

CHAPTER 16 Answers to Problems

Problem 16.2. Phenetics, cladistics, and a combination of the two, which is sometimes called evolutionary classification. Evolutionary classification is the most widely used approach. The most appropriate approach for evolutionary studies is cladistics (sometimes called phylogenetics) because it considers only evolutionary (i.e., phylogenetic) relationships among taxa.

Problem 16.4. Historical, present, and future diversity are all important to maintain. For example, maintenance of both ancient isolated lineages and current patterns of diversity are important for maximizing potential to generate future biodiversity, which is an important goal in conservation genetics (see Example 16.2).

Problem 16.6. Yes, there is clear evidence of phylogeographic structuring in (b). When we overlay the phylogeny (a) on to the geographic distribution map of haplotypes (b) we see phylogeographic structuring – i.e., phylogenetic distance is related to geographic distance such that the four different haplotypes occur in each of four different geographic areas (see overlap diagram below; see also Figure 16.12 for another example). Furthermore, the ancestral allele *w* occurs geographically (and phylogenetically) far from the derived allele *z*.

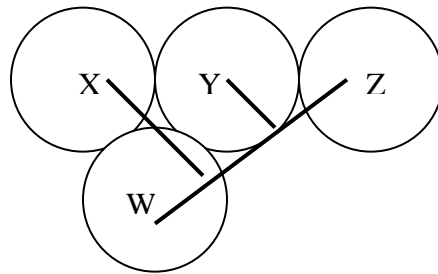
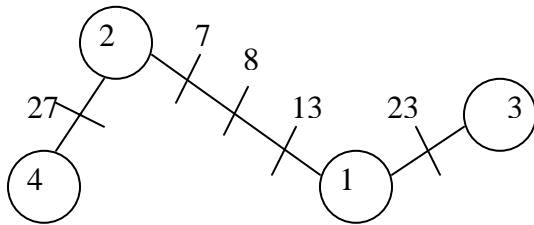


Figure (c) shows a geographic distribution of haplotypes with no phylogeographic structure in that different alleles (both ancestral *w*, and derived *y* and *x*) are widespread geographically with no apparent pattern relating to phylogeny.

Problem 16.8. A management unit (MU) often is defined as a population (or set of populations) that is *demographically independent* but that has (or recently has had) gene flow with other MUs (e.g., see Table 16.4). An ESU usually is defined as a population

(or set of populations) that is *evolutionarily independent* and that has not had recent gene flow with other ESUs. Further, MUs generally are not adaptively differentiated whereas ESUs typically are adaptively differentiated. MUs often are identified as subunits within an ESU. Molecular markers can help identify MUs by identifying populations and boundaries between populations, and by quantifying the degree of genetic differentiation among populations.

Problem 16.10. (a)



((b) The sequence matches a major histocompatibility complex (MHC) class II gene (DRB).

Hemitragus jemlahicus, *Bos taurus*, *Ovis canadensis*, *Ovis dalli*, and *Capra hircus* all have this sequence. The following is part of an accession from GenBank:

```

LOCUS      AY706317                236 bp    DNA     linear   MAM 22-SEP-2004
DEFINITION Hemitragus jemlahicus MHC class II antigen (Heje-DRB) gene,
            Heje-DRB05 allele, exon 2 and partial cds.
ACCESSION  AY706317
VERSION    AY706317.1  GI:52221404
KEYWORDS   .
SOURCE     Hemitragus jemlahicus (Himalayan tahr)
  ORGANISM Hemitragus jemlahicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Hemitragus.
REFERENCE  1 (bases 1 to 236)
  AUTHORS  Schaschl,H., Wandeler,P., Suchentrunk,F., Obexer-Ruff,G. and
            Goodman,S.J.
  TITLE    Selection and recombination drive the evolution of MHC class II DRB
            diversity in ungulates
  JOURNAL  Unpublished
REFERENCE  2 (bases 1 to 236)
  AUTHORS  Schaschl,H., Wandeler,P., Suchentrunk,F., Obexer-Ruff,G. and
            Goodman,S.J.

```