Ecology, 78(8), 1997, pp. 2303–2315

EFFECT OF RESOURCE ENRICHMENT ON A CHEMOSTAT COMMUNITY OF BACTERIA AND BACTERIOPHAGE

BRENDAN J. M. BOHANNAN AND RICHARD E. LENSKI

Center for Microbial Ecology, Michigan State University, East Lansing, Michigan 48824 USA

Abstract. We determined the responses of a model laboratory community to resource enrichment and compared these responses to the predictions of prey-dependent and ratio-dependent food chain models. Our model community consisted of *Escherichia coli* B and bacteriophage T4 in chemostats supplied with different concentrations of glucose. We observed the following responses to enrichment: (1) a large and highly significant increase in the equilibrium population density of the predator, bacteriophage T4, (2) a small but significant increase in the equilibrium population density of the prey, *E. coli*, and (3) a large and highly significant decrease in the stability of both the predator and prey populations. These responses were better predicted by a prey-dependent model (altered to include a time delay between consumption and reproduction by predators) than by a ratio-dependent model. Enrichment had a large effect on evolutionary change in our system. Enrichment significantly decreased the amount of time required for mutants of *E. coli* that were resistant to predation by bacteriophage to appear in the chemostats. Enrichment also significantly increased the rate at which these bacteriophage-resistant mutants invaded the chemostats. These results were also better predicted by the prey-dependent model. Invasion by bacteriophage-resistant mutants had a large effect on the subsequent population dynamics of both predator and prey. Both the equilibrium density and stability of the *E. coli* population increased following invasion, and the population shifted from being primarily limited by predators to being primarily limited by resources. After invasion by the mutants, the T4 population decreased in equilibrium density, and the population cycled with an increased period. These results were compared to the predictions of a ratio-dependent model and a prey-dependent model altered to include T4-resistant mutants. The dynamics of this community were better predicted by the modified prey-dependent model; however, this model was more complex mathematically than the simpler ratio-dependent model.

Key words: bacteriophage T4; Escherichia coli; *population dynamics; predation; prey-dependent models; ratio-dependent models; resource enrichment.*

INTRODUCTION

The dynamics of predator–prey and other exploitative interactions have long been recognized as fundamentally important to the structure of ecological communities (Hairston et al. 1960, Paine 1966, Lubchenco 1978). Nonetheless, there remains considerable debate over such basic issues as the effects of resource enrichment on these interactions and how best to model these effects (Arditi et al. 1991*a*, Ginzburg and Akçakaya 1992, Diehl et al. 1993, Abrams 1994, Berryman et al. 1995). Classical predator–prey models (i.e., Lotka-Volterra models and modern variations thereof) make two controversial predictions concerning the effect of resource enrichment on prey and their predators. First, these models predict that enrichment will result in an increase in the equilibrium population density of the predator but have no effect on the equilibrium population density of the prey (Rosenzweig 1977). Second, classical predator–prey models predict that enrichment can destabilize a predator–prey pair, increasing the amplitude and period of population oscillations (Rosenzweig 1971).

These classical models are considered ''prey-dependent'' because they assume that the attack rate of predators depends only on the instantaneous density of prey. Some theorists have argued that the attack rate is often better modeled as a function of the ratio of prey to predator density (Arditi and Ginzburg 1989). Such ''ratio-dependent'' models make very different predictions concerning the effect of enrichment on prey and their predators. Enrichment is not predicted to be destabilizing, and the equilibrium population sizes of both predators and prey are predicted to increase in response to enrichment.

Proponents of ratio-dependent models have suggested that this approach is superior because it captures the effects of heterogeneity on predator–prey dynamics. Such heterogeneity could include differences in the time scales of feeding by predators and reproduction by predators, discontinuous prey reproduction, spatial heterogeneity, and heterogeneity in prey edibility (Arditi and Ginzburg 1989). The superiority of ratio-dependent models in these situations has been hotly de-

Manuscript received 3 June 1996; revised and accepted 10 May 1997.

bated (Oksanen et al. 1992, Diehl et al. 1993, Abrams 1994, Gleeson 1994, Akçakaya et al. 1995, Berryman et al. 1995). This debate has centered on whether ratio-dependent models do indeed capture the effects of heterogeneity, whether it is better to model heterogeneity by using a ratio-dependent model or by explicitly incorporating heterogeneity into a prey-dependent model, and what the trade-offs are in using these two approaches.

There have been a number of attempts to answer these questions using field systems. Most of these attempts have involved comparing trophic structure and/or trophic level biomass across natural gradients of productivity (e.g., Arditi et al. 1991*a*, Ginzburg and Akçakaya 1992, Hansson 1992, Oksanen et al. 1992, Persson et al. 1992) or measuring the response of a natural community to enrichment (e.g., O'Brien et al. 1992, Wootton and Power 1993, Stow et al. 1995). The results of these attempts have been inconclusive. In some studies prey-dependent models appeared to better predict the responses (Hansson 1992, Oksanen et al. 1992, Persson et al. 1992, Wootton and Power 1993), while in other studies the responses appeared to be better predicted by ratio-dependent models (Arditi et al. 1991*a*, Ginzburg and Akçakaya 1992, O'Brien et al. 1992, Schmitz 1993). The limitations inherent in using field systems to test these models have been well discussed in the literature (e.g., Power 1992). These limitations include difficulty determining whether populations are at or near equilibrium, problems with quantifying trophic level biomass, and difficulty defining the physical boundaries of food chains.

Some of these limitations can be circumvented by using laboratory model systems. Ecological experiments with model laboratory systems can bridge the gap between mathematical models and natural communities, by allowing the predictions of mathematical models to be rigorously examined in a biological system that is easily manipulated, replicated, and controlled before such models are applied directly to natural systems (Lawton 1995). Two attempts have been made to test prey-dependent and ratio-dependent models using laboratory model communities. In the first attempt, Harrison (1995) reanalyzed the classic experiments of Luckinbill (1973). Luckinbill observed that decreasing the concentration of nutrients in batch cultures of protozoan predators and prey increased the stability of the populations dramatically (although manipulating the interactions between predators and prey by thickening the media was also necessary to achieve persistence). Luckinbill was unable to compare equilibria between treatments because the predator populations went extinct in the higher nutrient treatment. However, in his reanalysis of these experiments, Harrison (1995) found no evidence for ratio-dependent predation.

In contrast, Balciunas and Lawler (1995) found that in batch culture both bacteriovorus protozoans and prey bacteria increased in abundance in response to increased nutrient input. However, they sampled the bacteria population only twice during their 52-d experiment (they were primarily interested in protozoan population dynamics); if the bacteria population cycled in response to predation, these estimates of population density could be inaccurate. In addition, Balciunas and Lawler used a heterogeneous population of bacteria in their experiments, and the increase in bacteria abundance could be due to an increase in the abundance of less edible members of the mixed population. Balciunas and Lawler found some evidence for predator mutual interference and could not rule out ratio-dependent predation in their system.

Although most predator–prey theory assumes a ''chemostat-like'' environment (i.e., continuous input of resources, constant mortality, etc.), both studies above used batch culture systems rather than chemostats. In batch culture, an aliquot of the culture is transferred at regular intervals to fresh culture medium. The effect of such serial transfer is potentially confounding; it was considered by Harrison (1995) to be the major reason that he was unable to get a close fit between some of Luckinbill's data and the predictions of mathematical models.

We have built on these previous attempts by using chemostat communities of bacteria and bacteriophage (viruses that feed on bacteria) to test prey-dependent and ratio-dependent models. We observed the response of these communities to resource enrichment and compared this response to quantitative predictions of prey-dependent and ratio-dependent models. Both predator and prey persisted in all replicates and we were able to estimate equilibrium densities and quantify stability for all populations. In addition, bacteria and bacteriophage have sufficiently short generation times that we were able to observe the effect of enrichment on the evolution of predator–prey interactions during the course of our experiment.

