

Propagule dispersal and population connectivity

Introduction

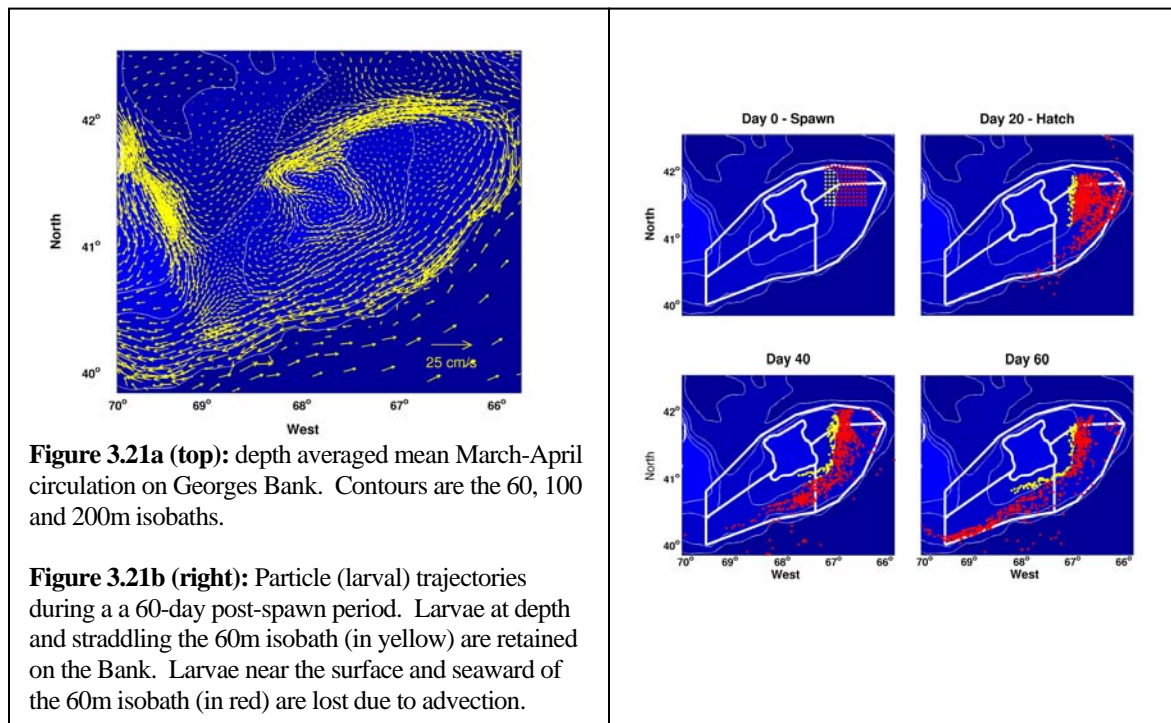
A fundamental goal of both ecology and conservation biology is to develop hypotheses explaining the abundance and distribution of species. A crucial step towards achieving this objective for marine taxa – particularly among those that possess either pelagic larvae or vagile adults that can potentially disperse hundreds of kilometers in ocean currents – is the identification of factors influencing rates of exchange, or connectivity, among populations. A wide variety of techniques are being used by MASC faculty, staff, and students to understand the dispersal and connectivity of marine plants and animals and the impact that immigration has on community structure and function.

I. Numerical current modeling

The use of spatially explicit individual based models (IBMs) has become a *de facto* tool in modeling studies of population dispersal (Werner et al. 2001). The utility of IBMs is that properties of ecological systems can be derived by considering the properties of individuals constituting them. Individual differences may be behavioral, physiological, or may arise from interactions among individuals. The differences result in unique life histories, which when considered as a whole give rise to growth and size distributions that provide a measure of the state of the population.

