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In This Issue

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Synergy of mutualism

The persistence of cooperation between species, or mutualism, despite clear incentives for members to "cheat," is a classic problem in ecology. Traditional explanations focus on short-term, pairwise relationships between partners, even though many mutualists interact with multiple species throughout a lifetime. Todd Palmer et al. (pp. 17234–17239) monitored annual survival, growth, reproduction, and ant occupancy of 1,750 *Acacia drepanolobium* trees over 8 years, and constructed demographic models that related the trees' lifetime fitness to occupation by four mutualistic species of ants. The authors discovered that the trees demonstrated greatest lifetime fitness when sequentially occupied by the set of all four ant species. As part of a set, even parasitic ants that weakened trees while providing low protection increased *Acacia* lifetime fitness relative to sole occupation by nondamaging highly protective ants. The long-term benefits depended on the timing and year-to-year consistency of occupation, the authors report. While one ant species sterilized the trees, these ants tended to consistently colonize and protect young trees for which survival was critical, and ants that invited herbivore attack helped to promote reproduction in older, better established trees. The authors suggest that mutualistic fitness may depend nonlinearly on duration, contrasting benefits and costs, and ontogenetic timing of partner interactions. — J.M.

Two ant species battle for possession of a host plant.

Reversible adhesion method mimics aphid feet

Researchers have long admired the ability of some insects and small animals to navigate steep angles and diverse surfaces. Many reports of biomimicry in adhesive materials focus on fibrillar structures like those found on gecko feet, but Seok Kim et al. (pp. 17095–17100) report a switchable adhesive surface inspired by aphids, which use sagging and retraction of foot pads to enlarge or diminish contact area with a surface to modulate adhesion. The researchers fabricated a soft square polymer stamp with pyramid-shaped structures at each corner and tested the stamp's ability to pick up and release silicon slides. When the researchers pressed the stamp firmly against a slide, the soft pyramid tips collapsed like the end of a foam football, maximizing the surface area between the two materials and allowing the slide to be retracted. After the slide was lifted, the polymer pyramids returned to their original shape, leaving only the tips in contact with the slide, which was easily transferred to another receiving surface. Tests indicated that contact area changes allow the stamp's adhesion strength to vary by 1,000 times. The authors suggest that the method may help researchers to improve the reliability and repeatability of transfer printing during electronic device fabrication. — J.M.

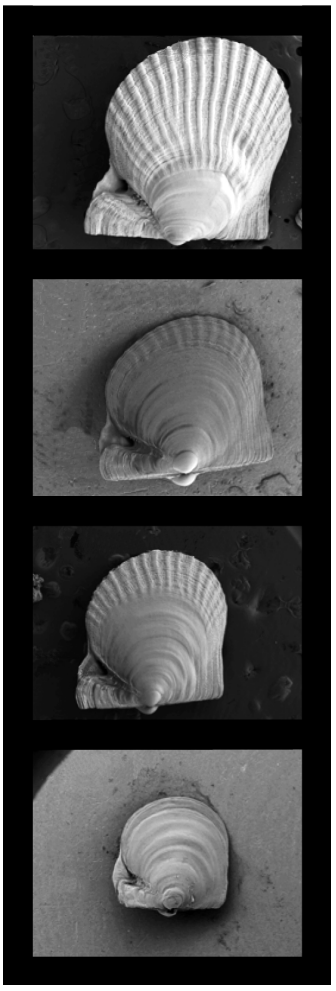


Image courtesy of Stephanie C. Talmage and Jim Quinn (Stony Brook University, Stony Brook, NY)

Individual scallop larvae.

Ocean acidification threatening shellfish larvae

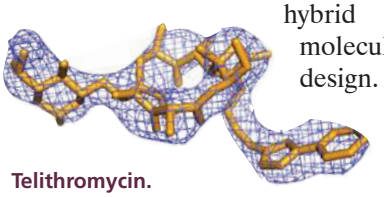
Previous studies have shown that rising atmospheric CO_2 levels have lowered the pH of the world's oceans. Stephanie Talmage and Christopher Gobler (pp. 17246–17251) conducted experiments to evaluate the past, present, and future impacts of ocean acidification on the larvae of two bivalve shellfish, *Mercenaria mercenaria* (Northern quahog) and *Argopecten irradians* (Atlantic bay scallop), that depend on ocean water pH to synthesize $CaCO_3$ shells. The authors report that larvae grown at preindustrial CO_2 concentrations of approximately 250 ppm had higher survival rates, grew faster, and displayed thicker and more robust shells than individuals grown at the modern concentration of about 390 ppm. Bivalve larvae that were grown at CO_2 concentrations above 400 ppm, which have been projected to occur later this century, exhibited malformed and eroded shells. The authors propose that ocean acidification during the past two centuries may be contributing to observed global declines of some bivalve populations, by interfering with the development and survival of larval shellfish. The findings may also provide insight into future evolutionary pressures of ocean acidification on marine calcifiers, according to the authors. — T.J.

Meta-analysis questions assumptions about predation and species diversity

Numerous studies have proposed theories for how predators maintain species diversity within communities of their prey. Most of these theories presuppose that the best competitor species are also the least able to defend against predation, but empirical evidence for this "competition–defense tradeoff" is limited. David Viola et al. (pp. 17217–17222) conducted a meta-analysis of 36 studies to examine the paradigm in plant communities, using a well-established mathematical model for the competition–defense tradeoff. As proxies for competitive ability and predator defense, the authors quantified species' responses to the experimental addition of resources and to the removal of predators, respectively. The authors report that negative relationships between competitive ability and defense, when present, influence species diversity as predicted by theory. But in a slight majority of cases, competitive ability and defense were positively correlated, indicating that the assumption of a competition–defense tradeoff in plant communities may not be broadly valid. The authors propose that while negative relationships between competition and defense can maintain species diversity, these relationships may be less common than thought. The findings support alternative theories in which the interaction between predation and competition can both enhance and reduce species diversity, according to the authors. — T.J.

Antibiotic-ribosome complex structure conserved across species

Antibiotics that inhibit ribosomal translation in bacterial cells have proven to be potent therapeutics, but the increasing prevalence of antibiotic-resistant pathogens has diminished these drugs' effectiveness. Recent studies have shown that structure-based drug design can potentially address resistance mutations by chemically linking pairs of known classes of ribosomal inhibitors, but discrepancies between crystallographic models of the structure of antibiotic-ribosome complexes have impeded hybrid molecule design.



Telithromycin.

To determine whether species-specific variation or experimental problems underlie these discrepancies, David Bulkley et al. (pp. 17158–17163) reexamined with crystallography the structure of the 70S ribosome of the eubacterium *Thermus thermophilus*, in complex with the macrolide antibiotics erythromycin, azithromycin, and telithromycin. The authors report that ribosomal structures in complex with *T. thermophilus* are indistinguishable from known complexes with the archaebacterium *Haloarcula marismortui*, and utilize contact points that are consistent with biochemical studies performed on *Escherichia coli*. The findings, according to the authors, support a mode of macrolide binding that is largely conserved across species, and may suggest that crystallography data quality and interpretation, rather than species specificity, explain the differences between published structural models. In addition, the authors identified a radically different structure of chloramphenicol in complex with *T. thermophilus* than the most widely accepted model. — T.J.