Diploid Genetics and Chromosomal Inheritance

A. Diploid Genetics

For each set of data below, determine the genotype of the parents in cross 1. Where it applies, indicate which phenotypes are dominant and which are recessive.

1. Mice I

a) cross 1: red-eyed mouse _____ **X** white-eyed mouse _____

gives F_1:   all red-eyed

cross 2: red-eyed F_1 **X** red-eyed F_1

gives F_2:   36 red-eyed
13 white-eyed

Cross 1: red eyes X white eyes gives all red eyes – a likely model is that eye color is controlled by one gene that has 2 alleles producing two phenotypes, red and white eyes. The red eyed phenotype is likely dominant. Therefore, choose appropriate symbols (one letter per gene, capital letter for allele with dominant phenotype):
•R - red allele. Dominant phenotype of red eyes.   •r - white allele. Recessive phenotype of white eyes.
Then: Cross 1 is: RR X rr ----> all Rr (all red eyes).   Cross 2 is: Rr X Rr ----> 3:1 red:white.
The predictions agree with the data.

b) cross 1: long-eared mouse _____ **X** short-eared mouse _____

gives F_1:   12 long-eared
10 short-eared

cross 2: long-eared F_1 **X** long-eared F_1

gives F_2:   36 long-eared
13 short-eared

Cross 1: long ears X short ears gives some long and some short ears – a likely model is that ear length is controlled by one gene with 2 alleles resulting in two phenotypes, long ears and short ears. From this data, we cannot determine which allele has the dominant phenotype.
Cross 2: long ears X long ears gives some long and some short ears – a likely model is that long ears is the dominant phenotype. Therefore, the appropriate symbols are: L - long ears and l - short ears .
Then: Cross 1 is: Ll X ll → 1:1 long ears: short ears   Cross 2 is: Ll X Ll → 3:1 long ears: short ears
The predictions agree with the data.

2. Flowers

cross 1: blue-flowered plant _____ **X** white-flowered plant _____

gives F_1:   all pale-blue-flowered

cross 2: pale-blue F_1 **X** pale-blue F_1

gives F_2:   27 blue49 pale-blue   24 white

Cross 1: blue flowers X white flowers gives all pale blue flowers – a plausible model is that color is controlled by one gene with 2 alleles, resulting in blue and white flowers, and that neither phenotype is dominant. This is an example of co- dominance. Then, BB- blue, B'B - white, BB'- pale blue phenotypes respectively.
Then: Cross 1 is: BB X B'B' → all BB', pale blue flowers.
*   Cross 2 is: BB' X BB' → 1:2:1 BB, blue flowers: BB', pale blue flowers: B'B', white flowers.*
The predictions agree with the data.

3. Blood Type

Blood type is determined by one gene that has three alleles:

   I^A - *allele associated with the A phenotype, co-dominant with the B phenotype*
   I^B - *allele associated with the B phenotype, co-dominant with the A phenotype*
   I^O - *allele associated with the O phenotype, recessive to both the A and B phenotype*

   a) cross 1: person, type A blood _____ **X** person with type B _____

      gives F$_1$:   all type AB blood

   cross 2: type AB F$_1$ **X** type AB F$_1$

      gives F$_2$:   2 type A
                        4 type AB
                        1 type B

Then:
<u>*Cross 1 is: $I^A I^A$ X $I^B I^B$ →all type $I^A I^B$*</u>
<u>*Cross 2 is: $I^A I^B$ X $I^A I^B$ →1:2:1 types A:AB:B (note **skewed ratio** with small number of progeny)*</u>

   b) cross 1: type A blood _____ **X** type B _____

      gives F$_1$:   2 type A blood
                        3 type AB blood
                        1 type B blood
                        2 type O blood

Then:
*Cross 1 is: $I^A I^O$ X $I^B I^O$----> 1:1:1:1 types A:B:AB:O (note **skewed ratio** with small number of progeny)*
The predictions agree with the data.

4. Mice II

   cross 1: tail-less mouse _____ **X** normal mouse _____

      gives F$_1$:   10 tail-less
                         9 normal

   cross 2: tail-less F$_1$ **X** tail-less F$_1$

      gives F$_2$:   10 normal
                        21 tail-less
                        9 dead

Tail-lessness and lethality are controlled by one gene with two alleles:
   T allele - dominant tail-less phenotype; recessive lethal phenotype
   t allele - recessive normal-tail phenotype; dominant viable phenotype

therefore:
   TT - tail-less and dead   *Tt - tail-less and alive*   *tt - normal-tail and alive*

Then:
Cross 1 is: Tt X tt→ 1:1 Tt (tail-less) : tt (normal)
Cross 2 is: Tt X Tt→1:2:1 normal:tail-less:dead
The predictions agree with the data.
Note that usually in such problems the number of dead animals is not reported, but needs to be inferred from the rest of the data (i.e. "missing" phenotype or numbers of progeny, i.e. ratios that don't make sense).

B. Chromosomes and Recombination

1. What is the physical basis of the genetic inheritance?
Genes are fragments of DNA that encode when, where, and what product (protein or functional RNA) is to be made. Genes are assembled together into chromosomes. During cell division chromosomal segregation can be observed with a microscope. Chromosomes are inherited from parents. Thus, sexually reproducing diploid organisms get one copy (allele) of each gene from each parent and pass one allele on to each of their offspring at random. These alleles are passed on the chromosomes inherited from each parent.

2. Why is sexual reproduction a powerful source of variation?
Sexual reproduction allows for great diversity and fast change (through bringing together genetic information from two parents). Gamete production in meiosis ($2n \rightarrow 4n \rightarrow 2n \rightarrow n$) allows for reshuffling of parental genetic information through independent segregation of chromosomes.

3. Why was it evolutionarily advantageous to develop the ability to recombine chromosomes?
Recombination—the exchange of parts of chromosomes between homologous pairs of chromosomes—increases the rate of reshuffling of parental genetic information compared with the independent segregation of chromosomes alone.
Faster reshuffling of genetic information means more variation in the population. In turn, that leads to better survival for a species because, for any change in the environmental conditions (selective pressure), it increases the chances that an individual will arise that is better suited to the new conditions (selective advantage). This individual and the individual's offspring will have be more likely to survive and procreate under the new conditions, and, thus, greater proportion of the population will end up with the advantageous allele in the future.

Think about the following question for next time (we will talk about it in Section 16):
Recombination can occur anywhere along the length of the chromosome. However, we have been relying on the fact that genes are inherited as discreet units. How do we reconcile these two things? (Hint: think about what usually is the difference between two alleles of the same gene.)