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BUREAU OF CRIMINAL APPREHENSION: Scientist sees DNA flaws in database

BY AMY BECKER

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Flaws in a state Bureau of Criminal Apprehension database affect expert testimony in criminal cases that feature complex DNA evidence, one scientist says.

Closely related people were included in the population databases, said Dr. Dan Krane, an associate professor of biological science at Wright State University in Dayton, Ohio. Those databases are used to make key calculations about matching DNA evidence to criminal defendants.

Krane says the BCA needs to track down the related pairs of people in the database and delete one from each set.

His research came to light in a recent Washington County District Court hearing about whether the current DNA testing method used by the BCA is an accepted science. While Judge Stephen Muehlberg awaits briefs in that matter, Krane is preparing a paper that describes what he calls flaws in the BCA's database.

His work hasn't yet been published or duplicated, so it's too soon for his peers to have thoroughly dissected it. Some other scientists are skeptical about the significance of his findings, yet they acknowledge that Krane's work is focusing on a "problematic" area of DNA evidence.

FROM SUSPECT TO CONVICT

Krane first looked at the BCA's population data when asked by defense lawyers to testify in connection with the murder trial of Tony Allen Roman Nose in July 2001. Roman Nose was convicted of killing Jolene Stuedemann, 18, of Woodbury, and is serving a life sentence in prison. That is, unless Minnesota's high court refuses to accept the current DNA testing method.

First, an overview of how a drop of blood becomes damning testimony.

The sample is taken from the scene to the laboratory, where scientists make multiple copies of particular snips of genetic information. Versions of the genetic material — called alleles — are measured at key locations, called a locus, or loci in the plural. Those measurements result in a

series of numbers. The BCA looks at two alleles at each of 12 loci, resulting in 24 numbers to define a person's genetic fingerprint.

Those numbers are then compared against the BCA population database — 649 people representing African-American, Caucasian, Hispanic and American-Indian populations. BCA staff can just type in the 24 numbers and the computer will calculate the odds of finding that profile in a randomly chosen, unrelated individual.

Krane's study of the BCA database focused on samples that contained DNA from multiple people. He learned two things that surprised him: One, that three-way mixtures can be mistaken for two-way mixtures more often than he had expected; and two, that the BCA data contained a discrepancy that changed his results.

It has generally been believed that it's exceedingly rare to confuse a three-way mixture of DNA with a two-way mixture. Krane's work with the BCA database shows it could happen about 5.5 percent of the time, which would be significant in court, he said.

"I was like, 'Wow!' It was a much larger number than I expected," Krane said. But he took the inquiry a step further. "I wondered: What would happen randomly?"

So he used the same data but split apart the information to make it random.

THE PEZ DISPENSER

Krane describes his test this way. Imagine you have four Pez dispensers with four kinds of candy. If the first candy is red, does that mean it's more likely the next candy will be red? In his experiment, Krane got two answers.

The colors of the candy correspond to the alleles and the location of individual pieces of candy corresponds to the loci where those alleles are found.

Krane essentially examined the sequence of candy in each dispenser in the first test. Then, he took all the candies out of the dispensers, scattered the candies and replaced them in no particular order. Then he compared those patterns and trends with his first look at the Pez dispensers. He should have gotten the same results, but they were slightly different.

His results showed three-way mixtures can masquerade as two-way mixtures 5.3 percent of the time in a random sample vs. 5.5 percent in the original BCA database. That surprised him for two reasons, he said.

It showed that experts in general might have been underestimating mixture interpretations. It also showed the BCA database wasn't as random a sampling of Minnesotans as it was intended to be, Krane said.

BCA representatives already carefully couch their testimony to avoid overstating their findings,

Krane said.

"They are already cautious about this. They may want to be more cautious," he said.

Krane is conducting a similar study on a larger database from the Federal Bureau of Investigation, and his findings so far are comparable, he said.

"These problems with confusing two-way mixtures with three-way mixtures are more common than we thought, and that's what a jury needs to understand," Krane said. "In some (criminal cases), it's going to be important."

"It illustrates the difficulty interpreting unknown mixed samples," said Christine Funk, one of Roman Nose's attorneys. Mixed samples played a key role in his prosecution.

THEORIES OF RELATIVITY

Others disagree with Krane. Paul Scoggin, a Hennepin County prosecutor, goes no further than this: "I consider it a red herring, because the scientific community hasn't accepted what he has to say."

John Fristik, the assistant Washington County attorney who prosecuted Roman Nose, said Krane is merely trying to "tramp down" the statistics to aid the defense. "I'm satisfied the BCA is exercising enough caution in reporting its numbers."

Jim Iverson, a forensic science supervisor with the BCA, said many other scientists have examined the database without finding any significant statistical variation.

But because of how the database was created — with samples from the Memorial Blood Bank of Minneapolis — he couldn't rule out the possibility that related people were included.

"Is it possible we have relatedness in the database? It probably is (possible)," he said. "The entire argument doesn't affect the results at the end of the day. A match is a match."

Experts interviewed for this story said it's best to remove relatives from the database if possible. Yet two people said having relatives in the database wouldn't significantly change the calculations.

Databases will always have undetected relatives, said Dr. Ranagit Chakraborty, the Robert A. Kehoe professor and director of the center for genome information at the University of Cincinnati Medical Center in Ohio.

"If I knew who the relatives were, my recommendation would be to throw them out," Chakraborty said, but because of the way the BCA uses the database, he isn't concerned.

"The BCA approach is scientifically valid," he added.

Dr. George Carmody, an associate professor in the Carleton University biology department in Ottawa, Canada, vetted the BCA database in 1998. Having relatives in the database wouldn't necessarily change the calculations, he said.

"Even with a database of that size (649 people), if you put in a couple of full siblings, say, that's going to have very little impact on the frequencies you derive from these databases to do these calculations," Carmody said. In the club-footed but precise language of science, the odds of finding that profile in a random individual might shift from one in five trillion "to one in a trillion. That's not a dramatic change. That's still a rare occurrence of a profile."

Carmody carefully worked his way through a layperson's example illustrating his point, paused and offered an expert opinion often lost in Minnesota's current legal debate about DNA.

"The law is a pretty clumsy tool to apply to these" esoteric points of population genetics, he said.

Testimony amounts to a battle of experts and the subject quickly skitters beyond the reach of the average juror.

"You get into these areas where people who are not experts, are forced to make decisions," Carmody said.

Krane is exploring an interesting area of DNA research, Carmody added.

"I think mixture interpretation is the one area of DNA that may be problematic," Carmody said.

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