# Spatial scale and the processes structuring a guild of larval trematode parasites

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## **3.1 INTRODUCTION**

An individual host is a patch of habitat for a particular stage in the life cycle of a parasite (Price, 1980; Holmes and Price, 1986). It contains resources necessary for growth and development of this infecting stage, and for production of the next, usually dispersing, stage. Each individual host is an inherently bounded, discrete habitat, that is isolated from other similar habitat patches by an external environment that is inhospitable to the parasitic stage that infects the host.

As patches of parasite habitat, hosts are both self-reproducing and ephemeral. Excluding instances of vertical transmission and assuming life-long infection (as is the case for many parasitic infections of invertebrate hosts), empty patches are born via the recruitment of susceptible offspring to a host population, patches increase in size and change in a variety of other characteristics (e.g. morphology, biochemistry, etc.) during host ontogeny, and they disappear (along with their resident parasites) when the host dies. The rates at which these processes occur vary among host populations and in time.

In many ecological systems, the distribution and accessibility of resources vary with spatial and temporal scale, as do the processes that structure populations and communities (e.g. Andrewartha and Birch, 1954; Wiens, 1976; Price, 1980; Allen and Starr, 1982; Connell and Sousa, 1983; Dayton and Tegner, 1984; Sousa, 1984; Addicott *et al.*, 1987). Studies of processes

operating at different scales within systems of divided habitat patches have provided substantial insight in this regard. When strong asymmetrical interactions on the small scale, i.e. within a patch, preclude the coexistence of competitors, or of predators and their prey, the existence of multiple patches coupled by dispersal often promotes their coexistence on the larger scale (Hutchinson, 1951; Skellam, 1951; Huffaker, 1958; Cohen, 1970; Levins and Culver, 1971; Horn and MacArthur, 1972; Levin, 1974, 1976; Slatkin, 1974; Armstrong, 1976; Hastings, 1977, 1980; Caswell, 1978; Shorrocks *et al.*, 1979; Sousa, 1979; Lloyd and White, 1980; Atkinson and Shorrocks, 1981; Hanski, 1981, 1983; Ives and May, 1985; Murdoch *et al.*, 1985). Differential rates of dispersal among species, independent aggregation of species among patches, and an increased number of patches in the system enhance the likelihood that diversity will be maintained on the large scale, i.e. across all patches in the system.

The spatial scales of resources provided by hosts are hierarchical (Esch *et al.*, 1975; Margolis *et al.*, 1982; Holmes and Price, 1986; see also Chapter 1), and patterns and outcomes of interaction among parasites may vary among these scales. Nested levels in this hierarchy include: (a) tissues within a host, (b) an individual of a particular host species, (c) populations of a particular host species, and (d) communities of host species. The population of a particular parasite species that infects an individual host is called an infrapopulation; the collection of populations of different parasite species within a single host is an infracommunity. The assemblage of parasite species that infect a population of a particular host species is called a component community.

Populations of invertebrates that serve as intermediate hosts are commonly infected by several species of parasitic helminths (Denny, 1969; Wright, 1971; Brown, 1978; Rohde, 1982; Lauckner, 1980, 1983). To understand the processes that structure such assemblages of larval parasites better, I investigated patterns of species diversity of the helminths that infect the salt marsh snail, *Cerithidea californica*, at two different spatial scales. This parasite assemblage is composed solely of larval digenetic trematodes. Because the members are taxonomically similar and exploit a common resource, the assemblage is more appropriately referred to as a guild (*sensu* Root, 1967) than a community. The smaller of the two scales examined in this study is that of the individual snail, which potentially supports an infraguild of larval trematodes. The larger scale is that of the local host population and its component guild of parasites.

This chapter primarily examines patterns and processes at the second, larger scale, but summarizes what is known concerning structure and dynamics at the individual host scale. The latter is the subject of Chapter 3. Here, I examine several characteristics of local host and parasite populations that may influence the diversity of component guilds of larval trematodes. These characteristics include host population density, size/age distribution, location, and rates of host and parasite recruitment. The study is restricted to infections by redia and sporocyst stages of trematodes that use *Cerithidea* as first intermediate host.

# 3.2 PATCH DYNAMICS AND COMPLEX PARASITE LIFE CYCLES

The digenetic trematodes that infect Cerithidea have life cycles typical of most parasitic helminths (see below). There is an obligate sequence of intermediate and definitive hosts; transmission is effected either by freeliving motile larvae or by encysted larvae that are ingested by the host. The complex life cycles of Digenea effectively isolate the patches of habitat afforded by individuals of the same host species, since the stages that infect one such individual cannot be directly transmitted to another. Therefore, in the case of the intermediate snail host, the rate of establishment of new redial and sporocyst infections within a local snail population depends on: (a) the abundance of infective stages (i.e. miracidia) in the local environment, (b) the rate at which hosts come into contact with these stages or ingest them, and (c) the susceptibility of the individual snails that comprise the local host population. The availability of infective stages is mainly determined by processes external to the local host population, e.g. the abundance and habitat use of the definitive hosts, and physical characteristics of the local aquatic environment including water flow, chemistry, temperature, turbidity, depth, etc. These physical characteristics may influence movement and survival of the infective stages. Differential production or mortality during the dispersal phase will cause rates of establishment to differ among species of parasites.

