



Forensic familial searching: scientific and social implications

Nanibaa' A. Garrison¹, Rori V. Rohlf's² and Stephanie M. Fullerton³

Familial searching in forensic genetic testing is raising concerns in the United States.

“
We advocate greater public transparency in terms of the methods used as well as with regard to the outcome of specific investigations”

In July 2010, a new forensic technique called familial searching gained public attention after the capture of a man alleged to be the ‘Grim Sleeper’: a serial killer who had evaded arrest in the United States for 25 years. DNA obtained from a discarded pizza crust was genetically matched to the alleged killer’s son, whose DNA profile was stored in the California offender database. Here, we consider the intersection of scientific and social concerns raised by the increasing use of familial searching. This consideration is especially urgent in light of oral arguments presented in the US Supreme Court in February — currently awaiting a decision — over the legality of archiving DNA from arrested suspects.

In standard forensic genetic testing, methodological assumptions that underpin the interpretation of a complete match have been well explored. There is usually high confidence that the 13 complete matches at the loci used in direct individual identification are not coincidental. By contrast, the genetic profiles of family members are expected to match only partially, and coincidental partial matches between unrelated people are likely to be more common¹. This increased uncertainty makes familial searching more prone to errors.

The scientific methods used and assumptions made can have a disproportionate impact on the likelihood of error. For example, a reference population must be used to assess the likelihood of a coincidental partial match between unrelated individuals. If the reference population does not accurately represent the genetic background of the individuals in question, a partial match may appear to be more suggestive than it actually is, leading to the inappropriate investigation of unrelated individuals². Typical population assumptions used in such work appear to have a disproportionate impact on individuals from groups that are not always represented by the reference populations, such as Native Americans. Similarly, some familial searching methods are based on a consideration of the number of matching genetic markers rather than on the strength of evidence that a partial match shows for a specific relationship³. Such lower-precision methods more

often result in mistaken identification of unrelated individuals as genetic relatives.

Moreover, because current forensic databases substantially over-represent individuals of particular ethnic groups (for example, in the United States, African Americans and Latinos), those communities are disproportionately exposed to errors associated with familial searching. As such, members of these groups will more often be targeted by familial searching, risking unjust exposure to criminal investigation and potentially exacerbating over-representation⁴.

It is essential to carry out a detailed investigation of the methods, including studying successes and failures associated with familial searching methodologies that are currently being used by different forensic laboratories. Unfortunately, it is challenging to undertake such analysis because of the great diversity of familial searching methods used in different jurisdictions (for example, in the United States, federal, state, county and city), the relative paucity of information available about those methods and restricted information on the content of DNA databases.

We advocate greater public transparency⁵ in terms of the methods used as well as with regard to the outcome of specific investigations, including providing data about observed false-positive rates and about the number of familial searches conducted without identification of possible genetic relatives. This information will facilitate outside analysis and broaden public awareness and discussion. Comprehensive, deliberative, community-based discussions about the scientific and social implications of familial searching will be essential to delineate boundaries around acceptable and unacceptable uses of forensic technologies.

1. Bieber, F. R., Brenner, C. H. & Lazer, D. *Science* **312**, 1315–1316 (2006).
2. Rohlf's, R. V., Fullerton, S. M. & Weir, B. S. *PLoS Genet.* **8**, e1002469 (2012).
3. Balding, D. J., Krawczak, M., Buckleton, J. S. & Curran, J. M. *Forens. Sci. Int. Genet.* **7**, 52–54 (2013).
4. Greely, H. T., Riordan, D. P., Garrison, N. A. & Mountain, J. L. *J. Law Med. Eth.* **34**, 248–262 (2006).
5. Krane, D. E. *et al. Science* **326**, 1631–1632 (2009).

Competing interests statement

The authors declare no competing financial interests.

¹Stanford Center for Biomedical Ethics, Stanford University School of Medicine, Stanford, California 94305, USA.

²Department of Integrative Biology, University of California Berkeley, Berkeley, California 94720, USA.

³Department of Bioethics and Humanities, University of Washington School of Medicine, Seattle, Washington 98195, USA. Correspondence to N.A.G. e-mail:

nanibaa@stanford.edu

doi:10.1038/nrg3519

Published online 4 June 2013