THE "HYBRID BRIDGE" HYPOTHESIS: HOST SHIFTING VIA PLANT HYBRID SWARMS

The mechanisms by which herbivorous insects acquire or shift to new host varieties or species are basic to understanding the evolution of plant-herbivore interactions. These mechanisms should also apply to plant parasites, pathogens, and perhaps even pollinators. Presently, host shifting is explained by either preadaptation or mutation hypotheses that require herbivores to make a single jump in shifting from one host species to another. Preadaptation hypotheses suggest that herbivores are preadapted to shift onto new host species but are prevented from doing so by the absence of these host species. When the barrier to shifting is removed following changes in either the herbivore's or the host's distribution (Tabashnik 1983; Thomas et al. 1987), a shift may result. In contrast, when herbivores are not preadapted to a host, one or more key mutations must occur to allow the herbivore to recognize and survive on the new host species (Bush 1974, 1975; Futuyma 1983; Jermy 1984).

These hypotheses do not consider the potential importance of naturally occurring hybrid plants that morphologically, genetically, and spatially bridge gaps between parental species and may allow herbivores to shift in a series of gradual steps. Based on our studies of insect distributions on cottonwood trees, we propose the "hybrid bridge hypothesis," which argues that the presence of plant hybrid intermediates facilitates host shifting by herbivores such that host shifting is more likely to occur in their presence than in their absence. Although we limit the present discussion to plant hybrids, a recent study by Le Brun et al. (1992) suggests that *Barbus meridionalis* × *barbus* fish hybrids may play a similar role in facilitating host shifting by gill parasites between the parental species.

The hybrid bridge hypothesis is not mutually exclusive of either preadaptation or mutation hypotheses and likely enhances both. For example, when allopatric distribution of plant species is the only barrier to host shifting, preadaptation hypotheses predict that herbivorous insects are stymied in shifting from one species to another unless their distributions become sympatric. However, if these plants hybridize such that the gap between their distributions is "spatially bridged" by hybrid intermediates (see, e.g., Potts 1986; DePamphilis and Wyatt 1989; Keim et al. 1989), herbivores could shift onto the new host species via these intermediates even though the plant species remain allopatric.

Similarly, hybrids may bridge the "morphological and/or genetic gaps" between plant species so that herbivores experience novel morphologies and genomes in a series of gradual steps. Because hybrid swarms may include individual plants with all possible combinations of the parental genomes (i.e., pure parentals,

 F_1 's, and complex backcrosses with varying proportions of each genome), herbivores colonizing these hybrids encounter various levels of the novel host's genome without having to shift directly onto the novel host species. This may be particularly important where the factors controlling successful host shifts are polygenic; hybrid plants can permit a gradual shift toward the new host as the necessary mutations accumulate.

To understand how plant hybrid intermediates may facilitate a host shift, consider a hypothetical situation in which host shifting requires a single mutation in an insect coupled with its previous exposure to the new host. This situation is not implausible as there is evidence to suggest that survival on new hosts is under the control of one or a few genes (Hatchett and Gallun 1970) and that previous exposure to a host species induces a preference for that host (Jermy et al. 1968; Jaenike 1982; Boer and Hanson 1984; Papaj and Prokopy 1988). In our example, insects on the old host that acquire the mutation to survive on the new host do not recognize it as "food," having never encountered it before, and the host shift is thwarted. However, if hybridization occurs between old and new host species, hybrid intermediates may have the recognition cues and survival factors for both plant species. Thus, when the mutation enabling survival on the new host arises, either before of after hybrids are colonized, insects on hybrid hosts gain the necessary exposure to recognition cues of the new host and can subsequently shift to the new host species.

If hybridization were rare, its potential role in host shifting would be greatly diminished; however, hybridization between plant species is common and well documented. For example, *Betula* species hybridize widely in Europe (Lotsy 1925, 1931), as do species of *Geum* and *Salix; Melandrium* in Sweden; *Nothofagus* in New Zealand; and *Pinus, Quercus, Gilia, Iris,* and *Diplacus* in western North America (see Grant 1981). *Eucalyptus* hybridize in Australia (Griffin et al. 1988), and *Crataegus* (Phipps 1984) and *Populus* (Eckenwalder 1984) hybridize extensively in North America. Past hybridization events are thought to account for 30%–80% of extant plant species (Stace 1987; see references in Wendel et al. 1991).

