Study Guide Mendelian Genetics
Unless otherwise noted, assume 2n = 2x.

1. Match the most correct definition with each of the following words:
    a) Gene
    b) Locus
    c) Allele

    d) Place on a chromosome where a gene is found and this place will (usually) be the same on two homologous chromosomes.
    e) DNA sequence associated with a particular phenotype.
    f) The form of the gene that is found at the locus in each of the two homologous chromosomes.

2. Explain to your partner/spouse/best friend why the % heterozygosity at a locus decreases by half with each generation of selfing and how this relates to inbreeding depression.

3. Show how you could get a 1:1 phenotypic ratio in F1 progeny and in doubled haploid progeny from an F1, depending on the allelic state of the parents used to make the cross.

4. If you study inheritance using only doubled haploids, why can't you determine if an allele is dominant or recessive?

5. In a chi square test, it is imperative that you use the correct degrees of freedom. Say you calculate a chi square value of 9. What conclusions will you make if you test goodness of fit at 2 df vs. 6 df?

6. What about those other genomes: chloroplasts and mitochondria. From what did they evolve? Why don't we use chi square tests to test the expected vs. observed ratios for traits encoded in these genomes? If chloroplasts in monocots usually show maternal inheritance, why are doubled haploids produced through anther culture green?

The reading – key points from Komatsuda et al.

1. What does the wild type (dominant, Vrs1) allele encode?
2. What do recessive (vrs1) alleles encode?
3. Why are there (apparently) more possible recessive alleles than dominant alleles at this locus?