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The Y chromosome in forensic analysis and paternity testing

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Abstract The male specificity of the human Y chromosome makes it potentially useful in forensic studies and paternity testing, and markers are now available which will allow its usefulness to be assessed in practice. However, while it can be used confidently for exclusions, the unusual properties of the Y mean that inclusions will be very difficult to make: haplotypes are confined within lineages, so population sub-structuring is a major problem, and many male relatives of a suspect will share his Y chromosome. Y haplotyping is most likely to find application in special instances, such as deficiency cases in paternity testing and in the analysis of mixtures of male and female DNA, or in combination with autosomal markers.

Key words Y chromosome · Polymorphism · Haplotype · Exclusion · Paternity testing

Introduction

Normal human males possess a Y chromosome, and normal females do not. The Y exists to determine maleness by specifying the development of the testis early in embryogenesis. This specialised role of the chromosome lends it some unique properties, which have attracted the attention of researchers who are interested in understanding human genetic history [see refs. 1, 2 for reviews]. As well as this, the Y is of potential use in forensic and paternity studies. The vast majority of violent crimes are committed by males: currently 93% of crimes of violence against the person, and 99% of sexual offences in England and Wales [3]; therefore a crime-scene sample left by a culprit will usually be informative when typed with Y-specific markers. Where male assailant and female victim DNAs are mixed, as in rape cases, these markers will give specific information on the assailant. Where the paternity of a son is in question, comparison of the Y chromosomes can be a simple way of excluding an alleged father.

Despite these potential uses, there are serious limitations which also arise from the special properties of the Y chromosome. In this review we will describe these properties, and the different classes of polymorphic marker which are available, discuss the suitability of these markers for forensic studies, and explore the problems which are associated with their use. Although we concentrate here on the Y, in practice Y-chromosomal markers are most unlikely to be used in isolation without other evidence; combining the Y with other systems will obviate many of the problems which we describe, and provide new and useful tools for forensic and paternity analysis.

Special features of the Y chromosome

The sex-determining function of the Y chromosome means that it is paternally inherited and haploid. Because of this haploidy, most of the chromosome does not recombine with any other at meiosis (Fig. 1). These properties have important consequences for its population genetics, since Y chromosomes are passed down from father to son unchanged except by the gradual accumulation of mutations. In principle it is possible to reconstruct the histories of paternal lineages by comparing modern Ys, using DNA polymorphisms. The aim is to build phylogenetic trees, and to find out about population histories [1]. Such studies are now yielding useful information, and complement data on human evolution which come from mitochondrial DNA (mtDNA) and from autosomes.

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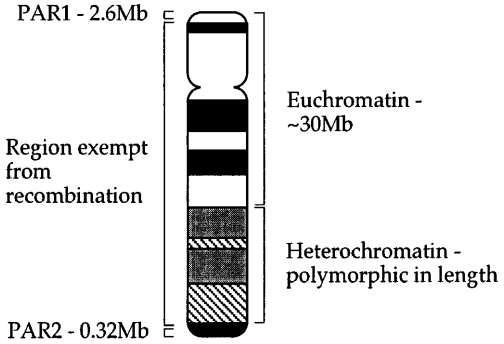

Fig. 1 Idiogram of G-banded human Y chromosome. Recombination takes place between the Y and the X only in the two pseudoautosomal regions (PAR1 and PAR2), and not in the majority of the chromosome which lies between them

Y polymorphisms and the Y chromosome tree

Binary polymorphisms

The Y chromosome is large, and bears many different polymorphisms of many different kinds. Even if we concern ourselves only with those which can be assayed by the polymerase chain reaction (PCR), the variety of polymorphisms is impressive. Base substitutions and the YAP [4] *Alu* element insertion have very low mutation rates (about 5×10^{-7} per site per generation for base substitutions [5]). Given that there are now more than 2×10^9 Y chromosomes in the human population, then it is clear that in any modern generation the same substitution at the same site is expected to take place in some individuals in the world; however, such parallel substitutions will exist at extremely low frequencies unless they occurred long ago. Thus base substitutions will usually provide markers representing unique mutational events, and are likely to be plentiful. For example, three base substitutions were found in a 2.6 kb region sequenced from 16 individuals [5]. If the euchromatin of the Y (see Fig. 1) is 30 Mb in size, then we expect there to be of the order of thousands of such base substitutions in the modern population of Ys. These markers are binary in nature, and can sometimes define very large groups of chromosomes in the population, but these definitions are robust, in that chromosomes sharing given substitutions are extremely likely to be related by descent. They are the best markers for constructing trees of Y chromosomes, and an example of such a tree is shown in Fig. 2. The nodes of this tree are Y-chromosomal haplotypic groups (or 'haplogroups') which are each defined by the allelic states at 18 unique or rare event markers. The tree includes an example of a parallel substitution which has risen to high frequency, and which is shown as a closed part of the tree (reticulation). The tree's resolution is low, but this will improve as more markers are discovered.