We predict that host shifting will be affected by the pattern of plant hybridization as this determines the degree to which hybrid genotypes span the genetic gap between plant species. For example, in the progression from F_1 sterility, to unidirectional introgression, to bidirectional introgression, the genetic gaps between parental species diminish to form a continuum of intermediates. This point is illustrated in figure 1, beginning with a hypothetical system of nonhybridizing plant species A and B (fig. 1A). If these species hybridize to produce sterile F_1 offspring, all hybrids contain 50% of the genomes of the parental species (fig. 1B) (see, e.g., Ownbey 1950; Cook 1979; Weber and Campbell 1989). The production of sterile F_1 hybrids should facilitate host shifting, but two large genetic gaps remain. An intermediate form of hybridization known as unidirectional introgression occurs when fertile F_1 's backcross only to one of the parental species to produce a continuum of hybrid genotypes from that parent to F_1 's, but a large genetic gap remains between F_1 's and the other parental species (fig. 1C) (see, e.g., Crawford 1974; Jones 1978; Keim et al. 1989). This pattern should

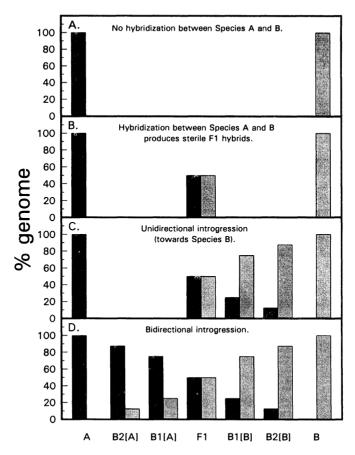


Fig. 1.—The various patterns of hybridization that result in different morphological and genetic gaps between species. A, In the absence of hybridization the gap between species A and B is greatest, and current models of host shifting assume this is the general pattern. B, When hybridization between species A and B produces sterile F_1 's, the gap between species is reduced to two smaller gaps. C, Unidirectional hybridization to B produces a continuum of hybrid genotypes between B and F_1 hybrids, but a large gap remains between F_1 's and A. D, Bidirectional introgression produces a complete morphological and genetic continuum of hybrids from A to B with no gaps.

facilitate host shifting halfway between the two species, but the remaining gap still represents a barrier to host shifting in gradual steps. Last, F₁ hybrids may backcross to both of the parental species in a pattern of bidirectional introgression resulting in a complete continuum of hybrid genotypes (fig. 1*D*) (see, e.g., Potts and Reid 1985; Potts 1986; Warwick et al. 1989). A genetic continuum with no gaps should be most likely to facilitate host shifting.

As hybrids also typically have intermediate morphologies, the above arguments, based on hybrids bridging genetic gaps, should also apply to hybrids

bridging morphological gaps (see, e.g., Potts and Reid 1985, 1988; Keim et al. 1989). This should be especially true when the morphologies of the hybridizing species are as different as cottonwoods (Keim et al. 1989) or the more extreme *Eucalyptus* described by Potts and Reid (1985, 1988).

TESTING THE HYBRID BRIDGE HYPOTHESIS

Existing studies do not show an overall pattern of herbivore distribution in hybrid zones. Insect species and their densities have been reported as being greater on hybrid plants than on the parental plant species (Drake 1981; Whitham 1989; Whitham et al. 1991). Similar reports occur for parasites of animal hybrids (Sage et al. 1986; Dupont and Crivelli 1988). However, other studies have found that herbivore densities may be the same or lower on hybrids than on the parental species (McClure 1985; Boecklen and Spellenberg 1990). In other cases, herbivore species and numbers on hybrid hosts reflect the degree to which hybrids resemble the parental species (Manley and Fowler 1969; Roskam and van Uffelen 1981).

These mixed results can be partially attributed to a lack of specific knowledge in these diverse systems. Studies do not always compare the performance and distribution of herbivores on hybrid hosts relative to their pure hosts (Caldbeck et al. 1978; Burkot and Benjamin 1979; Abrahamson et al. 1990). Furthermore, different categories of hybrids are not usually distinguished even though their susceptibilities to herbivores may be very different. For example, F₁ hybrids may be highly resistant while backcross hybrids may be susceptible (Paige et al. 1990), so valid comparisons between different hybrid systems need to consider hybrid category. For these reasons, all we can clearly conclude from the current literature is that insect herbivores can incorporate hybrid plants into their host range. Consequently, our development and discussion of the hybrid bridge hypothesis are restricted primarily to the galling insects of cottonwoods for which the pattern of hybridization is known.

