047



IN THE FLORIDA SUPREME COURT

STATE OF FLORIDA, :

Petitioner, :

v. : CASE NOS. 87,530, 87,543

MICHAEL GIBSON, :

Respondent. :

_____ :

ON DISCRETIONARY REVIEW
FROM THE FIRST DISTRICT COURT OF APPEAL

# RESPONDENT'S BRIEF ON THE MERITS

STEVEN A. BEEN
Florida Bar No. 335142
Public Defender's Office
Leon County Courthouse
301 South Monroe Street
Tallahassee, Florida 32301
(904) 488-2458

ATTORNEY FOR APPELLANT

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RESPONDENT'S BRIEF ON THE MERITS

PRELIMINARY STATEMENT ON ISSUES PRESENTED

The state has briefed only one issue in this Court, the issue raised by the certified question. Although the certified question, whether an attempted felony murder conviction vacated per State v. Gray, 654 So.2d 552 (Fla. 1995), may be reduced to, or retried on, a lesser included offense, is the same here as in Wilson v. State, 660 So. 2d 1067 (Fla. 3d DCA 1995), rev.granted, 668 So.2d 664 (Fla. 1996), and Alfonso v. State, 661 So.2d 308 (Fla. 3d DCA 1995), rev. granted, 668 So.2d 603 (Fla. 1996), the result in this case may not necessarily be determined by the result in Wilson and Alfonso, if those cases are decided first. In this case, the jury was not instructed on any lesser included offenses. Also, in this case, the evidence was insufficient to sustain a conviction for attempted felony murder, as it was defined before Gray.

Respondent Gibson has briefed a second issue, dealing with the admissibility of DNA evidence when the expert witness has

deviated from the National Research Council's prescribed procedure for determining the statistical significance of a DNA match. The Court has jurisdiction over this issue based on the certification of the Gray issue. See Feller v. State, 637 So. 2d 911 (Fla. 1994): "Having jurisdiction on the basis of the certified questions, we have jurisdiction over all issues." 637 So. 2d 914.

The DNA issue in this case is similar to the second question certified by the First District in Vargas v. State, 640 So. 2d 1139 (Fla. 1st DCA 1994), (Vargas I), reached in this Court only by Justice Overton, joined by Justice Wells, dissenting in State v. Vargas, 667 So. 2d 175 (Fla. 1995), (Vargas II). Given the increasing use of DNA evidence in criminal trials, the DNA issue raised in this case is significant and worthy of the Court's attention, and is actually of greater importance to the outcome of this case than is the Gray question. Respondent requests that the Court address the DNA issue and not be limited to the issue raised by the certified question.

## STATEMENT OF THE CASE AND FACTS

Respondent asserts no disagreement with the state's Statement of the Case and Facts, but supplements it with additional record material, pertaining to both Issue I and Issue II.

Michael Gibson was charged by information with armed burglary, armed kidnapping, attempted first degree felony murder, armed robbery, and four counts of armed sexual battery. (R1). Count III, charging attempted felony murder, alleged that Gibson had attempted to kill a human being, by shooting, during the perpetration of a sexual battery. (R2). The evidence showed:

On December 20, 1993, at about 6:45 a.m., [redacted] returned to her home in the Indian Oak apartment complex, 1800 Jackson Bluff Road, in Tallahassee. (51-53). Two or three minutes later the doorbell rang. (T53). She opened the door and saw a figure around the corner. (T54). As the man approached the door, she could see that he had on a baseball cap, and for a split second, she could see his face. (T54-55,79). She tried to close the door, but the man lunged and stuck his foot in the door. (T55). She tried to push the door closed, but the man put his hand around the door, and she could see he was holding a silver, metallic gun. (T55). She finally stopped pushing. (T55). When the man got into the apartment, she saw that he was wearing a bandanna over his face. (T57). He had apparently put on the bandanna during the struggle with the door. (T57). He was also wearing gloves. (T55).

Inside the apartment, the man demanded B 's purse, took money, stereo equipment, and other property, and committed four acts of sexual battery, two oral and two vaginal. (T56,57,62-64,66-69). Before the first sexual battery, while the man was unzipping his pants, the gun went off, and B was shot; the bullet penetrated her breast, but not her chest cavity. (T59, 277-278).[1] At first, she was not sure she had been shot. (T60). The emergency room physician testified that death can result from an injury to the breast alone. (T272). He said he would not have expected B to die from this injury, but that it is possible to bleed to death from such an injury; he put the odds at a few percentage points. (T278-279).

After the attacker left, B looked out her window and saw a figure dressed in black, in a light yellow two-door hatch-back, with license plate number starting with "L." (T69). She identified Gibson from a photographic line-up approximately nine days after the crime, and she identified Gibson in the courtroom. (T65,86-87). Also, she testified that the attacker was wearing a black baseball cap with no insignia, gold tomahawk earrings, a watch with visible coils and springs, black leather combat boots,

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[1]In the fact statement of the state's answer brief in the district court, the state also referred to the gun having "gone off."

> When the defendant grabbed her breast and began to unzip his pants, she told him not to touch her and the gun went off. (T59).

State's Answer Brief filed in First District, p. 4.

There was no evidence that Gibson shot the gun intentionally, and all the evidence is consistent with the gun having gone off by accident.

dark gloves, and she said the bandanna the man was wearing was a western style with a white diamond design. (T73-76). She examined the cap, watch, boots, gloves, and bandanna found in Gibson's apartment and testified they were identical to the items she saw on her attacker. (T73-76,155-159). The police found the watch in the pocket of pants in Gibson's room, the boots in Gibson's closet, the bandanna in Gibson's bedroom, the gloves behind a couch in the living room, and the baseball cap in the bedroom of Gibson's cousin, Julius Bennett. (T155-159). A witness who knew Gibson said she had seen him at a party the night before, wearing a tomahawk earring. (T135-136).

The bullet that struck B was recovered. (T144). It was determined to have been fired by a gun that Martin Geleta testified he had last seen on October 17, when he left it at the home of Gibson and Gibson's cousin, Julius Bennett. (T103-106, 140-141,286-289). Charles Brown testified that the last he saw the gun was before Thanksgiving, when he saw it on a shelf in Gibson's room. (T117-119).

Brown also testified that the night of December 19, he, Gibson, and others were at a Christmas party in Killearn. (T111-112). They were riding in Brown's 1984 Fiesta, with tag number LKA4402. (T113-115). Brown, Gibson, Julius Bennett, and a man named Mark Morris, ended up at Gibson's Prince Manor apartment that night. (T113,120). Gibson and Morris went to sleep first. (T113). Brown testified that he normally kept his car keys in his pocket, but when he woke up at 7:26 a.m. on December 20, his

keys were on a table in front of him. (T113,115). The front door of the apartment was open, and Gibson was outside, on his way back in. (T115-116). Brown's car was by the front door, where he had left it the night before. (T116,122-123). B was shown a photograph of Brown's Fiesta, and testified it looked like the car she saw the attacker driving. (T70).

After Gibson's arrest, he was questioned by the police in a recorded interview. (T145-146). Gibson stated that at about 1:30 a.m. on December 20, he left his apartment briefly to make a phone call to Deanna Ingram, returned and went to sleep, and did wake up until about noon. (T353-359). He stated that he had last seen the pistol left by Charles Brown several days before, when it was under the seat of Brown's car. (T368-369). He acknowledged that the watch seized at the apartment belonged to him. (T360-361). Deanna Ingram testified that at about 5:00 a.m. on December 20, her doorbell had rung, and she had seen Gibson through the peephole; she had not spoken to him or let him know she was home. (T126-129).

Semen, pubic hair, and fibers were collected from B 's body and from her clothing and bedding. (T144,147-150,246,274, 297). The semen was determined to have come from a type O secretor; Gibson is a type O secretor, as is 36% of the population. (T321,324). There was also testimony that a microscopic comparison of a pubic hair left at the scene of the crime with Gibson's pubic hair disclosed no differences, so the pubic hair could have been left by Gibson, although the

statistical significance of this match was unknown (246-253,258). Nylon fibers recovered from the victim's clothing and bedding were compared with the nylon fibers of the gloves seized from Gibson's apartment, and were found to be identical, indicating that the fibers could have come from the gloves. (296-306).

A DNA comparison was also made, and Gibson moved before trial to exclude the testimony of the state's DNA witness, Dr. James Pollack, based on Frye v. United States, 293 F. 1013 (D.C.Cir.1923), on the ground that Dr. Pollack had failed to follow the National Research Council procedure for determining the statistical significance of a DNA match. (R33-35). The motion relied on Vargas I, on the National Research Council's publication, DNA Technology and Forensic Science (1992) (hereafter "NRC Report"),[2] and on the pre-trial deposition of Dr. Pollack, as authority for the contention that Dr. Pollack's method of determining the statistical significance of the DNA match did not have Frye general acceptance. (R33-35). Gibson also moved before trial for recognition of the NRC report as an authoritative treatise for the purpose of cross-examining Dr. Pollack. (R31). The motion to recognize the NRC report as authoritative was granted. (R157).

At pre-trial hearings on the motion to exclude the DNA testimony, the state announced that it would present only

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[2]The NRC report was addressed by both parties in the trial court, but the report itself was not made a part of the record. Chapter 3 of the NRC report, "DNA Typing: Statistical Basis for Interpretation," is attached to this brief, for the convenience of the Court.

statistics derived from the more conservative approach suggested by the district court in Vargas I. (R171). Dr. Pollack testified he used two different procedures to calculate the probability that the DNA of a randomly selected person would match the DNA left at the scene of the crime, the binning method, and the modified ceiling principle recommended by the National Research Council in the NRC Report. (T172-179). He testified that the binning method is generally accepted in the "forensic community," although "there are those that feel that [the binning method is] not conservative enough." (T174). Dr. Pollack testified that the modified ceiling principle is generally accepted in the "scientific community," but that forensic scientists think the method is too conservative and he does not accept it; the modified ceiling principle is what the National Research Council has asked for, however, and what the "First DCA was seeking in the Vargas ruling," and he presents results based on it when called upon to do so. (T176-178). Dr. Pollack had also testified for the state in the Vargas case. (T171-172,186).

With the binning method, Dr. Pollack determined that, using the FBI's black population database, the chances of a match were one in six billion, using the Caucasian database, the chances were one in 900 million, and using the Hispanic database, the chances were one in two billion. (T172-173). With the modified ceiling principle, Dr. Pollack calculated the chance of a match to be one in twenty million. (T176).

Dr. Pollack described the modified ceiling approach as: (1)

determining the database frequency of each allele; (2) adjusting the frequencies by substituting 10% for any database frequency that is lower than 10%; and (3) then multiplying the adjusted frequencies to determine a final probability. (T175-176). Dr. Pollack conceded that the National Research Council procedure included an additional, initial step of determining whether the DNA profile of the sample left at the scene matched any of the samples in the database, and he conceded that he had failed to perform that initial part of the procedure. (T181-182; NRC Report, p. 91). He asserted that it was impossible for him to compare the DNA from the scene with the samples in the FBI database, but he conceded that the comparison could have been done by the FBI. (T183-184). He maintained that not performing the comparison had no effect on his results, but he conceded that he did not know if the DNA left at the scene would match any of the FBI's samples, and that if it did, this would change his results. (T183-184). Dr. Pollack was not asked, and did not testify, that the National Research Council's procedure, without the first step, is a generally accepted method of determining the probability of a random DNA match.

The prosecutor argued for denial of the defense motion by asserting that Dr. Pollack had followed the more conservative method suggested by Vargas I. (R178-179; T185-186). Defense counsel argued that Dr. Pollack's failure to compare the DNA profile of the sample with the samples in the FBI's database made the resulting statistics inadmissible. (T185). The judge denied

the defense motion to exclude Dr. Pollack's testimony. (T186-187).[3]

With the jury present, Dr. Pollack testified that DNA in semen left at the scene of the crime was compared with DNA in blood samples taken from both Gibson and from the victim's boyfriend, Chris Gordon. (T192). Five probes were used; the allele detected by each probe indicated a match with Gibson and no match with Chris Gordon (T198-200). Dr. Pollack said that "using an extremely conservative approach," the probability of selecting a person at random whose DNA matched the DNA profile of the sperm left at the scene would be approximately one in twenty million. (T201).

