

FIGURE 18.1 Three kinds of coevolution. In each pair of graphs, the horizontal axis represents evolutionary time (t), and the vertical axis shows the state of a character (z) in one or more species of parasites (P, with character z_p , upper graphs) and in one or more species of hosts (H, with character z_H , lower graphs). These could also represent predator and prey species or mutualistically interacting species. The characters (z) mediate the effect of the interaction on individuals' fitness. (A) Specific coevolution, in which each of two species imposes selection on the other, as indicated by the arrows. (B) Guild coevolution, in

which each of several P species interacts with each of several H species. It is assumed that a character in each species in a guild evolves similarly, although at different rates. (C) Escape-and-radiate coevolution. Several P species interact with several H species, one of which evolves a major new defense. P species previously associated with this host become extinct. The host lineage diversifies. Later, a P lineage, formerly associated with different hosts, adapts to the host clade and diversifies. The phylogenies of the P and H clades need not match (see Figure 18.2).

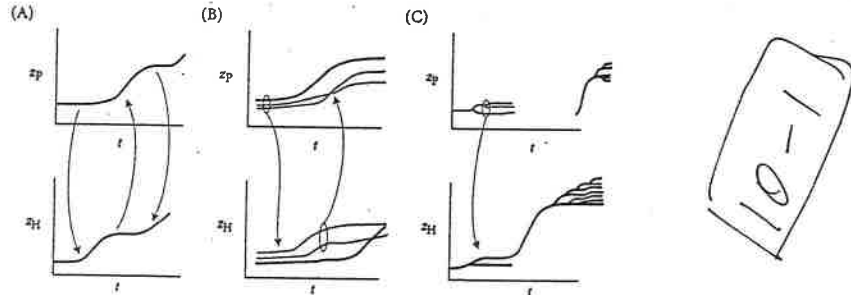


FIGURE 18.2 Congruent and incongruent phylogenies of hosts (black lines) and host-specific parasites or mutualists (colored lines). Each parasite lineage is specialized on the host with which it is closely associated in the diagrams. (A) Largely congruent phylogenies are due to several instances of concordant speciation, which may be due to the parasite-host interaction (cospeciation) or not. Host lineage B' is free of parasites, perhaps due to the evolution of a new defense or to its invasion of a new geographic region, unaccompanied by its parasite. (B) Discordant phylogenies of interacting species. The parasite lineage, derived from one associated with an entirely different host, "colonized" the host clade and diversified after the host clade had diversified (see the diagram of "escape-and-radiate coevolution" in Figure 18.1). (After Mitter et al. 1991.)

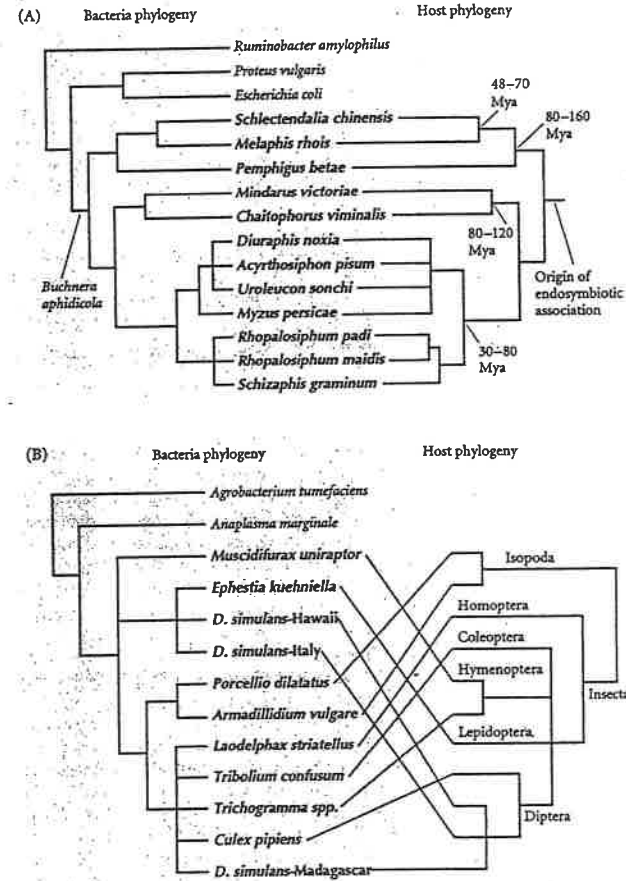
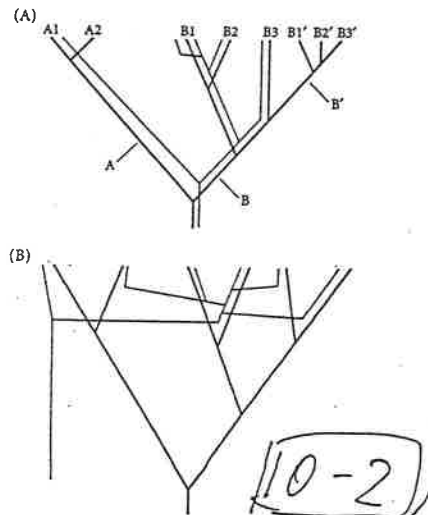


