Forensic Genetics

Module 16 – Session 2

STR Typing

- Mutations
 - $\,\circ\,$ Slipped Strand Mispairing
- PCR-CE Analysis and Anomalies
- Peak Height Variability
 - \circ Template
 - $\circ~\text{Degradation}$
 - $\,\circ\,$ Locus Specific Amplification Efficiency
 - \circ Stutter
- Mixtures
 - Heterozygous Balance

Considering the SSM mechanism, which one is most likely to occur?

- Increase in repeat length
- Decrease in repeat length
- Both equally likely



Source: Microsatellites: simple sequences with complex evolution (Ellengren, 2004).

Contractions are energetically favorable



What is the third step of the PCR process?

- Annealing
- Elongation
- Denaturation

PCR Steps



High molecular weight alleles are to drop out than low molecular weight alleles?

- More likely
- Less likely
- Equally likely

Degradation



Which allele is expected to stutter most?

- [ATAC]8
- [ATAC]12
- [AT]12

Stutter Characteristics

The characteristics shared by mutations and stutter are considerable:

- Rates increase with number of repeat units
- Rates are inversely correlated with repeat unit length
- Stutter usually involves insertion or deletion of a complete repeat unit

Mixtures

Most forensic stains contain DNA from different individuals. The number of contributors (NoC) is usually unknown.



Source: The interpretation of low level DNA mixtures (Kelley et al., 2012)

Mixtures

Mixing proportions can range over contributors.



Number of Contributors

The NoC can technically be any number. Some guidelines:

- \circ Use maximum allele counts (MAC) method: NoC ≥ MAC/2
- $\,\circ\,$ Use stutter rates
- $\,\circ\,$ Use the heterozygote balance

These may need modification when multiple effects play a role.

Heterozygote Balance

Two peaks of heterozygous alleles will show variability resulting from stochastic variations.

Understanding this variability can help the interpretation of mixtures and low template DNA:

- To classify combinations of alleles as possible or impossible for mixtures
- For LTDNA, if imbalanced peaks may have led to alleles not exceeding thresholds

Suppose there is a crime committed on a remote island with a population of size 101. A suspect Q is found to match the crime scene profile. What is the probability that Q is the source of the profile, assuming that:

- All individuals are equally likely to be the source.
- The DNA profiles of all the other individuals are unknown.
- We expect 1 person in 100 to possess this observed profile.

Source: Weight-of-Evidence for Forensic DNA Profiles (Balding & Steele, 2015)

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In addition to *Q*, we expect one other individual on the island to match. So, even though the profile is rare, there is only a 50% chance that *Q* is the source.



The Island Problem – Odds Version

Recalling the odds form of Bayes' theorem:

$$\frac{\Pr(H_p|E)}{\Pr(H_d|E)} = \frac{\Pr(E|H_p)}{\Pr(E|H_d)} \times \frac{\Pr(H_p)}{\Pr(H_d)},$$

with

$$\Pr(H_p) = \frac{1}{101} \qquad \Pr(E|H_p) = 100\%$$
$$\Pr(H_d) = \frac{100}{101} \qquad \Pr(E|H_d) = 1\%,$$

yielding prior odds of $\frac{1}{100}$ and a likelihood ratio of 100. Combining this gives posterior odd of 1, or equivalently, a 50%/50% chance.

The Island Problem – Odds Version

A more general formula can be derived by writing:

$$\Pr(H_p|E) = \frac{\Pr(E|H_p) \Pr(H_p)}{\Pr(E|H_p) \Pr(H_p) + \Pr(E|H_d) \Pr(H_d)}$$

$$=\frac{1}{1+\frac{\Pr(E|H_d)}{\Pr(E|H_p)}\frac{\Pr(H_d)}{\Pr(H_p)}}$$

Note that it is assumed that H_p and H_d are mutually exclusive and collectively exhaustive.

The Island Problem – Odds Version

When N denotes the number of individuals on the island other than the suspect, and p is the profile probability of the observed DNA sample:

$$\Pr(H_p|E) = \frac{1}{1+Np}$$

Extreme oversimplification of assessing the weight of evidence:

- Uncertainty about \boldsymbol{N} and \boldsymbol{p}
- Effect of searches, typing errors, other evidence
- Population structure and relatives

The Island Problem – Searches

Now suppose Q was identified through a search, with the suspect being the only one among 21 tested individuals who matches the crime scene profile.

- How does this knowledge affect the probability of being the source?
- What is the general expression for the probability of being the source, using k for the number of individuals who have been excluded?

How does knowledge about Q being identified through a search affect the probability of being the source?

- It decreases
- It increases
- It stays the same

The Island Problem – Searches

In this case we can exclude individuals from our pool of possible donors, such that our prior odds will slightly increase.

Out of the N-k = 80 individuals, we expect another 0.8 matches, yielding a probability of being the source of $1/1.8 \approx 56\%$. Or, in formula:

$$\mathsf{Pr}(H_p|E) = \frac{1}{1 + (N-k)p},$$

where setting k = 0 gives the original expression and k = N gives $Pr(H_p|E) = 1$.