At the conclusion of the evidence, defense counsel moved for judgment of acquittal as to attempted felony murder on the grounds that there had been no evidence of an intentional overt act that reasonably could have caused death. (T393-396). The prosecutor argued that pointing a loaded gun at a person is an overt act, and that if the gun goes off, that could cause death. (T397). Defense counsel pointed out that if pointing a loaded gun at someone was an overt act that could cause death, then every armed robber would be guilty of attempted felony murder, even if the gun did not go off. (T397). The trial judge ruled that pointing a loaded gun at a person's chest is an overt act

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[3]The testimony of a different expert witness to a DNA comparison by a different method was excluded by the trial court based on a discovery violation. (T1-32). No issue arising from that ruling has been asserted on appeal.

sufficient to establish attempted felony murder, and the motion was denied. (T398-399).

At the charge conference, there was discussion about possible lesser offenses included in attempted felony murder, but neither the state nor Gibson requested that the jury be instructed on any. (T411-415,425). The jury was not instructed on any lesser offenses included in attempted felony murder, and none were indicated on the verdict form. (R48;T491).

The judge gave the definition of attempted felony murder from the standard instructions, with no reference to shooting:

> Before you can find the defendant guilty of attempted first-degree felony murder, the State must prove the following two elements beyond a reasonable doubt: First, Michael Gibson did some overt act which could have caused the death of [redacted] but did not. And, two, the act was committed as a consequence of and while Michael Gibson was engaged in the commission of burglary, kidnapping, robbery or sexual battery.

(T491).

Gibson was convicted as charged of all counts except kidnapping. (R44-58,T508-509). He was sentenced to life in prison on all counts except armed robbery, on which he was sentenced to forty years. (R74-91;T268-269).

## SUMMARY OF ARGUMENT

Issue I. Double jeopardy bars a new trial on a charge of attempted first degree murder. The proof of attempted felony murder was insufficient because there was no proof of an intentional overt act that reasonably could have caused death. Pointing a gun at the victim was an intentional act, but this alone could not cause death. The evidence was also insufficient to prove attempted premeditated murder, as there was no proof of premeditation and no proof of intent to kill. Double jeopardy prevents the state from trying an attempted first degree murder charge on a felony murder theory, failing to prove the crime, and then trying the same crime again on a different theory.

Issue II. The state's DNA expert should not have been allowed to testify that there is a one in twenty million chance that a person chosen at random would have DNA that matched the profile of the DNA of the perpetrator. Gibson properly raised a Frye objection prior to trial and supported his objection with authorities. The state failed to satisfy its burden of proving that its expert's methods were generally accepted in the scientific community. The state's evidence showed that the method prescribed by the National Research Council is generally accepted, but the state failed to show that its expert's deviation from the NRC method was generally accepted.

## ARGUMENT

ISSUE I NO NEW TRIAL IS WARRANTED ON THE ATTEMPTED FELONY MURDER CONVICTION VACATED PER STATE v. GRAY BECAUSE: (1) THE EVIDENCE OF ATTEMPTED FIRST DEGREE MURDER WAS INSUFFICIENT, SO RETRIAL IS BARRED BY DOUBLE JEOPARDY; (2) NO LESSER OFFENSES WERE SUBMITTED TO THE JURY SO RETRIAL IS BARRED BY FLA. R. CRIM. PROC. 3.151; (3) THERE ARE NO LESSER OFFENSES NECESSARILY INCLUDED IN ATTEMPTED FELONY MURDER AND IN THIS CASE THERE ARE NO PERMISSIVE LESSER INCLUDED OFFENSES. CONVICTION OF LESSER INCLUDED OFFENSES WITHOUT A NEW TRIAL, IF THERE WERE LESSER OFFENSES, IS NOT AUTHORIZED BY STATUTE WHEN THE CONVICTION IS REVERSED FOR A REASON OTHER THAN INSUFFICIENCY OF THE EVIDENCE.

A. The evidence of attempted first degree murder was insufficient, so retrial is barred by double jeopardy.

The state acknowledges that when a conviction is reversed for insufficiency of the evidence, discharge is required by the double jeopardy clause. Burks v. United States, 437 U.S. 1, 98 S. Ct. 2141, 57 L. Ed. 2d 1 (1978). At trial, the state argued only the felony murder theory of attempted first degree murder. Gibson's counsel moved for judgment of acquittal and argued that the evidence was insufficient, and the motion was denied. After the trial, this Court issued the Gray decision, holding that there is no such crime as attempted felony murder. Gray appeared to offer complete relief from Gibson's attempted murder conviction, so the sufficiency issue was not asserted at the district court, and the district court vacated the conviction solely on the basis of Gray. The evidence was insufficient, however, to establish attempted first degree murder, either attempted felony murder as defined in Amelotte v. State, 456

So.2d 448 (Fla. 1984), or attempted premeditated murder, and respondent now asks this Court to affirm the reversal of the conviction on the ground of insufficiency as well.

Amelotte defined attempted felony murder:

> We find that attempted felony murder is a crime in Florida ... The essential elements of the crime are the perpetration of or the attempt to perpetrate an enumerated felony, together with an intentional overt act, or the aiding and abetting of such an act, which could, but does not, cause the death of another.

456 So.2d 448. The evidence here was insufficient because it failed to establish "an intentional overt act ... which could ... cause the death of another." The evidence failed to prove that the perpetrator intended to fire the gun, as the parties below recognized. The trial judge denied the motion for judgment of acquittal based on her ruling that pointing a loaded gun at a person's chest is an overt act within the meaning of attempted felony murder. As defense counsel pointed out, such an interpretation would make armed robberies into attempted murders, even when the gun is not discharged. Though, as this Court recognized in Gray, there were substantial problems with the reasoning of Amelotte, it would be unreasonable to conclude that Amelotte meant to make run-of-the-mill armed felonies, when no-one is attacked and no-one is hurt, into attempted murder. Amelotte must have meant by an intentional overt act that could have caused death, an act of actual attacking, such as shooting or stabbing, that could reasonably be expected to cause serious injury. Pointing a gun at a person, though criminal and

dangerous, will not itself cause death. The evidence of attempted felony murder must be held to have been insufficient.

The evidence was also insufficient to establish attempted first degree murder on a premeditation theory. There was no evidence of premeditation and no evidence of intent to kill. The state did not rely on attempted premeditated murder, and did not assert that the evidence was sufficient to establish attempted premeditated murder. Now, however, the state seeks a ruling that it be allowed to bring Gibson to trial again, on a premeditation theory.

Attempted premeditated murder and attempted felony murder are alternate forms of a single crime, attempted first degree murder. The state has tried to convict Gibson of attempted first degree murder, and it has failed. The double jeopardy bar prevents the state from trying again with a different theory of this same crime. Trying Gibson for attempted first degree murder again, this time on the premeditation theory, is barred by the prohibition of double jeopardy under the federal and Florida constitutions.

B. No lesser offenses were submitted to the jury so retrial is barred by Fla. R. Crim. Proc. 3.151.

The certified question asks if a new trial is permitted on lesser included offenses of attempted felony murder, none of which were submitted to the jury. Rule 3.151 provides:

> (a) Related Offenses. ... [Two] or more offenses are related offenses if they are triable in the same court and are based on the same act or transaction or on 2 or more

connected acts or transactions.

...

(c) Dismissal of Related Offenses after Trial. When a defendant has been tried on a charge of 1 of 2 or more related offenses, the charge of every other related offense shall be dismissed on the defendant's motion unless a motion by the defendant for consolidation of the charges has been previously denied, or unless the defendant has waived the right to consolidation, or unless the prosecution has been unable, by due diligence, to obtain sufficient evidence to warrant charging the other offense or offenses.

(d) Plea. A defendant may plead guilty or nolo contendere to a charge of 1 offense on the condition that no charges of other related offenses be instituted. Should the court find that the condition cannot be fulfilled, the plea shall be considered withdrawn.

Respondent is not aware of any case in which this Court has applied rule 3.151(c), but the district courts have considered the rule, and have applied it in several cases. State v. Harris, 357 So. 2d 758 (Fla. 4th DCA 1978), is the leading case. Harris entered a plea to reckless driving in county court and was later charged in circuit court with an aggravated assault arising from the same incident. He moved to dismiss based on rule 3.151. A panel including then Judge Anstead, relying on the commentary to the American Bar Association standard from which rule 3.151 was taken, held that subsection (c) applies only when the defendant has actually gone to trial. When the defendant enters a plea, subsection (d) applies, and related offenses are barred only if the plea agreement so provides. When there has been a trial, under subsection (c), related offenses must be dismissed. State v. Feldman, 362 So. 2d 481 (Fla. 1st DCA 1978), and Malik v.

State, 640 So. 2d 224 (Fla. 5th DCA 1994), are to the same effect.

In Dixon v. State, 486 So.2d 67 (Fla. 4th DCA 1986), the rule was used to bar untried related offenses. Dixon allegedly conspired in Broward County to transport marijuana to Atlanta. He was arrested in Martin County with marijuana in his car, tried in Martin County for trafficking in marijuana, and convicted of possession. The later charge of conspiracy to traffic in marijuana filed in Broward County was an untried related offense, so the district court held it was barred by rule 3.151(c).

In Wright v. State, 518 So.2d 475 (Fla. 4th DCA 1988), the defendant was tried for aggravated battery, and convicted of aggravated assault. The aggravated assault conviction was reversed because aggravated assault is not a lesser offense included in aggravated battery, and thus should not have been submitted to the jury. On retrial, the state amended the information to charge aggravated assault, and the district court allowed this. In Wright, the aggravated assault charge had been submitted to the jury, so it was tried, and rule 3.151(c) did not bar trying it again, after a reversal on appeal.

In this case, the state could have tried any lesser offense of attempted felony murder in the first trial, by requesting that the lesser offenses be submitted to the jury. As State v. Johnson, 601 So.2d 219 (Fla. 1992), holds, the state may insist on the submission of lesser included offenses over the defendant's objection. Instead, the state here opted to give the

jury the choice of attempted felony murder, or acquittal. Under subsection (c) of rule 3.151, Gibson has only been tried on the charge of attempted felony murder. The lesser included offenses of attempted felony murder are related offenses under rule 3.151. Because they are related offenses on which Gibson has not been tried, rule 3.151(c) bars prosecution for any such offenses.

The state may argue that rule 3.151 does not bar a new trial on lesser included offenses because the trial of lesser included offenses was implicit in the trial of attempted felony murder. This would be a tenuous construction of rule 3.151. If lesser included offenses could be said to have been implicitly tried, however, this implication should be limited to necessarily included offenses. By definition, every element of a necessarily included offense is also a necessary element of the main offense. Thus, when the jury considers whether the elements of the primary offense were proved, the jury is also considering whether the elements of the necessary lesser were proved. See Brown v. State, 206 So. 2d 377 (Fla. 1968). Permissive lesser offenses, on the other hand, contain at least one element that is not a necessary element of the primary offense. Thus, there is no reason for the jury to consider whether the elements of a permissive lesser have been proved, unless the jury is instructed on the lesser. In this sense a permissive lesser that is not instructed on has not been tried.

C. There are no lesser offenses necessarily included in attempted felony murder, and in this case there are no permissive

lesser included offenses.