Rates of contact between host and parasite may also be influenced by the behaviour of each. If infective stages are transmitted by ingestion, host feeding habits will affect the rate at which new infections are acquired. If infective stages actively seek hosts using environmental gradients (e.g. light intensity) that are correlated with host abundance, or chemical cues from the host, rates of encounter will be higher. Miracidia appear to employ both of these mechanisms, although behavioural responses to host exudates are only observed when the larva is in close proximity to its host (Wright, 1959, 1971; Ulmer, 1971; Cable, 1972; Chernin, 1974; Shiff, 1974; MacInnis, 1976; Brown, 1978; Smyth and Halton, 1983).

The susceptibility of hosts may vary with the species or genetic strain of parasite and with host characteristics such as age, sex, and genotype (Richards, 1976; Meuleman *et al.*, 1987). Susceptibility may also be affected by host nutritional state, which may, in turn, be influenced by host population density.

## 3.3 THE SYSTEM: CERITHIDEA CALIFORNICA AND ITS TREMATODE PARASITES

Details of the life history of *Cerithidea californica* are summarized in Sousa (1983). Dense populations of this deposit-feeding gastropod inhabit pickleweed (*Salicornia virginica*) marshes and adjacent high intertidal (+1.2–2.1 m mean lower low water) mudflats and tidal creeks in protected bays and estuaries along the Pacific coast of North America. The species' range extends from Tomales Bay (Marin Co., California) to central Baja, California, Mexico (Macdonald, 1969a, b). The snail is iteroparous and its larvae undergo direct development within benthic egg strings. Egg laying begins in late March or April, hatching starts by June and continues into August.

*Cerithidea* is first intermediate host to at least 18 species of digenetic trematodes in California (Martin, 1955, 1972; Yoshino, 1975). In Bolinas Lagoon (Marin Co., California), the site of this study, 15 species of trematodes were found in the seven annual samples of snail populations on which this chapter is based (Table 3.1). The life cycles of all but one of these species appear to follow the typical digenean sequence (Shoop, 1988): egg, free-living miracidium, intramolluscan sporocyst or redia stage, free-living

Family	Species
Cyathocotylidae	Mesostephanus appendiculatus cvathocotvlid #2*
Echinostomatidae	Acanthoparyphium spinulosum Echinoparyphyum sp.* Himashla shiqadana
Heterophyidae	Euhaplorchis californiensis Phocitremoides ovale
Microphallidae	microphallid #1* microphallid #2*
Notocotylidae	Catatropsis johnstoni
Philopthalmidae	Parorchis acanthus
Renicolidae	<i>Renicola buchanani</i> renicolid #2* renicolid #3*
Schistosomatidae	Austrobilharzia sp.*

 Table 3.1 Larval trematodes that infect Cerithidea californica

 in Bolinas Lagoon. The identities of species marked with an

 asterisk have yet to be determined

cercaria, encysted metacercaria stage in a poikilothermic second intermediate host (invertebrate or fish), and finally, development from an ingested metacercaria, of a parasitic adult worm in the definitive vertebrate host. The life cycle of *Austrobilharzia* sp. is the only exception to this pattern; the metacercaria stage is absent and the definitive host is infected directly by a cercaria. The definitive hosts for most of the trematodes are probably birds, but there is little information concerning the distribution of adult trematodes among potential avian or mammalian hosts that inhabit the study area.

# **3.4 METHODS**

# **Study sites**

The study was conducted in Bolinas Lagoon, located 24 km NW of San Francisco, California (37°55'N, 122°41'W). *Cerithidea* populations and their parasites were sampled at two sites within the lagoon. One site is adjacent to the mouth of Pine Gulch Creek (hereafter PGC site) which flows into the lagoon on its western edge, and the other is at the northeast corner of Kent Island (hereafter KI site). The sites are designated 'B' and 'C' respectively, on the map of the lagoon that appears in Stenzel *et al.* (1976), and are about 750 m apart. The freshwater flowing from the creek at PGC is an important resource for birds. Densities of wintering, migrant waterfowl and roosting gulls and terns are much higher at this site than at KI which lacks a source of freshwater. Some of these birds are probably definitive hosts of trematodes that infect *Cerithidea*.

The sites also differ in sediment characteristics. The surface sediment at PGC is a poorly sorted, very fine sandy mud and has a considerably higher organic content than the surface sediment at KI which is a well sorted, fine to medium sand (Ritter, 1969; Sousa, unpublished data). This variation in sediment quality is related to hydrological and biological differences between the sites. KI is closer to the mouth of the lagoon and to its main channel, so that tidal currents are relatively stronger, and deposition of fine particles is less, as compared to PGC. In addition, KI is inhabited by a dense population of ghost shrimp, Callianassa californiensis. While feeding and burrowing, Callianassa extensively rework the sediment, extracting or resuspending fine particulate matter, leaving a sandy, organically poor sediment (MacGinitie, 1934). In contrast, PGC has a depositional environment. Tidal currents at this site are slow and eddying. It receives a substantial input of allochthonous detrital matter and fine sediment from the creek, particularly following heavy winter rains. Bioturbation is minimal since *Callianassa* is not present at the site, possibly because the silty sediment at PGC is unsuitable for burrow construction, or because the ghost

shrimp cannot tolerate the sharp reductions in salinity associated with high, winter, creek flow (Sousa and Gleason, 1989).

