I. A cross between an A, arg+ and an a, arg- strain of Neursopora crassa gave the asci patterns 1-7 in the numbers indicated in the table below (ascospore pairs are shown).

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<thead>
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<th></th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<td>a, +</td>
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<td>125</td>
<td>100</td>
<td>36</td>
<td>2</td>
<td>4</td>
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a) Label the ascus type, (PD, NPD, TT) in the box below the numbers of each type.

b) Calculate the distance between each of the genes and its centromere.

A/a; \( \frac{1}{2} \cdot \frac{(36+2+4+6)}{400} = 6 \text{ cM} \); arg +/−: \( \frac{1}{2} \times \frac{(100 + 2 + 4 + 6)}{400} = 14 \text{ cM} \)

c) Are the mating type and arg genes on the same chromosome? How do you know?

No; NPDs are as common as PDs, (NPDs would need 4 strand DXO if genes linked)

d) An unusual ascus was found that had in order the spore pairs: A, +; A, +, a, +, a, arg. What can account for this ascus?

Most likely gene conversion of an arg- to and arg+ allele, but a reverse mutation could give this result.

2. When a yellow haploid strain of Aspergillus was fused with a white haploid, some of the strings of conidia spores produced by mitosis in the primary sterigmata were green and were found to be diploids. When the green diploids were grown, some sterigamata were found to produce strings of white and yellow conida, others had strings of white and green conida, but no yellow and green strings were observed. Surprisingly, when some of the white or yellow spores were tested, many were found to still be diploid and this was always the case when green and white spores were produced. Overall, there were about twice as many cases with white diploids from the white and green sectors as from the yellow and white sectors. Formulate a hypothesis and genetic map that will account for these observations.

Green diploid means w+/w and y+/y provides all enzymes to make green, so if a diploid has:

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+---y
w---+
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mitotic recombination between y and the centromere would give yellow and white 2N sectors while a XO between y and w would give green and white sectors.
3) Predict the phenotypic ratios in progeny of a self fertilization of a Ppp trisomic tomato plant, assuming:
a) a single P is sufficient to cause pointed leaves whereas those with no P are rounded and that both disomic eggs and pollen are viable:

    gametes would be 1P : 2p 2 Pp : 1 pp so 27 of 36 or ¾ would be pointed

b) at least 2 P’s are required for pointed leaves whereas other genotypes are rounded, and where disomic eggs are viable but not disomic pollen:

    since only the P and 2p male gametes function, 3ould be pointed to 15 round.

4) Three Drosophila populations are found to be homozygous for the following polytene chromosome banding patterns, where the letters and numbers represent distinguishable bands along chromosomes I and II and • is the centromere:

  pop. 1  A—B•−C—D—E  1—2—3•−4—5—6—7
  pop. 2  A−B•−C—D−E  1—2—5—4•−3—6—7
  pop. 3  A−B•−C—6—7  1—2—5—4•−3—D—E

Show chromosome pairing in hybrids between each pair of populations, and predict the fertility of hybrid males and females

  (need to show figures, paired gene for gene, as described below)
  Pops 1 and 2 --> linear for the abcde chromosome, inversion loop for chrom 1-7.
  Expect 50 % sterility in females (since the centromere is in the inversion (pericentric) there is no bridge so no lag to steer duplicated/deletion gametes to polar bodies). Male Drosophila have no XO's so only the 2 parental arrangements would be transmitted.

  Pops 2 and 3, translocation (cross shaped pairing configuration) of the 2 chromosomes would lead to semisterility (50%) in both sexes assuming adjacent and alternate segregation are equal.

  Pop 1 and 3 would have a translocation (cross shape) and pericentric inversion (loop inside a loop), keeping genes aligned. That would predict 50% sterility in male and 75% in females.

  Is it possible to predict which of the species is “ancestral” or an intermediate so far as these chromosomes

  Either 2 was ancestral and gave rise to the others in independent events or 2 is an intermediate between 1 and 3, either of which could be ancestral.
5) For the situation where R’R’ = red, R’R = pink and RR = white
a) You find a plot of annual self-fertilizing flowers that has 49% red, 2% pink and 49% white. What are the allele frequencies, how many years, at a maximum, have the flowers been growing and what was the original distribution if that maximum is correct. What is the current F value?

