Problem Set 8
Genetics 371
Winter 2010

1. In a population exhibiting Hardy-Weinberg equilibrium, 23% of the individuals are homozygous for a recessive character. What will the genotypic, phenotypic and allelic frequencies be for the next generation?

2. Red hair (autosomal recessive) is found in approximately 4% of people in Norway. If we assume that the Norwegian population is in Hardy-Weinberg equilibrium,
(a) What are the frequencies of the red hair (r) and the non-red hair (R) alleles?
(b) What is the frequency of heterozygotes?
(c) What proportion of all marriages stand a chance of having a child with red hair?

3. Two average sized parents have three children. The first child is very short, the second child is very tall, and the third child is average sized.

(a) Explain the inheritance pattern of height in this pedigree. In particular, how is it possible for these parents to have both a very short and a very tall child?

(b) The parents decide to have a fourth child. Is it most likely to resemble the first, second, or third child? Why?

3. A particular early-onset, form of cancer in humans was mapped to two genes, CA18 and CA19, located on chromosomes 14 and 9, respectively. A new extended family showing inheritance of this same form of cancer was recently detected. A small portion of the pedigree is shown on the next page, and the results from LOD score analysis using this family is shown in the table below.

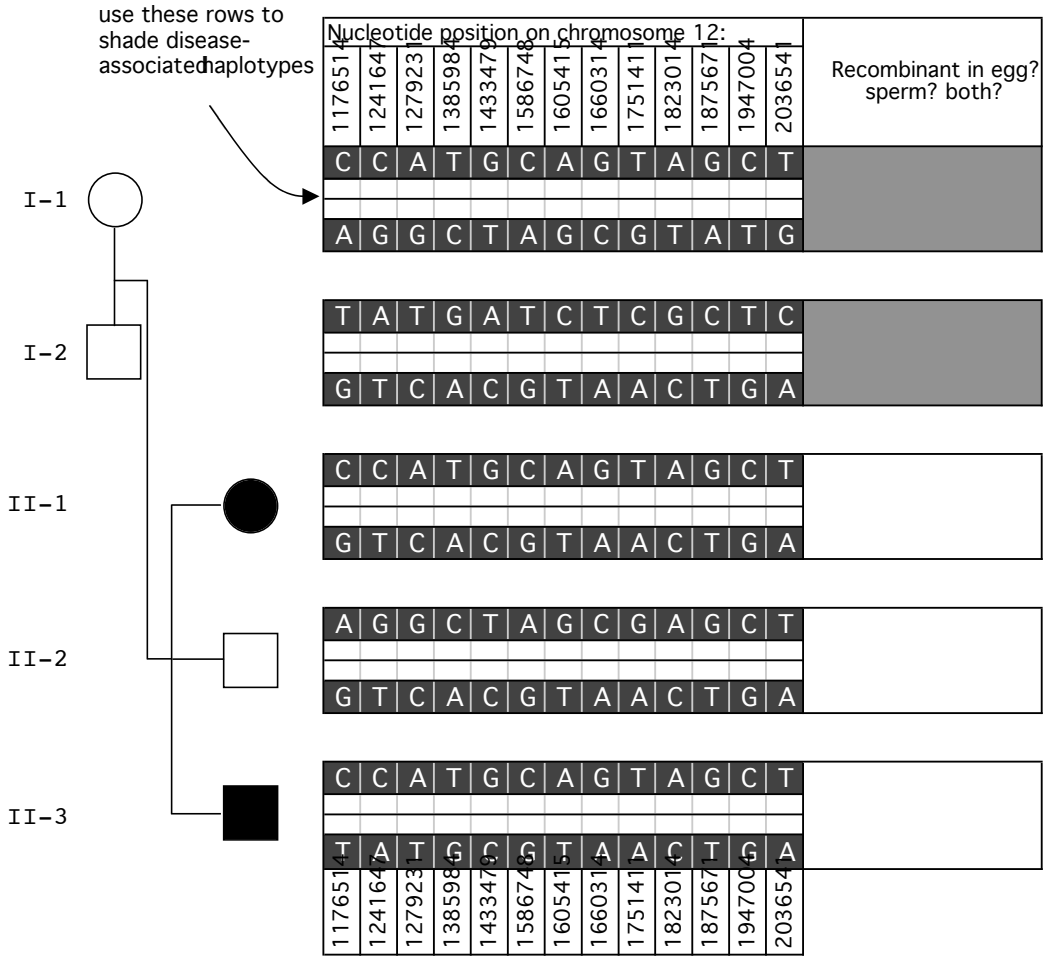
Polymorphic site	LOD score for $\theta = 0.05$
D14S16 (tightly linked to CA18)	–2.92
D9S722 (tightly linked to CA19)	–3.01
D12S1030 (on chromosome 12)	6.24

(a) What is the likely mode of inheritance of this cancer predisposition (autosomal or sex-linked; recessive or dominant)?

(b) Why did these LOD score results prompt the researchers to begin a search for yet another cancer gene?

(c) To map this new gene (called CA20), the researchers genotyped members of this extended family by hybridizing their DNA samples to allele-specific oligonucleotide microarrays. The genotyping results for DNA flanking marker D12S1030 on chromosome 12 are shown to the right of each member in the pedigree. Filled pedigree symbols = affected individuals. Each row represents one haplotype; only the Watson strand base is shown at each single-nucleotide polymorphic locus.

- For each parent, identify each disease-bearing homologue by shading its haplotype. (Use the center blank rows for each individual to show your shading.)
- For each child, shade part or all of each homologue as necessary to indicate recombinant vs. non-recombinant haplotypes. Indicate the recombinant gamete, if any: egg, sperm, or both.



(d) Circle the option below that best represents the location of CA20:

Between 1176514 and 2036541 Between 1433479 and 1751411

Between 1385984 and 1823014 Between 1433479 and 2036541

(e) Postulate a mechanism that results in early onset cancer that is consistent with your mode of inheritance.

4. A breeding experiment was performed on pure lines of tomatoes differing in fruit weight. The plants were all grown in a controlled environment chamber providing equal environmental conditions for all individuals as far as humanly possible. The results were as follows:

Parental lines A 24 g x B 32 g

F1 28 g

F2

Weight (g)	Number of plants
36	2
34	14
32	60
30	108
28	140
26	114
24	52
22	18
20	2

Show how a quantitative genetics model can explain these results, and give

(a) A general statement of your model (how many loci and whether alleles are additive, dominant, or recessive).

(b) Genotypes of the parents and F1.

(c) The effect of each "active" allele on the phenotypic value.

(d) Explain the frequencies of the 20 g and the 36 g F2 classes

5. In Friday's class, we discussed a statistic to quantify population genetic structure. What is it and how do you interpret it?