

NOTE

Genetic control of feeding preference in the herbivorous amphipod *Ampithoe longimana*

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ABSTRACT: The feeding preferences of individuals within a single species of marine consumer can differ because of variation in ontogeny, physiological state and environmental conditions; yet genetic variation can also play a central (largely undescribed) role. This study describes the nature of the genetic inheritance of feeding preference in the herbivorous amphipod *Ampithoe longimana*. Two populations known to have strong feeding preference for the chemically rich seaweed *Dictyota menstrualis* (from North Carolina, USA) were crossed to an F₂ generation with 2 populations known to have lower preference for the seaweed (i.e. from Connecticut and Massachusetts), and all parental and hybrid lines were assayed for their feeding preferences. F₁ hybrids of *A. longimana* populations with high and low *D. menstrualis* preference displayed preferences intermediate to both parental lines, and there were no persistent differences among sexes in the inheritance of *D. menstrualis* preference in the F₁ or F₂ generations. These results suggest that feeding preference for *D. menstrualis* is likely a polygenic trait inherited in a largely additive manner on autosomes. The presence of substantial polygenic control of feeding preference among this and perhaps other marine consumers suggests that the genetic potential for local adaptation of this trait may be more common than currently appreciated.

KEY WORDS: Feeding preferences · Seaweed-herbivore interactions · Quantitative genetics · Chemical defense · *Ampithoe longimana* · *Dictyota menstrualis* · Hybrid

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Marine consumers are often picky about the foods they eat, especially when their prey produce formidable arrays of chemical, nutritional and morphological deterrents. There is broad interest in understanding the forces influencing the evolution of these feeding preferences (see reviews in Horn 1989, Hay 1996, Choat & Clements 1998, Duda & Palumbi 1999, Targett & Arnold 2001), in part because they play central roles in determining the structure of marine biotic communities (Lawrence 1975, Lubchenco & Gaines 1981, Duffy & Hay 2000), in the evolution of specialization of small

consumers to larger hosts (Hay & Fenical 1988, Vermeij 1992), and in the coevolution of consumer and prey (Vermeij 1994).

A survey of this literature leaves 2 major impressions. The first is that the feeding preferences of most consumers do not vary substantially within a species; nearly all of these studies compare species rather than populations or sub-populations (cf. Denno & McClure 1983, Bernays & Chapman 1994). The second impression is that where variation in feeding preference within a single species of consumer is documented, the variation is largely environmentally or ontogenetically induced, rather than being the consequence of genetic differences (e.g. Palmer 1984, Moran & Arrontes 1990, Trowbridge 1991, Cronin & Hay 1996, Rovero et al. 1999). These patterns may reflect the reality for most marine consumers, or, there may be a substantial, but largely unrecognized, genetic component to the variation in feeding preferences found within some marine consumers.

The lack of information on the genetics of feeding preference among marine consumers is surprising, given that the genetic control underlying feeding preference provides a 'picture of evolutionary possibility' or constraint by influencing the course and the rate of future evolutionary trajectories (Via 1990). Further, since shifts to new hosts or prey items are commonly initiated by behavioral adaptations (Jaenike & Holt 1991), understanding the nature of the genetic inheritance of feeding preferences can help predict the responses of local biotic communities to human-induced perturbations, such as when non-native prey and consumer species are introduced (Travis & Futuyma 1993, Ruiz et al. 2000).

In this paper, I identify and describe the nature of the genetic control underlying the feeding preferences of the herbivorous amphipod *Ampithoe longimana*, a small crustacean (adults <2 cm long) found in shallow waters of the northwest Atlantic Ocean. In North

Carolina, USA, the amphipod is found on seaweeds from several taxonomic classes, but it prefers brown seaweeds of the tropical genus *Dictyota*; these seaweeds produce diterpene alcohols that deter most herbivores but have minimal effects on *A. longimana* (Hay et al. 1987, Duffy & Hay 2000, Cruz-Rivera & Hay 2001). As with most herbivores having broad distributions (see Strong et al. 1984), the geographic range of the amphipod extends beyond that of its preferred host plants. *Dictyota* species are rarely found northward of the North Carolina/Virginia border, while populations of *A. longimana* extend northward through at least the Gulf of Maine. In 2 recent studies, Sotka & Hay (2002) and Sotka et al. (2003) found that populations of *A. longimana* sympatric with *Dictyota* had higher affinity for, and fitness on, *Dictyota* than did populations outside the seaweed's geographic endpoint. These population-level differences were mediated by genetic differences in the ability to tolerate diterpenoid-rich secondary metabolites produced by the seaweed (Sotka & Hay 2002).

