TABLE 2.3 *Values of the coefficient of relatedness (r_{IJ}) for different relationships*

Relationship	r_{IJ}
Self and monozygotic (identical) twins	1.0
Parents and offspring	0.5
Grandparents and offspring	0.25
Full siblings	0.5
Half siblings	0.25
Aunt or uncle to niece or nephew	0.25
First cousins	0.125

individual's genes come from each parent. The value of r_{IJ} for full-siblings is also 0.5, but only on average, because each sibling received half of their genes from each of the same pair of parents, but the haploid set of genes that is put in each parental gamete is a random sample of half the parental genome due to recombination. More distant coefficients of relatedness can be calculated as products. For example, because parents and offspring share half their genes, the r_{IJ} for grandparents and offspring is the product of the two coefficients ($0.5 \times 0.5 = 0.25$). Table 2.3 gives values of the coefficient of relatedness for a variety of different relationships.

Dole and Ritland (1993) estimated F using seven allozyme loci in natural populations of two species of monkey flower. *Mimulus guttatus* is primarily **outcrossing** (outbreeding), while *M. platycalyx* is primarily selfing (Figure 2.15). As expected, F was much higher in the latter, averaging 0.54 compared to an average F of 0.17 for *M. guttatus*.

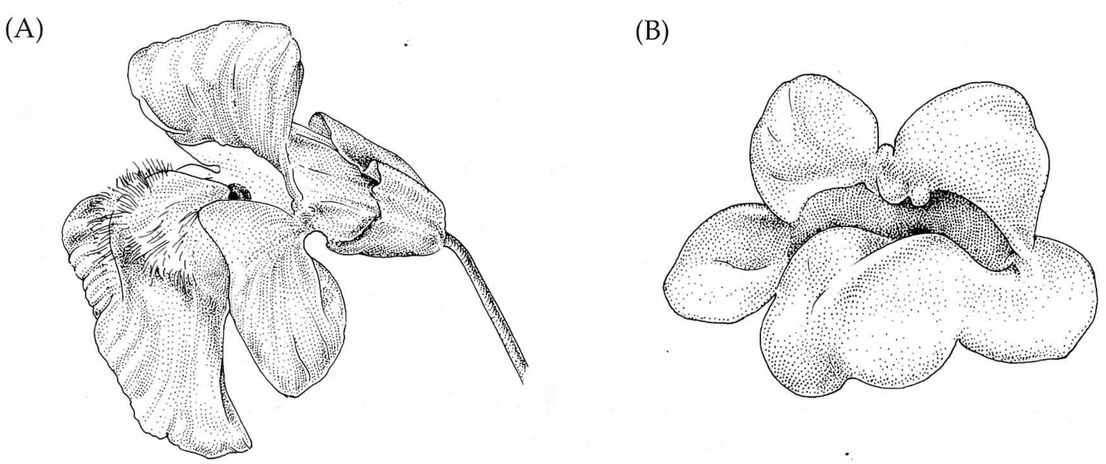


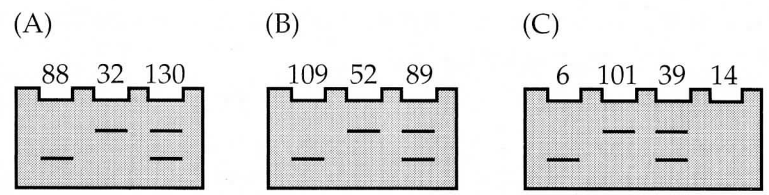
Figure 2.15 Flowers of (A) *Mimulus guttatus* and (B) *M. platycalyx*.

Inbreeding can also be estimated and studied directly using pedigrees. This approach is very useful if detailed pedigrees are known for the study organism, but this information is rarely available in natural populations, especially since paternity can often be uncertain. Pedigree analysis is described in detail in the population genetics books listed in the Suggested Readings at the end of this chapter.

The most important effect of the genome-wide increase in homozygosity caused by inbreeding is called **inbreeding depression,** which refers to a decrease in fitness that often accompanies inbreeding. Inbreeding and inbreeding depression are important in a number of contexts, and therefore will be discussed further in later chapters.

PROBLEMS

Whenever a statistical test is needed, report the test statistic (e.g., value of chi-square), the P-value and explain what the statistical result means biologically. The following electrophoresis gel diagrams are used in Problems 2.3 and 2.5. Above each lane is the number of individuals in the population sample with the banding pattern illustrated.



2.1 Spitze (1993) reported the following numbers of genotypes at the *PGI* locus in the *Daphnia* population in Nothing Pond:

SS	11
SS-	55
S-S-	61

a. What are the observed genotype and allele frequencies?

b. Given the observed allele frequencies, what are the genotypic frequencies expected under Hardy-Weinberg? Using a chi-square test, how well do the observed genotypic frequencies agree with the Hardy-Weinberg expectations?

2.2 Calculate F for the *Daphnia PGI* locus in the Ojibway Pond (page 35; note that there are data for *PGM* in the text as well) and the Nothing Pond (Problem 2.1 above) populations. What is a possible biological interpretation of these data? Explain your reasoning.

2.3 Gels A and B show banding patterns from RFLP markers in two related plant species.

a. Estimate allele and genotypic frequencies and test for HWE in each species.

b. Estimate F for each species.

c. What is a possible biological interpretation of the data from parts a and b? Explain your reasoning.

2.4 RAPD and AFLP markers have only two genotypes—presence or absence of a band. When a band is present, the genotype can be homozygous or heterozygous. Therefore, only the band-absent (null) genotype can be scored definitively. In a study of a selfing plant (*Medicago truncatula*), Bonnin et al. (1996) reported band-presence at a frequency of 0.59 at their RAPD locus B6-600 in a population from Aude, France.

a. Assuming HWE, what are the frequencies of the two alleles and the three genotypes?

b. Because this is a selfing plant, assume HWE is not valid. Is your estimate of the frequency of the band-present allele an over- or underestimate? Explain your reasoning.

2.5 Gel C shows the banding patterns from two AFLP markers (the upper and lower sets of bands).

a. Estimate the frequency q of the null allele of each of the two AFLP markers assuming HWE.

b. Estimate the percentage of *band-present* individuals (not the overall frequencies) that are heterozygous at each of the two markers. What biological principle does the difference between these two percentages illustrate?

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