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DNA Only Hope for Closure

Many families face an unhappy reality

By Laurie Garrett
STAFF WRITER

As families line up to provide DNA samples to help identify the bodies of loved ones, experts say it's become increasingly clear that many may be forced to find closure in the simple fact that an object retrieved from the Twin Towers debris contains genetic material matching their samples.

Such a report, a grim product of the new biotechnology era, may not satisfy the religious or emotional needs of many. To a remarkable degree, though, it will be accurate and final.

"We've been able to get genetic signatures and DNA out of materials that have been sitting in museums for hundreds of years," said Dr. Stephen O'Brien of the National Cancer Institute in Bethesda, Md. "The oldest I know of is saber-toothed tiger DNA from the La Brea tar pits, dating past 10,000 years. I think if samples [at Ground Zero] are collected up to Christmas, and if it's bigger than a marble, 80 or 90 percent of it will work."

To O'Brien, who probably has performed more DNA matching work than any living scientist, the scale of the World Trade Center effort is "mind-boggling."

Still, "It's doable," he said. "It's just not pretty."

Indeed, experts say that by Christmas, the number of tissue samples expected to be collected could exceed half a million. In most cases, city and federal officials say, tissue and flesh samples now being removed from Ground Zero are the only available evidence that a body existed.

Dr. Charles Hirsch, New York City's medical examiner, said Saturday that thousands of DNA samples are being collected from blood relatives so that investigators can match those samples genetically with tissue found on the scene. Additionally, probers are gathering DNA samples gleaned from such personal items as toothbrushes, combs or razors.

Hirsch said any human tissue that's found at the excavation site is first processed at the city medical examiner's office. The tissue in the best shape is then shipped to Myriad Labs in Salt Lake City for genomic DNA analysis. Smaller or degraded samples go to Celera Corp. and Applied Biosystems in Rockville, Md., which has the ability to do more sensitive mitochondrial DNA analysis.

It's been five months since Celera and the National Institutes of Health announced completion of the Human Genome Project. Now, grieving families of World Trade Center victims will benefit from the newly gained knowledge.

In particular, scientists will look at so-called STRs, or short tandem repeat sequences in DNA. About half of the human genome is made up of these repeating sequences of information, O'Brien explained. While the locations of these sequences are the same from person to person, their contents can sometimes change.

Mistakes occur in the genetic lettering, O'Brien said, "and you get misreads [called stutters] on the DNA."

Stutters are the most common mutations in human DNA. Scientists use a standardized technique to determine how frequently any individual combination of stutters is likely to occur. They then match the mutation patterns in the tissue sample against DNA gleaned from a sample to determine if they match.

When you don't have a sample of an individual's DNA to work with "you use DNA from parents, children, or siblings," O'Brien said. "In that case, the match won't be as close, and you have to compute whether a statistical association exists."

Mitochondrial match-ups are more difficult to determine. There are some 10,000 organelles inside human cells, called mitochondria. They hold the DNA of a person's mother, half the DNA information found in the individual's genome.



Newsday Photo / Jim Ose

At Fresh Kills on Staten Island, investigators comb debris from the World Trade Center for traces of victims' bodies.

Because those genetic packages are 10,000 times more plentiful than the full chromosomal package, scientists rely upon them when a sample is damaged or deteriorated. There are limits, however: This method only tells you "what your mother's DNA was, or your maternal lineage," O'Brien explained. "So you can end up with a whole clan with identical mitochondrial DNA."

If that's not good enough, scientists turn to so-called SNPs, or single nucleotide polymorphisms. This method develops a very individualized DNA fingerprint, but it's painstaking work, and at least three times as many SNPs must be analyzed to glean as precise a DNA fingerprint as STR work provides. SNPs analysis looks for individual, isolated DNA letters that vary greatly in the human population.

Once the genetic material is analyzed, results are entered into a computer for a final match, a process known as "infomatics." So taxing are the computational needs that yesterday the city medical examiner's office was stymied, awaiting sophisticated new software.

Ultimately, however, none of the painstaking lab and computational efforts will pan out if there are problems with the initial sample, experts said, and the medical examiner's office insisted yesterday that rescue personnel have been briefed about how to collect samples and the need to specifically catalogue where they were found.

There are ways to separate DNA that may have been accidentally mixed with that of a rescue worker, a spokesman for the medical examiner's office said, but it can make the job more difficult.

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