Galling Arthropods on Cottonwoods

Along the drainage of the Weber River in northern Utah, Fremont cottonwood, *Populus fremontii*, grows at elevations of about 1,300-1,500 m, and narrowleaf cottonwood, *Populus angustifolia*, grows at elevations of about 1,400-2,300 m. Between the communities of Riverdale and Mountain Green, there is a 13-km zone where these species overlap in distribution and hybridize. In this hybrid swarm DNA analyses of trees have identified the pattern of hybridization as unidirectional; F_1 individuals are produced that, in turn, backcross only to narrowleaf cottonwood (Keim et al. 1989). Thus, the form of this swarm is similar to that shown in figure 1C, where species A and B correspond to Fremont and narrowleaf cottonwood, respectively.

This system provides a critical test of the hybrid bridge hypothesis because the unidirectional pattern of introgression generates both a distinct genetic and morphological gap and also a continuum of genotypes and morphologies at the same site. The hypothesis predicts that host shifting is more likely to occur between narrowleaf cottonwood and F_1 hybrids because of the presence of a contin-

uum of intermediates. However, the lack of intermediates between F_1 hybrids and Fremont cottonwood leaves a large gap that could represent a barrier to host shifting. Thus, our a priori prediction was that hybrid intermediates would facilitate host shifting from narrowleaf to F_1 's but the gap between F_1 's and Fremont would inhibit shifting between these latter two groups.

Data on herbivore distributions were collected using timed censuses on 30 trees in each of four morphological categories: Fremont, F₁'s, backcross hybrids, and narrowleaf. Trees were categorized based on a combination of plant traits that had been identified using DNA analyses and experimental crosses between known parents (Keim et al. 1989). Because these categories are not equally distributed in the hybrid zone, sampling was designed to reduce potential site effects. For example, approximately equal numbers of trees from the center and either end of the 13-km hybrid zone were sampled for each category. Reproductively mature trees were surveyed for 2 min for each herbivore species. Since trees ranged in height from 5 to 30 m, the portion surveyed for each tree was standardized by examining only the lowest 3 m of foliage on all sides of the tree.

Gall-forming herbivores were surveyed because they are typically host-specific and were not likely to be found on both cottonwood species, their distinct galls allowed accurate censusing, and their galls were a long-term record of their presence even after the herbivore was gone. Surveys were conducted in late July and early August, when gall formers had produced their galls yet before leaf abscission occurred. The eight species censused were not select examples from our survey; they represented all of the galling herbivores surveyed indigenous to either Fremont or narrowleaf.

The distribution of galling herbivores supports three distinct predictions of the hybrid bridge hypothesis. First, the prediction that galling herbivores are unable to shift from Fremont onto F_1 hybrids, because of the absence of backcross intermediates, is supported by the distributions of the galling species surveyed indigenous to Fremont. None of the leaf-galling aphids *Pachypappa pseudobursa*, *Pemphigus populicaulis*, *Pemphigus populitransversus*, and *Pemphigus* sp. had successfully shifted from Fremont to F_1 's or beyond to narrowleaf cottonwood (fig. 2). Although characteristic signs of their failed galls were found on F_1 's, which signified that these aphids naturally encounter and recognize hybrid trees as hosts, each species has thus far been unsuccessful in shifting from Fremont onto F_1 hybrids.

The second prediction, that the presence of backcross intermediates enables herbivores to shift from narrowleaf onto F_1 hybrids, is fulfilled by each of the galling species surveyed indigenous to narrowleaf. Three leaf-galling aphid species (*Pemphigus populiglobuli*, *Pemphigus betae*, and *Thecabius populimonilis*) and a bud-galling mite (*Aceria* sp.) have successfully shifted across backcross intermediates onto F_1 hybrids (fig. 3).