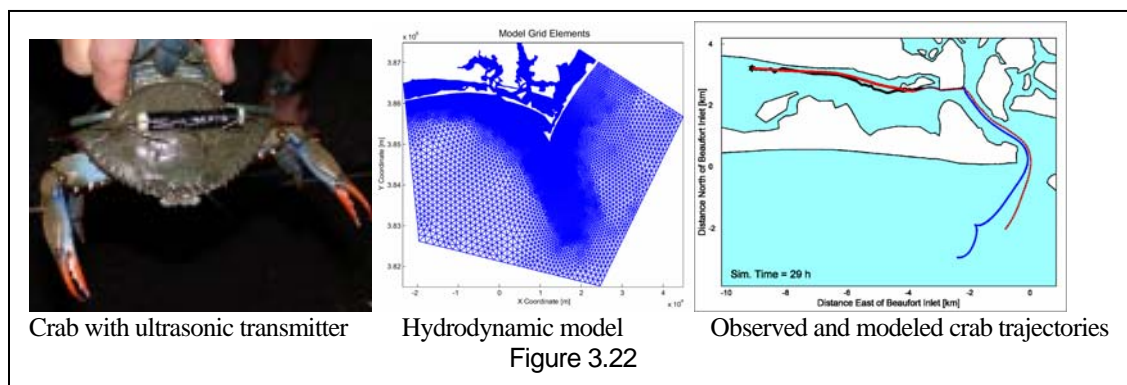
The spatial distribution of a species' abundance is a key focus of these modeling studies and includes the response of populations to horizontal spatial heterogeneity, e.g., as physical and biological conditions at lower trophic levels change, how does the spatial distribution of fished populations change? An example from the NW Atlantic GLOBEC Bank Program is the modeling study of the population regulation mechanisms of cod and haddock. Models of early life histories of cod and haddock (developed in the Ocean Processes Numerical Modeling Laboratory; Werner, Blanton, Pehrson and Aretxabaleta) have coupled advanced ocean circulation models and field data to determine the effects of realistic temporal and spatial variation of currents, turbulence, light, prey, etc., on their behaviorally modified trajectories and growth. The explicit consideration of realistic spatial heterogeneity provided an additional factor that contributed to the differentiation among individuals, to variances in population structure and regulation, and ultimately to our understanding recruitment process through the determination of retention and loss mechanisms, as well as food limitation. Realistic model flow-fields (Fig. 3.21a) are used to compute particle trajectories simulating the transport and dispersal of the early life stages of target species. The simulated larvae can individually behave in response to physical, chemical or biological cues. In this manner, unique time-histories and trajectories are constructed for each larva. For the particular case of Georges Bank, on-bank retention is predicted for larvae located inside the 60m isobath and below the surface wind-driven layer (Fig. 3.21b). Extensions to this work includes, among others, being able to make quantitative statements about the success of the later life stages of the species (i.e., the recruitment to the fishery), and to establish mechanistic links with

processes occurring at longer space- and time-scales, such as the decadal and basin-scale fluctuations associated with the North Atlantic Oscillation.



II. Observing and modeling the blue crab spawning migration

The Luetlich lab is studying the migration of female blue crabs *Callinectes sapidus* from adult habitats in North Carolina estuaries to coastal larval release (“spawning”) locations. During this migration, ovigerous crabs use ebb-tide transport, a vertical migratory behavior in which crabs ascend into the water column during ebb tides and descend to the bottom during flood tides, to move seaward. The lab is using a variety of methods for this work: tracking



migratory crabs with ultrasonic telemetry, tethering crabs in a local estuary to observe vertical ascent patterns, and coupling models of crab behavior to a hydrodynamic model of local

estuaries. These NSF-funded studies are being used to determine the relationship of vertical migrations to local currents, the influence of vertical migrations on horizontal transport, migratory trajectories in the estuaries, spatial patterns in migratory success, the residence times of crabs in different estuarine regions, and larval release locations.