Microsatellites and minisatellites

As well as these binary markers there are more rapidly mutating multi-allelic loci: 23 microsatellites [1, 6–8],

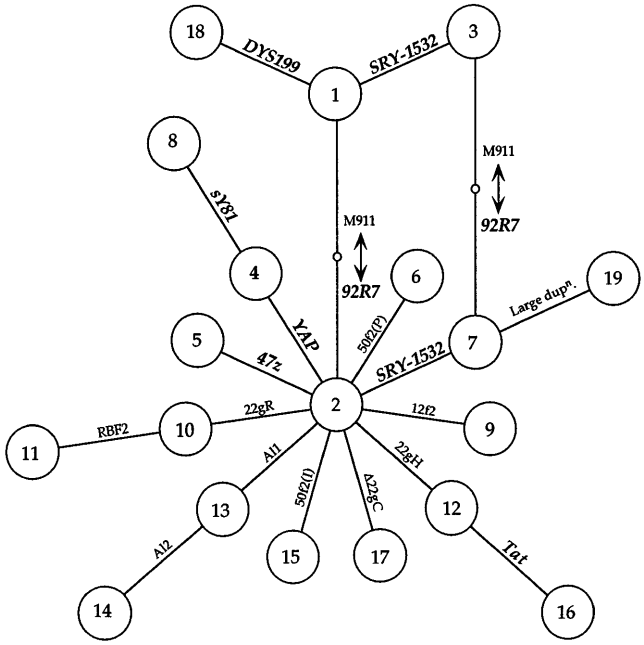

Fig. 2 Unrooted parsimony tree of 19 Y chromosome haplogroups. Large circles represent haplogroups, and single lines between these represent single mutation events. The tree, which is based on one published previously [1], was constructed using 18 polymorphisms (including base substitutions, insertion/deletions, and RFLPs) thought to represent unique or very rare events in human evolution. Names of polymorphisms are given next to branches, and those in bold italic type can be typed by PCR. Because of recurrence among the polymorphisms SRY-1532, 92R7, and M911 (unpublished data), part of the tree is shown as a reticulation. A full description of polymorphisms used in tree construction will be given elsewhere (Arpita Pandya et al., manuscript in preparation), and interested readers are meanwhile asked to contact the authors

and a single minisatellite, MSY1 [9], which can be assayed by MVR-PCR [10], revealing a very large number of variant code structures. Pedigree studies using autosomal loci suggest that the mutation rate to new-length alleles at microsatellites is around 10^{-3} per locus per generation [11], and similar studies are now being carried out to estimate these rates at Y-specific loci (P. de Knijff, personal communication). The observed diversity at MSY1 [9] suggests a mutation rate in excess of 1% per generation, and techniques are available to measure this for specific alleles directly in sperm DNA [12].

While searches for further Y-specific minisatellites have not been successful [13], it is likely that more microsatellites remain to be discovered. How many do we expect to find? Based on observed frequencies in cosmid libraries, a trinucleotide repeat locus occurs about once every 180 kb in the genome as a whole [14]. The 30 Mb of the Y chromosome should therefore contain about 170 of these loci, and only 7 have been identified to date [7, 8]. However, evidence from the chromosomal assignment of 2931 microsatellites isolated from a library made from the DNA of a male [15] indicates that there are significantly fewer of these loci on the Y than are expected on the basis of its size; this is also true for those tetranu-

cleotide repeat classes which have been analysed [15, 16]. As well as this, in the set of Y-specific loci cloned by the Cooperative Human Linkage Center and deposited in the Genome Data Base, one tetranucleotide locus was found twice (DYS393/DYS395), and one tetranucleotide was the same as DYS19 (see [1]). Together with the observation that primers designed to amplify Y loci often co-amplify at least one other locus, which sometimes presents practical problems, then it may be that the number of useful Y loci is rather small.