I take advantage of this population-level variation in feeding preference in order to begin to describe its genetic control. Two sets of populations that display high tolerance for *Dictyota* (i.e. from North Carolina) were crossed to an F₂ generation with populations that had low tolerance (i.e. from Connecticut and Massachusetts), and all parental and hybrid lines were assayed for their feeding preferences. It would be difficult to predict the nature of this genetic control *a priori*, since the diversity of genetic mechanisms underlying feeding preferences among other herbivores ranges from being extremely complex to relatively simple (Bernays & Chapman 1994).

Materials and methods. Populations of the amphipod *Ampithoe longimana* were collected from 4 high-salinity sites along the eastern coast of the USA: Westport Point, Massachusetts (MA; 41° 32' N, 71° 05' W); Millstone, Connecticut (CT; 41° 16' N, 72° 09' W); Morehead City, North Carolina (MHC; 34° 41' N, 76° 46' W); and Wilmington, North Carolina (Wil; 34° 13' N, 77° 48' W). The 2 northern sites (CT and MA) are 90 km apart, the 2 southern sites (MHC and Wil) are 110 km apart, and ~900 km separate the 2 regions. Amphipods were collected from a variety of seaweed species that occur at all sites, primarily the brown seaweed *Ectocarpus* spp. and green ephemeral seaweeds (e.g. *Enteromorpha* spp. and *Bryopsis* spp.). Amphipods in North Carolina were never collected from *Dictyota* spp. or during times of the year when *Dictyota* is most abundant (i.e. warm summer months).

Approximately 100 to 200 individuals seeded our laboratory cultures, which were then allowed to interbreed for 4+ generations before the present experiment began (see Sotka & Hay 2002 for details). Nine to

12 virgin males and 12 to 13 virgin females from each site were placed into 1 of 8 breeding lines: pure lines of all 4 sites and sets of reciprocal F₁ hybrids for CT/MHC and MA/Wil pairs. A majority of these virgins (68%) was raised on *Dictyota menstrualis* or *D. ciliolata* and the rest were raised on *Enteromorpha* for another experiment. Since survival on the *Dictyota* spp. was uniformly high, it is unlikely that selection dramatically altered genetic variation that occurs among the populations (survivorship of CT and MA populations = 86.8%; of North Carolina populations = 87.7%).

Offspring of these breeding lines were raised to maturity on *Enteromorpha* and *Sargassum* at room temperature and ~30‰. Seawater in plastic tubs (~2 l) was aerated constantly, changed every 2 to 4 d by pouring through a Nitex screen (mesh size = 500 µm) to prevent passage of cultured amphipods, and replaced with filtered seawater collected from Bogue Sound, NC. There was 1 tub per population, and seaweeds were added when needed. All seaweeds added to the cultures were bathed in freshwater for at least 2 × 30 s intervals, which eliminated *Ampithoe longimana* (Holmlund et al. 1990). After approximately 4 wk, the amphipods were offered a feeding choice between pre-weighed pieces of tissue from *Dictyota menstrualis* and *Ulva* sp., a green seaweed not known to differ in palatability to any of these populations (Sotka & Hay 2002). Pieces were removed from each plant, blotted dry, weighed to the nearest milligram, and then placed in separate plastic bowls filled with ~200 ml of seawater. Approximately 50 mg (±10%) wetmass of each seaweed was added to the choice assay, and 2 to 3 adult amphipods were placed into each feeding assay bowl. For each individual plant, a paired bowl with seaweeds but without amphipods acted as a control for autogenic changes in plant mass unrelated to amphipod feeding. Replicates were stopped after the amphipods had consumed at least half of one plant piece or when 72 h had elapsed, whichever came first. Plant pieces were reweighed, and the change in wet mass of each piece was scaled to reflect autogenic changes (see Sotka & Hay 2002). Replicates were dropped from the subsequent analysis (~5% of all replicates) if the amphipods died during the assay or if the total mass of plant eaten was minimal (<10%). In order to quantify the feeding preference of an individual amphipod for *Dictyota*, the feeding rate on *Dictyota* was divided by the total feeding on *Dictyota* plus *Ulva*. Each breeding line was offered tissue from a single plant, allowing us to block by plant within ANOVA. All data used were normally distributed (Shapiro-Wilks *W*-test, *p* > 0.05) and homoscedastic (Bartlett's test, *p* > 0.05).