III. Larval dispersal in North Carolina estuaries: implications for fisheries management and marine reserve design

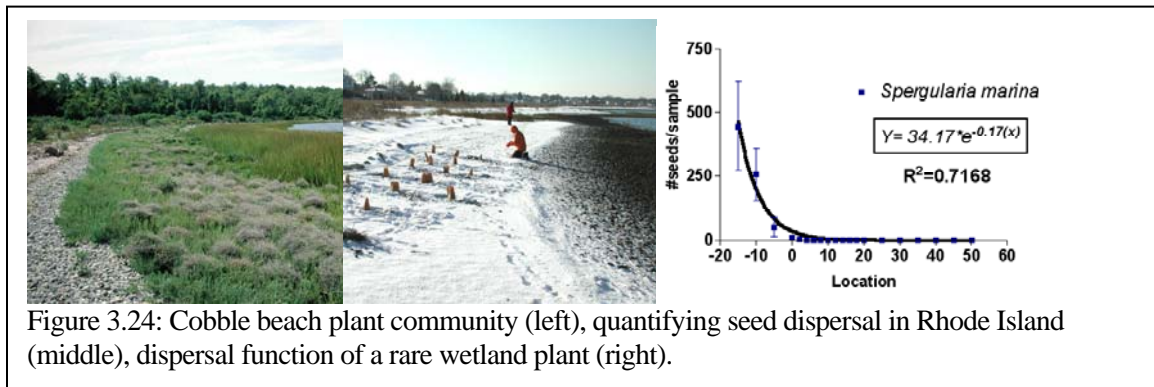
Members of three laboratories (Peterson, Moran, Marko) have been working on NSF-funded projects focused on the dispersal, population genetics, and larval biology of benthic marine invertebrates that exhibit evidence of recruitment limitation. Habitat forming (e.g., oysters) and commercially important species (e.g., oysters, bay scallops, hard clams) are of particular interest. Much of this work has been done either in collaboration and coordination with numerical modelling in Luettich and Werner's labs and with an aquaculturist at a community college in Morehead City. Physical models have been used as a starting point to explain patterns of larval supply, which can be tested indirectly with both ecological experiments (Peterson) and population genetic analyses of recruitment (Marko). Direct analysis of dispersal distances is also underway (Moran), through the development of fluorescent markers (Fig. 3.23) that can be incorporated into calcified larval structures that are retained in settled juveniles. These direct methods will not only reveal dispersal 'shadows' of marine species with pelagic larvae, but physically marked individuals recovered in experiments in NC estuaries can then be used to test statistical methods of population genetic stock identification.



IV. Seed dispersal in an estuarine plant metacommunity

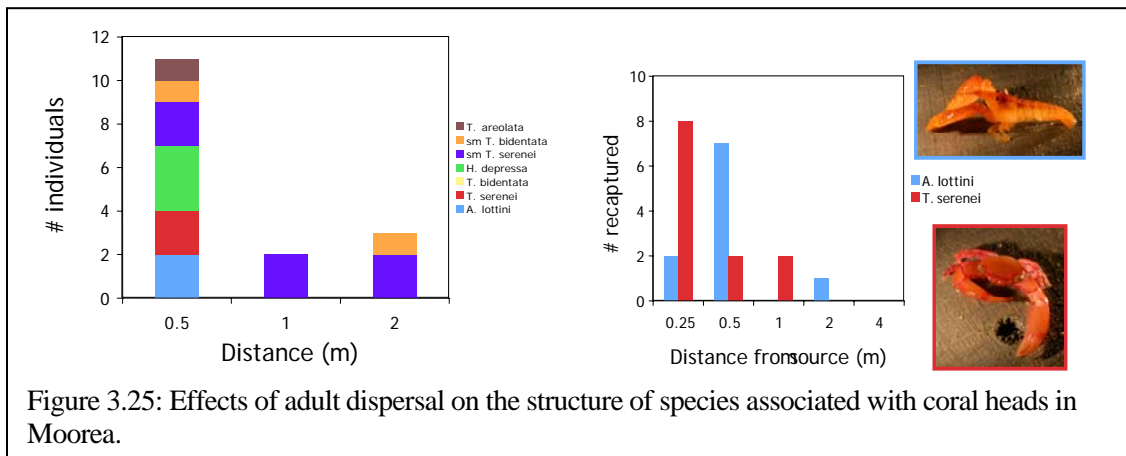
The Bruno lab has been working on dispersal in a New England cobble beach plant metacommunity since 1996. The main goal is to quantify the dispersal functions of all 12 constituent species, including annuals and perennial and both common and rare species. The role of current direction, habitat patch orientation and isolation, and patch size in controlling seed export and dispersal are all being quantified through yearly direct dispersal measurements. Dispersal functions of each species are then used in spatially explicit metacommunity models to test the effects of habitat patch quality, isolation, and density on metacommunity dynamics (Figure 3.24). This NSF-funded project will continue through

August 2005 and is being carried out in the Narragansett Bay National Estuarine Research Reserve.