Methods

Experimental system

Bacteria and bacteriophages have been proposed as ideal experimental systems for studying predator–prey dynamics (Campbell 1961, Lenski and Levin 1985) and have been successfully used as such by a number of researchers (Paynter and Bungay 1969, Horne 1970, Paynter and Bungay 1971, Chao et al. 1977, Levin and Lenski 1983, Lenski and Levin 1985, Lenski 1988*a*). Although bacteriophage–bacteria interactions have been traditionally modeled using prey-dependent models (Levin et al. 1977), they have a number of characteristics that could be modeled more simply using the ratio-dependent approach. Temporal heterogeneity is present, with bacteriophage feeding on bacteria on a time scale of seconds, but reproducing in bursts approximately every half hour. Heterogeneity in the sus-

ceptibility of bacteria to bacteriophage attack is common, evolving rapidly even in populations of bacteria started from a single clone (Lenski 1988*b*). There is strong evidence that the chemostat environment is not spatially homogeneous, and that growth by bacteria on the wall of a chemostat can have a profound effect on population dynamics (Chao and Ramsdell 1985). Growth on the vessel wall has been observed to act as a refuge for bacteria from bacteriophage, leading to greater population stability than predicted by prey-dependent models (Schrag and Mittler 1996).

Our experimental system consisted of *E. coli* B strain REL607 (Lenski et al. 1991) and the virulent bacteriophage T4 (kindly provided by L. Snyder) in glucose-limited chemostats. Our chemostat vessels are similar to those described by Chao et al. (1977). The media consisted of Davis minimal broth (Carlton and Brown 1981) supplemented with 2 μg thiamine hydrochloride/L and either 0.1 or 0.5 mg glucose/L of medium. These glucose concentrations were chosen because the predictions of the prey-dependent and ratio-dependent models differ dramatically within this range of concentrations. The volume of the chemostats was maintained at 30 mL, the flow rate at 0.2 turnovers per hour, and the temperature at 37°C. Three replicate chemostats at each glucose concentration were maintained simultaneously. Control chemostats, containing only *E. coli*, were established at each glucose concentration and maintained simultaneously with the treatment chemostats.

The population densities of *E. coli* and bacteriophage T4 were estimated twice daily by dilution and plating. *E. coli* cells were plated on Davis minimal agar supplemented with 2 μg thiamine hydrochloride/L and 4 mg glucose/mL of medium. Heat-killed cells were mixed with each sample to inactivate free bacteriophage prior to plating, as described by Carlson and Miller (1994). Bacteriophage T4 was plated on a lawn of *E. coli* using Davis minimal agar and the plate count technique described by Carlson and Miller (1994). We also estimated the population densities of *E. coli* mutants resistant to predation by bacteriophage T4. These T4-resistant cells were plated on Davis minimal agar supplemented as previously described. A concentrated bacteriophage T4 lysate was mixed with each sample to kill T4-sensitive *E. coli* prior to plating.

To estimate the population stability and equilibrium population densities of T4 and *E. coli*, we treated each chemostat as a single observational unit. We first calculated the mean and standard deviation of the T4 and *E. coli* population densities over time for each chemostat. We then estimated the stability of each population as the mean coefficient of variation across replicate chemostats (the lower the coefficient of variation, the higher the stability). We estimated the equilibrium density of each population as the grand arithmetic mean of population density across replicate chemostats. We determined that the arithmetic mean was superior to the geometric mean as an estimator of equilibria by analyzing simulated population data. The arithmetic mean estimated the equilibria of simulated data more accurately than the geometric mean, and it was not systematically biased.

E. coli mutants resistant to predation by bacteriophage T4 eventually appeared in all chemostats. To remove the influence of these mutants on stability and equilibria, we excluded the last two time points before the appearance of resistant mutants from our calculations. We also excluded the first two time points after inoculation, to allow time for the populations to reach equilibria. In addition to these estimates, we also estimated population stability and equilibria for the time period after the T4-resistant mutants had reached equilibrium in the higher glucose treatment (the experiment was terminated before they reached equilibrium in the lower glucose treatment).

We compared population stability and equilibria with *t* tests. One-tailed comparisons were used whenever the models made directional predictions. Prior to comparison we tested for homogeneity of variances. The data were log-transformed prior to comparison whenever the variances were found to be significantly different.

Mathematical models

We modeled our experimental system using modifications of the models developed by Levin et al. (1977). We solved these models analytically and examined the behavior of the models numerically using STELLA II simulation software (High Performance Systems 1994). Details of the models and the numerical simulations are included in the Appendix. A time-step of 0.05 h was used in the simulations. However, we ''sampled'' the output of each simulation every 12 h (the approximate sampling interval of our experiments) to produce the dynamical predictions shown graphically.

RESULTS

Ecological dynamics

Model predictions.—The predictions made by the ratio-dependent and prey-dependent food chain models for the ecological dynamics in our system are presented in Figs. 1 and 2. The predictions of the prey-dependent model vary depending on the concentration of glucose in the incoming media. At concentrations ranging from ≈0.08 mg/L to 1 mg/L, the prey-dependent model predicts that: (1) the equilibrium population density of T4 will increase in response to enrichment, and (2) the equilibrium population density of *E. coli* will not change in response to enrichment (Fig. 1A). We conducted our experiments within this input concentration range. As the glucose input concentration is lowered below this range the model predicts that the T4 population will become extinct first, and then the *E. coli* population. Above ~1 mg/L, neither population equi-

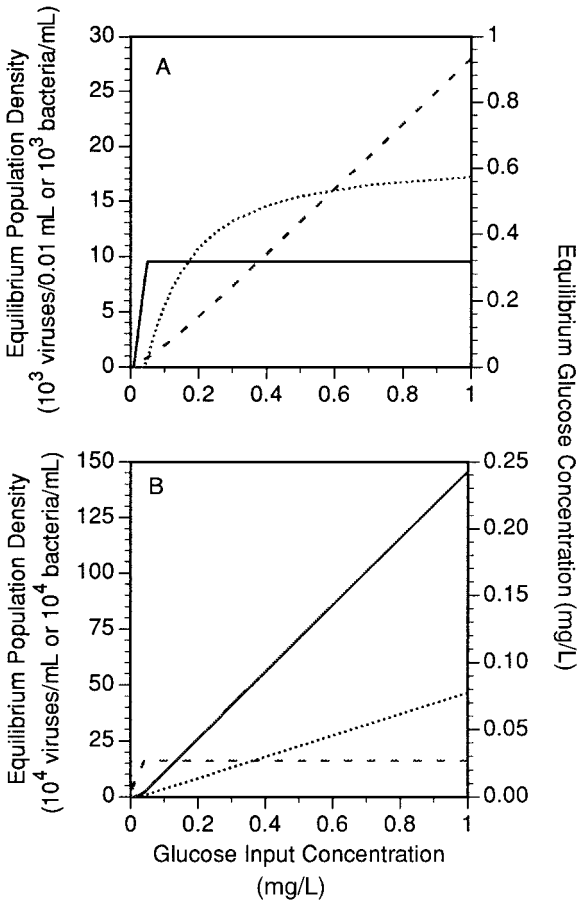

FIG. 1. Relationship between equilibria and glucose input concentration: (A) prey-dependent model (note that bacteriophage equilibria are divided by 100), (B) ratio-dependent model. Key: solid line = equilibrium population density of T4-sensitive *E. coli*, dotted line = equilibrium population density of T4, dashed line = equilibrium concentration of glucose.

librium is predicted to increase appreciably in response to enrichment. In addition, this model predicts that within the range of concentrations used in our experiment, both the T4 and *E. coli* populations will be less stable as glucose input concentration is increased (Fig. 2A and B).

In contrast, the ratio-dependent model predicts that the equilibrium population densities of both T4 and *E. coli* will increase in response to enrichment, regardless of the glucose input concentration range (Fig. 1B). The ratio-dependent model also predicts that the stability of the populations will not be affected by enrichment (Fig. 2D and E).

