DNA probe is available, the probe will hybridize only to the fragment with the complementary sequence to that probe, and if the probe is labelled with radioactivity, the fragment can be detected.

Suppose the probe hybridizes to a fragment 4500 base pairs long in one individual. There may be a polymorphic site for the restriction enzyme within this 4500 base pair fragment, and another individual may have that site. In this case, the enzyme will produce fragments of 1,500 base pairs and 3,000 base pairs, and depending on where the probe hybridizes in relation to the polymorphic site, one or two fragments will be detected.

Variable Number Tandem Repeat Loci (VNTR)

There is a special type of RFLP where the polymorphism is due not to the presence or absence of a restriction enzyme site, but rather to the variability in the distance between sites. Variable number tandem repeat regions (VNTR) are regions of DNA that are made up of identical units ("repeats") joined together like links in a chain. The numbers of repeats can vary widely between different individuals, and it is this variability that is exploited in forensic DNA typing. A probe to a VNTR locus detects bands that vary in size depending on the number of repeats present.

Two types of probe have been used. Alex Jeffreys developed the first of these type of probes, one that detects a large number of VNTR loci. The patterns of bands produced by this probe are very complicated. This disadvantage outweighs the advantage of their ability to detect extreme individual variability. Consequently, there has been a move to use probes that detect variations at a single VNTR locus. Using such probes still results in a great deal of variability at a VNTR locus, but

the pattern of bands is simpler. The power of the typing comes from examining several VNTR loci, each with a different probe, and combining the data obtained from all loci.

Performing DNA Typing

The techniques used for DNA typing are theoretically simple and require little in the way of sophisticated equipment. Nevertheless, this simplicity is deceptive because many steps are involved in the whole process. Reliable implementation requires rigorous controls. Inconclusive results and possibly false positives could be obtained if any of these steps are performed incorrectly.

Preparing DNA: DNA is first isolated from the evidentiary sample and purified using a combination of chemical methods. A small sample should be electrophoresed to check the quality of the DNA, and the amount of DNA should be measured with a fluorimeter. A control sample of high quality DNA should be processed in parallel to ensure that all stages of the procedure are working satisfactorily.

Restriction Enzymes: It is essential to have pure DNA because the next step - treating the DNA with a restriction endonuclease - may fail if impure DNA is used. The enzyme may not cut the DNA strands at all the available sites, resulting in an incomplete or partial digestion. Alternatively, the impurities may result in the DNA being totally destroyed. Following digestion with the enzyme, a small sample of the reaction mixture must be electrophoresed on a gel and stained

with ethidium bromide, a chemical that stains DNA. Properly digested DNA produces a characteristic picture, and partial digests and DNA degradation can also be detected at this stage. The test gels must be photographed, labelled and preserved in the laboratory records for the case.

Electrophoresis: Assuming the procedure is working well, the differing sized DNA fragments resulting from the action of the restriction enzyme must be separated by electrophoresis in an agarose gel. It is important to use the same amount of DNA and the same solutions for all the samples on a gel because these factors will alter the movement of the DNA fragments in the gel. It is also essential to include appropriate controls. These must include samples containing radioactive DNA fragments of known sizes that can be used for calibration. Samples of human DNA known to produce satisfactory data are used to control for subsequent stages. Evidentiary and suspect samples should be in adjacent lanes of the gel so that comparisons can easily be made. These gels must be photographed, labelled and preserved in the laboratory records for the case. Other controls may also be necessary to ensure that the DNA has migrated properly and that artifacts do not appear.

Southern Blotting: An agarose gel cannot be handled. Therefore, the DNA must be transferred to a more robust material. The preferred material is a sheet of positively charged nylon. An exact replica of the distribution of DNA in the gel is produced by overlaying the gel with the nylon sheet (called a

membrane or filter) and allowing capillary action to carry the DNA fragments from the gel onto the nylon where they become bound. This procedure is called Southern blotting or transfer. As a control, it is essential to check that the DNA has been transferred from the gel to the filter by restaining the gel with ethidium bromide and determining that no DNA remains in the gel. These gels must be photographed, labelled and preserved in the laboratory records for the case.

DNA Probes: The DNA probes used to detect the polymorphic fragments on the filter must be carefully prepared. The probes are small segments of DNA usually cloned into larger circular pieces of DNA called plasmids. Plasmids are able to replicate themselves inside bacteria, and they have to be isolated from the bacteria before they can be used. It is preferable to isolate the cloned probe segments from the plasmid DNA, but in any case a small sample of the probe should be run on a gel to check its purity. These gels must be photographed, labelled and preserved in the laboratory records for the case. The probe must be made radioactive. Before using the labelled probe on evidentiary samples, its quality must be checked by calculating its specific activity and by carrying out a test hybridization.