Haplotypic diversity

Micro- and minisatellites show large numbers of haplotypes throughout the tree, and cannot easily be used in tree-building by themselves [17, 18]. Similar microsatellite haplotypes and similar MSY1 codes can arise by chance, and if we were to group chromosomes on this basis alone, then distantly related chromosomes would sometimes be grouped together. When these markers are considered within a haplogroup defined using the binary markers, however, we see a genuinely related set of microsatellite haplotypes or MSY1 codes. Diversity is more or less restricted, depending on the age of the haplogroup. For example, haplogroup 16, which is relatively young, consists of chromosomes with closely related microsatellite haplotypes, while haplogroup 4, which is more ancient, contains much more diversity.

It is important to appreciate the effect that complete linkage has on haplotype diversity. If we consider ten binary polymorphisms, for example base substitutions, distributed on ten different autosomes, then, taking a haploid set, 2^{10} (= 1024) different states are possible. If, on the other hand, the ten are on the Y chromosome, then the maximum number of haplotypes we expect to observe is ten plus one, since the events have accumulated within lineages with no random assortment or recombination. We may see fewer if some chromosomes have gone extinct, and more if there has been recurrent mutation. The frequency of the haplotypes will usually depend on their ages provided that population size has behaved similarly since each was founded.

The situation with microsatellites is not as simple as this, since each locus is multi-allelic. If the mutation rate of a Y-specific locus is very low, then it behaves much like a base substitution. If the rate is high, then the correspondence of microsatellite allele size with the haplogroups defined by base substitutions breaks down. The extent to which this occurs depends on the mutation rate, and the number of generations to the most recent common ancestor for the haplogroup. While we observe very many different microsatellite haplotypes, we do not see as many as are expected on the basis of random association of loci (as would be the case with unlinked autosomal microsatellites), and this reflects the fact that common ancestors of the haplogroups are recent.

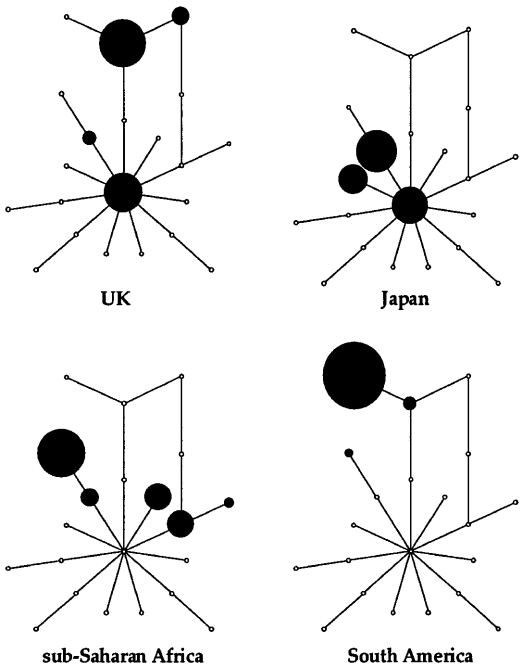

Fig. 3 Population sub-structuring of Y chromosomes. Distributions of the haplogroups within four indigenous populations are shown, using the framework of the tree given in Fig. 2. Areas of black circles are proportional to the frequency of each haplotype in each population. Data are from refs. 6, 20, 22, 23, 25 and 32, and from a forthcoming paper (Arpita Pandya et al., manuscript in preparation); in using some of the published data we have assumed that there have not been additional recurrent mutations

Population distribution of haplotypes

The subject of population sub-structuring is of central importance in forensic genetics. While there has been much debate in the case of unlinked autosomal markers [19], the problem is much more severe in the case of the Y chromosome. As has been discussed above, because of the lack of recombination, allelic states of markers are confined as haplotypes within lineages. When these lineages are themselves confined within populations as a consequence of their histories, then population diversity can be very low.