The species composition and abundance of foraging shorebirds also differs between the sites and appears to be related to the spatial variation in sediment and in the associated benthic invertebrates and fishes on which they prey (Stenzel *et al.*, 1976; Page *et al.*, 1979; Quammen, 1984). These birds are definitive hosts, and many of their prey are second intermediate hosts for some of the parasites that infect *Cerithidea* (Robinson, 1952; Russell, 1960a, b; Badley, 1979; Sousa, personal observation). Since shorebird species differ in diet, they probably harbour different infracommunities of parasites (Russell, 1960a, b). The differential use of lagoon habitats by bird species and variation in the abundances of second intermediate hosts between sites may combine to produce spatial differences in the abundance of infective stages of different trematodes.

At both study sites, snails are distributed as a series of subpopulations occupying shallow (5–15 cm deep) depressions or 'pans' in the surface of the mudflat which hold standing water at low tide. These pans range in size from slightly less than  $1 \text{ m}^2$  to  $20 \text{ m}^2$ . During most months of the year they are flushed daily by high tides.

At PGC, the pans are located along the interface of the tidal mudflats and the higher elevation, *Salicornia*-dominated marsh. Snails rarely move between them (Sousa, unpublished data) presumably because the emergent mudflats (which often consist of hard, dried plates of sediment) and the dense stands of pickleweed that border the pans, represent physical barriers to snail movement. As a consequence of this lack of adult migration and the absence of a planktonic stage in the snails' life history, the demographies of different subpopulations of snails at PGC vary greatly. They differ in size-distribution, rate of recruitment, density, and rate of parasitic infection (Sousa, unpublished data).

At KI, pans occur across the upper tidal mudflat as well as along the mudflat-marsh boundary as at PGC. At the start of the study, densities of ghost shrimp were low in these pans; however, over the course of the study shrimp populations gradually invaded about half the pans, excluding the snails. Their recruitment to the pans followed two stormy winters (1982 and 1983) when a significant amount of sedimentation occurred at the site; however, the precise mechanism(s) responsible for these shifts in local distribution are unknown. Areas between the pans have remained pockmarked with the conical sediment mounds that mark the burrow openings of a dense population of ghost shrimp. Snails are present in these surrounding areas, but at much lower densities than in the pans which are foci of snail feeding and reproduction. The *Callianassa*-dominated areas between the pans remain moist during most low tides, and few of the KI pans have vegetation around their edges. These features, as well as the fact that the

average distance between neighbouring KI pans is only half that of PGC pans (8 versus 16 m), probably account for the fact that rates of snail movement between subpopulation is at least three times greater at KI than PGC. As an apparent consequence of this greater exchange of migrants, demographic characteristics of different subpopulations at KI are very similar within any particular year, and they change quite synchronously over time (Sousa, unpublished data).

# **Sampling procedures**

In August of 1981, a total of 34 subpopulations of *Cerithidea* were selected for long-term monitoring of demographic parameters and parasitic infection, 19 at PGC and 15 at KI. The chosen pans comprised almost all of those that contained snails along the 315 m and 70 m of marsh edge habitat studied at PGC and KI, respectively.

These subpopulations were sampled each August from 1981 through to 1987. The snails were sampled with a 225 cm<sup>2</sup> scoop core which collected all sediment and benthic invertebrates to a depth of 2 cm, sufficient to collect all snails in the area. The contents of each scoop were sieved through 1 mm mesh in the field and returned to the laboratory for analysis. The length (apex to aperture) of each snail was measured to the nearest 0.01 mm, then each was dissected to determine its sex and what species of trematode, if any, infected it.

Five or ten scoop samples were collected from each pan, depending on the density of snails; the greater number was taken in sparser populations. The scoops were made at regularly spaced intervals along the length of a metric tape transecting each pool, parallel to its long axis. These samples provided estimates of snail density (both young of the year and older individuals) and biomass. To ensure an adequate sample size of snails  $\geq$  one year old, an additional sample of snails was collected from some pans. This supplemental sample was collected from one to three haphazardly chosen locations within a pool. Starting from the position of the first collected individual, all snails (excluding new recruits) were collected from the immediate area until the total sample numbered at least 100 individuals; a few collections fell short of this goal. Statistical tests verify that the size distributions of snails in these supplemental collections do not differ from those of  $\geq$  one year old snails in scoop samples taken in the same pans. For the following analysis of parasite assemblages, the scoop and supplemental samples of  $\geq$  one-year-old snails taken in a particular pan and year are pooled. Young-of-the-year snails collected in the scoop samples were never found to harbour trematode infections and are not considered in this analysis.