Because initial results suggested sex-linkage in the inheritance of *Dictyota* preference, the F₁ generation from crosses between CT and MHC populations were

allowed to breed for a month and *Dictyota* preference by the male and female offspring of F₁ hybrids (F₂ generation) were assayed as before. The blocked 2-way ANOVA tested whether sex, male source, or their interaction could explain variation in *Dictyota* preference. The data were normally distributed (Shapiro-Wilks *W*-test, *p* > 0.05) and homoscedastic (Bartlett's test, *p* > 0.05).

I made no attempt to quantify variation in chemistry within or between plants using liquid chromatography or mass spectrometry. Instead, I minimized the possibility that within-species variation biased the results in several ways. First, I collected *Dictyota* plants from a shallow subtidal jetty where the plants are always submerged and exposed to low densities of small grazers; desiccation and high densities of grazers are known to alter levels of chemical defenses (Cronin & Hay 1996a,b). Second, all plants were kept in running seawater at an ambient temperature for less than 24 h before the assays began. Finally, I ran feeding assays on

sets of breeding lines simultaneously (e.g. CT pure, MHC pure, and the 2 hybrid lines), which allowed me to offer similar tissue from a single plant to each line. This nearly eliminated the possibility that either within- or between-plant variation explained patterns in feeding preference.

Results. The feeding preferences for *Dictyota* expressed by parental and F₁ hybrid amphipods of northern (i.e. CT and MA) and southern populations (Wil and MHC) are presented in Fig. 1. CT individuals significantly preferred *Ulva* over *Dictyota*, while MHC individuals significantly preferred *Dictyota* over *Ulva* (Fig. 1a, left). Hybrids from Connecticut male and Morehead City female pairs (i.e. CT/MHC) ate *Dictyota* and *Ulva* at statistically indistinguishable rates, while hybrids from Morehead City male and Connecticut female pairs (i.e. MHC/CT) significantly preferred *Dictyota*. Interestingly, MHC/CT hybrids had a distribution significantly different from the mean parental line and more like the MHC parental line, suggesting male linkage in the trait (Fig. 1a, right; *Dictyota* preference ratio halfway between means of parental lines = 0.427; MHC/CT mean ± SE = 0.617 ± 0.070), though no analogous difference was present with CT/MHC hybrid distribution and mean of parental lines (CT/MHC mean ± SE = 0.458 ± 0.067). A 2-way ANOVA on relative preference for *Dictyota* indicated that an interaction between male and female source was not significant (Table 1; *p* = 0.070).

Crudely similar patterns were found with MA and Wil crosses (Fig. 1b). MA adults significantly preferred *Ulva* over *Dictyota*, while the Wil population significantly preferred *Dictyota* over *Ulva*. Hybrids from Massachusetts male and Wilmington female pairs (i.e. MA/Wil) ate *Dictyota* and *Ulva* at rates that could not be distinguished statistically, while hybrids from Wilmington male and Massachusetts female pairs (i.e. Wil/MA) significantly preferred *Dictyota*. No interaction between male and female source was detected by 2-way ANOVA (Table 1; *p* = 0.693), nor were there differences between either hybrid type and the mean preference of parental lines (*Dictyota* preference ratio halfway between means of parental lines = 0.521; MA/Wil mean ± SE = 0.509 ± 0.059; Wil/MA mean ± SE = 0.573 ± 0.045).