When we compare the distributions of the different Y-chromosomal haplogroups in different populations, we often see a remarkable degree of population specificity (Fig. 3). Examples are haplogroup 8, which is highly specific to sub-Saharan Africa [20], haplogroup 5 (Japanese; [21, 22]), and haplogroup 18 (Amerindians; [23]). Furthermore, when we examine particular populations, we can find instances where almost all members belong to a single haplogroup. Again, an example is the Amerindians, where 90% of Y chromosomes in South American indigenous populations belong to haplogroup 18 [23]. Low diversity results from fluctuations in the number of sons each male in a population has: some have many, while many have few or none. This natural variation can be exacerbated in some societies, past or present, by cultural

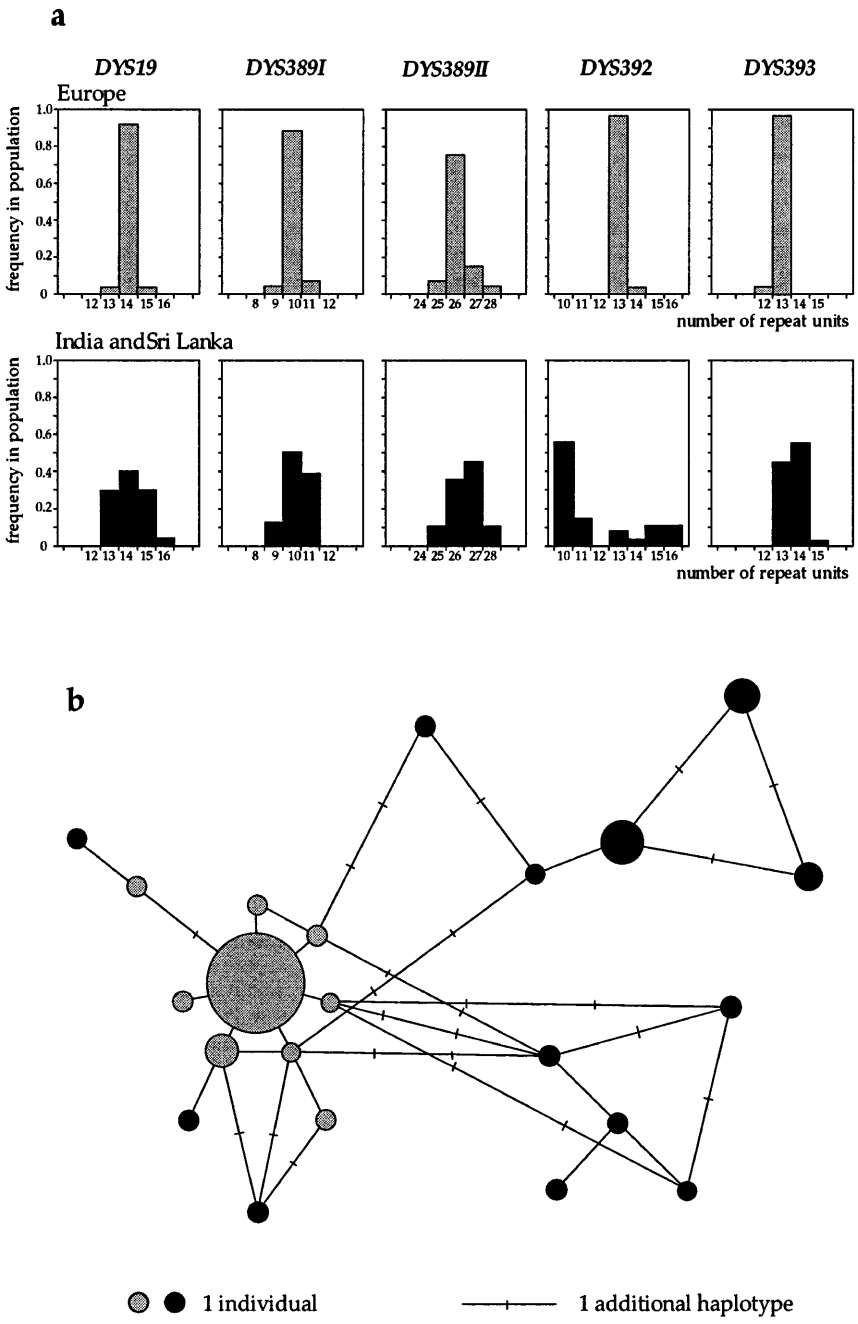

Fig. 4a, b Population sub-structuring of microsatellite haplotypes. **a** Haplogroup 1 chromosomes (Fig. 2) were defined as those containing the 92R7 T allele, SRY-1532 G allele and DYS199 C allele. The frequency of microsatellite alleles is shown for European (grey; $n = 27$) and Indian and Sri Lankan (black; $n \leq 29$) haplogroup 1 chromosomes using the nomenclature of ref. 8. **b** Network linking haplogroup 1 five-element microsatellite haplotypes from Europe (grey) and India and Sri Lanka (black). The network was constructed manually using the principle of parsimony, and assuming a single step mutation process. Microsatellite haplotypes are represented by circles with an area proportional to the number of chromosomes; mutational differences between haplotypes are represented by the lines joining the circles. Some haplotypes differed by more than one mutation; hypothetical intermediate haplotypes are indicated on the lines

constraints on mating practices. In these cases, then, Y chromosome analysis is of limited informativeness. If the haplotype of a suspect's Y chromosome were compared with those of a reference population, great care would have to be taken in the choice of the reference samples, and the ethnic divisions currently used in US databases, for example (Caucasian, Black, Hispanic, and 'other'), would not be ideal.

Because of their higher mutation rates, population specificity of microsatellite haplotypes is less marked, but can nevertheless be significant. Figure 4 shows an example of a combined base substitution and microsatellite analysis of some European, Indian and Sri Lankan Y chromosomes. The subset of chromosomes belonging to haplogroup 1 was first identified using base substitutions: it comprised 47% of the European and 22% of the Indian and Sri Lankan sample. The microsatellite alleles of the haplogroup 1 chromosomes were then examined. Greater diversity of allele sizes was seen in India and Sri Lanka than in Europe (Fig. 4a) and a similar result was obtained when a network linking the five-element microsatellite haplotypes was drawn (Fig. 4b): Indian and Sri Lankan haplotypes were scattered in the network, while European haplotypes were clustered in a distinct region. One explanation for this pattern would be that European haplogroup 1 chromosomes have been derived quite recently from an ancestral chromosome with the haplotype represented by the largest circle in Fig. 4b, perhaps reflecting a small