There are no necessarily included lesser offenses of attempted felony murder as it was defined in Amelotte and instructed on in this case. Under Amelotte, as discussed above, attempted felony murder is established by an intentional overt act that could have but did not cause death, during commission or attempted commission of one of the designated felonies for felony murder. Committing an overt act that could have caused death but did not is not even necessarily a crime, and does not imply any crime. Committing one of the felony murder felonies is a crime, but that crime is not necessarily included in attempted felony murder because for any particular designated felony, attempted felony murder could be committed by committing one of the other designated felonies. This is why felony murder and the underlying felony have been held to be separate crimes, conviction for both of which is permissible. State v. Enmund, 476 So. 2d 165 (Fla. 1985).

The state may argue that attempted second degree depraved mind murder is a necessarily included lesser offense of attempted first degree felony murder based on Linehan v. State, 476 So.2d 1262 (Fla. 1985). Logically, attempted second degree murder is not necessarily included in attempted felony murder, because attempted felony murder as defined in Amelotte did not require depraved mind or intent to kill. Linehan held, with a completed homicide, that second degree murder is a necessarily included offense of felony murder, but this holding was based on policy,

not because second degree murder is really included in felony murder. Scurry v. State, 521 So.2d 1077 (Fla. 1988):

> This Court, in Linehan made a policy determination that the same category one necessarily lesser included degrees of homicide of second-degree murder and manslaughter that were applicable for first-degree premeditated murder should also be applicable for first-degree felony murder. We adhere to that decision ...

521 So.2d 1078. The policy rationale of Linehan, though unstated, was apparently that a jury considering a case of capital murder should have the second degree murder option to use in the exercise of its pardon power, whether the capital murder charged is premeditated or felony murder. This consideration does not apply when the crime is non-capital attempted felony murder. Attempted second degree murder is not a necessarily included lesser offense of Amelotte attempted felony murder.

The state may argue that a new trial should be permitted on permissive lesser offenses. Permissive lesser offenses are those that are not necessarily included in the primary offense, but are charged by the language of the information or indictment and established by the evidence. Brown. The state has not indicated what crimes it may contend constitute permissive lesser offenses in this case. The possible permissive lesser offenses would be attempted second degree murder, attempted third degree murder, attempted manslaughter, aggravated battery, aggravated assault, battery, assault, and culpable negligence.

Since there is no offense of third degree murder other than felony murder, per Gray, there is no longer a crime of attempted

third degree murder. Thus attempted third degree murder can be readily eliminated.

As to attempted second degree murder and attempted manslaughter, each, after Gray, now includes an element of intent to kill. Gray essentially adopted Justice Overton's dissent in Amelotte. As that dissent recognized, there is no such thing as attempting to commit a homicide without an intent to cause death. An attempt to commit a crime includes the intent to accomplish the completed crime. Thus for any attempted homicide, intent to cause death must be an element of the crime.[4] This makes sense, and does not eliminate the differences among the different levels of attempted homicide. Attempted first degree murder requires a premeditated intent to cause death. Attempted second degree murder requires a depraved mind and an intent to cause death that need not be premeditated. Attempted manslaughter requires only intent to cause death. An example of an attempted homicide that fails to meet the elements of attempted second degree murder but

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[4]The most sensible understanding of Gentry v. State, 437 So. 2d 1097 (Fla. 1983), relied on by Amelotte, is not that attempted murder may be proved without proving intent to kill. Rather, Gentry held that attempts, including attempted second degree murder, are not specific intent crimes for the purpose of the voluntary intoxication defense, unless the completed crime would be a specific intent crime. Whether an offense is a specific intent crime for the purpose of the voluntary intoxication defense does not necessarily indicate what intent must be proved to establish the crime. See Linehan v. State, 442 So.2d 244 (Fla. 4th DCA 1983), aff'd, 476 So.2d 1262 (Fla. 1985). To the extent that Gentry indicates that attempted murder does not include the element of intent to kill, Gentry has been overruled by Gray.

establishes the elements of attempted manslaughter would be imperfect self-defense, i.e., using excessive force, with intent to kill, in response an attack that is insufficient to justify the response.

Attempted second degree murder is not a permissive lesser offense in this case because the information does not allege depraved mind, and because the evidence does not support the element of intent to kill. As discussed in the fact statement, the evidence is consistent with the perpetrator's gun having gone off accidentally as he prepared to commit sexual battery. For the same reason, the evidence does not support attempted manslaughter, so attempted manslaughter is also not a permissive lesser offense in this case.

Neither does the evidence prove either aggravated battery or battery, because an accidental shooting is not a battery. As the standard instructions on battery and aggravated battery state, an element of battery is that the touching or harming be intentional. Fla. Std. Jury Instr. Battery, Aggravated Battery.

The information does not charge aggravated assault or assault, as Count III does not allege that the victim was put in fear. Fla. Std. Jury Instr. Assault, Aggravated Assault. The information does not charge culpable negligence, section 784.05, Fla. Stat., as Count III does not allege negligence.

In sum, there are no necessarily included or permissive lesser offenses that could be retried, if such retrial were appropriate.

D. Conviction of lesser offenses without a new trial, if there were lesser offenses, is not authorized by statute when the conviction is reversed for a reason other than insufficiency of the evidence.

The certified question seems to ask whether the courts, upon vacating an attempted felony murder conviction, may enter a conviction for a lesser included offense, as is the practice under section 924.34, Fla. Stat., without another trial. In this case, there are no lesser included offenses, but attempted second degree depraved mind murder might be seen as a lesser statutory degree of attempted first degree felony murder, and section 924.34 applies to lesser degrees as well as lesser included offenses. Section 924.34 allows entry of a conviction, however, only for lesser offenses established by the evidence. As discussed above, attempted second degree murder was not established because there was no proof of intent to kill.

Even if there were a lesser degree or lesser included offense established by the evidence, if the attempted felony murder conviction were vacated only because attempted felony murder is a non-existent crime, and not for insufficiency of the evidence, entry of a conviction pursuant to section 924.34 would not be appropriate. Section 924.34, by its own terms, applies only "when the appellate court determines that the evidence does not prove the offense for which the defendant was found guilty ... ." Section 924.34 does not deal with the reversing of a conviction for any reason other than insufficiency of the

evidence. Extending section 924.34 beyond the application specified by its terms would violate the rule of strict construction in favor of the accused. Section 775.021(1), Fla. Stat.; Perkins v. State, 576 So.2d 1310 (Fla. 1991).

E. The state's brief does not supply any basis for disposing of Count III, attempted felony murder, other than by discharging respondent.

The state insists that it is not seeking a change in Gray's ruling that there is no crime of attempted felony murder or in Gray's holding that attempted felony murder convictions not yet final should be reversed on appeal. Yet the state claims that Gray violated three rules of statutory construction and was unfair to the state. In fact, Amelotte is the decision that violated the more important principles of statutory construction, creating a crime of attempted homicide that omitted the element of attempt. Gray gives no remedy to persons convicted of attempted murder under Amelotte, but who did not actually try to kill anyone, whose convictions were final before Gray.

The state asserts that the reversal of Amelotte should not taint convictions for lesser included offenses, or make it error to have instructed on lesser offenses. Of course, there were no instructions on lesser offenses in this case. The state does not indicate what offenses it thinks were lesser included offenses of attempted felony murder. As discussed above, there were none, not just because the concept of an offense included in a non-existent offense seems incongruous, but also because the crime as

defined by Amelotte does not include any lesser offenses.

The state points out that attempted first degree murder may be proved by establishing premeditation, without reference to attempted felony murder. How this is pertinent in this case, in which the information did not allege premeditation, the jury was not instructed on premeditation, and the evidence did not show premeditation, is not clear. The district courts that have considered attempted murder convictions that were submitted to the jury on attempted premeditated and attempted felony murder grounds, have remanded for a new trial on attempted premeditated murder. Humphries v. State, 20 Fla. L. Weekly D2634 (Fla. 5th DCA, Dec. 1, 1995); Harris v. State, 658 So.2d 1226 (Fla. 4th DCA 1995); Tape v. State, 661 So. 2d 1287 (Fla. 4th DCA 1995). Cooper v. State, 547 So.2d 1239 (Fla. 4th DCA 1989), rev.den., 560 So.2d 232 (Fla. 1990), cited by the state, reached the same result when the jury was instructed on both attempted manslaughter by act and the non-existent crime of attempted manslaughter by culpable negligence. These cases do not contradict Gibson's position that where only the non-existent theory was charged and submitted to the jury, and there are no lesser included offenses, and none were instructed on, discharge rather than remand for a new trial is required.

The state asserts that precedent requires that when a conviction is reversed because the crime does not exist, the remedy be remand for a new trial. All but one of the cases the state cites, however, involved conviction of attempt as a lesser

included offense of a crime that itself included attempts. State v. Sykes, 434 So. 2d 325 (Fla. 1983), is representative of all these cases. Sykes was charged with grand theft. Attempted grand theft was submitted to the jury as a lesser included offense. This was error because the definition of grand theft includes endeavoring to obtain someone else's property. Thus an attempt to commit grand theft is actually the same crime as grand theft, not a lesser offense. The Court in Sykes could have simply affirmed the conviction, after correcting the statutory degree to reflect that attempted grand theft is grand theft. This is what Justices McDonald and Adkins, dissenting, would have done. Alternatively, the Court could have reversed, not because attempted theft is a non-existent crime, but rather because erroneously telling the jury that attempted theft is a lesser crime interfered with the exercise of the jury pardon power. The majority, however, held that attempted grand theft is a non-existent offense, conviction of which is fundamental error. It was because conviction of attempted grand theft, whether a non-existent crime or not, required proof of every element of grand theft, that Sykes properly refused to construe the attempted theft conviction as an acquittal of theft. Thus, given the holding that attempted theft is a non-existent crime, retrial was the only sensible remedy. That Sykes and all the Sykes-type cases the state cited remanded for new trials says nothing about the issue here. Gibson's conviction of attempted felony murder did not establish the elements of any actual crime.

The one case the state cites that does not fall into the Sykes pattern is Hieke v. State, 605 So.2d 983 (Fla 4th DCA 1992). Hieke was charged with solicitation to commit first degree murder and convicted of solicitation to commit third degree felony murder, held to be a non-existent crime. Hieke remanded for retrial of the lesser included offense of aggravated battery or battery "as same were set forth on the verdict form." 605 So.2d 984. The rationale for this remedy was not discussed in Hieke, but in any event, Hieke did not remand for trial of lesser offenses other than the lessers that had been submitted to the jury in the first trial. In this case, as discussed above, there were no such lessers.

The state asserts that the double jeopardy clause does not constitute a bar when reversal of a conviction is on any ground other than insufficiency of the evidence. The evidence of attempted felony murder was insufficient, however, as discussed above. The state chose the crime to charge and the evidence to present, and it failed to prove the charged crime. The double jeopardy clause does operate as a bar to retrial in this situation.

Finally, the state asserts that Gray should be seen as equivalent to a prospective legislative repeal of the crime of attempted felony murder. This is not what Gray did. Gray recognized that Amelotte was wrongly decided. Gray holds that Justice Overton's dissent in Amelotte stated the more correct position. To Justice Overton, attempted murder without the

intent to kill was a logical impossibility. Gray is thus not a repeal; it is the correction of a misconception. In the most logical understanding of Gray, attempted felony murder has never been a crime.

ISSUE II THE TRIAL COURT ERRED IN OVERRULING RESPONDENT'S FRYE OBJECTION TO TESTIMONY ABOUT THE STATISTICAL SIGNIFICANCE OF A DNA MATCH WHEN THE STATE'S EXPERT OMITTED A STEP OF THE NATIONAL RESEARCH COUNSEL PROCEDURE AND THE STATE FAILED TO ESTABLISH THAT THE PROCEDURE USED, WITHOUT THE OMITTED STEP, IS GENERALLY ACCEPTED IN THE SCIENTIFIC COMMUNITY.