The third prediction is that herbivores that have shifted from narrowleaf onto F_1 's via backcross intermediates are unable to shift further from F_1 's to Fremont because of the absence of intermediates between these two categories. Again, for the galling species indigenous to narrowleaf that have all shifted to F_1 's, none have shifted onto Fremont (fig. 3). Each of the three predictions tested in this

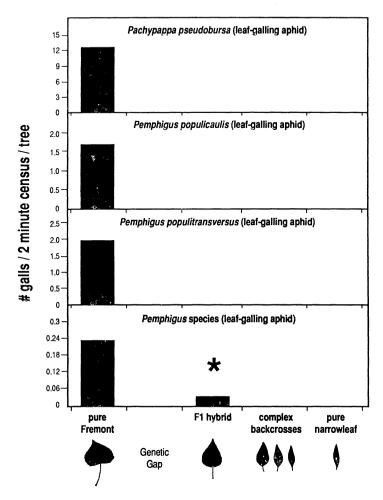


Fig. 2.—The distributions of four aphid species indigenous to Fremont cottonwood show that these species have not bridged the morphological and genetic gap to F_1 hybrids. The sole exception to this pattern (asterisk) was a single Pemphigus sp. gall found on an F_1 hybrid.

cottonwood system has been supported four times by different galling species, and the same patterns have been observed in a second year of censusing.

Although the above patterns support the hybrid bridge hypothesis, as an alternative hypothesis, dominance of narrowleaf genes affecting herbivore preference also could explain the observed distributions of galling insects (M. D. Rausher, personal communication). For example, if narrowleaf genes for these traits are dominant to those of Fremont, insects may perceive hybrids as "narrowleaf." This alternative could explain why galling species native to narrowleaf trees occur

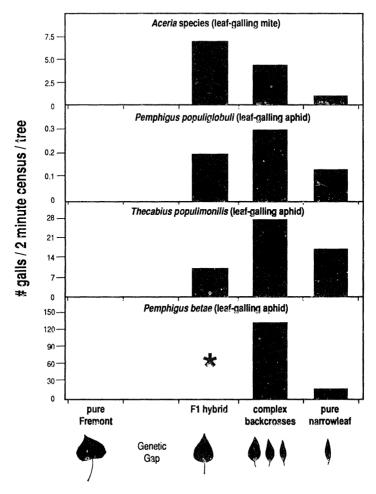


Fig. 3.—The distributions of four species (three aphids and one mite) indigenous to narrowleaf cottonwood show that these species have shifted to F_1 hybrids via hybrid intermediates, but they have not bridged the gap between F_1 's and Fremont cottonwood where hybrid intermediates are absent. (The *asterisk* indicates low densities of only 17 galls on 30 surveyed trees.)

on hybrids but do not occur on Fremont. It might also exlain why species native to Fremont are not observed on hybrids.

Two lines of evidence argue against this hypothesis. First, it is unlikely that the eight species studied (one mite and seven aphid species) use the same recognition cues to locate hosts and that all narrowleaf cues are dominant, although this has yet to be tested. Second, if insects perceive hybrid trees as "narrowleaf," colonization rates by these insects should be the same for the sympatric F_1 ,

backcross, and narrowleaf trees that co-occur in the hybrid zone. However, Moran and Whitham (1990) showed that the fall migrants of P. betae heavily colonize backcross hybrids, whereas F_1 hybrids are avoided.

DISCUSSION AND CONCLUSIONS

Assumptions

The hybrid bridge hypothesis has two basic assumptions. First, plants must hybridize, and hybridization must be common if this mechanism is more than just a rare occurrence. This assumption is met since hybridization is common to all major plant taxonomic groups (Grant 1971). Second, herbivores must have the capacity to shift onto hybrid hosts. This point is supported by our study and numerous others (e.g., Manley and Fowler 1969; Drake 1981; Roskam and van Uffelen 1981; McClure 1985; Whitham 1989; Boecklen and Spellenberg 1990; Whitham et al. 1991). Further, the use of hybrids by herbivores is not restricted to a single plant taxon but is widespread (e.g., the above citations include deciduous trees in North America, broadleaf evergreens in Australia, and conifers in Japan).

Predictions

Based on our initial tests of the hybrid bridge hypothesis, we make several predictions. First monophagous herbivores are more likely than polyphagous herbivores to benefit from the presence of a hybrid bridge for host shifting. These groups represent opposite ends of a gradient along which the value of hybrid intermediates in facilitating host shifts will change. Monophagous herbivores are best exemplified by gall formers, which are typically host-, organ-, and tissue-specific and are perhaps the most specialized guild of phytophagous insects (Shorthouse 1982). Because of the tight relationship necessary for the herbivore to elicit a galling response from its host plant, we predict that gall formers are the least likely of all feeding guilds to bridge the intervening genetic gap onto a new host species in the absence of hybrid intermediates. In contrast, polyphagous herbivores have already shown an ability to span genetic gaps between plant species by feeding on plants in different families, several genera, or distantly related species in the same genus.