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In most cases, snail subpopulations were dense enough that sampling was unlikely to have an impact on population dynamics. However, due to a variety of factors, but especially storm-related disturbance, the density of snails in certain pans sometimes fell to such low levels that I chose not to collect a sample for fear of affecting subsequent dynamics. Over the course of the seven years, a number of snail populations (and their component parasite assemblages) did become extinct due to physical and biological disturbances. For both these reasons, the number of subpopulations sampled at each site varied from year to year, and gradually diminished over the course of the study. By 1987, only 14 of the original pans sampled at PGC

		Unin	fected		Infect	ted by		
				1 sp	ecies	> 1 sp	pecies*	•
Site	Year	%	( <i>N</i> )	%	(N)	%	( <i>N</i> )	total N
PGC	1981	84.34	(3502)	15.44	(641)	0.22	(9)	4152
	1982	87.96	(2571)	11.87	(347)	0.17	(5)	2923
	1983	72.17	(1079)	26.96	(403)	0.87	(13)	1495
	1984	81.85	(1768)	18.01	(389)	0.14	(3)	2160
	1985	85.80	(1837)	13.97	(299)	0.23	(5)	2141
	1986	74.50	(1461)	25.09	(492)	0.41	$(\tilde{8})$	1961
	1987	66.33	(1186)	32.66	(584)	1.01	(18)	1788
KI	1981	74.07	(1631)	25.20	(555)	0.73	(16)	2202
	1982	89.96	(1505)	9.68	(162)	0.36	<b>)</b> (6)	1673
	1983	77.16	(456)	21.83	(129)	1.01	Ì6)	591
	1984	83.19	(886)	16.81	(179)	0.00	ÌÓ	1065
	1985	95.74	(1302)	4.19	(57)	0.07	à	1360
	1986	93.91	(1281)	6.09	(83)	0.00	ò	1364
	1987	94.72	(932)	5.18	(51)	0.10	(1)	984

**Table 3.2** Annual rates of trematode infection in  $\geq$  one-year-old *Cerithidea* californica at Pine Gulch Creek (PGC) and Kent Island (KI). Data from sampled subpopulations at each site are pooled

Average annual per cent uninfected and infected snails

	Uninj	fected		Infec	ted by	
			1 spe	ecies	> 1 sp	ecies*
Site	Mean	SD	Mean	SD	Mean	SD
PGC KI	78.99 86.96	8.07 8.86	20.57 12.71	7.74 8.55	0.44 0.32	0.36 0.40

\* All are double infections except for one triple infection at KI in 1981.

and seven of those at KI remained. The numbers of  $\geq$  one-year-old snails examined at each site during the seven censuses are listed in Table 3.2.

## **Measures of community structure**

This chapter examines the structure of the larval parasite assemblages infecting subpopulations of *Cerithidea*. For each yearly, pooled collection from a subpopulation (hereafter referred to as a sample of snails), I have estimated several measures of parasite guild structure (Table 3.3). The raw data from which these measures are calculated were the number of infections of each parasite species found in the sample of snails. For mixed species infections, the occurrence of each species was counted as if it were a single infection of that species; i.e. each species' total for the particular sample was incremented by one for every mixed species infection in which it occurred. Since mixed infections are exceedingly rare (see below), this protocol had little influence on the results.

Since the rate of parasitic infection varied among snail subpopulations (see below), as did the number of snails collected from each, the total number of infections (NI) found in each sample of snails varied considerably. Species richness (S), the number of species in an assemblage, is strongly affected by sample size (Hurlbert, 1971; Heck *et al.*, 1975; Simberloff, 1979). In an effort to reduce the effect of small sample size *per se*, samples with fewer than 30 snails or five infections were excluded from the analysis. However, this modification of the data alone did not eliminate a significant correlation in several years at both sites between S and ln NI

Measure	Symbol	Method of computation
Species richness	S	Total number of parasite species in sample
Expected number of species in a random sample of 15 infections	E(S <sub>15</sub> )	Calculated by rarefaction using multinomial formula of Heck <i>et al.</i> (1975)
Exponential of Shannon diversity index (Hill's (1973): $N_1$ )	Exp (H')	$\operatorname{Exp}\left(-\Sigma p_{i}^{'} \ln p_{i}\right)$
Reciprocal of Simpson's diversity index (Hill's (1973): N <sub>2</sub> )	$1/\Sigma p_i^2$	See symbol
Simple dominance (May, 1975)	Dom	<i>p</i> <sub>i</sub> of most abundant species in sample

**Table 3.3** Measures of parasite guild structure within snail subpopulations.  $p_i$  is the proportion of infections by parasite species i

able 3.3 for	s number of	
n a sample. See	relationships. n	alysis
per of infections i	ed linearity of the	Ill for statistical an
iess and the numl	infections improv	ze (n) was too sma
s of species richr	tion of number of	that the sample si
between measure	. Log transforma	. A dash indicates
3.4 Correlations	ation of measures	oulations sampled
Table	explan	lodqns