In Vargas I, the First District distinguished between the general scientific acceptance of the method of comparing DNA samples to determine whether there is a match, and the lack of general acceptance of the methods used for determining a match's statistical significance. Vargas I reviewed scientific and legal literature and concluded that there was too much controversy over the reliability of the method Dr. Pollack had used to determine statistical significance to say that his method met the Frye test. As Vargas I recognized, the determination of the frequency in the general population of a combination of DNA alleles found in a sample (a DNA profile) by determining the frequency of each allele in a small database, and then multiplying the frequencies, is based on unproved assumptions of allele independence and random mating with no sub-populations. Generating statistics without taking those sources of error into account does not meet the Frye test. Vargas I ordered a remand for a determination of whether a more conservative method, such as that suggested by the National Research Council, is generally accepted in the scientific community and thus meets the Frye test. The National Research Council's recommendations were designed to lessen the potential error due to the possibility that the allele

independence and no sub-population assumptions are incorrect. NRC Report, pp. 74-95.[5]

Vargas I certified a question as to whether the method Dr. Pollack had used, or the modified NRC method, met the Frye test. In Vargas II, a majority of this Court did not reach the certified question, because there was a dispositive suppression issue. Justice Overton, however, joined by Justice Wells, dissented on the suppression issue, and addressed the Frye question. Justice Overton stated that the unadjusted method of determining the statistical significance of a DNA match lacked general acceptance in the scientific community, as the First District had concluded, but also indicated that the NRC method did not seem to command general acceptance either. Justice Overton would have remanded for a new Frye hearing, because of the trial judge's errors in excluding defense evidence and in applying the wrong standard for determining admissibility.

In this case, neither side asserted that the National Research Council's procedure lacked general acceptance. The state presented testimony that purported to be based on the NRC method. The defense challenged that evidence because it omitted

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[5]In Hayes v. State, 660 So.2d 257 (Fla. 1995), this Court recognized that the National Research Council's disapproval of a DNA procedure is inconsistent with the procedure having general acceptance in the scientific community:

> When a major voice in the scientific community, such as the National Research Council, recommends that corrections made due to band-shifting be declared "inconclusive," we must conclude that the test on the tank top is unreliable.

660 So.2d 264.

the first step of the NRC procedure. The question here is whether the state satisfied its burden of showing that the NRC procedure, without the omitted step, is a method of determining DNA match significance that is generally accepted in the scientific community.

The party objecting to novel scientific evidence has the burden of making the objection prior to trial, and of supporting the objection with "authorities indicating there may not be general scientific acceptance of the technique employed." Correll v. State, 523 So.2d 562,567 (Fla. 1988), cert.den. 488 U.S. 871 (1988). Once the issue is raised, the burden to establish that the technique is generally accepted is on the party offering the evidence. As stated in Ramirez v. State, 651 So. 2d 1164 (Fla. 1995):

> In utilizing the Frye test, the burden is on the proponent of the evidence to prove the general acceptance of both the underlying scientific principle and the testing procedures used to apply that principle to the facts of the case at hand. The trial judge has the sole responsibility to determine this question. The general acceptance under the Frye test must be established by a preponderance of the evidence.

651 So. 2d 1168.

Appellant properly raised the issue below, by moving before trial to exclude the state's DNA evidence. (R33-35). The defense motion relied on the NRC report, and on Vargas I. The motion specifically identified the failure to comply with the first step of the NRC procedure as the basis for the request that the DNA

testimony be excluded. The defense motion was sufficient to indicate that there might not be general acceptance of the technique Dr. Pollack used, and was thus sufficient to raise the Frye issue.

The NRC report states:

> The multiplication rule is based on the assumption that the population does not contain subpopulations with distinct allele frequencies--that each individual's alleles constitute statistically independent random selections from a common gene pool.

NRC Report, 77.

> The key question underlying the use of the multiplication rule is whether actual populations have significant substructure for the loci used for forensic typing. This has provoked considerable debate among population geneticists ...
>
> Although mindful of the controversy, the committee has chosen to assume for the sake of discussion that population substructure may exist and provide a method for estimating population frequencies in a manner that adequately accounts for it.

NRC Report, 79-80.

The NRC report called for additional research, including studies of 100 randomly chosen members from fifteen to twenty relatively homogenous subpopulations. (NRC Report, 83). The NRC recommended an approach, designated the ceiling principle, to correct for problems with the assumptions underlying the calculation of profile frequencies, and the ceiling principle was to use the results of the subpopulation studies to be conducted. Dr. Pollack testified in this case that the subpopulation studies called for by the NRC report had not yet been done, to his

knowledge. (T180-181).

In the interim, the NRC recommended an approach designated the modified ceiling principle:

> Until ceiling frequencies can be estimated from appropriate population studies, we recommend that estimates of population frequencies be based on existing data by applying conservative adjustments:
>
> 1. First, the testing laboratory should check to see that the observed multilocus genotype matches any sample in its population database. ...
>
> 2. The testing laboratory should then calculate an estimated population frequency on the basis of a conservative modification of the ceiling principle ... The calculation should be carried out as follows:
>
> For each allele, a modified ceiling frequency should be determined by (1) calculating the 95% confidence limit for the allele frequency in each of the existing population samples and (2) using the largest of these values or 10%, whichever is larger. ...
>
> Once the ceiling for each allele is determined, the multiplication rule should be applied. The race of the suspect should be ignored in performing these calculations.

NRC Report, pp. 91-92.

Dr. Pollack testified that although the NRC prescribed procedure for the modified ceiling method was otherwise followed, the first step, checking to see if the multilocus DNA profile of the crime scene sample matched any sample in the database, was not done. Appellant's position, at trial and on appeal, is that the omission of this step deprives Dr. Pollack's statistical conclusion of Frye reliability, and that the results should therefore not have been admitted.

It was the state's burden, under Ramirez, to establish that

the technique used, without the first NRC step, was generally accepted in the scientific community. Dr. Pollack never testified that the NRC procedure without the omitted step is generally accepted. He did testify that he did not think the omitted step mattered:

> [REDIRECT]
> Q Dr. Pollack, you indicated you did not use that first step that was recommended.
> A That's correct.
> Q Does that affect the results that you would testify about?
> A In no way.
> Q Has no bearing whatsoever on it?
> A Other than the fact that that's an additional step that they recommended to look into the data bases that were originally prepared from individuals to see whether the profile that is in question here matches that in the data base. We don't have the ability to do that. We don't have the broad data from the FBI. So that's not something that we can do.
> Q So they have recommended something that's impossible and their recommendation does not affect your results and your opinion and your testimony here today?
> A In no way affects it.
> [RECROSS]
> Q If I could follow up. When you say it's impossible, it's not impossible to do. It could be done.
> A Not in my hands. It's impossible because I don't have the raw data.
> Q But, I mean, the raw data is accessible?
> A Not by me.
> Q Well I understand you can't see it. Is there any reason the scientists could not go up to wherever this is stored in Virginia and make these comparisons?
> A Oh, the comparison could be made by the FBI, yes.
> Q It could be done but just not by you?
> A Right.
> Q And you say that it would not affect your testimony but certainly if you found two or three matching patterns in the FBI data base that would make a difference.

A That, in my opinion, wouldn't happen.
Q I know that's your opinion but you said it wouldn't make any difference if you went up there and examined the data bases. It would make a difference if you found these patterns in the data base.
A Certainly, if it matched something in the data base, that would obviously change the results, yes.
Q Now you don't know whether it matches anything there or not?
A No. It's not something that I have done.

(T182-184).

The omitted step of the NRC procedure would have been a check on Dr. Pollack's conclusions. If he had taken the omitted step, and the perpetrator's DNA profile had not been found in the FBI data base, this would not have affected his results. If the omitted step had been done, and the profile was found to match more than one sample in the FBI data base, this would affect his conclusion.[6] Since Dr. Pollack conceded that, not having done the comparison, he could not say whether the pattern would be found in the FBI data base, his testimony is not that the omitted step had no effect. Rather, his testimony demonstrates that the omitted step could have changed the conclusion he testified to. In any event, Dr. Pollack's personal opinion as to the significance of the omitted step does not bear on the determinative question, whether the method Dr. Pollack used, without the omitted step, is generally accepted in the scientific

[6]Finding more than one sample that matched the perpetrator's DNA profile in a database of only about a thousand samples would cast doubt on Dr. Pollack's conclusion that the profile only occurs at a frequency of one in twenty million in the general population.

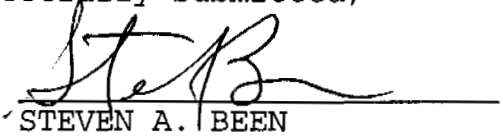
community. The state failed to meet its burden to show that Dr. Pollack's method was generally accepted. Thus, it was error to overrule Gibson's Frye objection.

This error was not harmless. Without DNA, the evidence implicating Gibson left room for doubt. The victim's identification of Gibson was questionable since she only saw her attacker's uncovered face for a split second. The stronger non-DNA evidence, the gun, car, boots, bandanna, watch, cap, and earrings, were all available to all of the men in Gibson's apartment, not just Gibson. Indeed, one of those men, Julius Bennett, as a relative of Gibson, is likely to share far more DNA with Gibson then would a person picked at random. NRC Report, 86-87. The testimony that the chance of a random match with the DNA in the sperm left at the scene was one in twenty million left the impression that, for all practical purposes, the DNA was Gibson's. That one in twenty million figure was the most compelling evidence presented. It cannot be said beyond a reasonable doubt that the one in twenty million testimony had no effect on the verdict. State v. DiGuilio, 491 So.2d 1129 (Fla. 1986).

## CONCLUSION

The attempted murder conviction should be vacated and Gibson discharged as to that count. The other convictions should be reversed and the case remanded for retrial.

Respectfully submitted,

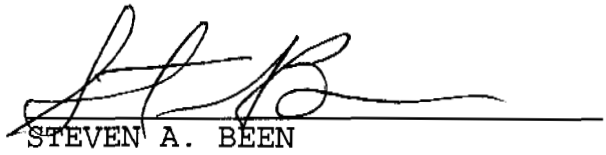


STEVEN A. BEEN
Florida Bar No. 335142
Public Defender's Office
Leon County Courthouse
Suite 401
301 South Monroe Street
Tallahassee, Florida 32301
(904) 488-2458

ATTORNEY FOR APPELLANT

## CERTIFICATE OF SERVICE

I HEREBY CERTIFY that a copy of the foregoing has been furnished by delivery to Assistant Attorney General Giselle Lylen Rivera, Office of the Attorney General, The Capitol, Plaza Level, Tallahassee, Florida, this 29th day of April, 1996.



STEVEN A. BEEN

IN THE FLORIDA SUPREME COURT

| | | |
|---|---|---|
| STATE OF FLORIDA, | : | |
| Petitioner, | : | |
| v. | : | CASE NOS. 87,530, 87,543 |
| MICHAEL GIBSON, | : | |
| Respondent. | : | |
| _____ | : | |

ATTACHMENT

DNA TECHNOLOGY IN FORENSIC SCIENCE
NATIONAL RESEARCH COUNCIL
1992

CHAPTER 3

DNA TYPING: STATISTICAL BASIS FOR INTERPRETATION

# 3

# DNA Typing: Statistical Basis for Interpretation

Can DNA typing uniquely identify the source of a sample? Because any two human genomes differ at about 3 million sites, no two persons (barring identical twins) have the same DNA sequence. Unique identification with DNA typing is therefore possible provided that enough sites of variation are examined.

However, the DNA typing systems used today examine only a few sites of variation and have only limited resolution for measuring the variability at each site. There is a chance that two persons might have DNA patterns (i.e., genetic types) that match at the small number of sites examined. Nonetheless, even with today's technology, which uses 3-5 loci, a match between two DNA patterns can be considered strong evidence that the two samples came from the same source.

Interpreting a DNA typing analysis requires a valid scientific method for estimating the probability that a random person might by chance have matched the forensic sample at the sites of DNA variation examined. A judge or jury could appropriately weigh the significance of a DNA match between a defendant and a forensic sample if told, for example, that "the pattern in the forensic sample occurs with a probability that is not known exactly, but is less than 1 in 1,000" (if the database that shows no match with the defendant's pattern is of size 1,000).