FIGURE 18.3 Phylogenies of some arthropods and their associated bacteria. In both diagrams, names of bacteria are in normal type and names of arthropod species are in boldfaced type. The bacterial phylogeny shows the relationship among the bacteria isolated from the species of arthropods indicated in boldface. (A) The phylogeny of bacteria included under the name *Buchnera aphidicola* is perfectly congruent with that of their aphid hosts. Several related bacteria were included as outgroups in this analysis. The estimated ages of the aphid lineages are based on fossils and/or biogeography. (B) The phylogeny of *Wolbachia* bacteria from various arthropods is not highly congruent with the phylogeny of their hosts, implying that the bacteria have been transferred among arthropod lineages. (After Moran and Baumann 1994.)

TABLE 18.2 Gene-for-gene interactions between a parasite and its host

ONE-LOCUS INTERACTION			
PATHOGEN GENOTYPE	HOST GENOTYPE		
	RR	Rr	rr
VV	- ^a	-	+ ^b
Vv	-	-	+
vv	+	+	+

TWO-LOCUS INTERACTION				
PATHOGEN GENOTYPE	HOST GENOTYPE			
	R ₁ -R ₂ ^a	R ₁ -r ₂ r ₂	r ₁ r ₁ R ₂ ^a	r ₁ r ₁ r ₂ r ₂
V ₁ -V ₂ ^a	-	-	-	+
V ₁ -v ₂ v ₂	-	-	+	+
v ₁ v ₁ V ₂ ^a	-	+	-	+
v ₁ v ₁ v ₂ v ₂	+	+	+	+

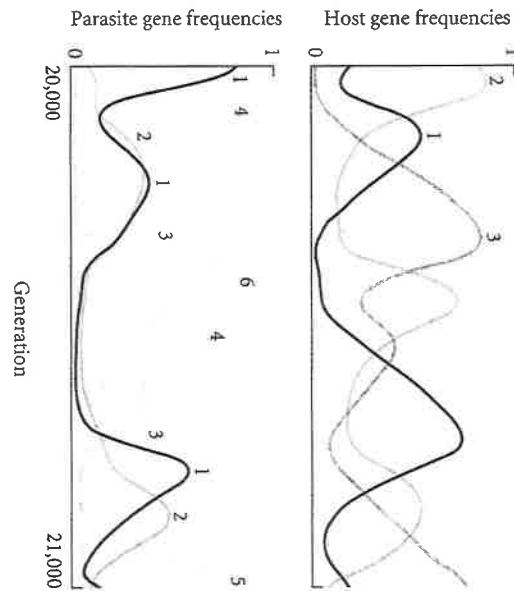
Source: Frank (1992).

^a- indicates that the host genotype is resistant to the pathogen genotype.

^b+ indicates that the pathogen genotype can grow on a host of a given genotype (i.e., the pathogen is virulent and the host is susceptible).