2% was 4 was 8 was 16 was 32 was 64 (max) so 5 generations of selfing. The allele frequencies are 0.5 each and would stay the same. Thus the original population would have 18 red : 64 pink : 18 white. Since the heterozygosity fell from 64 to 2, the loss of heterozygosity is 96.875% which is = to the current F value.

b) A gardener plants 50 red and 50 pink annuals of a random mating variety. Each generation for 3 years he removes any plants with white flowers before they release pollen. What are the starting and following frequencies of the R’ and R alleles. If the culling of whites is stopped after 3 cycles what will be the color distribution in the next generation? How long will it take to reach Hardy-Weinberg equilibrium?
Starting (50 red to 50 ink) f(R’) = ¾ and f(R) = ¼; selfing the first year would give

9/16 red : 6/16 pink and 1/16 white. If the white is eliminated the f(R’)is 12/15 or 4/5 and the f(R) = 1/5.

These frequencies would produce 16/25 red : 8/15 pink : 1/25 white the next year.

Eliminating the white would leave 20/24 R’ alleles and 4/24 R or f(R’)= 5/6 and f(R) = 1/6

The next round would lead to 6/7 R’ and 1/7 R alleles and random mating would give 36/49 R’R’ : 12/49 R’R : 1/49 RR which would occur in 1 generation and remain the same after that. (H-W equilibrium).

c) A population is observed over several years to have a ratio of 42 red : 36 pink : 22 white. Is the population at equilibrium? What is a likely basis for the observed ratio?

For allele frequencies 0.6 R’ ; 0.4 R; the expected distribution is 36% red : 48% pink and 16% white. The ratios suggest that there is ‘overdominance’, ie selection in favor of the heterozygote. (It is not legitimate to do a Chi-square test simply based on ratios, which was what was provided.). If the population is already at equilibrium, the relative fitness of the two homozygous classes could be calculated (0.44 for R’R’ and 0.51 for RR, but that is not clear in the problem as stated.)
6) Two relatively closed societies, one on an island off Spain and another a religious sect in Canada have unusually high rates of colon cancer associated with different defects in \( APC \), a gene that functions in tumor suppression. The Canadian defect is a large deletion in the promoter region and the Spanish island defect is a 5 base deletion in the coding region. Since \( APC \) is also required for normal development, it seems unlikely that homozygous defective individuals survive to reproduce. Speculate as to why these clearly detrimental defects persist in these populations.

These data strongly suggest a “founder effect” with different mutations becoming common in the initial small populations and remaining there simply by chance, although since in both cases the lethal remains in the population there may be cases where heterozygotes out-reproduce homozygous normal. Since colon cancer likely occurs after reproduction has ended in most cases, the defective allele will diminish very slowly.

7) Approximately 16 per million Japanese have acatalasemia, a homozygous recessive condition which seems to have no detrimental effects, unless perhaps the individual contracts gangrene. A) What fraction of the population is expected to be heterozygous?

\[
F(a) = q = (16/10^6)^{1/2} = 4 \times 10^{-3} \text{ and } p = 0.996, \text{ so } 2pq = \text{ approx. } 0.008
\]

B) What are the odds (approximate is fine) that at least 1 of a child's 4 grandparents will be heterozygous?

Approx 4 \times 0.008 or 3.2%

C. Two brothers from this population marry 2 sisters and a son from one marriage marries a daughter from the other (double first cousins). What is the \( F \) value for a child from the latter marriage?

\[
X \\
F \text{ for } X = 4(1/2)^5
\]

D. What is the likelihood the child will have acatalasemia?

\[
Q^2 + Fpq \text{ which is essentially } Fpq \text{ or } 0.0005
\]
8. In several naturally self pollinated crops, the use of cytoplasmic male sterility to produce fertile hybrids actually utilizes 3 ‘lines’, generally referred to as A, B and R lines. The A line has sterile cytoplasm [S] and is rf1/rf1, the B line has Normal [N] cytoplasm and is rf1/rf1 while the R line is [N] Rf1/Rf1, i.e., it is homozygous for the dominant gene or genes needed to restore fertility. Given that the B line is essentially genetically the same as the A line, what is its role in hybrid production?