To say that two patterns match, without providing any scientifically valid estimate (or, at least, an upper bound) of the frequency with which such matches might occur by chance, is meaningless.

Substantial controversy has arisen concerning the methods for estimating the population frequencies of specific DNA typing patterns.[1-14] Questions have been raised about the adequacy of the population databases on which frequency estimates are based and about the role of racial and ethnic origin in frequency estimation. Some methods based on simple counting produce modest frequencies, whereas some methods based on assumptions about population structure can produce extreme frequencies. The difference can be striking: In one Manhattan murder investigation, the reported frequency estimates ranged from 1 in 500 to 1 in 739 billion, depending on how the statistical calculations were performed. In fact, both estimates were based on extreme assumptions (the first on counting matches in the databases, the second on multiplying *lower* bounds of each allele frequency). The discrepancy not only is a question of the weight to accord the evidence (which is traditionally left to a jury), but bears on the scientific validity of the alternative methods used for rendering estimates of the weight (which is a threshold question for admissibility).

In this chapter, we review the issues of population genetics that underlie the controversy and propose an approach for making frequency estimates that are independent of race and ethnic origin. This approach addresses the central purpose of DNA typing as a tool for the identification of persons.

## ESTIMATING THE POPULATION FREQUENCY OF A DNA PATTERN

DNA "exclusions" are easy to interpret: if technical artifacts can be excluded, a nonmatch is definitive proof that two samples had different origins. But DNA "inclusions" cannot be interpreted without knowledge of how often a match might be expected to occur in the general population. Because of that fundamental asymmetry, although each new DNA typing method or marker can be used for investigation and exclusion as soon as its technical basis is secure, it cannot be interpreted with regard to inclusion until the population frequencies of the patterns have been established. We discuss the issues involved in estimating the frequency of a DNA pattern, consisting of pairs of alleles at each of several loci.

### Estimating Frequencies of DNA Patterns by Counting

A standard way to estimate frequency is to count occurrences in a random sample of the appropriate population and then use classical statistical formulas to place upper and lower confidence limits on the estimate. Because estimates used in forensic science should avoid placing undue weight on incriminating evidence, an upper confidence limit of the frequency should be used in court. This is especially appropriate for forensic DNA typing, because any loss of power can be offset by studying additional loci.

To estimate the frequency of a particular DNA pattern, one might count the number of occurrences of the pattern in an appropriate random population sample. If the pattern occurred in 1 of 100 samples, the estimated frequency would be 1%, with an upper confidence limit of 4.7%. If the pattern occurred in 0 of 100 samples, the estimated frequency would be 0%, with an upper confidence limit of 3%. (The upper bound cited is the traditional 95% confidence limit, whose use implies that the true value has only a 5% chance of exceeding the upper bound.) Such estimates produced by straightforward counting have the virtue that they do not depend on theoretical assumptions, but simply on the sample's having been randomly drawn from the appropriate population. However, such estimates do not take advantage of the full potential of the genetic approach.

### Estimating Frequencies of DNA Patterns with the Multiplication Rule (Product Rule)

In contrast, population frequencies often quoted for DNA typing analyses are based not on actual counting, but on theoretical models based on the principles of population genetics. Each matching allele is assumed to provide statistically independent evidence, and the frequencies of the individual alleles are multiplied together to calculate a frequency of the complete DNA pattern. Although a databank might contain only 500 people, multiplying the frequencies of enough separate events might result in an estimated frequency of their all occurring in a given person of 1 in a billion. Of course, the scientific validity of the multiplication rule depends on whether the events (i.e., the matches at each allele) are actually statistically independent.

From a statistical standpoint, the situation is analogous to estimating the proportion of blond, blue-eyed, fair-skinned people in Europe by separately counting the frequencies of people with blond hair, people with blue eyes, and people with fair skin and calculating their proportions. If a population survey of Europe showed that 1 of 10 people had blond hair, 1 of 10 had blue eyes, and 1 of 10 had fair skin, one would be wrong to multiply these frequencies to conclude that the frequency of people with all three traits was 1 in 1,000. Those traits tend to co-occur in Nordics, so the actual frequency of the combined description is probably higher than 1 in 1,000. In other words, the multiplication rule can produce an underestimate in this case, because the traits are correlated owing to population substructure—the traits have different frequencies in different population groups. Correlations between those traits might also be due to selection or conceivably to the action of some genes on all three traits. In any case, the example illustrates that correlations within subgroups—whatever their origin—bear on the procedures for estimating frequencies.



Unlike many of the technical aspects of DNA typing that are validated by daily use in hundreds of laboratories, the extraordinary population-frequency estimates sometimes reported for DNA typing do not arise in research or medical applications that would provide useful validation of the frequency of any particular person's DNA profile. Because it is impossible or impractical to draw a large enough population to test calculated frequencies for any particular DNA profile much below 1 in 1,000, there is not a sufficient body of empirical data on which to base a claim that such frequency calculations are reliable or valid per se. The assumption of independence must be strictly scrutinized and estimation procedures appropriately adjusted if possible. (The rarity of all the genotypes represented in the databank can be demonstrated by pairwise comparisons. Thus, in a recently reported analysis of the FBI database, no exactly matching pairs of profiles were found in five-locus DNA profiles, and the closest match was a single three-locus match among 7.6 million basepair comparisons.)[13]

The multiplication rule has been routinely applied to blood-group frequencies in the forensic setting. However, that situation is substantially different: Because conventional genetic markers are only modestly polymorphic (with the exception of human leukocyte antigen, HLA, which usually cannot be typed in forensic specimens), the multilocus genotype frequencies are often about 1 in 100. Such estimates have been tested by simple empirical counting. Pairwise comparisons of allele frequencies have not revealed any correlation across loci. Hence, the multiplication rule does not appear to lead to the risk of extrapolating beyond the available data for conventional markers. In contrast, highly polymorphic DNA markers exceed the informative power of protein markers, so multiplication leads to estimates that are less than the reciprocal of the size of the databases.

### Validity of Multiplication Rule and Population Substructure

The multiplication rule is based on the assumption that the population does not contain subpopulations with distinct allele frequencies—that each individual's alleles constitute statistically independent random selections from a common gene pool. Under this assumption, the procedure for calculating the population frequency of a genotype is straightforward:

- Count the frequency of alleles. For each allele in the genotype, examine a random sample of the population and count the proportion of matching alleles—that is, alleles that would be declared to match according to the rule that is used for declaring matches in a forensic context. This step requires only the selection of a sample that is truly random with reference to the genetic type; it does not appeal to any theoretical models.

It is essential that the forensic matching rule be precise and objective—otherwise it would be impossible to apply it in calculating the proportion of individuals with matching alleles in the population databank. And it is essential that the same rule be applied to count frequencies in the population databank, because this is the only way to determine the proportion of random individuals that would have been declared to match in the forensic context. (In the context of forensic applications, an estimate of the probability of a match in DNA typing has been termed conservative if on the average it is larger than the actual one, so that any weight applied to the estimate would favor the suspect. Thus, some laboratories use a more conservative rule for counting population frequencies than for forensic matches—an acceptable approach, because it overestimates allele frequency. The converse would not be acceptable.)

• Calculate the frequency of the genotype at each locus. The frequency of a homozygous genotype a1/a1 is calculated to be $p_{a1}^2$, where $p_{a1}$ denotes the frequency of allele a1. The frequency of a heterozygous genotype a1/a2 is calculated to be $2p_{a1}p_{a2}$, where $p_{a1}$ and $p_{a2}$ denote the frequencies of alleles a1 and a2. In both cases, the genotype frequency is calculated by simply multiplying the two allele frequencies, on the assumption that there is no statistical correlation between the allele inherited from one's father and the allele inherited from one's mother. The factor of 2 arises in the heterozygous case, because one must consider the case in which allele a1 was contributed by the father and allele a2 by the mother and vice versa: each of the two cases has probability $p_{a1}p_{a2}$. When there is no correlation between the two parental alleles, the locus is said to be in Hardy-Weinberg equilibrium. We should note that in forensic DNA typing, a slight modification is used in the case of apparently homozygous genotypes. When one observes only a single allele in a sample, one cannot be certain that the individual is a homozygote; it is always possible that a second allele has been missed for technical reasons. To be conservative, most forensic laboratories do not calculate the probability that the sample has two copies of the allele (which is $p_{a1}^2$), but rather the probability that the sample has at least one copy (which is $2p_{a1}$) leaving open the possibility of a second allele. We endorse this procedure.)

• Calculate the frequency of the complete multilocus genotype. The frequency of a complete genotype is calculated by multiplying the genotype frequencies at all the loci. As in the previous step, this calculation assumes that there is no correlation between genotypes at different loci; the absence of such correlation is called linkage equilibrium. (Some authors prefer to reserve the term linkage equilibrium for loci on the same chromosome and to use the term gametic phase equilibrium for loci on different chromosomes.) Suppose, for example, that a person has genotype a1/a2, b1/b2, c1/c1. If a random sample of the appropriate population shows that the frequencies of a1, a2, b1, b2, and c1 are approximately 0.1, 0.2, 0.3, 0.1, and 0.2, respectively, then the population frequency of the genotype would be estimated to be [2(0.1)(0.2)][2(0.3)(0.1)][(0.2)(0.2)] = 0.000096, or about 1 in 10,417.



Again, the validity of the multiplication rule depends on the absence of population substructure, because only in this special case are the different alleles statistically uncorrelated with one another.

In a population that contains groups with characteristic allele frequencies, knowledge of one allele in a person's genotype might carry some information about the group to which the person belongs, and this in turn alters the statistical expectation for the other alleles in the genotype. For example, a person who has one allele that is common among Italians is more likely to be of Italian descent and is thus more likely to carry additional alleles that are common among Italians. The true genotype frequency is thus higher than would be predicted by applying the multiplication rule and using the average frequency in the entire population.

To illustrate the problem with a hypothetical example, suppose that a particular allele at a VNTR locus has a 1% frequency in the general population, but a 20% frequency in a specific subgroup. The frequency of homozygotes for the allele would be calculated to be 1 in 10,000 according to the allele frequency determined by sampling the general population, but would actually be 1 in 25 for the subgroup. That is a hypothetical and extreme example, but illustrates the potential effect of demography on gene frequency estimation.

### Basis of Concern About Population Substructure

The key question underlying the use of the multiplication rule is whether actual populations have significant substructure for the loci used for forensic typing. This has provoked considerable debate among population geneticists: some have expressed serious concern about the possibility of significant substructure,[2,4,9,10] and others consider the likely degree of substructure not great enough to affect the calculations significantly.[1,3,6,8,11-13]

The population geneticists who urge caution make three points:

1. Population genetic studies show some substructure within racial groups for genetic variants, including protein polymorphisms, genetic diseases, and DNA polymorphisms. Thus, North American Caucasians, blacks, Hispanics, Asians, and Native Americans are not homogeneous groups. Rather, each group is an admixture of subgroups with somewhat different allele frequencies. Allele frequencies have not yet been homogenized, because people tend to mate within these groups.

2. For any particular genetic marker, the degree of subpopulation differentiation cannot be predicted, but must be determined empirically.

3. For the loci used for forensic typing, there have been too few empirical investigations of subpopulation differentiation.

In short, those population geneticists believe that the absence of substructure cannot be assumed, but must be proved empirically (see Lewontin and Hartl[10]). Other population geneticists, while recognizing the possibility or likelihood of population substructure, conclude that the evidence to date suggests that the effect on estimates of genotype frequencies are minimal (see Chakraborty and Kidd[12]). Recent empirical studies concerning VNTR loci[13, 14] (Weir, personal communication, 1991) detected no deviation from independence within or across loci. Moreover, pairwise comparisons of all five-locus DNA profiles in the FBI database showed no exact matches; the closest match was a single three-locus match among 7.6 million pairwise comparisons.[13] These studies are interpreted as indicating that multiplication of gene frequencies across loci does not lead to major inaccuracies in the calculation of genotype frequency—at least not for the specific polymorphic loci examined.