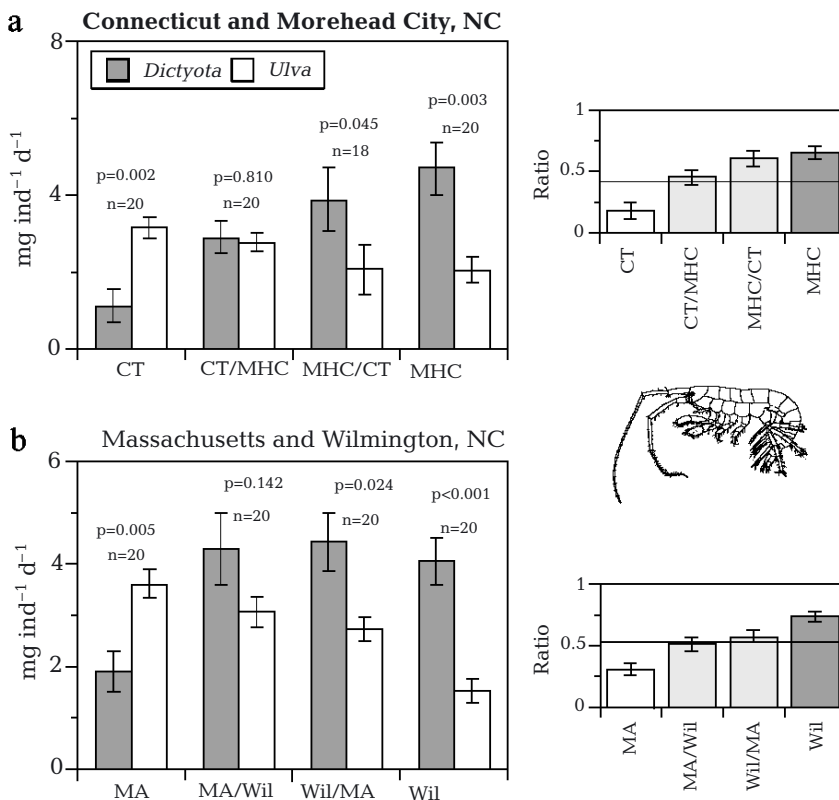


Fig. 1. *Amphiphoe longimana*. Feeding preference for *Dictyota* exhibited by parental populations and their F₁ hybrids. (a) One set of hybrids created from Connecticut (CT) and Morehead City, NC (MHC) populations and (b) a second set created from Massachusetts (MA) and Wilmington, NC (Wil) populations. P-values are taken from paired *t*-tests. Two-way ANOVAs on *Dictyota* preference with male and female source as independent variables are shown in Table 1. For hybrids, the male source is given before female source (e.g. CT/MHC signifies CT males and MHC females). Right panels show ratios of feeding rate on *Dictyota* divided by total feeding on *Dictyota* and *Ulva*

To confirm or refute the presence of male-linkage in the MHC and CT crosses, F_1 hybrids were left to interbreed for a month, and their F_2 progeny were assayed for feeding preferences. Females from the MHC/CT crosses significantly preferred *Dictyota*; all other groups ate *Dictyota* and *Ulva* at rates that could not be distinguished statistically (Fig. 2). A direct test of relative consumption of *Dictyota* found no interaction among sex and source of male genetic material (Table 2). Thus, the suggestion from the MHC/CT crosses that sex-linkage is present in this trait (Fig. 1a, Table 1) could not be confirmed using the Wil/MA crosses (Fig. 1b, Table 1) nor the F_2 generation (Fig. 2, Table 2). Sex linkage in herbivore preference for host plants is known for a marine isopod (Jormalainen et al. 2001) and terrestrial insects (e.g. Thompson 1988); however, the present evidence suggests the effect in *Ampithoe longimana*, if any, is neither strong nor persistent.

