Microarray analysis can identify unsuspected incest

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Researchers using DNA microarrays to diagnose developmental disabilities or congenital anomalies in children may unexpectedly identify that some have been conceived through incest. This raises social and legal issues that institutions and the scientific community must address, said researchers from Baylor College of Medicine in a report that appears in the current issue of the journal *Lancet*.

"We have discussed these issues with legal and ethics experts at Baylor and Texas Children's Hospital, and we are considering how best to handle them," said Dr. Arthur Beaudet, chair of molecular and human genetics at BCM and a senior author of the report. In most states, clinicians are required to report suspicions of child abuse. If it is suspected that the pregnancy was the result of abuse, then that will need to be reported to child protective services and, potentially, law enforcement. The responsibility of the physician is less clear when the mother is an adult, he said. It may depend on her age and family circumstances when she became pregnant.

These findings have social implications as well. The mother may deny that the incest took place, or she may be fearful for the safety of herself and her child if it comes to light.

Scientists identify cases of possible incest through what they call an "absence of heterozygosity." In most instances, an infant receives roughly half of his or her genes from the mother and half from the father. This is called heterozygosity. In the case of incest, family

members, who already share much of their genetic code, each contribute to the genetic material of a child. This will result in absence of heterozygosity in the genes of that child. In other words, children conceived through incest have large blocks of DNA in which genes inherited from the mother and the father are identical.

"In some cases, these regions can account for as much as one-fourth of the genome," said Beaudet. The most common cause for this is that the child was conceived by first-degree relatives, such as a father and a daughter or a brother and a sister.

Because disabilities are frequent in children born of incestuous liaisons, they may come to the attention of experts seeking to identify the source of their problems. The use of single nucleotide polymorphism-based (SNP-based) arrays, usually to identify small deletions or duplications in the genome, can also identify these large identical chunks of DNA.

Beaudet and his co-authors, Drs. Christian P. Schaaf, Daryl A. Scott and Joanna Wiszniewska, all of BCM, recommended that health care institutions establish a committee to discuss these issues and draft practice guidelines that deal with issues of consent, disclosure of results and reporting. Existing ethics committees associated with the American College of Medical Genetics, the American Society of Human Genetics and the European Society of Human Genetics could also draft such guidelines, they said.

More information: http://www.thelancet.com/

Provided by Baylor College of Medicine