Although mindful of the controversy, the committee has chosen to assume for the sake of discussion that population substructure may exist and provide a method for estimating population frequencies in a manner that adequately accounts for it. Our decision is based on several considerations:

1. It is possible to provide conservative estimates of population frequency, without giving up the inherent power of DNA typing.

2. It is appropriate to prefer somewhat conservative numbers for forensic DNA typing, especially because the statistical power lost in this way can often be recovered through typing of additional loci, where required.

3. It is important to have a general approach that is applicable to any loci used for forensic typing. Recent empirical studies pertain only to the population genetics of the VNTR loci in current use. However, we expect forensic DNA typing to undergo much change over the next decade—including the introduction of different types of DNA polymorphisms, some of which might have different properties from the standpoint of population genetics.

4. It is desirable to provide a method for calculating population frequencies that is independent of the ethnic group of the subject.

## Assessing Population Substructure Requires Direct Sampling of Ethnic Groups

How can one address the possibility of population substructure? In principle, one might consider three approaches: (1) carry out population studies on a large mixed population, such as a racial group, and use statistical tests to detect the presence of substructure; (2) derive theoretical principles that place bounds on the possible degree of population substructure; and (3) directly sample different groups and compare the observed allele frequencies. The third offers the soundest foundation for assessing population substructure, both for existing loci and for many new types of polymorphisms under development.



In principle, population substructure can be studied with statistical tests to examine deviations from Hardy-Weinberg equilibrium and linkage equilibrium. Such tests are not very useful in practice, however, because their statistical power is extremely low: even large and significant differences between subgroups will produce only slight deviations from Hardy-Weinberg expectations. Thus, the absence of such deviations does not provide powerful evidence of the absence of substructure (although the presence of such deviations provides strong evidence of substructure).

The correct way to detect genetic differentiation among subgroups is to sample the subgroups directly and to compare the frequencies. The following example is extreme and has not been observed in any U.S. population, but it illustrates the difference in power. Suppose that a population consists of two groups with different allele frequencies at a diallelic locus:

| | A | a |
|---|---|---|
| Group I | 0.5 | 0.5 |
| Group II | 0.9 | 0.1 |

If there is random mating within the groups, Hardy-Weinberg equilibrium within the groups will produce these genotype frequencies:

| | AA | Aa | aa |
|---|---|---|---|
| Group I | 0.25 | 0.50 | 0.25 |
| Group II | 0.81 | 0.18 | 0.01 |

Suppose that Group I is 90% of the population and Group II is 10%. In the overall population, the observed genotype frequencies will be

$$AA = (0.9)(0.25) + (0.1)(0.81) = 0.306$$
$$Aa = (0.9)(0.50) + (0.1)(0.18) = 0.468$$
$$aa = (0.9)(0.25) + (0.1)(0.01) = 0.226$$

If we were unaware of the population substructure, what would we expect under Hardy-Weinberg equilibrium? The average allele frequencies will be

$$A = (0.9)(0.5) + (0.1)(0.9) = 0.54$$
$$a = (0.9)(0.5) + (0.1)(0.1) = 0.46$$

which would correspond to the Hardy-Weinberg proportions of

AA = (0.54)(0.54) = 0.2916
Aa = 2(0.54)(0.46) = 0.4968
aa = (0.46)(0.46) = 0.2116

Even though there is substantial population substructure, the proportions do not differ greatly from Hardy-Weinberg expectation. In fact, one can show that detecting the population differentiation with the Hardy-Weinberg test would require a sample of nearly 1,200, whereas detecting it by direct examination of the subgroups would require a sample of only 22. In other words, the Hardy-Weinberg test is very weak for testing substructure.

The lack of statistical power to detect population substructure makes it difficult to detect genetic differentiation in a heterogeneous population. Direct sampling of subgroups is required, rather than examining samples from a large mixed population.

Similarly, population substructure cannot be predicted with certainty from theoretical considerations. Studies of population substructure for protein polymorphisms cannot be used to draw quantitative inferences concerning population substructure for VNTRs, because loci are expected to show different degrees of population differentiation that depend on such factors as mutation rate and selective advantage. Differences between races cannot be used to provide a meaningful upper bound on the variation within races. Contrary to common belief based on difference in skin color and hair form, studies have shown that the genetic diversity between subgroups within races is greater than the genetic variation between races.[15] Broadly, the results of the studies accord with the theory of genetic drift: the average allele frequency of a large population group (e.g., a racial group) is expected to drift more slowly than the allele frequencies of the smaller subpopulations that it comprises (e.g., ethnic subgroups).

In summary, population differentiation must be assessed through direct studies of allele frequencies in ethnic groups. Relatively few such studies have been published so far, but some are under way.[16] Clearly, additional such studies are desirable.

### The Ceiling Principle: Accounting for Population Substructure

We describe here a practical and sound approach for accounting for possible population substructure: the ceiling principle.[9] It is based on the following observation: The multiplication rule will yield conservative estimates, even for a substructured population, provided that the allele frequencies used in the calculation exceed the allele frequencies in any of the population subgroups. Accordingly, applying the ceiling principle involves two steps: (1) For each allele at each locus, determine a *ceiling frequency* that is an upper bound for the allele frequency that is independent of the ethnic background of a subject; and (2) To calculate a genotype frequency, apply the multiplication rule, using the ceiling frequencies for the allele frequencies.



How should ceiling frequencies be determined? We must balance rigor and practicality. On the one hand, it is not enough to sample broad populations defined as "races" in the U.S. census (e.g., Hispanics), because of the possibility of substructure. On the other hand, it is not feasible or reasonable to sample every conceivable subpopulation in the world to obtain a guaranteed upper bound. The committee strongly recommends the following approach: Random samples of 100 persons should be drawn from each of 15-20 populations, each representing a group relatively homogeneous genetically; the largest frequency in any of these populations or 5%, whichever is larger, should be taken as the ceiling frequency. The reason for using 5% is discussed later.

We give a simplified example to illustrate the approach. Suppose that two loci have been studied in three population samples, with the following results:

| | Population 1 | Population 2 | Population 3 |
|---|---|---|---|
| Locus 1 | | | |
| Allele a | 1% | 5% | 11% |
| Allele b | 5% | 8% | 10% |
| Locus 2 | | | |
| Allele c | 3% | 4% | 4% |
| Allele d | 2% | 15% | 7% |

For the genotype consisting of a/b at locus 1 and c/d at locus 2, the ceiling principle would assign ceiling values of 11% for allele a, 10% for allele b, 5% for allele c, and 15% for allele d and would apply the multiplication rule to yield a genotype frequency of [2(0.11)(0.10)][2(0.05)(0.15)] = 0.00033, or about 1 in 3,000. Note that the frequency used for allele c is 5%, rather than 4%, to reflect the recommended lower bound of 5% on allele frequencies. Because the calculation uses an upper bound for each allele frequency, it is believed to be conservative given the available data, even if there are correlations among alleles because of population substructure and even for persons of mixed or unknown ancestry. This is more conservative, and preferable, to taking the highest frequency calculated for any of the three populations.

The ceiling principle reflects a number of important scientific and policy considerations:

- The purpose of sampling various populations is to examine whether some alleles have considerably higher frequencies in particular subgroups than in the general population—presumably because of genetic drift. It is

matches at such alleles that might be accorded too much evidentiary weight, if the general population frequency were used in calculating the probability of a match.

• Determining whether an allele has especially high frequency does not require a very large sample. A collection of 100 randomly chosen people provides a sample of 200 alleles, which is quite adequate for estimating allele frequencies.

• Genetically homogeneous populations from various regions of the world should be examined to determine the extent of variation in allele frequency. Ideally, the populations should span the range of ethnic groups that are represented in the United States—e.g., English, Germans, Italians, Russians, Navahos, Puerto Ricans, Chinese, Japanese, Vietnamese, and West Africans. Some populations will be easy to sample through arrangements with blood banks in the appropriate country; other populations might be studied by sampling recent immigrants to the United States. The choice and sampling of the 15-20 populations should be supervised by the National Committee on Forensic DNA Typing (NCFDT) described in Chapter 2.

We emphasize, however, that it is not necessary to be comprehensive. The goal is not to ensure that the ethnic background of every particular defendant is represented, but rather to define the likely range of allele frequency variation.

• Because only a limited number of populations can be sampled, it is necessary to make some allowance for unexamined populations. As usual, the problem is rare alleles. Genetic drift has the greatest proportional effect on rare alleles and may cause substantial variation in their frequency. Even if one sees allele frequencies of 1% in several ethnic populations, it is not safe to conclude that the frequency might not be five-fold higher in some subgroups.

To overcome this problem, we recommend that ceiling frequencies be 5% or higher. We selected this threshold because we concluded that allele frequency estimates that were substantially lower would not provide sufficiently reliable predictors for other, unsampled subgroups. Our reasoning was based on population genetic theory and computational results, and we aimed at accounting for the effects of sampling error and for genetic drift. The latter consideration was especially important, because it scales inversely with effective population size (i.e., small populations have larger drift) and because it accumulates over generations. The use of such a ceiling frequency would correspond to a lower bound of 5% on allele frequencies. Even if one observed allele frequencies of about 1%, one would guard against the possibility that the frequency in a subpopulation had drifted higher by using the lower bound of 5%. Thus, the lowest frequency attributable to any single locus would be 1/400 (1/20 × 1/20). In any case, it seems reasonable not to attach much greater weight to any single locus.



• The ceiling principle yields the same frequency for a genotype, regardless of the suspect's ethnic background, because the reported frequency represents a maximum for any possible ethnic heritage. Accordingly, the ethnic background of an individual suspect should be ignored in estimating the likelihood of a random match. The calculation is fair to suspects, because the estimated probabilities are likely to be conservative in their incriminating power.

Some legal commentators have pointed out that frequencies should properly be based on the population of possible perpetrators, rather than on the population to which a particular suspect belongs.[17,18] Although that argument is formally correct, practicalities often preclude use of that approach. Furthermore, the ceiling principle eliminates the need for investigating the perpetrator population, because it yields an upper bound to the frequency that would be obtained by that approach.

Some have proposed a Bayesian approach,[19-21] to the presentation of DNA evidence. However, this approach, focusing on likelihood ratios, does not avoid the kinds of population genetic problems discussed in this chapter. The committee has not tried to assess the relative merits of Bayesian and frequentist approaches, because, outside the field of paternity testing, no forensic laboratory in this country has, to our knowledge, used Bayesian methods to interpret the implications of DNA matches in criminal cases.

• Although the ceiling principle is a conservative approach, we feel that it is appropriate, because DNA typing is unique in that the forensic analyst has an essentially unlimited ability to adduce additional evidence. Whatever power is sacrificed by requiring conservative estimates can be regained by examining additional loci. (Although there could be cases in which the DNA sample is insufficient for typing additional loci with RFLPs, this limitation is likely to disappear with the eventual use of PCR.) A conservative approach imposes no fundamental limitation on the power of the technique.

## DETERMINING ALLELE FREQUENCIES IN A POPULATION DATABANK

For forensic purposes, the frequency of an allele in a laboratory's databank should be calculated by counting the number of alleles that would be regarded as a match with the laboratory's forensic matching rule, which should be based on the empirical reproducibility of the system. This matching rule must account for both the quantitative reproducibility of forensic

measurements in the testing laboratory and the quantitative reproducibility of the population measurements in the laboratory that generated the databank. In addition, the matching rule should reflect that one is making inter-gel comparisons, which are typically less precise than intra-gel comparisons.

The above approach is sometimes referred to as "floating bins," in that one counts the alleles that fall into a "bin" centered on the allele of interest. Most forensic laboratories in this country use the slightly different approach of "fixed bins":[22] One first aggregates alleles into a predetermined set of bins. Given an allele in a forensic case, one must then compute its frequency by adding the frequencies of all the bins that contain any alleles that fall within the window specified by the laboratory's forensic matching rule. (All bin frequencies must be added; it is not enough to take the largest of the bin frequencies.) This fixed-bin approach is acceptable and might be more convenient in some settings, because examiners need only consult a short table of bin frequencies, rather than search an entire databank.