   The B line is needed to “maintain” the A line: since it cannot self pollinate, this provides a mechanism for producing seed for crossing and also for introducing different genes if needed through continuous backcrossing with the a line as the female parent.

9. A statement in the text says ‘Natural selection has a much greater effect on traits with high narrow-sense heritabilities than on traits with low narrow sense heritabilities.’ Explain why (or why not, if you disagree) including why h² rather than H² was mentioned when considering changing gene frequencies in natural selection.

   Since h² shows the additive genetic component, a large value obviously means much of the differences seen can be attributed to differences in genetic makeup among individuals in the population. Since every allele of an additive gene “contributes” to the trait under selection, all are subject to selection. If H² was used, some alleles such as a recessive in a heterozygous individual could not be selected, even if advantageous and might be carried along even if detrimental.

10 a). A 2009 article in the International Journal of Plant Genomics reported the following data on 5-day height of cowpea seedlings resulting from a high school science fair project. The variance seen in 15 pots (4 plants per pot) of one cultivar was 1.09. The variance seen from 15 other randomly selected naturally inbred varieties, also grown at 4 plants per pot, was 2.28. What type of heritability value can be calculated from these data and what is that value?

   Ve is estimated from the variation seen in the single cultivar at 1.09
   Vt or Vp, is estimated from the 15 genetically different cultivars at 2.28
   Vg thus is 2.28 – 1.09 or 1.19 and H² is 1.19/2.28 or 0.552

b) The average tail length in a large mouse colony was measured at 9.7 cm. When the 10 males and females with the longest tails (average = 14.3 cm) were mated, the average tail length in those progeny was 13 cm. What type of heritability value can be calculated from these data and what is that value?

   The realized gain or R is 13 – 9.7 or 3.3
   The selection differential S is 14.3 – 9.7 or 4.6  h² is 3.3/4.6 = 0.72
11. DNA sequencing revealed about 120 transposable element families in Drosophila, of which approximately 100 are retrotransposons. It has also been found that Drosophila produces a number of PIWI-interacting or pi-RNAs, small (26-31 bases) RNAs encoded at multiple sites in the genome. When expressed in the presence of PIWI proteins, the pi-RNAs have been shown to cause silencing of many retrotransposons. Speculate in the origin of the pi-RNA genes and propose a mechanism that allows them to silence retrotransposons.

The likely origin if the microRNAs is from the transposons themselves, either from reverse transcription of their own mRNA or from deletions etc that remove much of the functional gene. It's possible that these fragments might interfere with transcription/translation of the retrotransposons for silencing, but given their size and similarity to the component that trigger RNAi, this is a more likely (and actual in this case) explanation. (PIWI proteins carry the microRNAs to the RISC complex).

12. An AAaa tetraploid plant is self fertilized. Assuming all diploid gametes are equally viable in both eggs and pollen, what fraction, if any, of the progeny will have the aaaa genotype? Show your rationale.

If A is near the centromere, there will be a $\frac{1}{2} \times \frac{1}{3}$ chance for either AA or aa gametes, the remainder will be Aa. In that case, 1 in 36 (2.778%) will end up as aaaa.

If A is far from the centromere there is a $\frac{1}{2} \times \frac{3}{7}$ that two a’s will end up at the same pole in which case the $\frac{3}{14}$ from each parents will give 4.6 % aaaa progeny.

13. Early embryonic Hox-c13 expression in mice was found in the nails and tail by Godwin and Capecchi (1998). Later studies showed Hox-c13 was also expressed in various tissues, including hair follicles throughout the body; in fact Hox-c13 knockouts lost hair all over their bodies. How do these observations fit with the expected pattern of expression of HOX genes?

Hox genes are typically expressed in a spatial and temporal order along the ‘head to tail’ axis of a developing embryo. A KO thus typically has an effect on the part of the body that develops from that segments, including moving the later segments forward. Thus the nails and tail defects seem typical, but not the ‘whole body’ lack of hair. As it turns out, the hox13c gene is also expressed in the developing hair follicles giving it an added function to its role in the array of Hox genes.