Second, hybridizing plant species will share more herbivores than nonhybridizing species, for example, cynipid gall wasps on oaks (*Quercus* sp.). Oaks frequently hybridize within a subgenus but not between subgenera, which reflects the distribution of cynipid wasps that usually attack only one or a few closely related oak species, always within the same subgenus (Cornell and Washburn 1979). However, this pattern may merely reflect the genetic similarity of the hybridizing species and not the fact that they hybridize. To test the prediction critically, comparisons need to be made of the herbivores of two plant species at sites where they hybridize and at other sites where they do not.

Third, the pattern of hybridization allows for specific predictions. When the hybrid bridge is symmetrical (i.e., when F_1 sterility or bidirectional introgression

occurs), F_1 's should have the same number of herbivore species in common with both of the parental species. When the bridge is asymmetrical (i.e., when unidirectional introgression occurs), F_1 's will share more herbivore species with the parent to which introgression occurs than with the parental species with which hybridization does not occur, which is supported by the present study.

Implications

The hybrid bridge hypothesis may have important implications for the preservation of biodiversity. First, by bridging the spatial, morphological, and/or genetic gaps between parental species, hybrids could have a greater species richness than either of the parents because the hybrids can accumulate the fauna of both parents (e.g., hybrid fish, Dupont and Crivelli 1988; hybrid plants, Whitham et al. 1991; but see Boecklen and Spellenberg 1990). This fauna includes not only herbivores and pathogens but also their associated predators and parasites. Therefore, by conserving hybrid zones, it can be argued that we preserve both important centers of plant evolution and focus points of biodiversity (Whitham et al. 1991).

Second, by facilitating host shifting, hybrid zones may also promote speciation. Host shifting has been suggested as one way (Bush 1969, 1974, 1975) in which sympatric speciation could occur through habitat diversification (see also Maynard Smith 1966; Tauber and Tauber 1977; Felsenstein 1981; Rice 1987). Because the new host represents an environment distinct from the old host, herbivore populations on old and new hosts may be subject to divergent selection pressures that could then lead to reproductive isolation, race formation, and eventual speciation. Thus, if hybrid zones are centers of plant speciation, they may also be centers of insect speciation as well. For example, Moran and Whitham (1988) have suggested that race formation in the leaf-galling aphid Pemphigus betae may, in part, be a consequence of hybridization between Fremont and narrowleaf cottonwood. In the hybrid zone where susceptible hosts are common, this aphid annually alternates between cottonwoods and herbaceous plants. In the pure narrowleaf zone where trees are more resistant, P. betae remains almost solely on herbaceous plants. Reciprocal transfer experiments in the field and the performance of aphid clones in the lab argue that the differences in these life cycles are genetically based (Moran and Whitham 1988; Moran 1991). If hybrids facilitate host shifting and host shifting leads to genetic differentiation, then hybrid zones could also play a role in insect speciation.

ACKNOWLEDGMENTS

We thank K. Christensen, N. Cobb, R. DeClerck-Floate, G. W. Fernandes, C. Gehring, J. Maschinski, S. Mopper, P. Price, M. Rausher, P. Service, D. Siemens, S. Stein, and three anonymous reviewers for their valued comments. We greatly appreciate the use of facilities provided by PacifiCorp during our field seasons. Financial support was provided by National Science Foundation (NSF) grants BSR-8906391, BSR-8918380, BSR-9107042, U.S. Department of Agriculture (USDA) grant 91-37302-6224, and a Sigma Xi Grant-in-Aid of Research.

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KEVIN D. FLOATE*
THOMAS G. WHITHAM

DEPARTMENT OF BIOLOGICAL SCIENCES NORTHERN ARIZONA UNIVERSITY FLAGSTAFF, ARIZONA 86011-5640

Submitted September 27, 1991; Revised April 13, 1992; Accepted April 23, 1992

* Present address: Agriculture Canada Research Station, PO Box 3000, Main, Lethbridge, Alberta TIJ 4B1, Canada

Editor: Mark D. Rausher