Hybridization: The polymorphic DNA fragments are detected by hybridizing the radioactive probe with the filter. The probe hybridizes to just the fragments with its complementary sequence out of all the millions of fragments on the filter. The filters are washed under very carefully defined conditions of temperature

and salt concentration to remove non-hybridized probe. The stringency of this washing is very important to avoid non-specific binding of the probe. With experience, adequate washing can be crudely determined by using a Geiger Counter.

Autoradiography: Following washing, the filters are dried and sandwiched with an X-ray film. The radioactively labelled fragments expose the X-ray film and reveal their exact position. After an appropriate length of time, the film is developed. This is the critical stage for the most stringent quality control. The autoradiograph will show whether the whole procedure has been performed properly. It is essential that the film be reviewed by several people to determine if it is adequate for interpretation. In forensic applications as in medical genetics, sub-optimal autoradiographs must be rejected and not interpreted. The size of a fragment on the film is determined by measuring how far the band has moved along the gel. Small fragments move longer distances than large fragments. The position of bands on the autoradiographs must be determined, although the way in which this should be done varies substantially from laboratory to laboratory.

Re-Probing: The filter must then be treated to remove the radioactive probe so that the filter can be hybridized with a second probe to detect another polymorphism. Stripping the probe must be done carefully or else the DNA bound to the filter may be removed. Following stripping and before hybridization, the film should be exposed to X-ray film to ensure that all the previous

probes have been removed. Otherwise, confusion will arise if fragments labelled by two different probes appear on the same autoradiograph.

Record-Keeping: It will be clear from this brief description that the procedure is complex and there are many points at which things may go wrong. It is essential that complete records be kept of all laboratory procedures for each step in each case. All data must be kept whether the particular step was a success or failure. All reasons for modifying a procedure must be recorded.

Problems with Laboratory Procedures

There are several unique methodological problems associated with DNA analysis for forensic use:

Probes: The Variable Number Tandem Repeat (VNTR) probe is commonly used in forensic DNA analyses. In contrast to most probes used in clinical applications, the VNTR recognizes a continuum of band sizes rather than discrete bands. Thus, discrimination between alleles is difficult at best. To use these probes for forensic purposes, most laboratories group these bands representing alleles into bins that contain a short range of sizes. Currently there is no consensus among the forensic community or among the laboratories performing these tests on how large these bins should be; the size of the bin, however, influences calculations of the probability and the determination of whether any two individuals' DNA match or does not match. Moreover, there is some disagreement about the appropriate

methodology for measuring band size. Most laboratories use a digitizer to measure band sizes; however, at least one laboratory may be relying solely on visual observation for evaluating a match.

Artifacts that affect DNA migration: There are several artifacts that affect DNA migration through a gel. Since the degree of migration is used as a measure of the size of the DNA fragment, it is critically important to determine whether there is any band shifting due to various environmental conditions such as heat, contaminants in the sample, unevenness in the gelling procedure, unevenness in the position of the electrodes, bacterial contamination, etc.

Two methods are currently being proposed to evaluate this situation. The first uses nonpolymorphic probes of various sizes to determine the degree of band shifting. If the nonpolymorphic probe recognizes the bands at the same position in all lanes, it can be assumed that no band shifting has occurred. If band shifting is observed, however, it may be difficult to determine if there is a match or a non-match since band shifting is often not uniform.

The second method is to mix the unknown sample with that of the suspect. If the two samples are identical, they will migrate to the exact same location. If they are not identical, they will most likely separate depending on the resolution of the gel system.

Both methods are valid; however, the mixing system requires enough DNA for a second sample, which is often unavailable in forensic cases.

Quality of DNA: Because of the nature of the forensic sample, the DNA may often degrade, lessening its quality. This makes DNA analysis more difficult, especially when the probe used detects higher molecular weight fragments. To avoid this problem, laboratories are screening their sample DNAs prior to analysis to determine if they are suitable for the Southern blotting technique. Unfortunately, these screening systems are not entirely successful at determining the degradation of the human-part of the DNA samples since they also display bacterial DNA. The use of nonpolymorphic human probes that detect high molecular weight human DNA bands of comparable sensitivity has been proposed as one solution.