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A computer simulation of genetic changes at a resistance locus in a host (top) and a virulence locus in a parasite (bottom). The host is diploid and has three alleles; the parasite is haploid and has six alleles. Each parasite genotype can overcome the defenses of one of the six host genotypes (e.g., parasite P_1 can attack host H_1H_1). Both populations remain polymorphic, and fluctuate irregularly in genetic composition. (After Seger 1992.)

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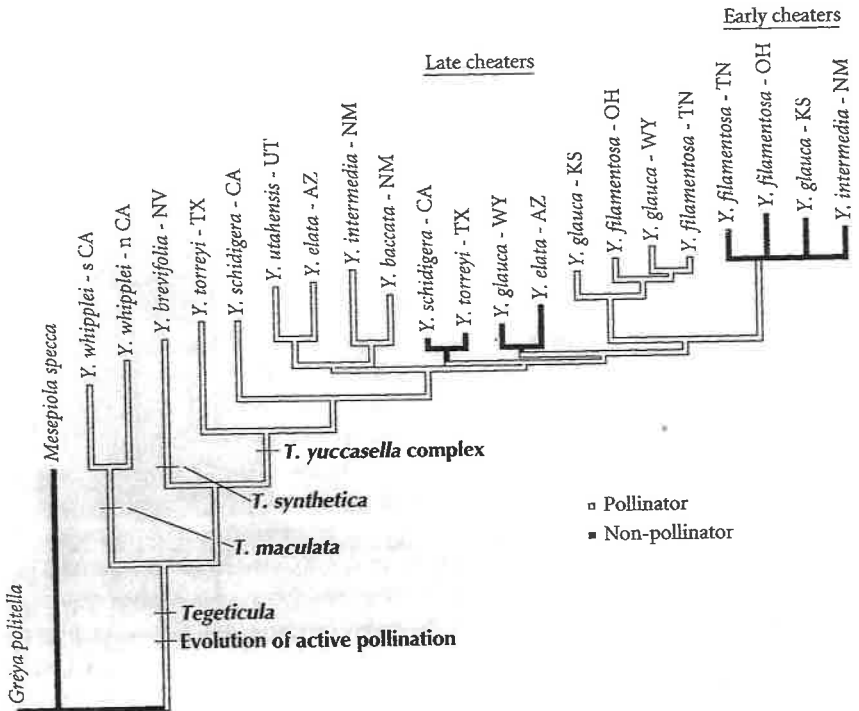
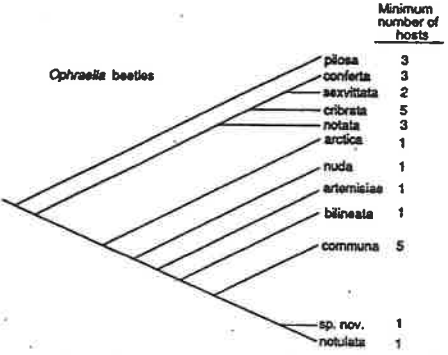


FIGURE 18.18 Phylogeny of the yucca moth genus *Tegeticula*, and two closely related genera. The *Tegeticula* populations in this phylogenetic analysis are labelled by the name of the host (*Yucca* species) from which they were collected. Three *Tegeticula* species are named; species limits in the *T. yuccasella* complex are uncertain. Most *Tegeticula* taxa actively pollinate (open branches in the phylogeny). Three lineages (solid branches), denoted "late cheaters" and "early cheaters," lay eggs in *Yucca* flowers, but do not pollinate. The phylogeny indicates that they have evolved from pollinating ancestors. (After Pellmyr et al. 1996a.)

PHYLOGENY OF SPECIALIZATION



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Fig. 4.2. Phylogeny of specialization in the beetle genus *Ophraella*. Data from Futuyama 1991 and Futuyama and McCafferty 1990.