## IMPLICATIONS OF GENETIC CORRELATIONS AMONG RELATIVES

Because of the laws of Mendelian inheritance, the genotypes of biological relatives are much more similar than those of random individuals. Parent and child share exactly one identical allele at every locus, sibs share an average of one identical allele per locus, and grandparent and grandchild share an average of 0.5 identical allele per locus. (Here, identical refers to identity by descent from a common ancestor. Relatives can share additional alleles simply by chance.) These facts have important consequences for DNA typing:

• The genetic correlation between relatives makes it possible to carry out parentage and grandparentage testing. Paternity testing with DNA typing is already an active industry in the United States, and grandmaternity testing (with mitochondrial DNA, as well as nuclear genes) has been used in Argentina to reunite families with children who were abducted during the military dictatorship in the 1970s.[23,24] Relatedness testing involves a question analogous to that asked in identity testing: What is the chance that a randomly chosen person in the population would show the degree of relatedness expected of a relative? The same basic methods of population genetics apply, as discussed earlier.

• The ability to recognize relatedness poses a novel privacy issue for DNA databanks. Many states are starting to compile databanks that record patterns of DNA from convicted criminals, but not from other citizens, with the hope of identifying recidivists. When a biological sample is found at the scene of a crime, its DNA pattern can be determined and compared with a databank. If the unidentified sample perfectly matches a sample in the convicted-criminal databank at enough loci, the probable perpetrator is likely to have been found. However, a different outcome could occur: the sample might match no entry perfectly, but match some entry at about one allele per locus. Depending on the number of loci studied, one could have a compelling case that the source of the sample was a first-degree relative (e.g., brother) of the convicted criminal whose entry was partially matched. (In practice, four loci would not suffice for this conclusion, but 10 might.) Such information could be sufficient to focus police attention on a few persons and might be enough to persuade a court to compel a blood sample that could be tested for exact match with the sample.



To put it succinctly, DNA databanks have the ability to point not just to individuals but to entire families—including relatives who have committed no crime. Clearly, this poses serious issues of privacy and fairness. As we discuss more fully later (Chapter 5), it is inappropriate, for reasons of privacy, to search databanks of DNA from convicted criminals in such a fashion. Such uses should be prevented both by limitations on the software for search and by statutory guarantees of privacy.

• Finally, the genetic correlation among relatives warrants caution in the statistical interpretation of DNA typing results. Our discussion above focused on the probability that a forensic sample would by chance match a person randomly chosen from the population. However, the probability that the forensic sample would match a relative of the person who left it is considerably greater than the probability that it would match a random person. Indeed, two sibs will often have matching genotypes at a locus—they have a 25% chance of inheriting the same pair of alleles from their parents and a 50% chance of inheriting one allele in common (which will result in identical genotypes if their other alleles happen to match by chance). Roughly speaking, the probability of a match at k loci will be approximately $(0.25 + 0.5p + 2p^2)^k$ in the general population, where p is the average chance that two alleles will match (i.e., the apparent homozygosity rate). Using p = 10% per locus for illustration, the probability that two sibs match at two loci would be about 10% and at four loci about 1%. Even for DNA profiles consisting entirely of very rare alleles (p~0%), the probability that two sibs will match at two loci is about 6% and at four loci about 0.3%. In short, the probability that two relatives will have matching genotypes is much greater than for two randomly chosen persons. Whenever there is a possibility that a suspect is not the perpetrator but is related to the perpetrator, this issue should be pointed out to the court. Relatives of a suspect could be excluded, of course, by testing their genotypes directly, provided that their DNA could be obtained.

## IMPLICATIONS OF INCREASED POWER OF DNA TYPING COMPARED WITH CONVENTIONAL SEROLOGY

Questions about the population genetics of DNA markers remain open, but it is clear that the forensic scientist's discriminatory power has been substantially expanded with the advent of DNA markers. Indeed, forensic laboratories are routinely finding cases in which a suspect is included through conventional serology but later excluded through testing with DNA markers. The FBI reports, for example, that some 33% of suspects that match evidence samples according to conventional serology turn out to be excluded through DNA typing (J. W. Hicks, presentation to committee, 1990). Such outcomes represent a dramatic success of the new technology and often lead to the exoneration of innocent suspects.

## LABORATORY ERROR RATES

Interpretation of DNA typing results depends not only on population genetics, but also on laboratory error. Two samples might show the same DNA pattern for two reasons: two persons have the same genotype at the loci studied, or the laboratory has made an error in sample handling, procedure, or interpretation. Coincidental identity and laboratory error are different phenomena, so the two cannot and should not be combined in a single estimate. However, both should be considered.

Early in the application of the DNA approach, results from nonblind proficiency studies suggested a high rate of false positives due to laboratory error. One commercial laboratory reported one false match in 50 samples in each of the first two blind proficiency tests conducted by the California Association of Crime Laboratory Directors (CACLD).[25] The error was attributed to incorrect sample loading in the first test and to mixing of DNA samples (because of reagent contamination) in the second. Another commercial laboratory reported no false positives in the two CACLD tests, but is reported to have made errors related to sample mixup in actual casework in *New York v. Neysmith*[26] and in the matter of a dead infant found in the Rock Creek area of Erie, Ill.[27] A third commercial laboratory made one error in 50 samples in the first CACLD test, but none in later blind trial testing. Estimates of laboratory errors in more recent practice are not available because of the lack of standardized proficiency testing.

Proficiency testing has also revealed important instances of false negatives. In the second CACLD test, the second laboratory cited failed to detect that two samples were 1:1 mixtures from two donors. Similarly, the first laboratory cited failed to detect several 1:1 mixtures and, in one case, reported that a stain from one person was a mixture. Those results raised serious questions about the reliability of interpretation of mixed samples.



Especially for a technology with high discriminatory power, such as DNA typing, laboratory error rates must be continually estimated in blind proficiency testing and must be disclosed to juries. For example, suppose the chance of a match due to two persons' having the same pattern were 1 in 1,000,000, but the laboratory had made one error in 500 tests. The jury should be told both results; both facts are relevant to a jury's determination.

Laboratory errors happen, even in the best laboratories and even when the analyst is certain that every precaution against error was taken. It is important to recognize that laboratory errors on proficiency tests do not necessarily reflect permanent probabilities of false-positive or false-negative results. One purpose of regular proficiency testing under standard case conditions is to evaluate whether and how laboratories have taken corrective action to reduce error rates. Nevertheless, a high error rate should be a matter of concern to judges and juries.

Reported error rates should be based on proficiency tests that are truly representative of case materials (with respect to sample quality, accompanying description, etc.). Tests based on pure blood samples would probably underestimate an error rate, and tests based primarily on rare and extremely difficult samples (which might be useful for improving practice) would probably overestimate. Although the CACLD proficiency test was less than ideal (being open, rather than blind, and not requiring reporting of size measurements), the materials appear to have been representative of standard casework.

## TOWARD A FIRM FOUNDATION FOR STATISTICAL INTERPRETATION

Statistical interpretation of DNA typing evidence has probably yielded the greatest confusion and concern for the courts in the application of DNA to forensic science. Some courts have accepted the multiplication rule based on the grounds of allelic independence, others have used various ad hoc corrections to account for nonindependence, and still others have rejected probabilities altogether. Some courts have ruled that it is unnecessary even to test allelic independence, and others have ruled that allelic independence cannot be assumed without proof. The confusion is not surprising, inasmuch as the courts have little expertise in population genetics or statistics.

In reaching a recommendation on statistical interpretation of population frequencies, the committee balanced the following considerations:

- DNA typing should be able to provide virtually absolute individual identification (except in the case of identical twins), provided that enough loci are studied and that the population-genetics studies are developed with

appropriate scientific care. The importance of this long-term goal justifies substantial investment in ensuring that the underlying population-genetics foundation is firm.

- Statistical testimony should be based on sound theoretical principles and empirical studies. Specifically, the validity of the multiplication rule in any application depends on the empirical degree of population differentiation for the loci involved. Adequate empirical data must be collected, and appropriate adjustments must be made to reflect the remaining uncertainties.
- It is feasible and important to estimate the degree of variability among populations to determine ceiling frequencies for forensic DNA markers and to evaluate the impact of population substructure on genotype frequencies estimated with the multiplication rule.
- Careful population genetics is especially important for the development and use of databanks of convicted-offender DNA patterns. Whereas the comparison of an evidence sample to a single suspect involves testing only one hypothesis, the comparison of a sample to an entire databank involves testing many alternative hypotheses. Special attention must thus be paid to the possibility of coincidental matches.

On the basis of those considerations, the committee reached conclusions, which now will be discussed.

### Population Studies to Set Ceiling Frequencies

In view of the long-term importance of forensic DNA typing, the population-genetics foundation should be made as secure as possible. Accordingly, population studies should be promptly initiated to provide valid estimation of ceiling frequencies, as described above. Specifically, variation in allele frequencies should be examined in appropriately drawn random samples from various populations that are genetically relatively homogeneous. The selection, collection, and analysis of such samples should be overseen by the National Committee on Forensic DNA Typing (NCFDT) recommended in Chapter 2.

Given the effort involved in drawing appropriate population samples and the continuing need to type new markers as the technology evolves, the samples should be maintained as immortalized cell lines in a cell repository; that would make an unlimited supply of DNA available to all interested investigators. We note that preparation of immortalized cell lines through transformation of lymphoblasts with Epstein-Barr virus is routine and cost-effective. Transformation and storage can be handled as contract services offered by existing cell repositories, such as the NIH-supported repository in Camden, N.J.



Such a cell repository would be analogous to that of the international consortium Centre d'Etude du Polymorphisme Humain (CEPH)[28] created in 1983. It holds some 1,000 samples from 60 reference families, which are used for genetic mapping of human chromosomes. The cell lines have played an essential role in the development of the human genetic-linkage map. The existence of a common resource has also promoted standardization and quality control through the ability to recheck samples. (We should note that the CEPH families themselves are not appropriate for studying population frequencies, because they represent closely related people in a small number of families.)

Substantial benefits will accrue to forensic DNA typing through the availability of a reference collection that can be maintained at an existing facility like the ones at the Coriell Institute of Medical Research and the American Type Culture Collection. Although there is an initial investment in collecting, transforming, and storing cells, the cost will be more than repaid in the broad and continued availability of well-chosen samples for population studies of newly developed DNA typing systems and the ability of investigators to confirm independently the DNA typing that was done in another laboratory.

### Reporting of Statistical Results

Until ceiling frequencies can be estimated from appropriate population studies, we recommend that estimates of population frequencies be based on existing data by applying conservative adjustments:

1. First, the testing laboratory should check to see that the observed multilocus genotype matches any sample in its population database. Assuming that it does not, it should report that the DNA pattern was compared to a database of N individuals from the population and no match was observed, indicating its rarity in the population. This simple statement based on the counting principle is readily understood by jurors and makes clear the size of the database being examined.

2. The testing laboratory should then calculate an estimated population frequency on the basis of a conservative modification of the ceiling principle, provided that population studies have been carried out in at least three major "races" (e.g., Caucasians, blacks, Hispanics, Asians, and Native Americans) and that statistical evaluation of Hardy-Weinberg equilibrium and linkage disequilibrium has been carried out (with methods that accurately incorporate the empirically determined reproducibility of band measurement) and no significant deviations were seen. The conservative calculation represents a reasonable effort to capture the actual power of DNA typing while reflecting the fact that the recommended population studies have not yet

For each allele, a modified ceiling frequency should be determined by (1) calculating the 95% upper confidence limit for the allele frequency in each of the existing population samples and (2) using the largest of these values or 10%, whichever is larger. The use of the 95% upper confidence limit represents a pragmatic approach to recognize the uncertainties in current population sampling. The use of a lower bound of 10% (until data from ethnic population studies are available) is designed to address a remaining concern that populations might be substructured in unknown ways with unknown effect and the concern that the suspect might belong to a population not represented by existing databanks or a subpopulation within a heterogeneous group. We note that a 10% lower bound is recommended while awaiting the results of the population studies of ethnic groups, whereas a 5% lower bound will likely be appropriate afterwards. In the context of the discussion of the ceiling principle, the higher threshold reflects the greater uncertainty in using allele frequency estimates as predictors for unsampled subpopulations.

