LETTER TO JMG

Inadvertent diagnosis of male infertility through genealogical DNA testing

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Key points

- Commercial Y chromosome testing for genealogical purposes is increasing in popularity and is employing an increasing number of polymorphic markers, raising the possibility of the detection of Y chromosomal deletions in clients.
- Here we show that commercially used markers detect AZFa and AZFc deletions associated with male infertility in general population samples.
- Companies should avoid markers in the commonly deleted regions of the chromosome, and meanwhile their clients should be warned of the possibility and implications of the inadvertent diagnosis of infertility.

AZFc deletions are the commonest of the classes found in infertile men, with a frequency estimated to be 1 in 4000. We found three deletions in 2574 English males, and can add to these an additional 681 males (mostly from the Iberian peninsula) typed for PN25 in whom we would have expected to detect some deletions had there been any. The frequency we find, three in 3255, is not significantly different from 1 in 4000 (p = 0.20, Fisher exact test).

AZFa deletions are particularly rare, constituting 1–2% of all pathogenic Y chromosomal deletions, and have a likely population frequency of less than 1 in 100 000. We found one deletion in 69 Inuit males, but including 5303 additional undeleted chromosomes from many, mostly Eurasian, populations typed with AZFa region microsatellites in our laboratory, the observed incidence is one case in 5374. A large database (see Roewer et al and http://www.yhrd.org) of ~23 000 Y chromosomal microsatellite haplotypes includes DYS389I, DYS385, and DYS464,15 lying within the r1–r4 ampliconic regions,16 and contributors would therefore be expected to detect AZFa deletions, although it is possible that such "incomplete" haplotypes would not be submitted. The database contains no examples with null alleles at this locus. Notably, we have found no examples of AZFb deletions, intermediate in frequency between AZFa and c deletions, in our population studies (n = 5374); these14 would be expected to lack several microsatellites, including the widely typed DYS385 and DYS392.

While the typing of the binary marker PN25, in the AZFc region, is not being offered commercially, at least one major testing company types the highly informative multi-locus microsatellite, DYS464,17 lying within the r1–r4 ampliconic repeats, and also absent in the three AZFc males we have identified (fig 1A). Microsatellites within the AZFa and b regions are typed by all companies carrying out commercial Y

METHODS

Samples were collected with informed consent and relevant ethical approval from the Leicestershire Research Ethics Committee (ref. 5796) and the Committee for Scientific Investigations in Greenland (ref. 505-16).

Deletion analysis was carried out using standard PCR techniques; primer sequences and conditions are given in original references cited for markers in the text below.

RESULTS

As part of a Y chromosomal haplotyping study of 2574 English males ascertained on the basis of surname and geographical origin, we included the binary marker PN25 which defines an important haplogroup, R1b, common in Western Europe. The PN25 polymorphism is an A to C transversion in one of three copies of the PN25 sequence, which lie in the three ampliconic repeat units g1, g2, and g3 of the AZFc region on Yq (fig 1A). In three unrelated males PN25 sequences were absent, and analysis of markers across the AZFc region showed a pattern of presence or absence consistent with these males carrying ~3 Mb deletions caused by non-allelic homologous recombination (NAHR) between the b2 and b4 repeats, previously observed in 47 of 48 deletion patients.

In a population study of 69 Greenlandic Inuit males, we typed a set of 19 Y-specific microsatellites and a number of binary markers on the Y chromosome. In one male nine of 19 microsatellites and a single binary marker, M173, failed to amplify (fig 1B). Since all of these markers lie in the AZFa region on Yq, this is consistent with this male carrying an AZFa deletion. Testing of further loci in and around the region confirmed this, and showed that the deletion has arisen through a mechanism observed in the majority of AZFa cases; that is, by NAHR between directly repeated HERVs 780 kb apart and flanking the AZFa region.

DISCUSSION

AZF deletions are normally ascertained by testing the DNA of men with idiopathic infertility, and estimates of their frequencies are derived from clinical data. Here, we have ascertained deletions in an unbiased way.
chromosome testing (fig 1B). Such testing will therefore lead to the detection of AZF deletions and thus an inadvertent diagnosis of likely infertility (some AZF deleted males have been reported to father children). Recent identification of 166 new Y-specific microsatellites brings the total number known to over 200, and with so many to choose from it would be easy to avoid markers within the AZF intervals of the chromosome. There certainly seems no good reason for continued commercial typing of the AZF marker DYS464, which in any case offers problems of interpretation because of its multilocal nature. Markers within the AZFa and b regions are so well established, however, that it is unlikely that they will be abandoned—a problem mitigated by the comparative rarity of these classes of deletions. Testing companies routinely inform their customers of the possibility of detecting non-paternity; while they continue to type the regions, users are warned that these markers are not neutral with respect to fertility.

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ELECTRONIC-DATABASE INFORMATION

The URL of the Y-STR Haplotype Reference Database is http://www.yhrd.org.

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