Site				PGC							KI		· · · · · ·	
Year	81	82	83	84	85	86	87	81	82	83	84	85	86	87
Correlation	of:													
1. S and 1n	(number	r of infec	stions)											
r	0.65	0.87	0.42	0.78	0.38	0.47	-0.07	0.32	0.72	0.91	0.09	0.34	0.94	0.42
и	19	15	14	13	14	13	14	15	14	7	8	7	×	9
$P^{\mathrm{a}}$	* *	* * *	+	* * *	+	+	su	su	* *	* *	su	su	* * *	su
2. E (S <sub>15</sub> ) at	nd 1n (nu	umber of	infectic	(suc										
r	0.17	0.07	0.61	-0.07	-0.20	-0.53	-0.60	0.33	I	0.91	-0.10	I	I	I
u	15	11	13	×	10	10	13	15	7	4	8	0	1	0
d	su	su	*	su	su	+	*	su	I	*	su	I	1	I
<sup>a</sup> All probabi	lities in ta	ble are oi	ne-tailed:	: ns ≥ 0.1	0, + < 0.	10, * < (	).05, ** < (	.01, *** <	< 0.001.					

(Table 3.4). Rarefaction procedures were then used (Heck et al., 1975) to estimate the expected number of trematode species in a sample of 15 infections (E  $(S_{15})$ ) drawn randomly from the collection of infections found in each sample of snails. The multinomial-based formula of Heck et al. (1975) was applied since the infections within each collection of snails is likely to be a very small fraction of those within an entire subpopulation of snails, numbering in the thousands of individuals. In this situation, the successive collection of infected snails is unlikely to affect the relative abundance of infections by different parasites within the snail subpopulation. The sampling and estimation procedures also meet the criteria outlined by Sanders (1968) and Simberloff (1979): (a) the samples are taxonomically similar and come from the same habitat, (b) the method of sampling was consistent for all pans and years, and (c) (E  $(S_{15})$ ) was computed by interpolation, not extrapolation. As a result of this rarefaction procedure, the sample sizes for analyses of relationships between (E  $(S_{15})$ ) and host population characteristics were smaller than those for other measures of guild structure, since snail samples containing fewer than 15 infections were not included in the former data set. The correlation between (E  $(S_{15})$ ) and ln NI is clearly weaker than between S and ln NI (Table 3.4). Partial correlations between (E  $(S_{15})$ ) and ln Ni with mean length of snails in the sample held constant were not significant in any year, at either site.

The other measures of parasite guild structure (Table 3.3) were chosen for their ease of interpretation (Hill, 1973; Peet, 1974; May, 1975). The two diversity measures, Exp(H') and  $1/\Sigma p_i^2$ , differ in their sensitivity to changes in the relative importance of species (Hurlbert, 1971; Peet, 1974). The first index is most sensitive to changes in rare species, while the second is more responsive to changes in common species.

# **3.5 THE ANALYSIS**

## Patterns at the level of the individual host

Several lines of evidence indicate that strong antagonistic interactions between larval parasite species occur within individual snails. Circumstantial evidence comes from the observation that mixed-species infections by larval trematodes are exceedingly rare in *Cerithidea* populations. Martin (1955) made 12 monthly collections of adult *Cerithidea* from a salt pond in Upper Newport Bay, California and reported the frequencies of different categories of infection for the pooled collection of monthly samples. A statistical analysis of these pooled data indicates that mixed-species infections were fewer than would be expected under the null hypothesis that parasites are randomly and independently distributed among snails (Chapter 4). This result suggests negative interactions between species of parasites, but the pooled nature of the data set complicates interpretation of the statistical pattern of negative association. Heterogeneity in the relative abundance of parasite species among the monthly samples alone could produce such a pattern, without any direct interaction between species. Indeed, Martin (1955) found seasonal variation in the prevalance of infection, as did Yoshino (1975) for *Cerithidea* populations in Goleta Slough, California. Cort *et al.* (1937) were among the first to identify this problem with analyses of parasite associations based on heterogeneous data sets.

Mixed species were also very rare in the seven annual samples from Bolinas Lagoon (Table 3.2). Of 4462 infected snails examined during the seven censuses, only 91 (2%) were infected by more than one species. I have statistically compared the observed and expected numbers of mixed infections for each pan within a given year. This pan by pan analysis of samples collected in the same month of each year reduces the influence of spatial and temporal heterogeneity in parasite abundance discussed above. Due to the large number of parasite species involved and relatively low frequencies of infections per species, the expected numbers of mixedspecies infections are often too small for the application of standard analyses for discrete data, e.g. contingency tables. Instead, I used Monte Carlo simulations (Sokal and Rohlf, 1981) to estimate the probability of the observed number of mixed infections under the null hypothesis of random, independent assortment of parasites among hosts. The results of this analysis agree with that of Martin's (1955) data discussed above; within a number of snail subpopulations in any given year, the frequency of snails infected by more than one species of larval trematode is less than would be expected by chance (Sousa, in prep).

Such negative associations are not proof of direct antagonistic interactions among species. One alternative explanation is that miracidia of one parasite species may actively avoid, or be unable to infect, snails that are already parasitized by a different species (for a discussion of possible mechanisms of indirect antagonism see Lim and Heyneman, 1972).