Discussion. Recent studies documented that the herbivorous amphipod *Ampithoe longimana* held substantial genetic variation in its feeding preference for the seaweed *Dictyota menstrualis*. This was partitioned both within- and among-populations (Sotka & Hay 2002, Sotka et al. 2003). The nature of the inheritance of the feeding preference was unknown. Here, a series of lab-based rearing and feeding assays determined that this polygenic trait is probably inherited in a largely additive manner on autosomes. F_1 hybrids of *A. longimana* populations with high *Dictyota* preference (i.e. from North Carolina) and low *Dictyota* pref-

Table 1. *Ampithoe longimana*. Two-way ANOVA on relative preference for *Dictyota menstrualis* using data from parental and hybrid strains. Source refers to the site from which the male or female parent originated. Degrees of freedom (df), mean sums of squares (MS), F -ratios and p -values are indicated. MA: Massachusetts; CT: Connecticut; MHC Morehead City, NC; Wil: Wilmington, NC

Source	CT, MHC and hybrids				MA, Wil and hybrids			
	df	MS	F	p	df	MS	F	p
Block	19	0.116	1.55	0.105	19	0.035	0.67	0.836
Male source	1	1.969	26.26	<0.001	1	1.212	24.43	<0.001
Female source	1	0.443	5.90	0.018	1	0.662	13.34	0.001
Male \times Female	1	0.256	3.41	0.070	1	0.008	0.16	0.693
Error	55	0.075			57	0.050		

erence (i.e. from Connecticut and Massachusetts) displayed *Dictyota* preferences intermediate to both parental lines (Fig. 1), indicating the additive nature of the trait. There were no persistent differences among sexes in the inheritance of *Dictyota* preference in the F_1 (Fig. 1) or F_2 generations (Fig. 2), suggesting that the trait is autosomally inherited, rather than sex-linked. Note that these effects are almost certainly genetic, since non-genetic effects were minimized; there were no previous exposures to *Dictyota*, and parents were taken from lab-based cultures maintained for 4+ generations.

For *Ampithoe longimana*, there may be an evolutionary consequence for the lowered preference for *Dictyota* among hybrids, relative to the North Carolina parental line. In North Carolina, *A. longimana* is one of few consumers that can tolerate *Dictyota* and its diterpene alcohols; other consumers are strongly deterred by the diterpene alcohols produced by the plant (Hay et al. 1987, Duffy & Hay 1994, Stachowicz & Hay 1999, Cruz-Rivera & Hay 2003). As a consequence, a strong

host preference for the chemically defended *Dictyota* provides *A. longimana* a refuge from omnivorous fishes. Sotka & Hay (2002) indicate that, as a consequence of this selection, populations within the range of *Dictyota* have higher feeding preference for, and fitness on, *Dictyota* than do populations from outside the range of *Dictyota*.

Since populations that are sympatric and allopatric with *Dictyota* may be exchanging migrants (Sotka et al. 2003), individuals from populations with low tolerance for *Dictyota* are potentially hybridizing with individuals from populations with higher tolerance for *Dictyota*, and vice versa. Because the *Dictyota* preferences of hybrids are lower than preferences of North Carolina genotypes, hybrids may not take advantage of the refuge provided

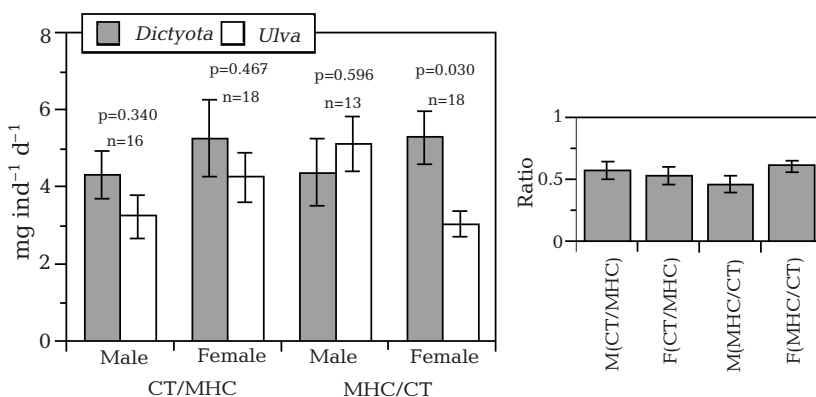


Fig. 2. *Ampithoe longimana*. Feeding preference for *Dictyota* exhibited by males (M) and females (F) of the Connecticut (CT) and Morehead City, NC (MHC) F_2 hybrids. p -values are taken from paired t -tests. A 2-way ANOVA on *Dictyota* preference with sex and male source as independent variables is shown in Table 2. Right panel shows feeding rate on *Dictyota* divided by total feeding on *Dictyota* and *Ulva*