number of founding Y chromosomes contributing to the European population. Its significance for forensic purposes is that even microsatellite haplotypes in outbred populations can show specificity, although more diversity would be expected if additional microsatellite loci were examined.

Forensic and paternity testing considerations

The potential uses of Y chromosome typing in forensic and paternity studies have been outlined above. Given their high levels of diversity and the fact that the technology is well-established, microsatellites are likely to be the markers of choice. As microsatellite haplotypes accumulate, our knowledge about population sub-structure will increase too. If information about other classes of polymorphisms, such as base substitutions, is also collected then the sub-structures of particular haplogroups will be illuminated, and when microsatellite haplotyping shows that two samples have identical haplotypes, then the typing of base substitutions might be useful in defining the haplogroups to which they belong.

Practical considerations of Y markers

Because they are typed using small PCR amplicons, Y-specific microsatellites are well suited to the analysis of degraded DNA samples. Base substitutions can also be typed in degraded DNA by designing PCR primers which amplify a small region containing the polymorphic site. Although amplification of whole MSY1 minisatellite alleles (1.7–2.7 kb) is not necessary for MVR-PCR, their characteristic structures (i.e. large clusters of like repeat units) mean that the results obtained from degraded DNA, in which only a few repeats from each end of the allele can be typed, are often likely to be uninformative. However, in cases where DNA quality is not a problem, the very high diversity of MSY1 becomes an advantage: codes at this one locus are more diverse and informative than haplotypes derived using ten microsatellite loci [9, Mark Jobling et al., manuscript in preparation].

Exclusions

As with other DNA-based typing systems, the finding that a suspect has a different Y chromosome haplotype to the culprit is good reason to exclude the suspect. Similarly, in a paternity test, a difference at a Y-linked locus will convincingly demonstrate non-paternity, and with a higher exclusion probability than for an analogous autosomal locus [24]. The only issue that needs to be considered here is mutation, and this applies only to paternity. Mutation rates for microsatellites are low enough for this to be a minor problem, but if the difference is in a single repeat unit change at a single locus, then analysis at further Y-specific microsatellites (or, indeed, autosomal loci) could be carried out.