A second alternative explanation for the rarity of mixed infections is that parasite species may preferentially infect hosts of different size, although this pattern itself might be an evolutionary response to negative interactions in the past, i.e. niche partitioning (MacArthur and Levins, 1967; but see Connell, 1980). *Cerithidea* infected by different trematode species do differ in mean length (Sousa, 1983; Sousa and Gleason, 1989; see also Chapter 4), but the ranges of snail lengths in which the different species are found overlap considerably. While these distinctive patterns of distribution may reduce rates of interspecific interaction, two lines of evidence indicate that intramolluscan antagonistic interactions do occur, and that they are strongly hierarchical in outcome (Sousa, in prep.). While dissecting snails from the annual samples, I have observed a number of mixed infections in which rediae of one species are preying on rediae, sporocysts, or cercariae of another. These interactions are hierarchical: species with large rediae dominate, especially *Himasthla* and *Parorchis*. Redial species of intermediate size are, in turn, dominant over species with small rediae or sporocysts. I have also examined temporal patterns of parasite species replacement in marked snails carrying known infections that have been released in the field and recaptured at a later date. These sequences of replacement are also strongly hierarchical. Species with large rediae (*Himasthla* and *Parorchis*) most frequently invade and displace infections by other species; in contrast, infections by these two species are very rarely invaded and, if so, only by the other member of the pair.

In summary, the rarity of mixed-species infections, direct observations of hierarchical antagonism between co-occurring species, and the record of hierarchical species replacement over time, all suggest that negative interspecific interactions among larval trematodes occur at the scale of the individual snail, the infraguild (i.e. infracommunity) level. The next section addresses the question of whether these interactions are common enough to affect the structure of the component guild (i.e. component community) of parasites within a subpopulation of snails.

# Patterns at the level of the host subpopulation

## Hypotheses and predictions

In this section, I present two alternative hypotheses which may explain parasite guild structure at the level of the host population in this system. The first hypothesis is that the hierarchical, negative, interspecific interactions seen at the infraguild level strongly influence component guild structure. The second is that the spatial and temporal patterns of parasite recruitment and the duration of host exposure, rather than interspecific competition, are the primary determinants of guild structure at the component level.

Infraguild interactions will affect the structure of component parasite guilds if the host resource is sufficiently limiting that a few antagonisticallydominant species of parasites come to monopolize the infections. These conditions could result in two ways: (a) from high rates of recruitment and infection by these dominant species, or (b) from low rates of recruitment of new hosts to the population and the gradual accumulation of infections by the dominant parasites with time. If intramolluscan antagonism was the primary determinant of component-level structure, the following patterns would be predicted. First, assuming that the mean length of snails in a population is an index of mean age, species richness and diversity should exhibit a hyperbolic relationship when plotted against mean length of snail. Young populations composed predominantly of small snails will have only been exposed to infective parasite larvae for a short time. Therefore, only a small number of parasite species will have had the opportunity to infect them, and those parasite species with the highest recruitment rates will be most abundant. Species richness and diversity of parasite guilds infecting such snail populations will be low. At the opposite extreme, populations composed primarily of larger, older snails will have been exposed to infective miracidia for a relatively long time. For this reason, and the fact that infections appear to be life-long in *Cerithidea* (Sousa, 1983, in prep.), prevalence of infection should be high in these older populations and antagonistic interspecific interactions common. These interactions should result in most snails being infected by a few dominant trematode species, and diversity should decline. The highest species richness and diversity should be seen in populations of intermediately-sized snails which are old enough to have accumulated several parasite species, but are not so old that one or a few species have had sufficient time to dominate the majority of the infections. The pattern for species dominance should be the mirror image of that for species richness and diversity. This hypothesized hyperbolic relationship is analogous to that predicted by the Intermediate Disturbance Hypothesis for patterns of species diversity in assemblages of free-living organisms (Connell, 1978; Sousa, 1984).

The assumption that snail length is an index of snail age is certainly true in a relative sense (i.e. snails grow longer with time); however, the precise age of a snail cannot be predicted from its length. For example, snail growth can be stunted under conditions of high density. As a result, in populations of different density, snails of the same age may differ by several mm in length. In addition, parasitic infection can alter snail growth rate, either slowing or accelerating it depending on the species of trematode (Sousa, 1983, unpublished data). As a consequence, while a strong relationship between size and age exists, there is undoubtedly some variation in it.

A second prediction from the interspecific interaction hypothesis is that all else being equal, the species richness and diversity of parasites should increase with greater variation in host size within a snail subpopulation, since the distributions of different species among host size classes are heterogeneous (see references cited earlier). Partitioning of hosts by size may promote coexistence of parasite species by reducing the rates at which they antagonistically interact.

A third prediction is that, all else being equal, parasite species richness and diversity should be higher in host populations with a greater availability of uninfected, susceptible individuals since the frequency of mixed-species infections and antagonistic interactions should be lower under these conditions.

Under the second general hypothesis, a very different pattern of component guild structure is predicted. If rates of parasite recruitment and infection are low relative to the rate at which uninfected, susceptible new hosts recruit, the number of open patches of host resource may never become so limited that intramolluscan interactions would reduce the diversity of the component guild. Further, mortality of old, infected hosts may limit the accumulation of infections by dominant species. Under these conditions, an equilibrium assemblage, dominated by a few species would seldom if ever develop. Species richness and diversity would rise monotonically with mean snail age (length) as parasite species and infections accumulate with time. These indices of guild diversity might even display a faster than linear increase with mean length of snails in a subpopulation, if the range of mean host sizes is sufficiently large. This is because a snail's rate of growth slows with increasing length (Sousa, unpublished data); therefore, the mean age of a host population increases as a power function of mean length.