Quantity of DNA: Sample sizes are often small and inadequate for suitable analysis. In certain cases, the bands present in the evidentiary lane are on the borderline of resolution by visual or mechanical means. Moreover, often the test cannot be repeated for confirmation due to the limitations of the sample. Interpretations are consequently difficult. Sometimes a longer exposure of the gel to the X-ray film can resolve the bands that are difficult to see. There is a sensitivity limit, however, that cannot be corrected by any length of exposure.

Some laboratories are developing new techniques that work with smaller samples. Based on a new procedure called the polymerase chain reaction, these techniques are now being used in paternity exclusion cases and in some forensic cases. They are quite different from the DNA analysis based on the Southern blotting technique and may have an entirely different set of methodological problems. Forensic scientists should consider saving a small amount of any evidentiary sample for possible future use with this new technology.

Quality control: There are no widely accepted criteria for quality control or proficiency testing in DNA analysis of forensic samples. It is consequently unclear whether forensic laboratories use appropriate quality control and assurance techniques. If not, the laboratories' results are suspect. For example, if samples are mislabelled, contaminated, or used incorrectly, different DNA band sizes or additional DNA band sizes could be identified.

To remedy this problem, the FBI runs a known human tissue sample at the same time as the evidentiary sample. If the results with the known sample are incorrect, the data obtained from the evidentiary sample is disregarded.

Another way, used by the forensic as well as the clinical and medical communities, to ensure quality control is to insist that each laboratory performing such tests be evaluated periodically by proficiency testing techniques - preferably blind proficiency testing techniques. These techniques involve the

shipment of known samples that are similar to the ones the laboratory would normally receive. The laboratory then evaluates these samples under the same conditions and with the same personnel as they use for forensic samples. Their results could later be compared with results of other laboratories receiving the same samples. These tests should be blind, that is, the laboratory should not know whether the samples were test samples or actual forensic case samples.

Population genetics: Population studies are an integral part of any forensic DNA analysis. Without a knowledge of the frequencies of certain alleles as represented by DNA band size in a population, it is impossible to predict the probability of a match or a non-match. While several laboratories are now performing more population studies, only one population study from one private company has so far been published in a peer-reviewed journal, and this study has been seriously challenged by its own peer reviewer.

There are several problems with the population studies being conducted. The statistics used in other population studies with single-copy probes to analyze genes with a low degree of polymorphism may not be applicable to forensic studies that employ a highly polymorphic VNTR probe. There is very little information on this subject, and it is thus difficult to evaluate

the methodology. Disagreement exists over the size of the population bases needed to accurately forecast DNA band size frequencies. Moreover, frequencies may vary by ethnicity or by subpopulations within the larger racial or ethnic population.

APPENDIX III: FINANCING THE DNA NETWORK

This report calls for the eventual establishment of three regional laboratories, one of which will be located in New York City, where rent and other costs may be higher than in other areas of the State. While the staffing patterns will probably vary between the laboratories, our cost estimates are based on an equal distribution of resources between the regions. The Advisory Committee will determine the final allocation of resources among the regions.

The estimates include several distinct categories: personal service, with each laboratory staffed with a highly-skilled and experienced supervising scientist, two serologists, two technicians and one stenographer; equipment, which in many cases will involve one-time only start-up costs; rent, although it may be possible to find space for one or more of the laboratories at low or no cost; reagents and supplies; training; administrative costs; and travel and other non-personal services expenses.

In deriving our cost estimates, we considered the experience of other jurisdictions.

ESTIMATED ANNUALIZED EXPENSES
PER DNA LABORATORY

Personal Services:

1 Supervisor	SG-25 =	$ 47,000
2 Serologists	SG-20 =	72,000
2 Lab Technicians	SG-12 =	47,000
1 Stenographer	SG-09 =	20,000
Total Personal Service		$186,000

Non-Personal Services:

Equipment:	$90,000	
Supplies & Reagents:	60,000	
Training:	30,000	
Rent:	30,000	
Administrative:	50,000	
Miscellaneous:	10,000	
Total Non-Personal Services	$270,000	
TOTAL PER LAB:	$456,000	
3 REGIONAL LABS:	$1,368,000	

These estimates are for full-year funding once the three regional laboratories are fully operational. First year funding requirements will be minimal, probably less than $50,000. The initial costs will be limited primarily to financing the cost of the Advisory Committee and Scientific Review Board's meetings and training sessions. Second year costs will be limited to the cost of a single laboratory, with remaining laboratories established in subsequent years.

Additional costs will be incurred in establishing DNA databanking capabilities. At this time, in anticipation of the resolution of the privacy concerns addressed in this report, the

State should make at least a minimal investment by beginning to address some of the technological issues inherent in creating a DNA databank.