V. Dispersal and recruitment limitation in invertebrate metacommunities

Members of the Bruno lab are also working on the effects of dispersal and connectivity on community structure in a variety of invertebrate metacommunities. For example, recent work at IMS has tested the effect of recruitment limitation and propagule flux on community composition and richness. If mobile invertebrate communities are saturated, then increasing the number and richness of immigrants should not affect resident richness, but could alter composition. They are also working in Moorea (Figure 3.25) and Mexico, using obligate inhabitants of branching corals (e.g. shrimp and crabs) as a model system to test several metacommunity models.



VI. Molecular genetic analyses of population structure, recruitment, and migration

Members of Peter Marko's lab routinely use molecular genetic tools to make inferences about the dispersal of marine organisms. Single snapshots of population structure, however, have proven inadequate for understanding the magnitude of dispersal over ecological



Figure 3.26: Deployment of larval collectors in sea grass beds.

timescales because most classical population genetic analyses yield values of gene flow that are time-averaged over thousands of generations. Thus, the approach the Marko lab has taken is to conduct genetic analyses across multiple generations and also compare the genetic composition of different life history stages, making possible inferences about the origins of new individuals recruiting into local populations. In-depth genetic analyses also make possible estimates of effective population size, which are vital for understanding the demographic significance of immigration estimates. Current work in the lab includes collaboration with Dr. Laura Rogers-Bennett (CA Dept. of Fish and Game) on the population structure of demersal fishes on the west coast of the US. One student is also working in collaboration with an animal behaviorist, Dr. Peter Klimley (UC Davis), to understand the genealogical structure within schools of migrating pelagic sharks in the Sea of Cortez and to compare population genetic estimates of dispersal to movement patterns of individuals documented with satellite tags.

VII. Larval dispersal and life history evolution: Lindquist lab

Long-distance larval dispersal vs. philopatry (i.e., remaining near the maternal adult) is an important life-history dichotomy that has substantial implications for levels of genetic exchange among populations. Thus, a better understanding of the factors affecting life-history evolution among marine species has utility for developing management and conservation strategies. Numerous hypotheses have been proposed regarding the selective forces, trade-offs, and constraints leading to the evolution of these different reproductive/dispersal strategies and their suites of associated traits. Research by the Lindquist group has shown that unpalatable secondary metabolites effectively protect larvae of diverse taxa of sessile marine invertebrates against predators. Regardless of their taxonomic affiliation (from sponges to tunicates), chemically defended larvae exhibit a combination of traits suggesting that their risk of predation is low: large size, bright coloration, daytime spawning, vulnerable morphology, and virtually no ability to elude predators. Further, chemically defended larvae tend to occur among brooding species and settle only minutes to hours after their release, although their large size would suggest they have energy reserves sufficient for a lengthy planktonic existence. Because their predation risk has been minimized, chemically defended larvae likely exhibit traits not associated with predator avoidance but that have a distinct selective advantage at other life stages. As examples, (i) large larvae become large juveniles and size is directly correlated with survival; (ii) daytime spawning allows chemically defended larvae to use strong photic cues to direct their settlement to refuges against grazers and UV exposure, typically shaded cracks and crevices in the substrate; and (iii) quick larval settlement places juvenile in a habitat that proved favorable for growth and reproduction.

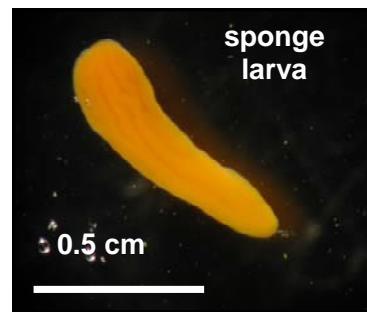


Figure 3.27