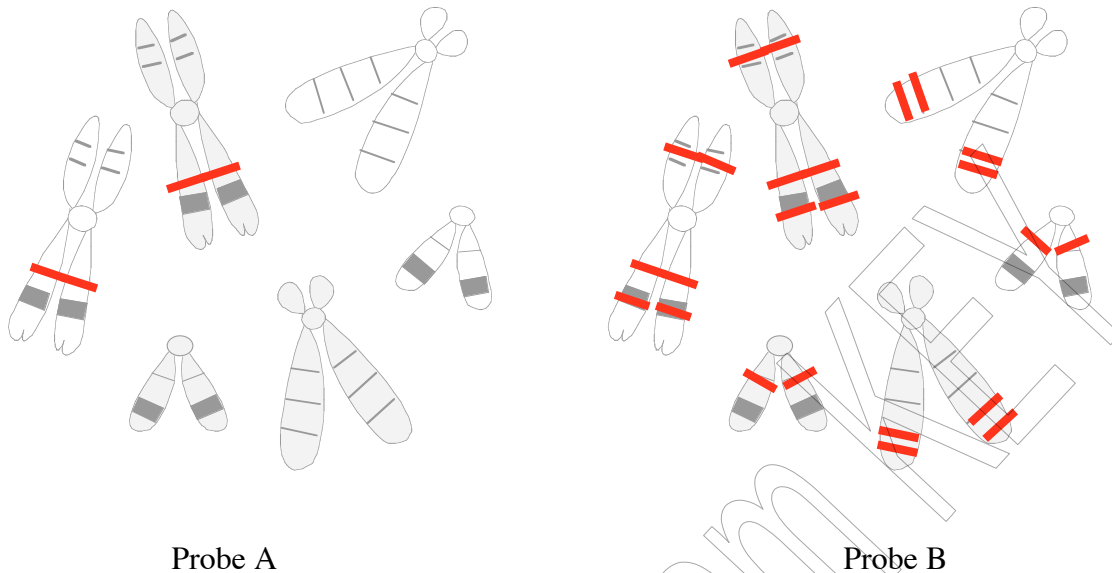


1A)

EcoRI insert: The human DNA contains a sequence that is polymorphic and repeated throughout the genome.

Fragment A: The A sequence is unique in the genome. If the restriction sites are polymorphic, Brad is homozygous for a 3.0 kb allele.

Fragment B: Fragment B contains the polymorphic repeat.

1B)

Note: the signal for probe A can appear on ANY of the chromosomes, but it MUST appear only as a single band on that chromosome, on its sister chromatid, and on the two sisters of its homologue (in the same location).

The signal for probe B should appear at many sites, but again it should be consistent on the sister chromatids and homologues.

1C) The A fragment contains a region that is transcribed abundantly in brain, very little in heart, and moderately in liver. The liver transcript is either alternatively spliced or has a different transcription start or termination site, since it is larger than the transcripts found in brain and heart.

The B fragment is not expressed at detectable levels in these three tissues.

2A) Autosome (individuals with single bands that appear darker on the gel are homozygous).

2B) The PstI site is polymorphic; it is present in some individuals and not in others.

2C) The maternal grandmother is heterozygous for the alleles producing the 3 kb and 2 kb bands.

2D) No; both parents have the 3 kb allele.

2E) Celie could be adopted, since she shares no marker with either parent. Alternatively, the EcoRI enzyme might have cut the DNA in that lane, but for some technical reason, PstI did not).

2F) Cut the DNA with PstI alone and compare to the DNA of others whose bands are not unusual. If hypothesis A is true, the digest will give a certain size band that is the same size as is present in everyone else. If B, that band will be 10 kb larger than the band in everyone else.

Alternatively, you could sequence the EcoRI site and look for a change.