Table 2. *Ampithoe longimana*. Two-way ANOVA on relative preference for *Dictyota menstrualis* using data from F₂ hybrids of Connecticut (CT) and Morehead City, NC (MHC) populations. Source refers to the site from which the male parent originated. Degrees of freedom (df), mean sums of squares (MS), *F*-ratios, and *p*-values are indicated

Source	df	MS	<i>F</i>	<i>p</i>
Block	9	0.129	2.43	0.036
Sex	1	0.095	1.79	0.192
Male source	1	0.006	0.10	0.750
Sex × Male source	1	0.090	1.69	0.204
Error	27	0.053		

by *Dictyota*, and could therefore become more susceptible to predation by omnivorous fishes (cf. Duffy & Hay 1991, 1994). If such selection against hybrids is present, it could potentially impede the introgression of low-preference alleles into North Carolina populations, and help to maintain geographic differentiation in feeding behavior (Endler 1977, Barton & Hewitt 1985). This hypothesis has a clear empirical test that will be pursued in the future.

Among other marine consumers, there are precious few data on the nature of inheritance of feeding preference. In the herbivorous amphipod *Gammarus palustris*, slight changes in the feeding preferences for the green seaweeds *Ulva* and *Enteromorpha* are correlated with allelic variation in a single digestive enzyme (Borowsky et al. 1985, Guarna & Borowsky 1993, 1995), but it is clear that much of the phenotypic variation remains unexplained and is likely polygenic in origin. Another example may come from *Peramphithoe parmerong*, a marine amphipod that displays significant family-level variation in performance on *Padina* and *Sargassum* (Poore & Steinberg 2001). If this variation in juvenile performance is mediated by their feeding behaviors, as it is for *Ampithoe longimana* (see Sotka & Hay 2002), then one can infer genetic variation in the feeding preferences of *P. parmerong*. Third, preferences for different habitats (wood debris, *Fucus distichus*, or rhizomes of marsh grass) in the estuarine amphipod *Eogammarus confervicolus* are clearly under polygenic control (Stanhope et al. 1992), though it is unclear to what extent such habitat preferences reflect feeding preferences. Thus, several amphipod species, including *A. longimana*, display feeding preferences that are probably under polygenic control and, as such, each should be able to evolve local adaptations in preference. The fact that some (Stanhope et al. 1993, Sotka & Hay 2002) but not all (e.g. Poore & Steinberg 2001) of these species displayed local adaptation in behavior suggests that factors (e.g. environmental stability, strength of selection, gene flow) other than the nature of the genetic control may more strongly determine its evolution.

It remains to be seen whether such genetic variation in feeding preferences is commonplace among marine consumers. In the examples listed above, the detection of genetic variation required the use of small, shallow-water amphipods (<2 cm) that were raised for generations under controlled laboratory environments in a fairly short period of time (the generation time of *A. longimana* is ~3 wk). I am not aware of unequivocal examples of genetic variation in feeding preference among larger consumers (e.g. fishes and urchins), in part because such questions are rarely asked. Instead, marine ecologists interested in within-species variation in feeding preferences of large (and small) consumers investigate the influences of ontogeny (e.g. Palmer 1984, Pennings 1990, Clements & Choat 1993, Micheli 1997, Rovero et al. 1999, Muñoz & Ojeda 2000), the consumers' recent history (e.g. Moran & Arrontes 1990, Trowbridge 1991, 1997, Cronin & Hay 1996, Thacker et al. 1997), prey availability (e.g. Pennings et al. 1993, Kennish et al. 1996), or prey quality (see Hay 1996 for review). Large consumers may or may not have substantial genetic variation in feeding preferences, but testing this will likely require the application of newer, molecular-based techniques to assess its extent (Ritland 2000, Thomas et al. 2000).

Acknowledgements. Funding was provided by a National Science Foundation Dissertation Improvement Grant (IBN-0073073), American Museum of Natural History Lerner-Grey Memorial Fund for Marine Research, and a University of North Carolina at Chapel Hill—Paul Hardin Dissertation Completion Fellowship to E.E.S. Thanks go to N. Lindquist and R. Whitlatch for allowing me to invade their lab spaces and to 2 anonymous reviewers for comments.

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