Short Tandem Repeat-based identification of individuals and parents

History of parentage proof

The use of genetic systems to analyze parentage began shortly after the description of ABO blood groups, which were also used in forensic exclusion. The scientific value of parentage analysis is, strictly speaking, exclusion; one can never absolutely prove that there is no other man or woman in the world who could be the father or mother.

HBO blood groups: The **classification of human blood based on** the inherited properties of red blood cells (erythrocytes) as determined by the presence or absence of the antigens A and B, which are carried on the surface of the red cells. Persons may thus have type A, type B, type O, or type AB blood.

Chaplin parentage parentage proof

Chaplin was ordered to pay child support, although the genetic proof that he could not have been the child's father was available to the court (10). In the absence of mutation, the presence in a child of an allele not seen in the alleged parent
is absolute proof that the alleged parent is not the
true parent.

Allele: is a variant form of a gene. Some genes have a variety of different forms, which are located at the same position, or genetic locus, on a chromosome. Humans are called diploid organisms because they have two alleles at each genetic locus, with one allele inherited from each parent.

How is parentage determined?

parentage is assigned when alleles are shared between the child and the alleged parent, although it is formally possible that another individual who carries all or most of the shared alleles could be the true parent.

What Short tandem repeat offers...

Short tandem repeat loci offer the opportunity to study enough loci to satisfy all but the most absurd requirements for exclusion or proof of parentage, because the loci used are highly polymorphic and there are a great many loci available for testing parentage (12,13).

Short tandem repeats (STRs): are **short repeated sequences of DNA (2–6 bp)** that account for approximately 3% of the human genome (Lander et al., 2001). The number of repeat units is highly variable among individuals, which offers a high power of discrimination when analyzed for identification purposes.

Principles of Parentage Analysis

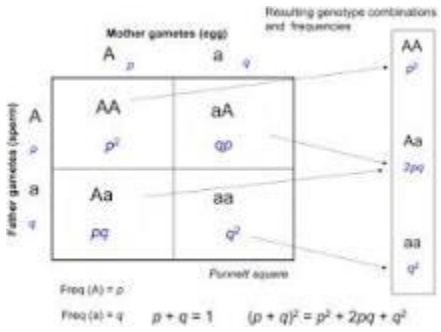
The basis of parentage analysis is very simple: a child must receive, in the absence of mutation, one allele matching each parent. For example, in a simple case, a mother who is a genotype 10,12 and a father who is a 9,14 may produce children of the following types: 9,10 9,12 10,14, and 12,14. If the specific genotype of a child is known, say it is 10,14, and the genotype of the parent contributing one allele, usually the mother, is also known, we may identify the allele that must have come from the other questioned parent. In this case, the mother is known to be a 10,12; the egg must have been a 10. The true father must have contributed a sperm carrying the 14 allele. When the true father is known to be a heterozygote or an alleged father is identified as a heterozygote, he has a 50:50 chance of fathering a child with each of his alleles. In this case, a heterozygous male with a 14 allele will produce a child carrying his 14 allele ½ of the time. If we switch focus from a specific male to the entire population of possible fathers, we can say only that the true father must carry the 14 allele. Thus the chance

of randomly drawing the true father from the population of possible fathers is simply the frequency of the 14 in this population. The analysis of parentage is formally equivalent to the inclusion/exclusion algorithm used in forensic identification and the examples discussed in the introduction.

Genotype: The genetic constitution (genome) of a cell, an individual, or an organism. The genotype is distinct from the expressed features, or phenotype, of the cell, individual, or organism. The genotype of a person is **that person's genetic makeup**. It can pertain to all genes or to a specific gene.

Other possibilities

The two possibilities: (a) true father is identified, or (b) father is randomly drawn from the population of possible fathers, may be tabulated as a Punnett square in the first case, and as part of a tabulation of all possible matings and children for a multiallelic locus in the second case. The full table for the biallelic or binomial case is presented in Table 3. For the Punnett square or true father case, we write the frequency of eggs across the top of the square and the frequency of sperm along the left side of the square. The 50:50 probability that a specific child will be produced by this heterozygous man.



The Punnett square: is **a table in which all of the possible outcomes for a genetic cross between two individuals with known genotypes are given**. In its simplest form, the Punnett square consists of a square divided into four quadrants as in the figure above.

Heterozygous: The presence of two different alleles at a particular gene locus. A heterozygous genotype may include one normal allele and one mutated allele or two different mutated alleles (compound heterozygote).

A multiallelic site: is a specific locus in a genome that contains three or more observed alleles, again counting the reference as one, and therefore allowing for two or more variant alleles.

Locus: A locus is a set of points, in geometry, which satisfies a given condition or situation for a shape or a figure. The plural of the locus is loci. ... The word locus is derived from the word location.

Probability of Paternity

Assuming only that the child has a father, we may split the pool of possible fathers into the alleged father and all other possible fathers, that is all men carrying the required allele seen in the child. The probability of paternity (PP) for the alleged father is, in this formulation, the probability that he fathered this child (AF) divided by the sum of the probability that he fathered the child (AF) plus the probability that some other male fathered the child (O):

$PP = (AF)/[(AF) + (O)] \times 100\%.$

For the above example:

$PP = (1/2)/[(1/2) + (1/10)] = 0.83 \times 100\% = 83\%.$

Parentage Independence

The power of STR analysis resides in the polymorphism seen at individual loci and in the number of loci tested. The frequencies may be multiplied to estimate the expected frequency of a multilocus haplotype contributed to the child by the questioned parent, but this multiplicative estimation is only legitimate if the alleles at a locus and among loci are inherited independently, that is, Hardy-Weinberg and linkage equilibrium must be established for data bases used in parentage analysis.

STR analysis: is a tool in forensic analysis that evaluates specific STR regions found on nuclear DNA. ... These STR loci (locations on a chromosome) are targeted with sequence-specific primers and amplified using PCR. The DNA fragments that result are then separated and detected using electrophoresis.

Polymorphism: Polymorphism involves one of two or more variants of a particular DNA sequence. The most common type of polymorphism involves variation at a single base pair. Polymorphisms can also be much larger in size and involve long stretches of DNA.

The Hardy-Weinberg model: enables us to compare a population's actual genetic structure over time with the genetic structure we would expect if the population were in Hardy-Weinberg equilibrium (i.e., not evolving).

Genetic equilibrium: is a condition where a gene pool is not changing in frequency across generations. ... **Hardy-Weinberg equilibrium** is a principle assuming that both allele and genotype frequencies would remain constant in a randomly-mating population to achieve genetic equilibrium.

Problem of Mutation and False Exclusion

While false exclusion, based in mosaicism, etc, is a formal possibility in genotypic analysis, it is not frequently encountered. Mutation rates for many STR loci are fairly high and meiotic mutations will be detected in the children. One way to handle mutation is to use an estimate of the mutation rate as the probability that the alleged father contributed this nonmatching allele.The data still favor the hypothesis of parentage for the alleged parent, but incorporating the mutant allele makes the case much less convincing. The method does, however, have the distinct advantage of being fairly realistic, and estimated rates are available for some STR loci (e.g.,http:// www.cstl.nist.gov/div831/strbase/mutation.html).