Once the ceiling for each allele is determined, the multiplication rule should be applied. The race of the suspect should be ignored in performing these calculations.

Regardless of the calculated frequency, an expert should—given with the relatively small number of loci used and the available population data—avoid assertions in court that a particular genotype is unique in the population. Finally, we recommend that the testing laboratory point out that reported population frequency, although it represents a reasonable scientific judgment based on available data, is an estimate derived from assumptions about the U.S. population that are being further investigated.

As an example, suppose that a suspect has genotype A1/A2, B1/B2 at loci A and B and that three U.S. populations have been sampled in the current "convenience sample" manner and typed for these loci. The likelihood of a match for this two-locus genotype would be estimated as follows:

| | Population 1 | Population 2 | Population 3 | Derived frequency |
|---|---|---|---|---|
| | 750 persons | 500 persons | 200 persons | |
| Locus A | | | | |
| Allele A1 | 0.003 | 0.013 | 0.042 | Use 0.10 |
| Allele A2 | 0.112 | 0.086 | 0.124 | $0.124 + 0.032 = 0.156$[a] |
| Locus B | | | | |
| Allele B1 | 0.004 | 0.007 | 0.014 | Use 0.10 |
| Allele B2 | 0.228 | 0.078 | 0.218 | $0.228 + 0.021 = 0.249$[a] |
| Loci A and B combined | | $[2(0.10)(0.156)][2(0.10)(0.249)] = 0.001554$ | | |

[a]The upper 95% confidence limit is given by the formula $p + 1.96\sqrt{p(1-p)/N}$, where p is the observed frequency and N is the number of chromosomes studied.



A frequency of 0.001554 corresponds to about 1 in 644 persons. Addition of two loci with about the same information content would yield a four-locus genotype frequency of about 1 in 414,000 persons. Of course, if fewer than four loci were interpretable, as is common in forensic typing, the estimated genotype frequency would be much higher.

Significantly more statistical power for the same loci will be available when appropriate population studies have been carried out, because the availability of data based on a more rigorous sampling scheme will make it unnecessary to take an upper 95% confidence limit for each allele frequency nor to put such a conservative lower bound (0.10) on each allele frequency. Assuming that the population studies do not reveal significant substructure, the 5% lower bound recommended earlier should be used.

Finally, once appropriate population studies have been conducted and ceiling frequencies estimated under the auspices of NCFDT, population frequency estimates can be based on the ceiling principle (rather than the modified ceiling principle discussed above). Such calculations can never be perfect, but we believe that such a foundation will be sufficient for calculating frequencies that are prudently cautious—i.e., for calculating a lower limit of the frequency of a DNA pattern in the general population. In addition, new scientific techniques (e.g., minisatellite repeat codings[29]) are being and will be developed and might require re-examination by NCDFT of the statistical issues raised here.

Our recommendations represent an attempt to lay a firm foundation for DNA typing that will be able to support the increasing weight that will be placed on such evidence in the coming years. We recognize that a wide variety of methods for population genetics calculations have been used in previous cases—including some that are less conservative than the approach recommended here. We emphasize that our recommendations are not intended to question previous cases, but rather to chart the most prudent course for the future.

## Openness of Population Databanks

Any population databank used to support forensic DNA typing should be openly available for reasonable scientific inspection. Presenting scientific conclusions in a criminal court is at least as serious as presenting scientific conclusions in an academic paper. According to long-standing and wise scientific tradition, the data underlying an important scientific conclusion must be freely available, so that others can evaluate the results and publish their own findings, whether in support or in disagreement. There is no excuse for secrecy concerning the raw data. Protective orders are inappropriate, except for those protecting individual's names and other identifying information, even for data that have not yet been published or for data

claimed to be proprietary. If scientific evidence is not yet ready for both scientific scrutiny and public re-evaluation by others, it is not yet ready for court.

### Reporting of Laboratory Error Rates

Laboratory error rates should be measured with appropriate proficiency tests and should play a role in the interpretation of results of forensic DNA typing. As discussed above, proficiency tests provide a measure of the false-positive and false-negative rates of a laboratory. Even in the best of laboratories, such rates are not zero.

A laboratory's overall rate of incorrect conclusions due to error should be reported with, but separately from, the probability of coincidental matches in the population. Both should be weighed in evaluating evidence.

## SUMMARY OF RECOMMENDATIONS

Although mindful of the controversy concerning the population genetics of DNA markers, the committee has decided to assume that population substructure might exist for currently used DNA markers or for DNA markers that will be used in the future. The committee has sought to develop a recommendation on the statistical interpretation of DNA typing that is appropriately conservative, but at the same time takes advantage of the extraordinary power of individual identification provided by DNA typing. We have sought to develop a recommendation that is sufficiently robust, but is flexible enough to apply not only to markers now used, but also to markers that might be technically preferable in the future. We point out that in using conservative numbers in the interpretation of DNA typing results, any loss of statistical power is often offset through typing of additional loci. The committee seeks to eliminate the necessity to consider the ethnic background of a subject or of the group of potential perpetrators.

- As a basis for the interpretation of the statistical significance of DNA typing results, the committee recommends that blood samples be obtained from 100 randomly selected persons in each of 15-20 relatively homogeneous populations; that the DNA in lymphocytes from these blood samples be used to determine the frequencies of alleles currently tested in forensic applications; and that the lymphocytes be "immortalized" and preserved as a reference standard for determination of allele frequencies in tests applied in different laboratories or developed in the future. The collection of samples and their study should be overseen by a National Committee on Forensic DNA Typing.
- Sample collection and immortalization should be supported by federal funds, in view of the benefits for law enforcement in general and for the convicted-offender databanks in particular.
- The ceiling principle should be used in applying the multiplication rule for estimating the frequency of particular DNA profiles. For each allele in a person's DNA pattern, the highest allele frequency found in any of the 15-20 populations or 5% (whichever is larger) should be used.
- In the interval (which should be short) while the reference samples are being collected, the significance of the findings of multilocus DNA typing should be presented in two ways: 1) If no match is found with any sample in a total databank of N persons (as will usually be the case), that should be stated, thus indicating the rarity of a random match. 2) In applying the multiplication rule, the 95% upper confidence limit of the frequency of each allele should be calculated for separate U.S. "racial" groups and the highest of these values or 10% (whichever is the larger) should be used. Data on at least three major "races" (e.g., Caucasians, blacks, Hispanics, Asians, and Native Americans) should be analyzed.
- Any population databank used to support DNA typing should be openly available for scientific inspection by parties to a legal case and by the scientific community.
- Laboratory error rates should be measured with appropriate proficiency tests and should play a role in the interpretation of results of forensic DNA typing.



## REFERENCES

1. Devlin B, Risch N, Roeder K. No excess of homozygosity at loci used for DNA fingerprinting. Science. 249:1416-1420, 1990.
2. Cohen JE, Lynch M, Taylor CE, Green P, Lander ES. Forensic DNA tests and Hardy-Weinberg equilibrium. (Comment on Devlin et al. Science. 249:1416-1420, 1990.) Science. 253:1037-1039, 1991.
3. Devlin B, Risch N, Roeder K. (Response to Cohen et al. Science. 253:1037-1039, 1991). Science. 253:1039-1041, 1991.
4. Lander ES. Research on DNA typing catching up with courtroom application. (Invited Editorial.) Am J Hum Genet. 48:819-823, 1991.
5. Wooley JR. A response to Lander: The courtroom perspective. Am J Hum Genet. 49:892-893, 1991.
6. Caskey CT. Comments on DNA-based forensic analysis. (Response to Lander. Am J Hum Genet. 48:819, 1991.) Am J Hum Genet. 49:893-905, 1991.
7. Chakraborty R. Statistical interpretation of DNA-typing data. (Letter.) Am J Hum Genet. 49:895-897, 1991.
8. Daiger SP. DNA fingerprinting. (Letter.) Am J Hum Genet. 49:897, 1991.
9. Lander ES. Lander reply. (Letter.) Am J Hum Genet. 49:899-903, 1991.
10. Lewontin RC, Hartl DL. Population genetics in forensic DNA typing. Science. 254:1745-1750, 1991.
11. Chakraborty R, Daiger SP. Polymorphisms at VNTR loci suggest homogeneity of the white population of Utah. Hum Biol. 63:571-588, 1991.

12. Chakraborty R, Kidd K. The utility of DNA typing in forensic work. Science. 254:1735-1739, 1991.
13. Risch N, Devlin B. On the probability of matching DNA fingerprints. Science. 255:717-720, 1992.
14. Weir B. Independence of VNTR alleles defined as fixed bins. Genetics, in press.
15. Lewontin RC. The apportionment of human diversity. Evol Biol. 6:381-398, 1972.
16. Deka R, Chakraborty R, Ferrell RE. A population genetic study of six VNTR loci in three ethnically defined populations. Genomics. 11:83-92, 1991.
17. Cavalli-Sforza LL, Bodmer WF. The genetics of human populations. San Francisco: W.H. Freeman, 1971.
18. Lempert R. Some caveats concerning DNA as criminal identification evidence: with thanks to the Reverend Bayes. Cardozo Law Rev. 13:303-341, 1991.
19. Evett I, Werrett D, Pinchin R, Gill P. Bayesian analysis of single locus DNA profiles. Proceedings of the International Symposium on Human Identification 1989. Madison, Wisconsin: Promega Corp., 1990.
20. Berry DA. Influences using DNA profiling in forensic identification and paternity cases. Stat Sci. 6:175-205, 1991.
21. Berry DA, Evett IW, Pinchin R. Statistical inferences in crime investigation using DNA profiling. J Royal Stat Soc. [Series C - Applied Statistics], in press.
22. Budowle B, Giusti AM, Waye JS, Baechtel FS, Fourney RM, Adams DE, Presley LA, Deadman HA, Monson KL. Fixed-bin analysis for statistical evaluation of continuous distributions of allelic data from VNTR loci, for use in forensic comparisons. Am J Hum Genet. 48-841-855, 1991.
23. DiLonardo AM, Darlu P, Baur M, Orrego C, King MC. Human genetics and human rights: identifying the families of kidnapped children. Am J Forensic Med Pathol. 5:339-347, 1984.
24. King MC. An application of DNA sequencing to a human rights problem. Pp. 117-132 in: Friedmann T, ed. Molecular Genetic Medicine. Vol. 1. New York: Academic Press, 1991.
25. California Association of Crime Laboratory Directors. DNA Committee, Reports to the Board of Directors: 1, August 25, 1987; 2, November 19, 1987; 3, March 28, 1988; 4, May 18, 1988; 5, October 1, 1988; 6, October 1, 1988.
26. Lander ES. DNA fingerprinting on trial. (Commentary.) Nature. 339:501-505, 1989.
27. The fallibility of forensic DNA testing: of proficiency in public and private laboratories. Part I. The private sphere. Sci Sleuth Rev. 14(2):10, 1990.
28. Dausset J, Cann H, Cohen D, Lathrop M, Lalouel J-M, White R. Centre d'Etude du Polymorphisme Humain (CEPH): collaborative genetic mapping of the human genome. Genomics. 6:575-577, 1990.
29. Jeffreys A, MacLeod A, Tamaki K, Neil D, Monckton D. Minisatellite repeat coding as a digital approach to DNA typing. Nature. 354:204-209, 1991.