The problem of inclusions

What evidential weight is to be given to the observation that a suspect shares a Y chromosome haplotype with a culprit, or a son with an alleged father? For autosomal systems, the major consideration is the frequency of the DNA profile in question in the population, and there follows from this the problem of which population should be analysed to derive this frequency. As has been discussed already, this is a much more serious difficulty for Y chromosome typing, and it seems reasonable to predict that claims of inclusion will be unacceptable in court on these grounds alone: if, as is commonly done, the probability of a randomly selected male sharing the haplotype of the suspect is given, then this is unlikely to be a low enough value to convince a jury. In an extreme example, at least 13 out of 111 unrelated Mongolian Buryat males (12%) carried the same ten-locus microsatellite haplotype [25].

However, there is a simpler and even more serious problem: in autosomal DNA profiling, the only individual who will have an identical profile to a suspect other than by chance is his identical twin - a rare occurrence. For the Y chromosome, identical haplotypes will exist if the suspect has brothers, sons, a father, paternal uncles and so on, which is not so rare. In many criminal cases it seems likely that this information will muddy the waters sufficiently for a jury to acquit if other evidence does not exclude the relatives.

Similar considerations apply to mtDNA, where, unless mutations have occurred, the same sequence will be shared by all members of a matrilineage. The high levels of mitochondrial D-loop variation, together with the high copy number, which allows the analysis of very small or degraded samples, do make mtDNA a very informative marker, and a useful tool in forensic studies. Nevertheless, it is of limited application in the identification of criminals [26], and most likely to be useful in identifying the victims of crimes [27, 28] or accidents. In general, there seems little reason to attempt to argue for identification of a suspect on the basis of Y or mtDNA evidence alone, but the information that these markers ‘failed to exclude’ would nonetheless be useful in an investigation.

Special cases

Despite these caveats, there are a number of special instances where Y chromosome analysis is likely to be particularly helpful. One is in deficiency cases in paternity testing, where the alleged father is not available [29]. Other relatives of the putative son, such as the sons of paternal uncles, can be tested with Y markers. If their Y chromosomes are not the same as his, then this gives an exclusion [30], although it is also possible that the non-paternity occurred in the previous generation.

In rape cases where the assailant's semen is mixed with cells from the victim, differential lysis of the cell types usually allows sperm nuclei to be separated from the female component [31]. When this cannot be done, and where autosomal markers are used in the analysis, the victim's profile must be subtracted from that of the assailant. In contrast, Y-specific analysis in such cases allows the assailant's haplotype to be determined simply. Y-chromosomal markers would also be particularly useful in analysing other kinds of mixtures, such as blood-blood, and blood-saliva, where differential lysis cannot be applied. In cases of multiple rape, the use of Y-specific microsatellites might allow the minimum number of assailants to be determined: although their individual haplotypes could not be deduced directly, analysis of haplotypes of detained suspects could show whether the mixed haplotypes were consistent with a match.

Deductions regarding population of origin

The high degree of population specificity of Y-chromosomal haplotypes might make it tempting to ask whether reasonable conclusions can be drawn about the ethnic origin of a culprit from a DNA sample. Suppose that a haplogroup 8 Y chromosome were identified in a sample from a UK crime scene: would investigating officers be justified in seeking a black suspect with origins in Africa (Fig. 3)? Contact has existed between sub-Saharan Africans and British for several centuries, and it is likely that haplogroup 8 chromosomes will be found at low frequency in the white population. In a published study, one was found in a group of ethnic Mayans [20]. The urban populations in which the forensic scientist often has to operate are very different from the anthropologist's indigenous sample sets, and the tight localisation of Y haplotypes, and the association with membership of a specific ethnic group, will break down: Y chromosomes are, after all, not the cause of any of the features which characterise particular groups. Nonetheless, it may be that in some cases, where the relevant frequencies of haplogroups are known, such information will be used in investigations. If this happens, it is important that the information is not misused to reinforce racial prejudices or stereotypes. Perhaps any such use and its consequences should be monitored by an independent body.

Y chromosomes are co-inherited with surnames in many societies, and, in an ideal world, a sufficiently detailed Y haplotype could give police officers the surname of the person who left a sample at a crime scene. To be realistic, however, the practicalities of haplotyping and the high frequency of non-paternity (itself an issue where Y typing is relevant) make this a highly fanciful scenario.