Conversely, species dominance should exhibit a monotonic decline with mean snail length. Neither variation in host size within a population, nor variation in the availability of uninfected, susceptible hosts would have a marked effect on guild structure, since the host resource is not limiting. Under these circumstances, guild structure would be determined primarily by temporal and spatial patterns of parasite recruitment. This situation is roughly equivalent to Wilson's (1969) non-interactive phase of community development. Price (1980) argues that this kind of nonequilibrium situation is typical of many, if not most, host-parasite systems.

## Results

Scatterplots (Figs 3.1–3.3) and correlation analysis (Table 3.5) reveal that in five of the seven annual samples from PGC, rarefied species richness (E (S<sub>15</sub>)), and at least one of the two diversity indices (Exp(H') and  $1/\Sigma p_i^2$ ) exhibited a significant monotonic increase with the mean length of snails in a subpopulation. There was no significant correlation between these variables in 1982 or 1987. Simple dominance (Dom) declined significantly and monotonically with mean snail length in three of the seven years (Table 3.5; Fig. 3.4); similar, but non-significant, negative relationships were detected in the other four. The combined probability (Fisher, 1954) for all seven years was highly significant for each of the above correlations (p < .001 in each case).

Patterns at KI were similar to those at PGC, but not as strong. The smaller number of subpopulations sampled at this site reduces the statistical power of the correlation analysis. This problem is aggravated by the fact that within any particular year, KI subpopulations varied little in mean length (Figs

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Site				PGC							KI			
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	0.55	0.40	0.40	0.61	0.73	0.66	0.34	-0.21	0.56	0.44	0.92	-0.44	0.66	0.65
$n^{\mathrm{b}}$	19	15	14	13	14	13	14	15	14	7	8	7	8	9
d	*	su	su	*	* *	*	su	su	*	su	* * *	su	+	su
3. $1/\Sigma p_i^2$														
r	0.48	0.31	0.30	0.69	0.74	0.67	0.43	-0.18	0.47	0.46	0.83	-0.43	0.57	0.75
d	*	su	su	* *	* *	*	su	su	+	su	*	su	su	+
4. arcsin D	mo													
r	-0.36	-0.26	-0.25	-0.69	-0.75	-0.63	-0.49	0.02	-0.24	-0.39	-0.54	0.25	-0.28	-0.79
d	us	su	su	* *	* *	*	+	su	su	us	su	su	su	+

<sup>a</sup> All probabilities in table are two-tailed:  $ns \ge 0.10$ , + < 0.10, \* < 0.05, \*\* < 0.01, \*\*\* < 0.001. <sup>b</sup> Sample sizes are the same for measures 2, 3, and 4 this table.



**Fig. 3.1** Plot of rarefied number of trematode species versus mean length of snails in a subpopulation at each study site. Each symbol represents the pooled sample of snails collected from an individual pan in the indicated year (see text for further explanation).

3.1–3.4), as discussed earlier. Even so, significant positive correlations between rarefied species richness or the indices of diversity and mean snail length were detected in two of the seven years. Simple dominance appeared to be negatively correlated with mean snail length, but this relationship was never statistically significant.

Figure 3.5 is identical to Fig. 3.4, but indicates which species of parasite was the most prevalent in each pan. Note that the predominant species differed considerably between sites, even though the number of parasite species infecting a host subpopulation of a given mean length did not differ between sites (Fig. 3.1). Also note that *Echinoparyphium* was a conspicuous dominant in those PGC populations whose size distributions were dominated by small snails.

No significant relationship was found in any year, at either site, between the standard deviation of snail length and any of the measures of parasite guild structure. The same was true for a partial correlation analysis of these



**Fig. 3.2** Plot of antilogarithm of Shannon diversity index versus mean length of snails in a subpopulation at each study site. Symbols as in Fig. 3.1.

variables with mean snail length held constant. Scatterplots of the variables did not reveal any hidden, non-linear relationships.

Similarly, only three out of 38 partial correlations (mean length held constant) between rarefied species richness, or the diversity indices, and the mean density of uninfected snails were statistically significant. Two of these significant correlations were positive, favouring the Antagonistic Interaction Hypothesis; the third was in the opposite direction.

When no adjustment for differences in mean snail length is made, species richness and diversity were sometimes negatively related to the density of uninfected hosts. Significant negative relationships of these measures to the density of uninfected snails were found at PGC in three of the seven years (1984–86; r ranged from -0.57 to -0.76, p < .05 or .01). These were years in which the proportionately fewer infections in dense, younger, populations of small snails were dominated by one parasite species, *Echinoparyphium*. In each of these years, simple dominance was also significantly correlated with the density of uninfected snails, but in the opposite direction



**Fig. 3.3** Plot of reciprocal of Simpson diversity index versus mean length of snails in a subpopulation at each study site. Symbols as in Fig. 3.1.

to the diversity measures (r ranged from 0.65 to 0.73, p < .05 or < .01). None of these relationships were significant in any year at KI, where *Echinoparyphium* infections never dominated a component guild (Fig. 3.5).