Empirical observations.—The dynamics of the T4 and *E. coli* populations are shown in Fig. 3 for representative chemostats with two different input concentrations of glucose. The populations persisted in all chemostats with apparent population cycles until the appearance of, and subsequent invasion by, T4-resistant bacteria. There was a large and highly significant increase in the equilibrium population density of bacteriophage T4 in response to enrichment ($t = 18.225$, df = 4, one-tailed $P < 0.0001$; Fig. 4A). The equilibrium population density of *E. coli* responded to enrichment with a small but significant increase ($t = 2.4699$, df = 4, one-tailed $P = 0.0345$; Fig. 4A). There was a large and highly significant decrease in stability (i.e., increase in coefficient of variation) for both T4 and *E. coli* populations in response to enrichment ($t = 4.6092$, df = 4, one-tailed $P = 0.0050$ for *E. coli*; $t = 4.3042$, df = 4, one-tailed $P = 0.0063$ for T4; Fig. 4B). In control chemostats without bacteriophage, the *E. coli* population increased in response to enrichment. Population stability was unaffected by enrichment in the control chemostats.

Fit of observations to mathematical models.—Qualitatively, the response of the predator and prey populations to enrichment was better predicted by the prey-dependent model than the ratio-dependent model. In response to enrichment: (1) the equilibrium population density of the predator increased, (2) the equilibrium population density of the prey changed slightly, and (3) the stability of both prey and predator populations decreased. However the quantitative agreement between the model and our data was far from perfect. The prey-dependent model predicted no change in the prey equilibrium; we observed a small but significant increase. The prey-dependent model predicted an increase in the predator equilibrium of approximately threefold; we observed approximately a 13-fold increase. The predator and prey populations were destabilized by increased resource input as predicted by the prey-dependent model, but the prey population did not go to extinction in the high-glucose treatment as the model predicted (Fig. 2B).

Evolutionary change

Model predictions.—The prey-dependent and ratio-dependent food chain models also make predictions regarding evolutionary change in our experimental system. Evolutionary change in our system can be thought of as occurring in two phases: (1) appearance of, and invasion by, T4-resistant mutants of *E. coli*, and (2) persistence of T4-resistant mutants following invasion. We will discuss the predictions for phase 1 first. Both models predict that T4-resistant mutants of *E. coli* can invade the chemostat provided that they can grow fast enough at the equilibrium glucose concentration to offset washout. However, the prey-dependent model predicts a substantially higher equilibrium glucose concentration than the ratio-dependent model (Fig. 1), resulting in much broader conditions for invasion by T4-resistant mutants. The prey-dependent model also predicts that the equilibrium glucose concentration will be proportional to the glucose input concentration and thus the rate of invasion by T4-resistant mutants will be faster in the higher glucose treatment. The ratio-

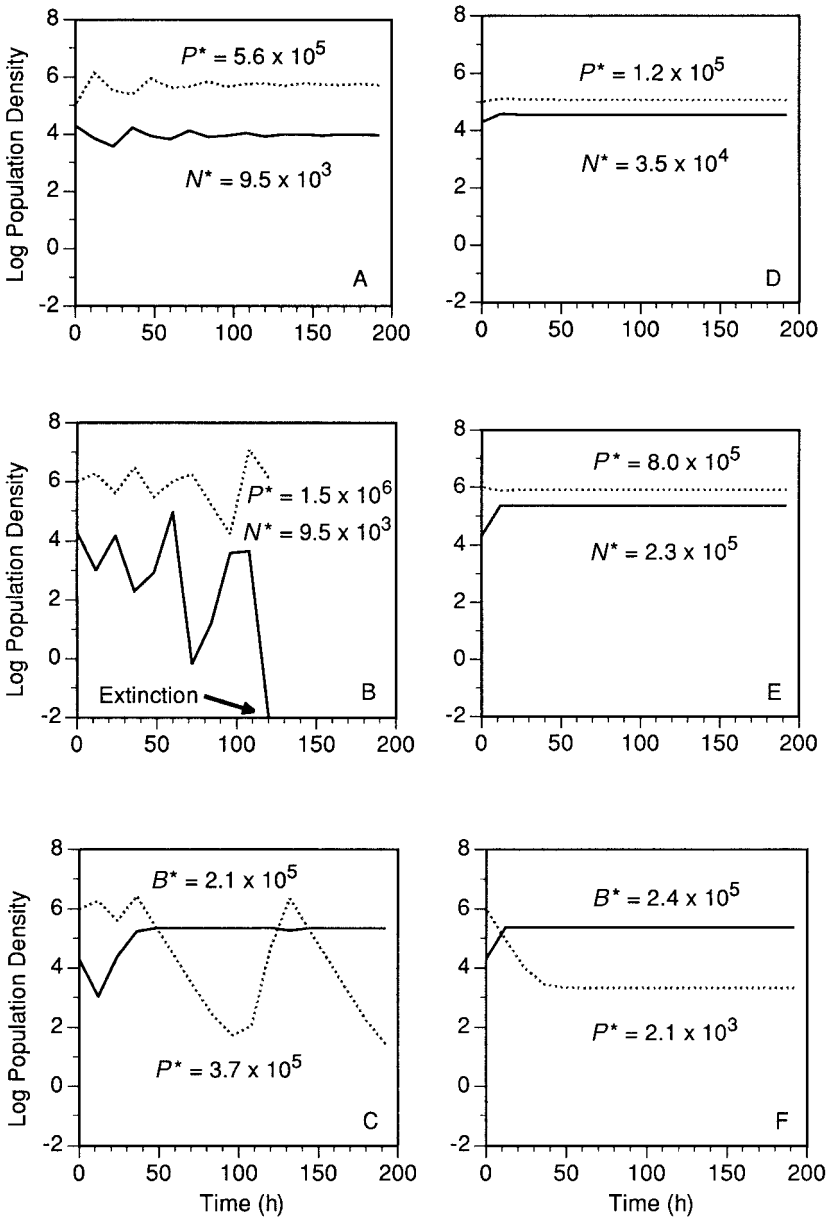

FIG. 2. Population equilibria and dynamics predicted by the models. Equilibria are from analytical solutions of the models; dynamics are from numerical simulations of the models, ''sampled'' at 12-h intervals. (A) prey-dependent model with a glucose input concentration of 0.1 mg/L, (B) prey-dependent model with a glucose input concentration of 0.5 mg/L, (C) prey-dependent model (altered to include heterogeneity in prey edibility) with a glucose input concentration of 0.5 mg/L, (D) ratio-dependent model with a glucose input concentration of 0.1 mg/L, (E) ratio-dependent model with a glucose input concentration of 0.5 mg/L, (F) ratio-dependent model (altered to include heterogeneity in prey edibility) with a glucose input concentration of 0.5 mg/L. Key: N^* = equilibrium population density of T4-sensitive *E. coli* (bacteria/mL), P^* = equilibrium population density of T4 (viruses/mL), B^* = equilibrium population density of total *E. coli* (T4-sensitive and T4-resistant combined; bacteria/mL); solid line = *E. coli* population dynamics, dotted line = T4 population dynamics. The population dynamics depicted are of log-transformed densities.

dependent model does not predict this relationship. Both models predict that enrichment could decrease the amount of time required for T4-resistant mutants of *E. coli* to appear in the chemostats, either because the growth rate of *E. coli* is increased by enrichment (prey-dependent model) or because the equilibrium population size of *E. coli* is increased by enrichment (ratio-dependent model).