In conclusion, despite the problems we have outlined, it is true, and is likely to remain true, that most violent offenders are males. As Y typing becomes more sophisticated, and as the culture of DNA databases becomes more widely accepted than it currently is, it may be seen as reasonable in the future to compile databases of Y haplotypes of all male offenders, and even of all males. For this to happen, the population genetics, as well as the technology, will need to advance.

Here we have stressed the uncertainties associated with Y chromosome haplotyping, and emphasised the special cases in which it is likely to be most widely used. However, it is important to make the distinction between the use of DNA evidence in court for the purposes of conviction, and its use in the exclusion of suspects, or in the identification of a suspect whose guilt or innocence could then be established using other evidence. Also, in practice Y-chromosomal analysis will be done in combination with autosomal markers, and thus provide useful extra options both in forensic studies and paternity testing.

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References

1. Jobling MA, Tyler-Smith C (1995) Fathers and sons: the Y chromosome and human evolution. Trends Genet 11:449–456
2. Mitchell RJ, Hammer MF (1996) Human evolution and the Y chromosome. Curr Opin Genet Dev 6:737–742
3. Home Office (1995) In: Criminal statistics England and Wales supplementary tables 1994, Vol. 2: Proceedings in the Crown Court. Government Statistical Service, London, pp 6–25
4. Hammer MF (1994) A recent insertion of an Alu element on the Y chromosome is a useful marker for human population studies. Mol Biol Evol 11:749–761
5. Hammer MF (1995) A recent common ancestry for human Y chromosomes. Nature 378:376–378
6. Mathias N, Bayés M, Tyler-Smith C (1994) Highly informative compound haplotypes for the human Y chromosome. Hum Mol Genet 3:115–123
7. Jobling MA, Samara V, Pandya A, Fretwell N, Bernasconi B, Mitchell RJ, Gerelsaikhan T, Dashnyam B, Sajantila A, Salo PJ, Nakahori Y, Disteche CM, Thangaraj K, Singh L, Crawford MH, Tyler-Smith C (1996) Recurrent duplication and deletion polymorphisms on the long arm of the Y chromosome in normal males. Hum Mol Genet 5:1767–1775
8. Kayser M, Caglià A, Corach D, Fretwell N, Gehrig C, Graziosi G, Heidorn F, Herrmann S, Herzog B, Honda K, Jobling M, Krawczak M, Leim K, Meyer E, Oesterreich W, Pandya A, Parson W, Piccinini A, Perez-Lezaun A, Prinz M, Szibor R, Teifel-Greding J, Weichhold G, de Knijff P, Roewer L (1997) Evaluation of Y chromosomal STRs: a multicenter study. Int J Legal Med 110:125–133
9. Jobling MA, Bouzekri N, Fretwell N, Dover GA, Jeffreys AJ (1996) Digital DNA typing of human paternal lineages. In: Boyce AJ, Mascie-Taylor CGN (eds) Molecular biology and human diversity. Cambridge University Press, Cambridge, pp 12–23
10. Jeffreys AJ, MacLeod A, Tamaki K, Neil DL, Monckton DG (1991) Minisatellite repeat coding as a digital approach to DNA typing. Nature 354:204–209
11. Weber JL, Wong C (1993) Mutation of human short tandem repeats. Hum Mol Genet 3:1123–1128
12. Jeffreys AJ, Tamaki K, MacLeod A, Monckton DG, Neil DL, Armour JAL (1994) Complex gene conversion events in germline mutation at human minisatellites. Nature Genet 6:136–145