3)

<u>Answer</u>	<u>Experimental questions:</u>	<u>Tools:</u>
<u>8, 9, 12, 13</u>	to determine if this sequence is transcribed?	1) FISH (Fluorescent <i>In Situ</i> Hybridization)
<u>1, 14</u>	to map this DNA molecule to a chromosome?	2) Colony hybridization of a dog genomic library
<u>1, 4, (2)</u>	to determine if the PCR fragment is repeated elsewhere in the dog genome	3) Sequence the PCR fragment and do a BLAST search of yeast and Drosophila databases
<u>3, 11, 14</u>	to see if it is homologous to DNA sequences in other organisms?	4) Southern blot of restriction-enzyme digested dog genomic DNA
<u>10</u>	to see if it is polymorphic in dog populations?	5) Insert the PCR fragment into a vector
<u>2</u>	to find a BAC clone containing this fragment?	6) Hybridize the PCR fragment to allele-specific oligonucleotides specific to this sequence
<u>7</u>	to determine if the PCR fragment contains a minisatellite	7) DNA sequencing of this particular PCR fragment
		8) Sequence the PCR fragment and do a BLAST search of dog EST libraries
		9) Northern blot
		10) PCR amplification of this fragment from different dogs
		11) Zoo blots
		12) Colony hybridization of a dog cDNA library
		13) Measure CpG frequency
		14) Sequence the PCR fragment and look by computer for syntenic regions in the human genome

4. 777 is DOMINANT.
 777 is NOT sex-linked.
 You cannot determine if 777 is on the second chromosome.
 You cannot determine if 777 is on the third chromosome.

Possible genotypes:

$$\frac{G}{Y} ; \frac{T}{777} ; \frac{F}{+} \quad \text{or} \quad \frac{G}{Y} ; \frac{T}{+} ; \frac{F}{777}$$

5A)

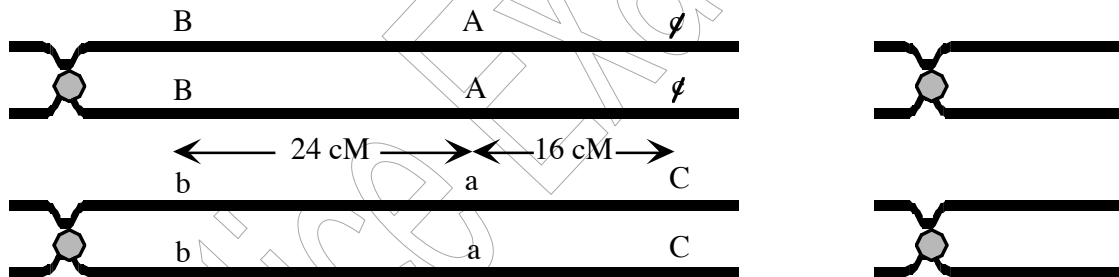
number of AB genotypes	9	10	3	3
number of BC genotypes	4	4	8	9
number of AC genotypes	2	2	10	11

5B) A-B linked? yes $6/25 = 24 \text{ cM}$

B-C linked? yes $8/25 = 32 \text{ cM}$

A-C linked? yes $4/25 = 16 \text{ cM}$

5C)



Double recombination events between B and C decrease the genetic distance between these loci such that the map distance appears to be 32 cM, rather than $24 + 16 = 40 \text{ cM}$.

6A) A locus – $1, 1 = (0.25)^2 = 0.0625$

B locus – $10, 11 = (\text{since each allele can come from either parent}) 2 (.2) (.3) = 0.12$

C locus – $23, 27 = (\text{since each allele can come from either parent}) 2 (.3) (.7) = 0.42$

Total frequency = $\square_A \times \square_B \times \square_C = (0.0625) (0.12) (0.42) = 0.00315$

The probability that the leaves in the truck are NOT from the oak tree at the murder scene is $1/0.00315$.

6B) By **examining more polymorphic loci** (assuming the leaves match), the odds that the truck leaves are not from the murder scene oak become vanishingly small.

7A) H1/h2

7B) 95%

7C) h3/h2

7D) 5%

7E) $(.95) (.95) = .9025 = 90.25\%$

7F) $(.05) (.05) = .0025 = 0.25\%$