To produce predictions for phase 2, we modified the prey-dependent model by adding an additional equation to describe the dynamics of the T4-resistant mutants (see Appendix). This model treats the resistant mutants

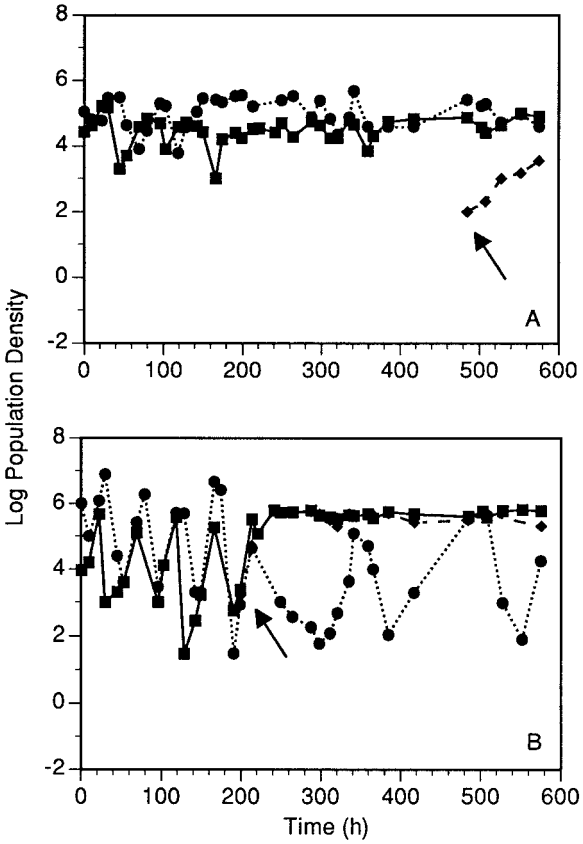

FIG. 3. Dynamics of *E. coli* and bacteriophage T4 populations in representative chemostats supplied with media containing different amounts of glucose. The population densities (viruses/mL or bacteria/mL) have been log-transformed. (A) 0.1 mg/L glucose, (B) 0.5 mg/L glucose. Key: solid line = total *E. coli* population, dotted line = T4 population, diamonds = T4-resistant *E. coli*; arrows indicate first detection of T4-resistant *E. coli*.

as a separate population and assumes that there is a trade-off between T4 resistance and competitive ability. Such a trade-off has been previously reported (Lenski 1988*a*) and has been shown to result in coexistence of bacteriophage-resistant and bacteriophage-sensitive *E. coli* when bacteriophage is present (Chao et al. 1977). We measured the magnitude of this trade-off in our system and it is similar to previously reported trade-offs (see Appendix). We also developed a ratio-dependent model of our system after invasion by fitting our ratio-dependent model to previously published observations of *E. coli* and T4 after invasion by T4-resistant mutants (see Appendix). This model combines the T4-resistant and T4-sensitive *E. coli* into one heterogeneous population.

When the pre- and postinvasion versions of each model are compared, several predictions emerge (compare Fig. 2B and C for the prey-dependent model, Fig. 2E and F for the ratio-dependent model). The ratio-dependent model predicts a 4% increase in the equilibrium population density of total *E. coli* (T4-sensitive and T4-resistant combined) following invasion, while the prey-dependent model predicts a 22-fold increase. The ratio-dependent model predicts no change in the stability of the total *E. coli* population following invasion; in contrast, the prey-dependent model predicts that the population will increase in stability. Both models predict a decrease in the population density of T4 following invasion; however, the ratio-dependent model predicts a decrease of ~400-fold, while the prey-dependent model predicts a decrease of ~4-fold. Neither model predicts that the stability of the T4 population will change following invasion. However, the ratio-dependent model predicts a stable equilibrium both before and after invasion by T4-resistant mutants, while the prey-dependent model predicts that the population will exhibit undamped oscillations both before and after invasion. In addition, the prey-dependent

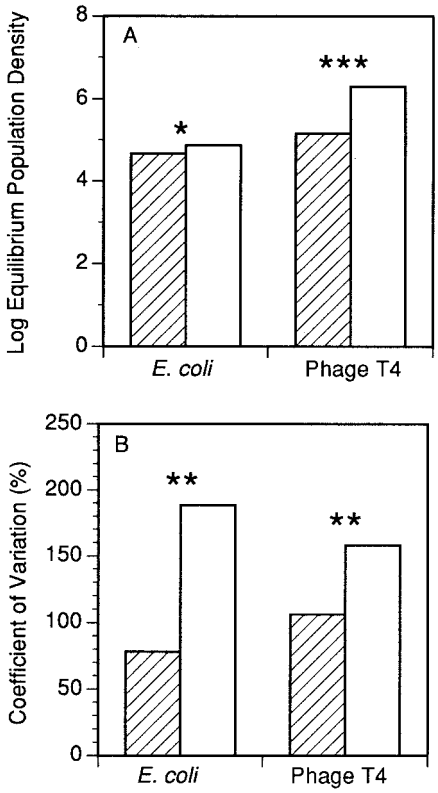

FIG. 4. Effect of glucose input concentration on equilibrium densities and population instability of *E. coli* and bacteriophage T4 populations interacting in a chemostat. Equilibrium population density is estimated as the grand mean of the mean population densities in three replicate chemostats. The equilibrium population densities (viruses/mL or bacteria/mL) have been log-transformed in this figure. Instability is estimated as the coefficient of variation of population densities averaged across three replicate chemostats. Stars indicate statistical significance: $*0.01 < P < 0.05$; $**0.001 < P < 0.01$; $*** P < 0.001$. (A) equilibrium density, (B) instability. Key: striped bars = 0.1 mg/L glucose treatment; open bars = 0.5 mg/L glucose treatment.

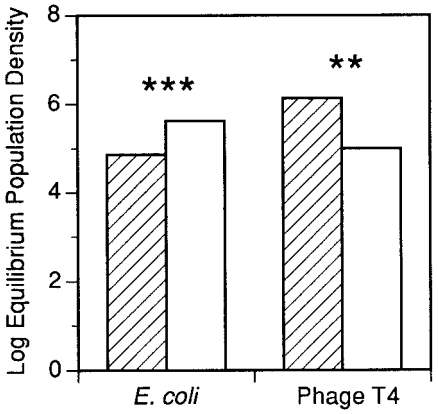

FIG. 5. Effect of invasion by T4-resistant mutants of *E. coli* on the equilibrium densities of total *E. coli* (T4-sensitive and T4-resistant cells) and bacteriophage T4 populations interacting in a chemostat. Equilibrium population density is estimated as the grand mean of the mean population densities in three replicate chemostats. The equilibrium population densities (viruses/mL or bacteria/mL) have been log-transformed in this figure. Stars indicate statistical significance: $**0.001 < P < 0.01$; $*** P < 0.001$. Key: striped bars = before invasion by T4-resistant mutants, open bars = after invasion by T4-resistant mutants.

model predicts that the T4 population oscillations will increase in period length following invasion.

Empirical observations.—T4-resistant bacteria were eventually detected in all treatment chemostats (they were not detected in control chemostats without bacteriophage). T4 was unable to make visible plaques on a lawn of these bacteria, indicating that the bacteria were completely resistant to predation by T4 (see also Lenski and Levin 1985). We tested these bacteria for genetic markers present in REL607. The T4-resistant bacteria were identical to REL607 and were therefore presumed to be T4-resistant mutants of REL607 (as opposed to contaminating bacteria). These mutants appeared significantly sooner in the high-glucose treatment than in the low-glucose treatment ($t = 8.999$, df $= 4$, one-tailed $P = 0.0004$). We calculated the rate of invasion of these mutants by first fitting a line to the log-transformed time series data for the mutants. Only those data points occurring before the mutants reached equilibrium were used. The slopes of the best fit lines were then compared between treatments. Only one replicate of the lower glucose treatment had a sufficient number of data points to determine the invasion rate; this was compared to the three replicates of the high-glucose treatment. The rate of invasion by these mutants was significantly faster in the high-glucose treatments than in the low-glucose treatments ($t = 7.1117$, df $= 2$, one-tailed $P = 0.0096$).

The invasion of the chemostats by T4-resistant mutants had a significant effect on the equilibrium density and stability of the *E. coli* population. The *E. coli* population increased dramatically in population density ($t = 10.944$, df $= 4$, one-tailed $P = 0.0002$, Fig. 5) and stability ($t = 7.8563$, df $= 4$, one-tailed $P = 0.0014$) following invasion. The equilibrium density of the total *E. coli* population after invasion was not significantly different from the equilibrium population density of *E. coli* in the control chemostat without bacteriophage (indicating that the population was now resource limited, rather than predator limited).