13. Fretwell N, Armour JAL, Jeffreys AJ, Dover GA, Jobling MA (1995) A search for Y-chromosome-specific minisatellites and microsatellites. Am J Hum Genet 57 [Suppl]:A163
14. Gastier JM, Pulido JC, Sunden S, Brody T, Buetow KH, Murray JC, Weber JL, Hudson TJ, Sheffield VC, Duyk GM (1995) Survey of trinucleotide repeats in the human genome: assessment of their utility as genetic markers. Hum Mol Genet 4: 1829–1836
15. Sunden SLF, Businga T, Beck J, McClain A, Gastier JM, Pulido JC, Yandava CN, Brody T, Ghazizadeh J, Weber JL, Duyk GM, Murray JC, Buetow KH, Sheffield VC (1996) Chromosomal assignment of 2900 tri- and tetranucleotide repeat markers using NIGMS somatic cell hybrid panel 2. Genomics 32:15–20
16. Sheffield VC, Weber JL, Buetow KH, Murray JC, Even DA, Wiles K, Gastier JM, Pulido JC, Yandava C, Sunden SL, Mattes G, Businga T, McClain A, Beck J, Scherpier T, Gilliam J, Zhong J, Duyk GM (1995) A collection of trinucleotide and tetranucleotide repeat markers used to generate high-quality, high-resolution human genome-wide linkage maps. Hum Mol Genet 4:1837–1844
17. Roewer L, Kayser M, Dieltjes P, Nagy M, Bakker E, Krawczak M, de Knijff P (1996) Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations. Hum Mol Genet 5:1029–1033
18. Cooper G, Amos W, Hoffman D, Rubinsztein DC (1996) Network analysis of human Y microsatellite haplotypes. Hum Mol Genet 5:1759–1766
19. Lander ES, Budowle B (1994) DNA fingerprinting dispute laid to rest. Nature 371:735–738
20. Seielstad MT, Hebert JM, Lin AA, Underhill PA, Ibrahim M, Vollrath D, Cavalli-Sforza LL (1994) Construction of human Y-chromosomal haplotypes using a new polymorphic A to G transition. Hum Mol Genet 3:2159–2161
21. Nakagome Y, Young SR, Akane A, Numabe H, Jin DK, Yamori Y, Seki S, Tamura T, Nagafuchi S, Shiono H, Nakahori Y (1992) A Y-associated allele may be characteristic of certain ethnic groups in Asia. Ann Hum Genet 56:311–314
22. Lin SJ, Tanaka K, Leonard W, Gerelsaikhan T, Dashnyam B, Nyamkhishig S, Hida A, Nakahori Y, Omoto K, Crawford MH, Nakagome Y (1994) A Y-associated allele is shared among a few ethnic groups of Asia. Jpn J Hum Genet 39:299–304
23. Underhill PA, Jin L, Zemans R, Oefner PJ, Cavalli-Sforza LL (1996) A pre-Columbian Y chromosome-specific transition and its implications for human evolutionary history. Proc Natl Acad Sci USA 93:196–200
24. Chakraborty R (1985) Paternity testing with genetic markers: are Y-linked genes more efficient than autosomal ones? Am J Med Genet 21:297–305
25. Zerjal T, Dashnyam B, Pandya A, Kayser M, Roewer L, Santos FR, Schiefenhövel W, Fretwell N, Jobling MA, Harihara S, Shimizu K, Semjidmaa D, Sajantila A, Salo P, Crawford MH, Ginter EK, Evgrafov OV, Tyler-Smith C (1997) Genetic relationships of Asians and northern Europeans revealed by Y-chromosomal DNA analysis. Am J Hum Genet: in press
26. Barreto G, Vago AR, Ginther C, Simpson AJG, Pena SDJ (1996) Mitochondrial D-loop signatures produced by low-stringency single specific primer PCR constitute a simple comparative human identity test. Am J Hum Genet 58:609–616
27. Gill P, Ivanov PL, Kimpton C, Piercy R, Benson N, Tully G, Evett I, Hagelberg E, Sullivan K (1994) Identification of the remains of the Romanov family by DNA analysis. Nature Genet 6:130–135
28. Ivanov PL, Wadhams MJ, Roby RK, Holland MM, Weedn VW, Parsons TJ (1996) Mitochondrial DNA sequence heteroplasmy in the Grand Duke of Russia Georgij Romanov establishes the authenticity of the remains of Tsar Nicholas II. Nature Genet 12:417–420
29. Pena SDJ, Chakraborty R (1994) Paternity testing in the DNA era. Trends Genet 10:204–209
30. Santos FR, Epplen JT, Pena SDJ (1993) Testing deficiency paternity cases with a Y-linked tetranucleotide repeat polymorphism. In: Pena SDJ, Chakraborty R, Epplen JT, Jeffreys AJ (eds) DNA fingerprinting: state of the science. Birkhäuser Verlag, Basel, pp 261–265
31. Gill P, Jeffreys AJ, Werrett DJ (1985) Forensic application of DNA 'fingerprints'. Nature 318:577–579
32. Hammer MF, Horai S (1995) Y-chromosomal DNA variation and the peopling of Japan. Am J Hum Genet 56:951–962