Paternity Testing

Chapter 23
Kinship and Paternity

• DNA analysis can also be used for:
  – Kinship testing – determining whether individuals are related
  – Paternity testing – determining the father of a child
  – Missing persons/mass disasters

• We are asking different questions than with Forensics
  – Forensics looks for direct ID match
  – Here we are looking for degrees of relationship
Types of Kinship Testing:

A) Paternity Testing:
Know child’s genotype, try to determine father

B) Reverse Parentage: 
Know parent’s genotypes, try to determine their child

Mendelian Segregation

• Since we know the relationship between the individuals in the test
  – Parent to child
  – Siblings, etc

• We use Mendel’s laws to calculate the amount of shared genetic material expected between individuals

• Then calculate how well data fits with the relationship expected
Mendelian Segregation

Rules of Inheritance:
1) Child has two alleles for each autosomal marker (one from mother and one from biological father)
2) Child will have mother’s mitochondrial DNA haplotype (barring mutation)
3) Child, if a son, will have father’s Y-chromosome haplotype (barring mutation)
Correlation Coefficient

- If you are looking at other relatives
- Use “Correlation Coefficient”

<table>
<thead>
<tr>
<th>Relationship</th>
<th>Percent Genes Shared</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monozygotic Twins</td>
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Paternity Index (PI)

- Likelihood that the alleles this child has came from the man being tested rather than another man at random

In other words:
- How good is this DNA profile for determining paternity?
- Depends on:
  - Number of markers genotyped
  - Heterozygosity of markers
Paternity Testing

• In US there are more than 300,000 disputed paternity cases each year
• Almost all of these cases involve:
  – A child
  – A mother
  – One or more alleged father (AF)
• Question asked is – does this man share all the alleles with the child?
Two possible results:

1. Inclusion:
   Tested man, Alleged Father, could be this child’s father

2. Exclusion:
   There is no way that the AF could be this child’s father
Obligate Paternal Allele

- The alleles the actual father MUST have
- Compare the child to the mom
- Whatever allele the mom does not have is the obligate paternal allele
- If mom and dad share alleles there will be less information
- More markers you type – eventually you will find unique alleles
Obligate Paternal allele

(B) Example

Obligate paternal allele

What genotype must the true father have?

Has to be (11,12)
if there is one father for all these children
Statistics

• PI = paternity index
• Ratio of the two probabilities:
  \[ \frac{p(\text{AF is the father})}{p(\text{A random man is the father})} \]
• Ratio then represents how much better the data (genotypes) fits with the hypothesis that the AF is the real father
• Larger ratio = more evidence that this man is the real father
Paternity Index

- \( PI = \frac{X}{Y} \)
- \( X \) = probability that the AF transmitted the obligate paternal alleles
- \( Y \) = probability that a random man could have transmitted the obligate alleles
- \( X = 1.0 \) if the AF is homozygous for the obligate paternal allele
- \( X = 0.5 \) if AF is heterozygous for the allele
Paternity Index

- $Y$ is determined from a population database
- $Y$ is the chance of any man in this population transmitting the obligate paternal allele
  - Based on the allele frequency of the allele
- PI is determined for each locus and then multiplied together to get CPI
  - Combined Paternity Index
Combined Paternity Index

- CPI = Combined Paternity Index
- CPI = the chances of seeing the entire DNA profile from the real father
- CPI > 100 = inclusion
- The AF has a 99 to 1 chance of being the father of this child
- In court this man would be considered the father of this child
Exclusion Probability

• Another statistic that can be calculated
• Combine the frequency of all the genotypes that would be excluded based on the child’s DNA profile
• Child = p alleles
• Everything else = q = 1 – p
  – Assuming no mutations
• How good is this child’s profile for excluding any men?
Mutations

• As we said before mutations do cause problems in paternity testing
  – Alleles will be different between parents and child

• STR loci have known mutation rates:
  – 1 to 4 per 1,000 (0.1 %)

• Non-paternity (exclusion) cannot be determined based on a single allele difference
Mutations

• More markers you genotype
• More chance for seeing a mutation event
  – Simple probability
• Therefore must see three or more differences in alleles before AF can be excluded
• “Two exclusion rule”
  – Two alleles different is not enough
  – Need to see at least three
Reference Samples

- Ideal situation = mother, accused father and child
- Complete parentage trios are not always available
- If the mom is missing the child can still provide information about the obligate alleles
  - Only you won’t be able to assign mother vs. father as contributor of the allele
Reference Samples

- Without a mom can still exclude and sometimes include the accused father
  - Will lose power to differentiate
- Can also determine genetic relationships from other relatives:

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Reference Samples

- If you are desperate for reference samples, you can use lineage markers.
- mtDNA and/or Y-STRs.
- This will increase the number of relatives that can be used as reference samples.
- But will add all problems discussed before:
  - Cannot use product rule.
  - Increased mutation rate.
  - Unable to pinpoint one person in family.
Reverse Parentage

• Trying to identify the remains from a mass disaster or missing persons without having that person’s DNA profile

• Question becomes – given the parent’s genotype is this their child?
  – Or their sibling, or nephew, etc

• If both parent’s DNA is available then this can be determined with great accuracy
Reverse Parentage

- Genotype both parents
- Then you know exactly what alleles their child must have
- Compare to victim’s DNA
Reverse Parentage

• Even if one or both parents isn’t available, identity can still be determined using close relatives.

• More relatives collected – the better the calculations will be.

Example – September 11th bodies:
  – Matched from reference samples taken from individuals homes (toothbrushes, hair, etc)
  – Or from closest relatives available.
Summary

• Statistics are not calculated the same when examining related individuals.
• Instead use known Mendelian relationships between individuals to determine the amount of shared genetic material that is expected.
• Calculate a statistic of how well the genotype data fits with the expected relationship between individuals.
Any Questions?

Read Chapter 24