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Old family secrets exposed

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Abstract

An elderly man and woman died after being burned in an automobile accident. DNA typing strongly confirmed that they were brother and sister. But further typing, on four additional presumed siblings, revealed some surprising and instructive genetic patterns. The additional information contradicts the original conclusion, and also reveals remarkably precise insights into events many years ago.

Keywords: Kinship likelihood ratio; Sibship; Excluding sibship; Family reconstruction

1. Introduction

Mr. F, age 73, and Mrs. G, age 56, were badly burned and later died. DNA analysis was used to identify them and their relationship. The identity of F was quickly resolved by comparison with his wife and children. G shared a total of 25 alleles with F in 17 of 19 tested autosomal forensic DNA systems, strongly suggesting sibship. Indeed, the likelihood ratio favoring them to be brother and sister, rather than unrelated, is 300. In a sense this settles the issue for G is surely the person who had always been presumed to be the sister of F. However, further evidence suggests that the truth is somewhere in between, that the relationships are not quite as the family had supposed.

It is a sound general principle that, when there is evidence that favors some explanation A over some explanation B with a sufficiently high likelihood ratio—here B is "unrelated," and 300 may be sufficiently high—the explanation B may be discarded. However, it is not sound to therefore conclude A. Possibly some other explanation, C, may exist that explains the data as well or better.

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2. Results and discussion

2.1. Excluding sibship

DNA examination of four further presumed siblings of F and G—Mrs. E (age 77), Mrs. D (age 66), Mr. C (age 63), and Mrs. A (age 60)—seemed superficially to confirm siblingship. Every pair shows allele-sharing characteristic of siblings. Moreover, in none of the 19 genetic systems were more than four distinct alleles observed among the six people, so at least the data survived the obvious rule that (mutations aside):

> A collection of people who have five or more alleles among them in any one genetic system cannot all be full siblings.

Nonetheless, there are ways to distribute only three or four alleles that cannot be explained by only two parents. If there are four distinct alleles and one child is homozygous, that is effectively the same as having five alleles. Similarly, if two children are differently homozygous (PP and QQ) all four alleles from the parents (PQ and PQ) are accounted for, so even a third allele in an additional child (e.g., QR) would contradict full sibship among the three children. A subtler fact is

> If three children have four alleles among them, and one allele occurs at least three times, the three children cannot all be full siblings.

This assertion is worth proving rigorously. Numerous instances of it occurred among the putative siblings. For example, in vWA the children F, A, and C had genotypes 14/17, 14/16, and 14/18, respectively. Assume, contrary to the assertion, that they are full siblings. Then among the three occurrences of the 14 allele, at least two occurrences—F and A for example—came from one particular parent. The complementary two alleles—17 and 16 in this example—thus comprise the genotype of the other parent, and, therefore, exclude that parent from being the parent of C. Assuming the contrary of the assertion thus leads to a contradiction, which proves the assertion.

The above rules describe all patterns among three children that exclude mutual sibship. However, I do not know whether, for any pattern of four genotypes that exclude mutual sibship, it is always possible to find a trio among them that already excludes it.

2.2. Two fathers

Occurrence of thrice-occurring alleles according to the pattern of the rule above suggests partitioning the children into two sets, corresponding probably to different fathers. (Official records indicate a single set of parents; different fathers seems more plausible.) There are three consistent arrangements. F can be a full sibling of E, or of A, or of both, but of no others. To decide among these possibilities, CSF1PO is informative and illustrative. F and E are 11/12, C and A are 10/12, the others are 12/12, which suggests the alignment: F and E have one father; C (along with G and D) and A have the other father. An exact likelihood ratio computation across all loci using the Symbolic Kinship Program

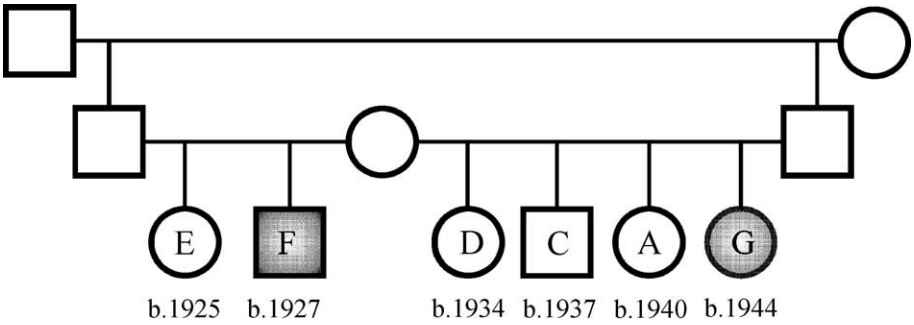

Fig. 1. The relationship among the children that is suggested by their DNA types.

[1] of DNA-VIEW [2] gives a likelihood ratio of at least 1,000,000 supporting this hypotheses over either of the others. Encouragingly, it groups the children by age: E and F are the oldest.

2.3. Related fathers

However, a mystery remains. The children manifest five distinct alleles in no system, and almost every pair, by likelihood ratio computation, looks more like full siblings than half. Therefore, I considered the possibility that the two fathers are brothers to one another, thus making the two cohorts of children "three-quarter siblings" to one another (Fig. 1).

Probably computations by the Kinship program support this speculation with a likelihood ratio of 6. (A parent–child relationship between the two fathers would explain the genetic data equally well.) Moreover, Y-chromosomal loci were eventually typed and both males F and C, with hypothetically different fathers, had the same haplotype.

References

[1] C.H. Brenner, Symbolic Kinship Program, Genetics 145 (1997) 535–542.
[2] C.H. Brenner, http://dna-view.com/dnaview.htm.