### **3.6 DISCUSSION AND CONCLUSIONS**

There is little evidence from this analysis that the antagonistic interactions between parasite species which occur within individual hosts have a strong impact on patterns of parasite species richness or diversity at the level of the host population. In particular, parasite diversity did not decline in older populations of hosts as would be predicted if uninfected hosts were a limited resource for parasites in such populations and infections came to be monopolized by a small number of antagonistically dominant species. In addition, neither the density of uninfected, susceptible hosts, nor the variation in host size within a snail subpopulation showed any relationship to



**Fig. 3.4** Plot of arcsin-transformed simple dominance index versus mean length of snails in a subpopulation at each study site. Symbols as in Fig. 3.1.

parasite diversity. Indeed, the percentage of hosts infected by larval trematodes is generally greater in populations comprised of larger, older individuals (for full data set: PGC: r = 0.46, n = 103, p < .001; KI: r = 0.86, n = 70, p < .001). Apparently the number of uninfected, susceptible hosts never becomes sufficiently limiting, given the rates of snail and parasite recruitment in this system, to drive parasite diversity downward. Instead, species richness and diversity rise monotonically with mean snail length, or roughly, the mean age of the host population. This is not to say that competition has no influence on the structures of the component parasite guilds examined in this study. Indices of guild structure such as those computed for this analysis hide the population dynamics of individual species; some species may well be less abundant at the component level as a consequence of infra-level antagonistic interactions. It is clear, however, that any such reductions are more than compensated for by increases in both the number and equitability of other parasite species in older host populations. The competitive interactions that prevent the coexistence of



Fig. 3.5 Plot of arcsin-transformed simple dominance index versus mean length of snails in a subpopulation at each study site. Symbols indicate dominant species of parasite in each subpopulation: *Acanthoparyphium* (filled circle), *Euhaplorchis* (open triangle), *Parochis* (filled triangle), *Echinoparyphium* (open square), cyanthocotylid #2 (filled square), *Catatropis* (open inverse triangle), *Himasthla* (filled inverse triangle), renicolid #2 (open diamond), microphallid #1 (filled diamond), co-domination by two or more species (open circle).

parasite species within individual hosts have far less impact on the structures of the component parasite guilds infecting subpopulations of hosts. The population dynamics of the different parasite species in each of the host subpopulations will be examined separately (Sousa, in prep.).

Under a condition of relatively unlimited resources, which appears to characterize the component level of this system, spatial and temporal variation in the abundance and/or infectivity of miracidial stages will be the primary determinant of component guild structure. The observations that the dominant parasite species differ markedly between the sites (Fig. 3.5) and that the relative prevalence of different parasite species fluctuates greatly from year to year (Sousa, unpublished data) support this interpretation.

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This study demonstrates that distinct processes are primarily responsible for the structure of assemblages of larval trematodes at different spatial scales; a similar conclusion has been reached for a number of assemblages of free-living organisms (see references cited earlier). If more than one species of parasite recruits to an individual snail, deterministic antagonistic interactions almost always result in the exclusion of one of the two species. Most larval trematodes exploit the gonad or digestive gland of their molluscan hosts (e.g. Wright, 1971; Brown, 1978; Kuris, 1974; Lauckner, 1980, 1983; Sousa, 1983), tissues which are not as easily partitioned as are the complex organ systems of the definitive vertebrate hosts (e.g. Crompton, 1973; Holmes, 1973; Kennedy, 1975; Bush and Holmes, 1983, 1986a, b). Consequently, parasite species rarely coexist on the small scale, and infraguilds are depauperate.

In contrast, the component guild of trematodes that infects populations of *Cerithidea* in Bolinas Lagoon appears to be structured largely by external processes, in particular those that determine spatial and temporal variation in the abundance of infective stages in the parasite life cycle. Interspecific antagonism on the small spatial scale does not have a detectable effect on patterns at this larger scale. Thus, it appears that very different processes determine the organization of larval parasite guilds at the two spatial scales examined in this study, the infra- and component guild levels of parasite resources.

Finally, it is apparent that the discrete, divided nature of resources provided by hosts promotes coexistence of parasite species on the large scale. This structure and the complex life cycle of the parasites preclude the direct spread between snails of asexual parasitic stages (rediae) of antagonistically dominant species. In effect, this provides a refuge for less aggressive parasites, similar to that demonstrated in Huffaker's (1958) classic study of predator-prey interactions in a patchy, experimental system. Independent aggregation of parasites among hosts, as a consequence of both asexual reproduction and differential exploitation of different-sized hosts, makes coexistence even more likely (Shorrocks *et al.*, 1979; Atkinson and Shorrocks, 1981; Dobson, 1985; Ives and May, 1985). In addition, the ephemeral nature of host patches, and the high rate at which new ones are created via host reproduction, make it all the more difficult for one or a few species to monopolize the host resource.

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