PSET 6 ANSWER KEY

1.

(a) first cousins once removed: (G & F or E & H)

$F = (1/2)^{\#\text{ generations to G}} \times (1/2)^{\#\text{ generations to F}} \times (1/4) * 4^{\text{([illegible])}}$

$= (1/2)^3 \times (1/2)^2 \times (1/4) * 4 \; \boxed{1/32} =$

first cousins twice removed: (E & J or F & I)

$F = (1/2)^2 \times (1/2)^4 \times (1/4) * 4 = \frac{1}{64}$

(b) second cousins: (G & H)

$F = (1/2)^3 \times (1/2)^3 \times (1/4) * 4 = \frac{1}{64}$

third cousins (I & J)

$F = (1/2)^4 \times (1/2)^4 \times (1/4) * 4 = \boxed{1/256}$

fourth cousins (K & L)

$F = (1/2)^5 \times (1/2)^5 \times (1/4) * 4 = \boxed{1/1024} =$

(c)

orange fingernails f/m random mating

orange fingernails f/m 4th cousin marriage

$= F \times f \times q = (1/1024) \times (0.1)(7 \times 10^{-6}) = 6.8 \times 10^{-10}$

$\therefore$ inbreeding $\approx$ $\boxed{13.95 \text{ times more likely}}$ to give orange finger nails

if $f = 0.01$: $F \times f \times q = 6.8359 \times 10^{-11}$

$\therefore$ inbreeding ≈ 1.40 times less likely to give orange nails

(2.)

(a) daughter #1: $F_1 = \boxed{0}$ (no homozygosity possible)

daughter # 2: $F_2 = (1/2)^1 \times (1/2)^2 \times 2 = \boxed{1/4} = 0.025$

(c) No

(d) Yes, for x-linked genes:

(i) back crossing to a patriarch means that the father always passes the trait to daughters

$F_t = (1) \times (1/2)^t \cdot 2 = \boxed{(1/2)^{t-1}}$

(ii) backcrossing to a matriarch means the fathers never pass the trait to sons

no calculations.

(e) $p = 0.8$, $q = 0.2$

White-fur animals $= p^2 + 2pq = 0.96$

3.

(a) $P_{res} = \frac{560+40}{10000} = 0.06$ $P_{spot} = \frac{560+8760}{10000} = 0.93$

$P_{sen} = \frac{8760+640}{10000} = 0.94$ $P_{stripe} = \frac{40+640}{10000} = 0.07$

Expected frequencies: (H_0 = alleles are in LE)

$P_{res,spot} = (0.06)(0.93)\times 10000 = 558$

$P_{res,stripe} = (0.06)(0.07)\times 10000 = 42$

$P_{sen,spot} = (0.94)(0.93)\times 10000 = 8742$

$P_{sen,stripe} = (0.94)(0.07)\times 10000 = 658$

$\chi^2 = \Sigma \frac{(O-E)^2}{E} = 0.632$, $df = 1$

$p > p_{0.05}$ ∴ we ~~a~~ reject H_0 & population is $\boxed{\text{not in LD}}$

(b) $P_{res} = 0.86$, $P_{sen} = 0.14$, $P_{spot} = 0.14$, $P_{stripe} = 0.86$

Expected freq:

$P_{res,spot} = 1204$ $P_{sen,spot} = 196$

$P_{res,stripe} = 7396$ $P_{sen,stripe} = 1204$

$\chi^2 = 8407$, $df = 1$

$p << p_{0.05}$ ∴ we can reject H_0 & population $\boxed{\text{is in LD}}$

(c) We suspect linkage between the res/sen & stripped/spotted genes. Selection by the parasite may skew allele frequencies in the S.E Asian population.

(d) $D = P_{sen,spot} P_{res,stripe} - P_{sen,stripe} P_{res,spot} = 0.11$

$D_{max} = \min\{P_{res} q_{spot}, q_{sen} p_{stripe}\} = \min\{0.1204, 0.1204\} = 0.1204$

$D' = \frac{D}{D_{max}} = \boxed{91\%}$

$r^2 = \frac{(0.11)^2}{(0.86)(0.86)(0.14)(0.14)} = \boxed{0.83}$

High D' & r^2 both support our suspicion of LD in the population. The striped gene likely "hitchhiked" on the resistant gene.

(e) European: $freq_{stripe} = 0.07$

Asian: $freq_{stripe} = 0.86$

(f) Assuming linkage b/w the loci, the selective pressure of the parasite may increase the freq of striped animals.

(g)

$P_{sen,spot} = \frac{(8760 + 2\times 1300)}{3\times 10000} = 0.38$

Similarly, $P_{sen,stripe} = 0.028$ $P_{res,spot} = 0.025$ $P_{res,stripe} = 0.568$

$P_{res,spot} = 0.02$

3g. $P_{Res\ spotted} = \frac{560 + 200}{10000 * 3} = .0253$

$P_{Res\ striped} = \frac{40 + 2 * 8500}{30000} = .568$

$P_{Sen\ spotted} = \frac{8760 + 2 * 1300}{30000} = .3787$

$P_{sen\ striped} = \frac{640 + 2 * 100}{30000} = .028$

$D = P_{AB} * P_{ab} - P_{Ab} * P_{aB}$

Check

$D = P_{sen\ striped} * P_{res\ spotted} - P_{sen\ spotted} * P_{res\ striped}$ A = Sen B = Striped a = Res b = spotted

$= (.028 * .0253) - (.3787 * .568$

$\boxed{D = -.214}$

3h. $D_{30} = (1-r)^{30} \cdot \boxed{-.214}$

31st generation

$D_{30} = (.9)^{30} \cdot \boxed{-.214} = \boxed{= -.0091}$