There was a moderate but significant decrease in equilibrium population density of T4 ($t = 11.199$, df $= 2$, one-tailed $P = 0.0039$, Fig. 5) following invasion. The T4 population continued to cycle even after equilibrium was reached by the T4-resistant *E. coli* in the higher glucose treatment (the experiment was terminated before T4-resistant *E. coli* had reached equilibrium in the lower glucose treatment). This persistence of T4 has also been observed by other researchers and has been attributed to the bacteriophage feeding on a minority subpopulation of T4-sensitive *E. coli,* which coexists with resistant cells because of a trade-off between resistance and competitive ability (Chao et al. 1977, Lenski and Levin 1985). Although we did observe a trade-off between resistance and competitive ability in our system, we were unable to detect the minority population of T4-sensitive cells, presumably because it was too small relative to the resistant population to detect directly. In two of the three replicate chemostats the period of T4 population oscillations increased following invasion. There were not enough data points in the third replicate to determine the period length after invasion.

Fit of observations to mathematical models.—Qualitatively, evolutionary change occurred in our system in a manner most consistent with the predictions of the prey-dependent model. The invasion by the mutants was faster in the higher glucose than lower glucose treatments, and, following invasion by the T4-resistant mutants: (1) the total equilibrium density of *E. coli* increased substantially, (2) the stability of the total *E. coli* population increased dramatically, (3) there was a moderate decrease in the equilibrium density of the T4 population, and (4) the T4 population continued to cycle, with oscillations longer in period than before invasion. Quantitatively, both models predicted the total equilibrium population density of *E. coli* within a factor of 2; however, the prey-dependent model better predicted the equilibrium population size of T4 (within a factor of 5) than did the ratio-dependent model (which underestimated the equilibrium by two orders of magnitude).

DISCUSSION

Currently there is considerable debate among ecologists over the strengths and weaknesses of ratio-dependent predator–prey models. This debate has centered on whether it is better to model the effects of heterogeneity on predator–prey dynamics using ratio-dependent models or by altering prey-dependent models. We believe that there are at least two important

reasons why these issues remain contentious. One reason is the profound difficulty of obtaining high-quality empirical data on predator–prey interactions. This is due at least in part to insufficient data to distinguish equilibrium from nonequilibrium dynamics and an inability to perform critical manipulative experiments to test key predictions of the alternative models. We have been able to circumvent each of these typical limitations by studying the dynamics of bacteria and their predatory bacteriophages in chemostats. We have population dynamics that extend for several hundred hours, equivalent to some 100 generations under the maximum generation time that is set by flow through the chemostat. We have manipulated the key variable (rate of resource input) while being confident that all other extrinsic factors (temperature, etc.) have remained unchanged.

A second reason for the lack of consensus on these issues may reflect the diverse goals of model builders and users in ecology. Levins (1966) distinguished three sometimes conflicting goals: realism, generality, and precision. Our own tastes favor a primary emphasis on mechanistic realism, but we recognize that others may prefer, for example, generality to enable robust inferences under conditions where it is not feasible to pursue a mechanistic understanding. Nonetheless, it seems worthwhile to us to ask whether (and in what respects) a more complex model that maintains mechanistic realism might perform as well as, or better than, a simpler model that ignores mechanism.

Temporal and spatial heterogeneity

The chemostat is often assumed to be an environment homogeneous in time and space, but this is an oversimplification. The presence of the vessel wall introduces spatial heterogeneity into the chemostat, and growth on the vessel wall can profoundly influence the dynamics of chemostat populations (Chao and Ramsdell 1985, Schrag and Mittler 1996). Moreover, temporal heterogeneity is present in chemostat communities of bacteria and bacteriophage because there is a latent period between prey consumption (i.e., infection) and predator reproduction (i.e., cell lysis) (Lenski 1988*b*). The effects of these heterogeneities can be modeled using a ratio-dependent model or by altering a prey-dependent model. The ratio-dependent model is presumed to capture the effects of temporal and spatial heterogeneity simply by virtue of the ratio-dependent functional response. The prey-dependent model is more complex, requiring additional terms to capture the effect of temporal heterogeneity; capturing the effects of spatial heterogeneity using this model would require even more complexity, and the inclusion of parameters not yet possible to estimate (see Appendix). Thus, with a chemostat community of bacteria and bacteriophage we can ask: Does a prey-dependent model that explicitly incorporates temporal heterogeneity (via a time delay) perform better than a ratio-dependent model that incorporates temporal heterogeneity phenomenologically? Does a prey-dependent model that ignores spatial heterogeneity perform better than a ratio-dependent model that incorporates spatial heterogeneity phenomenologically? And what are the trade-offs between these approaches?

The prey-dependent and ratio-dependent models make numerous distinct predictions with respect to the effects of resource enrichment on the dynamics of predators and prey. We estimated the response of chemostat populations of bacteriophage and bacteria to enrichment and compared the response to these predictions. In almost all respects, the predictions of the prey-dependent models were fulfilled, whereas those of the ratio-dependent model were not. In summarizing these points, we will gloss over one notable exception, which we will then discuss in greater detail.

Both models predicted that resource enrichment would cause the equilibrium population of the predator (bacteriophage T4) to increase substantially, as indeed we observed. The equilibrium ratio of predators to prey also increased substantially in response to resource enrichment, as predicted by the prey-dependent model but not the ratio-dependent model. Moreover, resource enrichment destabilized the interaction, producing greater temporal fluctuations of both prey and predator densities, an outcome predicted by the prey-dependent model but not the ratio-dependent model.

In addition to these effects on the equilibrium and stability properties of the system, as originally constituted, resource enrichment influenced the evolutionary dynamics of our system. Both models predicted (but for different underlying reasons) that T4-resistant bacteria might appear sooner at high than at low resource inputs, and indeed we observed that effect. However, resource enrichment also increased the rate at which resistant mutants subsequently invaded the sensitive bacterial population, as predicted by the prey-dependent model but not its ratio-dependent counterpart.

In short, the results of our experiments on resource enrichment in a simple microbial community provide very strong support for several distinct predictions of the prey-dependent model. At the same time, many predictions of the ratio-dependent model are flatly contradicted by our results. However, as we noted earlier, there is one exception. That is, we observed an increase in the density of sensitive bacteria in response to resource enrichment, a prediction of the ratio-dependent model but not the prey-dependent model. This result was just barely significant, with $P = 0.0345$ using a one-tailed test. We used a one-tailed test because, in all fairness, the ratio-dependent model makes a directional prediction (while the prey-dependent model predicts no effect). We can think of at least three possible reasons for this result. First, this significant difference could be due to chance (Rice 1989). We performed many statistical tests in this paper, and all of the other tests that were judged significant had associated *P* val-

ues of <0.01. Thus, it seems possible that a spuriously significant result would be obtained, and this one is the most likely candidate given its large *P* value and the fact that it alone contradicts a qualitative prediction of the prey-dependent model. However, when we correct for the number of comparisons using the Sequential Bonferroni method, this result remains significant (Sokal and Rohlf 1995).

The second potential explanation is that the difference between equilibria is actually larger and highly significant, but that this effect is masked by differences in mass per bacterial cell between treatments. We tracked population density over time rather than biomass because density is much easier to estimate accurately in our system. However, the prey-dependent model predicts that the growth rate of the bacteria population will increase with increasing glucose input, and faster growing bacterial cells tend to be larger (Bremer and Dennis 1987, Mongold and Lenski 1996). Thus, it is possible that the mass per bacterial cell could vary between our treatments, potentially affecting the accuracy of our estimates of equilibria. The relationship between cell mass and growth rate has been determined for our *E. coli* strain (Mongold and Lenski 1996), and the maximum growth rate difference possible between our treatments can be estimated from the prey-dependent model. Using these estimates, the cells in our 0.5 mg/L treatment could be no more than 15% larger than the cells in the 0.1 mg/L treatment. Even if we account for this potential cell mass difference in our estimates of equilibrium population densities of *E. coli*, the difference in equilibria between treatments and the significance of this difference increases only slightly. In addition, this slight increase in mass per cell would likely be offset by a concomitant increase in the adsorption rate of bacteriophage to the cell (because the cell would also be larger in volume and would thus be a bigger ''target'').