PHYLOGENY OF SPECIALIZATION

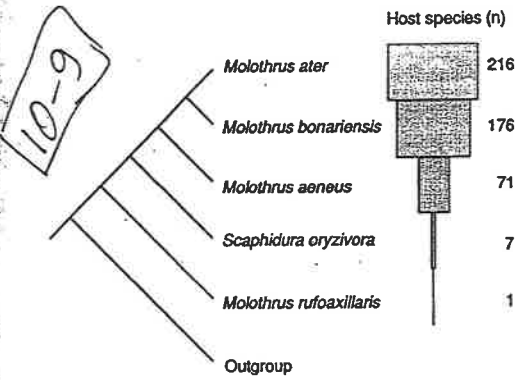


Fig. 4.4. Phylogeny of specialization in parasitic cowbirds, indicating evolution of host generalists from host specialists. Redrawn from S.M. Lanyon, "Interspecific Brood Parasitism in Blackbirds (Icterinae)," *Science* 255:77-79, copyright 1992 by the AAAS.

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10-10 65

Table 4.1. The range in the number of plant species used as hosts within each monophyletic group with two or more species within the moth subfamily Prodoxinae (yucca moths and allies)

Monophyletic group	No. of species	No. of species used per moth species
<i>Greya politella</i> group	2	2-7
<i>Greya punctiferella</i> group	4	1-4
<i>Greya solenobiella</i> group	5	1-5
<i>Tegeticula</i> spp.	3+	1-19 ^a
<i>Prodoxus</i> spp.	10	1-11
<i>Agavenema</i> spp.	2	1

Sources: Data from Davis 1967; Thompson 1987c; Davis, Pellmyr, and Thompson 1992; and Pellmyr and Thompson, unpublished.

^a*Tegeticula yuccasella*, which has been reported from at least nineteen *Yucca* species, is now considered to be a complex of sibling species, each with a much narrower range of hosts (Miles 1983; Addicott et al. 1990).

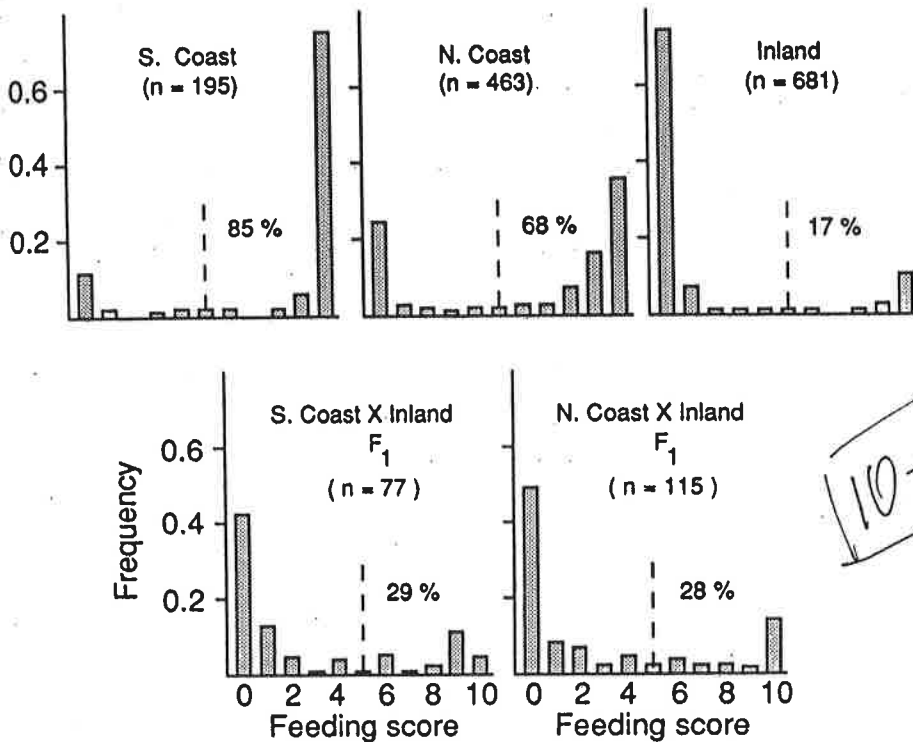


Fig. 5.2. Percentages of naive, newborn garter snakes (*Thamnophis elegans*) from coastal, inland, and laboratory hybrid populations showing preference for slugs (scores above 5) or avoidance of slugs (scores below 5). Redrawn from Arnold 1981b.