The third possible explanation is that this difference is due to the spatial heterogeneity present in our system. Recent research (Schrag and Mittler 1996) suggests that even in well-mixed chemostats, growth of *E. coli* on the vessel wall can shelter *E. coli* cells from predation by bacteriophage. Wall growth was not visible in our chemostats, but the growth need not be dense to make an impact. Other researchers have demonstrated theoretically (e.g., Abrams and Walters 1996) that the presence of prey refuges can lead to increases in equilibrium prey density in response to enrichment. Thus, the presence of such a physical refuge from predation could explain the slight increase in the equilibrium density of the sensitive prey population at higher resource inputs. The presence of such a refuge is ignored by our prey-dependent model; however, the ratio-dependent model is presumed to capture the effects of such heterogeneity in the ratio-dependent functional response (Arditi et al. 1991*b*, Arditi and Saiah 1992).

While the prey-dependent model accurately predicts many qualitative effects of resource enrichment not predicted by the ratio-dependent model, the quantitative agreement between the prey-dependent model and our empirical observations is far from perfect. For example, the equilibrium density of the predator population increases to a greater extent than is predicted by the prey-dependent model. According to the prey-dependent model, the five-fold experimental increase in the resource supply rate should have produced a threefold increase in the equilibrium density of the predator population, whereas we observed an increase of ~13-fold. And while the prey-dependent model predicts oscillations in prey and predator densities, as we observed, the model also predicts that these oscillations should be of increasing amplitude, leading to eventual extinction of one or both populations, whereas we did not witness any such extinctions. These quantitative discrepancies could be explained by the spatial heterogeneity in our system. Schrag and Mittler (1996) have shown, both theoretically and empirically, that wall growth can stabilize the oscillations of sensitive bacteria and their viral predators. By reducing the average vulnerability of the bacteria, and hence the average adsorption rate, wall growth might simultaneously increase the expected equilibrium density of both the prey and predator populations, as well as stabilize their interaction.

The ratio-dependent model did not provide a better quantitative fit to our experimental observations than the prey-dependent model. The ratio-dependent model predicted an approximately sevenfold increase in the prey and predator populations in response to enrichment; we observed an ~13-fold increase in predators and an ~1.5-fold increase in prey.

In summary, although the ratio-dependent model may have predicted the qualitative effects of enrichment on the equilibrium densities of predator and prey, it failed to predict the effects of enrichment on the stability of predator and prey populations, as well as the effects of enrichment on the evolution of prey defenses. A prey-dependent model altered to include temporal heterogeneity (in the form of a time delay) did a much better job, even though it ignored spatial heterogeneity in our system. But what of other forms of heterogeneity? For example, can the effects of heterogeneity in prey edibility be captured by the ratio-dependent model, as some have argued (Arditi et al. 1991*a*, Sarnelle 1994)? Or is it better to alter a prey-dependent model to include this heterogeneity? We can address this question with our system because heterogeneity developed in prey edibility due to the evolution of T4-resistant *E. coli.*

Heterogeneity in prey edibility

The presence of heterogeneity in prey edibility has been recognized by a number of ecologists as a factor that could alter the response of a food chain to enrichment (McCauley et al. 1988, Leibold 1989, Abrams

1993, Kretzschmar et al. 1993, Sarnelle 1994, Abrams and Walters 1996, Leibold 1996, Polis and Strong 1996). The addition of inedible (or less edible) individuals to a prey population has been shown theoretically to result in a shift in population regulation, from limitation primarily by predators to limitation primarily by resources (Leibold 1989, Abrams 1993, Leibold 1996). We observed this shift in our experimental system. The total *E. coli* population went from being primarily predator limited to primarily resource limited due to the evolution of T4 resistance.

The ratio-dependent model can easily capture the effect of heterogeneity in prey edibility (albeit phenomenologically) by changing the value of the coefficient in the functional response. In contrast, the prey-dependent model describes this heterogeneity mechanistically, but it requires the inclusion of a separate equation with multiple parameters to accomplish this. The prey-dependent and ratio-dependent models make numerous distinct predictions with respect to the effects of heterogeneity in prey edibility on the dynamics of predators and prey. In almost all respects, the predictions of the prey-dependent models were fulfilled by our experimental system, whereas those of the ratio-dependent model were not.

Qualitatively, both models predicted that the equilibrium density of the *E. coli* population would increase following invasion by T4-resistant *E. coli*; however, only the prey-dependent model predicted that the total *E. coli* population would increase in stability following invasion. Both models predicted that the equilibrium density of T4 would decrease following invasion by T4-resistant *E. coli*; however, only the prey-dependent model predicted that the T4 population would continue to cycle. Moreover, the prey-dependent model accurately predicted that the oscillations of the T4 population would increase in period in response to invasion. Quantitatively, both models adequately predicted the total population density of *E. coli* as well as the relatively high stability of the heterogeneous population. However, the prey-dependent model adequately predicted the equilibrium density of T4, while the ratio-dependent model underestimated the equilibrium density by orders of magnitude.

As was the case for temporal and spatial heterogeneity, the ratio-dependent model predicted the qualitative effects of heterogeneity in prey edibility on equilibrium population density, but it failed to predict the effects of heterogeneity in edibility on population stability. The prey-dependent model (altered to include heterogeneity in edibility) was superior, predicting not only the effect of heterogeneity on equilibria and stability, but even predicting the effect of heterogeneity in edibility on the period of population cycles. However, the prey-dependent model was much more complex, requiring not only additional parameters but an additional equation.

Mechanistic realism versus general applicability

Since it was first proposed by Arditi and Ginzburg, the idea that ratio-dependent models could parsimoniously model the effects of heterogeneity on predator–prey dynamics has been hotly debated. This debate has centered on whether the effects of heterogeneity could indeed be captured by such a simple model, and what the limitations of using this approach might be. Using a laboratory model system, we have demonstrated that although some qualitative effects of heterogeneity may be captured by a ratio-dependent model, this approach overlooks a number of important aspects of predator–prey dynamics. In particular, the effects of resource enrichment on population stability and evolution were not predicted by the ratio-dependent models. In contrast, the prey-dependent models did a superior job of predicting the response of our model system to enrichment, but at the cost of simplicity. The prey-dependent models are more complex than the ratio-dependent models and require detailed information about the communities of interest. It is certainly not possible always (perhaps even usually) to develop a fully mechanistic model of complex communities. Ratio-dependent models may be very useful, for example, to managers concerned with the effects of resource enrichment on the structure of complex communities. While ratio-dependent models may be sold as able to predict equilibrium responses in complex communities, they should also come with the explicit warning that certain complications may be missed (e.g., unstable equilibria) by virtue of the lack of mechanistic realism.

Acknowledgments

We thank J. Mongold and P. Sniegowski for valuable discussions and L. Ekunwe for technical assistance. We are grateful to P. Crowley, L. Ginzburg, G. Mittelbach, and two anonymous reviewers for comments on a previous draft of this paper. This research was supported by a National Science Foundation grant (DEB 912 0006) to the Center for Microbial Ecology.

Literature Cited

Abrams, P. A., 1993. Effect of increased productivity on the abundances of trophic levels. American Naturalist **141**: 351–371.

———. 1994. The fallacies of ''ratio-dependent'' predation. Ecology **75**:1842–1850.

Abrams, P. A., and C. J. Walters. 1996. Invulnerable prey and the paradox of enrichment. Ecology **77**:1125–1133.

Akçakaya, H. R., R. Arditi, and L. R. Ginzburg. 1995. Ratio-dependent predation: an abstraction that works. Ecology **76**:995–1004.

Arditi, R., and L. R. Ginzburg. 1989. Coupling in predator–prey dynamics: ratio-dependence. Journal of Theoretical Biology **139**:311–326.

Arditi, R., L. R. Ginzburg, and H. R. Akçakaya. 1991*a*. Variation in plankton densities among lakes: a case for ratio-dependent predation models. American Naturalist **138**: 1287–1296.

Arditi, R., N. Perrin, and H. Saiah. 1991*b*. Functional responses and heterogeneities: an experimental test with cladocerans. Oikos **60**:69–75.

Arditi, R., and H. Saiah. 1992. Empirical evidence of the

role of heterogeneity in ratio-dependent consumption. Ecology **73**:1544–1551.

Balciunas, D., and S. P. Lawler. 1995. Effects of basal resources, predation, and alternative prey in microcosm food chains. Ecology **76**:1327–1336.

Berryman, A. A., A. P. Gutierrez, and R. Arditi. 1995. Credible, parsimonious and useful predator–prey models—a reply to Abrams, Gleeson and Sarnelle. Ecology **76**:1980–1985.

Bremer, H., and P. P. Dennis. 1987. Modulation of chemical composition and other parameters of the cell by growth rate. Pages 1527–1542 *in* F. C. Neidhardt, editor. *Escherichia coli* and *Salmonella typhimurium*: cellular and molecular biology. American Society for Microbiology, Washington, D.C., USA.

Campbell, A. 1961. Conditions for the existence of bacteriophage. Evolution **15**:153–165.

Carlson, K., and E. S. Miller. 1994. General procedures. Pages 427–437 *in* J. D. Karam, editor. Molecular biology of bacteriophage T4. American Society for Microbiology, Washington, D.C., USA.

Carlton, B. C., and B. J. Brown. 1981. Gene mutation. Pages 222–242 *in* P. Gerhardt, editor. Manual of methods for general bacteriology. American Society for Microbiology, Washington, D.C., USA.

Chao, L., B. R. Levin, and F. M. Stewart. 1977. A complex community in a simple habitat: an experimental study with bacteria and phage. Ecology **58**:369–378.

Chao, L., and G. Ramsdell. 1985. The effects of wall populations on coexistence of bacteria in the liquid phase of chemostat cultures. Journal of General Microbiology **131**: 1229–1236.

Diehl, S., P. A. Lundberg, H. Gardfjell, L. Oksanen, and L. Persson. 1993. *Daphnia*-phytoplankton interactions in lakes: is there a need for ratio-dependent consumer-resource models? American Naturalist **142**:1052–1061.

Ginzburg, L. R., and H. R. Akçakaya. 1992. Consequences of ratio-dependent predation for steady-state properties of ecosystems. Ecology **73**:1536–1543.

Gleeson, S. K. 1994. Density dependence is better than ratio dependence. Ecology **75**:1834–1835.

Hairston, N. G., F. E. Smith, and L. B. Slobodkin. 1960. Community structure, population control and competition. American Naturalist **94**:421–425.

Hansson, L.-A. 1992. The role of food chain composition and nutrient availability in shaping algal biomass development. Ecology **73**:241–247.

Harrison, G. W. 1995. Comparing predator–prey models to Luckinbill's experiment with *Didinium* and *Paramecium*. Ecology **76**:357–374.

High Performance Systems. 1994. STELLA II version 3.0.5. High Performance Systems, Hanover, New Hampshire, USA.

Horne, M. T. 1970. Coevolution of *Escherichia coli* and bacteriophages in chemostat culture. Science **168**:992–993.

Kretzschmar, M., R. M. Nisbet, and E. McCauley. 1993. A predator–prey model for zooplankton grazing on competing algal populations. Theoretical Population Biology **44**:32–66.

Lawton, J. H. 1995. Ecological experiments with model systems. Science **269**:328–331.

Leibold, M. A. 1989. Resource edibility and the effects of predators and productivity on the outcome of trophic interactions. American Naturalist **134**:922–949.

———. 1996. A graphical model of keystone predators in food webs: trophic regulation of abundance, incidence and diversity patterns in communities. American Naturalist **147**:784–812.

Lenski, R. E. 1988*a*. Experimental studies of pleiotropy and epistasis in *Escherichia coli*. I. Variation in competitive fitness among mutants resistant to virus T4. Evolution **42**: 425–432.

———. 1988*b*. Dynamics of interactions between bacteria and virulent bacteriophage. Advances in Microbial Ecology **10**:1–44.

Lenski, R. E., and B. R. Levin. 1985. Constraints on the coevolution of bacteria and virulent phage: a model, some experiments, and predictions for natural communities. American Naturalist **125**:585–602.

Lenski, R. E., M. R. Rose, S. C. Simpson, and S. C. Tadler. 1991. Long-term experimental evolution in *Escherichia coli*. I. Adaptation and divergence during 2000 generations. American Naturalist **138**:1315–1341.

Levin, B. R., and R. E. Lenski. 1983. Coevolution in bacteria and their viruses and plasmids. Pages 99–127 *in* D. J. Futuyma and M. Slatkin, editors. Coevolution. Sinauer, Sunderland, Massachusetts, USA.

Levin, B. R., F. M. Stewart, and L. Chao. 1977. Resource-limited growth, competition, and predation: a model and experimental studies with bacteria and bacteriophage. American Naturalist **111**:3–24.

Levins, R. 1966. The strategy of model building in population biology. American Scientist **54**:421–430.

Lubchenco, J. 1978. Plant species diversity in a marine intertidal community: importance of herbivore food preference and algal competitive abilities. American Naturalist **112**:23–39.

Luckinbill, L. S. 1973. Coexistence in laboratory populations of *Paramecium aurelia* and its predator *Didinium nasutum*. Ecology **54**:1320–1327.

McCauley, E., W. W. Murdoch, and S. Watson. 1988. Simple models and variation in plankton densities among lakes. American Naturalist **132**:383–403.

Mongold, J. A., and R. E. Lenski. 1996. Experimental rejection of a nonadaptive explanation for increased cell size in *Escherichia coli*. Journal of Bacteriology **178**:5333–5334.

Monod, J. 1949. The growth of bacterial cultures. Annual Review of Microbiology **3**:371–394.

O'Brien, W. J., A. E. Hershey, J. E. Hobbie, M. A. Hullar, G. W. Kipphut, M. C. Miller, B. Moller, and J. R. Vestal. 1992. Control mechanisms of arctic lake ecosystems: a limnocorral experiment. Hydrobiologia **240**:143–188.

Oksanen, L., J. Moen, and P. A. Lundberg. 1992. The time-scale problem in exploiter–victim models: does the solution lie in ratio-dependent exploitation? American Naturalist **140**:938–960.

Paine, R. T. 1966. Food web complexity and species diversity. American Naturalist **100**:65–75.

Paynter, M. J. B., and H. R. Bungay. 1969. Dynamics of coliphage infections. Pages 323–335 *in* D. Perlman, editor. Fermentation advances. Academic Press, New York, New York, USA.

Paynter, M. J. B., and H. R. Bungay. 1971. Characterization of virulent bacteriophage infections. Science **169**:405.

Persson, L., S. Diehl, L. Johannson, G. Andersson, and S. F. Hamrin. 1992. Trophic interactions in temperate lake ecosystems: a test of food chain theory. American Naturalist **140**:59–84.

Polis, G. A., and D. R. Strong. 1996. Food web complexity and community dynamics. American Naturalist **147**:813–846.

Power, M. E. 1992. Top-down and bottom-up forces in food webs: do plants have primacy? Ecology **73**:733–746.

Rice, W. R. 1989. Analyzing tables of statistical tests. Evolution **43**:223–225.

Rosenzweig, M. L. 1971. Paradox of enrichment: destabilization of exploitation ecosystems in ecological time. Science **171**:385–387.

———. 1977. Aspects of biological exploitation. Quarterly Review of Biology **52**:371–380.
Sarnelle, O. 1994. Inferring process from pattern: trophic level abundances and imbedded interactions. Ecology **75**: 1835–1841.
Schmitz, O. J. 1993. Trophic exploitation in grassland food chains: simple models and a field experiment. Oecologia **93**:327–335.
Schrag, S. J., and J. E. Mittler. 1996. Host–parasite coexistence: the role of spatial refuges in stabilizing bacteria–phage interactions. American Naturalist **148**:348–377.
Sokal, R. R., and F. J. Rohlf. 1995. Biometry. Third edition. W. H. Freeman, New York, New York, USA.
Stow, C. A., S. R. Carpenter, and K. L. Cottingham. 1995. Resource vs. ratio-dependent consumer-resource models: a Bayesian perspective. Ecology **76**:1986–1990.
Vasi, F., M. Travisano, and R. E. Lenski. 1994. Long-term experimental evolution in *Escherichia coli*. II. Changes in life history traits during adaptation to a seasonal environment. American Naturalist **144**:432–456.
Wootton, J. T., and M. E. Power. 1993. Productivity, consumers, and the structure of a river food chain. Proceedings of the National Academy of Sciences (USA) **90**:1384–1387.

APPENDIX

Numerical simulations.—We examined the behavior of our mathematical models numerically using STELLA II simulation software (High Performance Systems 1994). The simulations were run using a time step of 0.05 h. We tested the sensitivity of the simulations to time step size by running replicate simulations at step sizes of 0.1, 0.05, and 0.025 h. Varying the size of the time steps had no detectable effect on the results of the simulations. We ''sampled'' the output of each simulation every 12 h (the approximate sampling interval of our experiments) to produce the predictions in Fig. 2.

Prey-dependent model.—This model explicitly includes a time delay between consumption of prey and reproduction by the predator. This model differs from the model of Levin et al. in that it ignores the dynamics of infected cells (we consider infected cells to instantaneously become ''dead'' cells in our experimental system because infected cells will not produce colonies when plated). This model also ignores spatial heterogeneity. Although theorists have developed prey-dependent models that include spatial heterogeneity (e.g., Abrams and Walters 1996), these models cannot be easily adapted to our experimental system because they require parameters that we cannot yet estimate (e.g., cell transfer rates between wall and liquid populations). The prey-dependent food chain model is as follows,

$$dC/dt = (C_0 - C)\omega - \varepsilon N\psi C/(K + C)$$

$$dN/dt = N\psi C/(K + C) - \alpha(N)P - \omega N$$

$$dP/dt = \beta e^{-\tau\omega}\{\alpha(N')P'\} - \alpha(N)P - \omega P$$

where C_0 = concentration of glucose in the reservoir, C = concentration of glucose in the chemostat, ω = flowrate, ε = reciprocal of the yield of the bacteria, N = population size of uninfected bacteria, ψ = maximum specific growth rate, K = resource concentration at which the bacteria grow at one-half ψ, $\alpha(N)$ = trophic function, P = population size of free bacteriophage, β = number of bacteriophage progeny per infected bacterial cell, τ = time lag between infection and release of bacteriophage progeny, $e^{-\tau\omega}$ = fraction of bacteria infected at time $t - \tau$ that has not washed out of the chemostat before releasing bacteriophage, N' = population size of uninfected bacteria at time $t - \tau$, and P' = population size of bacteriophage at time $t - \tau$.

The following parameter values were used for this model: C_0 = either 0.1 or 0.5 mg/L, $\omega = 0.2$ h^{-1}, $\varepsilon = 2 \times 10^{-6}$ μg (Lenski 1988*b*), $\psi = 0.7726$ h^{-1} (Vasi et al. 1994), $K = 0.0727$ mg/L (Vasi et al. 1994), $\alpha = 3 \times 10^{-7}$ mL/h (Lenski and Levin 1985), $\beta = 80$ viruses per bacterial cell and $\tau = 0.6$ h (Lenski and Levin 1985). The predictions for this model are presented in Figs. 1A, 2A and B.

Ratio-dependent model.—The ratio-dependent food chain model was similar to the prey-dependent model above with the exception that the trophic function $\alpha(N)$ was replaced with $\alpha(N/P)$. This model does not explicitly include a time delay, but it is presumed that the ratio-dependent functional response captures the effect of such temporal heterogeneity on predator–prey dynamics (Arditi and Ginzburg 1989). The model was as follows,

$$dC/dt = (C_0 - C)\omega - \varepsilon N\psi C/(K + C)$$

$$dN/dt = N\psi C/(K + C) - \alpha(N/P)P - \omega N$$

$$dP/dt = \beta\{\alpha(N/P)P\} - \alpha(N/P)P - \omega P.$$

The parameter values used for the ratio-dependent model were the same as for the prey-dependent model with the exception of α. In the ratio-dependent model, α has different units than in the prey-dependent model, and thus must be estimated differently. Using the same value of α as that used in the prey-dependent model would result in predicted equilibria for our system that are orders of magnitude different from preliminary results for our system. Therefore we estimated α by fitting the ratio-dependent trophic function to preliminary estimates of equilibria for our system at a glucose input concentration of 0.1 mg/L ($\alpha = 8.95 \times 10^{-3}$ h^{-1}). We used this value to predict the equilibria of our system at 0.5 mg/L and to produce the predictions depicted in Figs. 1B, 2D and E.

Prey-dependent model (postinvasion).—We used a modification of the prey-dependent model above to model our experimental system after T4-resistant mutants of *E. coli* had invaded the chemostats. This modified model consists of four differential equations,

$$dC/dt = (C_0 - C)\omega - \varepsilon N\psi C/(K + C) - \varepsilon_R R\psi_R C/(K_R + C)$$

$$dN/dt = N\psi C/(K + C) - \alpha(N)P - \omega N$$

$$dP/dt = \beta e^{-\tau\omega}\{\alpha(N'/P')\} - \alpha(N)P - \omega P$$

$$dR/dt = R\psi_R C/(K_R + C) - \omega R$$

where, in addition to the variables described above, R = population size of T4-resistant bacteria, ε_R = reciprocal of the yield of the T4-resistant bacteria, ψ_R = maximum specific growth rate of T4-resistant bacteria, and K_R = resource concentration at which T4-resistant bacteria grow at one-half ψ_R. In addition to the parameter values used in the prey-dependent model above, we used the following values: $\psi_R = 0.7027$ h^{-1} and $K_R = 0.123$ mg/L. These values were determined experimentally. ψ_R was estimated using the methods described by Vasi et al. (1994). We were unable to directly estimate K_R with consistent and meaningful results. Instead, we estimated K_R indirectly by first estimating the fitness of the T4-resistant mutants relative to their T4-sensitive ancestors in chemostats (as described by Lenski and Levin 1985). The average relative fitness was 0.575, similar to values previously reported by Lenski and Levin (1985). From the relative fitness value we estimated the growth rates of the T4-sensitive (μ) and T4-resistant (μ_R) *E. coli* at steady state in the chemostats. The

equilibrium glucose concentration in the chemostats (C^*) was assumed to be set by the superior competitor (the T4-sensitive *E. coli*). C^* was estimated from a rearrangement of the Monod (1949) model using parameters for the T4-sensitive *E. coli*,

$$C^* = K/(\psi/\mu - 1).$$

Finally, we estimated K_R from yet another rearrangement of the Monod model, in this case using parameters estimated for the T4-resistant *E. coli*,

$$K_R = C^*(\psi_R/\mu_R - 1).$$

The predictions of this model are summarized in Fig. 2C.

Ratio-dependent model (postinvasion).—Proponents of ratio-dependent models have argued that the ratio-dependent functional response incorporates the net effect of heterogeneity on population dynamics and that heterogeneous systems are more parsimoniously modeled by ratio-dependent models than by other types of models (Arditi and Ginzburg 1989). We tested this idea by developing a ratio-dependent model that combined the T4-sensitive and T4-resistant *E. coli* into one population that is heterogeneous in edibility. We used the same ratio-dependent model described above, with the exception that we fit the ratio-dependent trophic function to estimates of equilibria from previously published (Lenski and Levin 1985) observations of *E. coli* and T4 after invasion by T4-resistant mutants ($\alpha = 2.28 \times 10^{-5}$ h^{-1}). These observations were made in chemostats with glucose input concentrations of 300 mg/L. The predictions of this model are summarized in Fig. 2F.