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A Hawaiian dark

rumped petrel

LETTERS

edited by Etta Kavanagh

Ongoing Threats to Endemic Species

CAROLYN GRAMLING'S ARTICLE "HAWAII'S CORAL TREES FEEL THE STING of foreign wasps" (News Focus, 16 Dec. 2005, p. 1759) highlights the risk posed by a nonnative wasp. This is only the most recent example of the vulnerability of endemic Hawaiian species to foreign invaders (1). For example, the continued existence of the Hawaiian dark rumped petrel (Pterodroma phaeopygia sandwichensis) depends on control of nonnative predators at its breeding colonies. Such threats can at best be managed rather than eliminated. Continuing conservation management thus is necessary to maintain such species.

The need for ongoing management to maintain species is one characteristic of what has recently been defined as "conservation-reliant species" (2). Such species face threats that are pervasive, recurring, and cannot be eliminated (e.g., nest parasites, predators, and dependence on disturbance habitat regimes). Without species-specific management, conservation-reliant species are at risk of extinction.

The need for ongoing management runs counter to traditional assumptions. In the Endangered Species Act, for example, Congress assumed that, after a species is listed, the threats to its existence will be identified and eliminated so that the species can be taken off the list as recovered. This assumption is proving to be false (2).

Given projections of increased globalization with its resulting homogenization and the concomitant fragmentation of native habitats, the threats of nonnative species can only be expected to increase. Thus, the threat posed to the survival of the coral tree by nonnative wasps, rather than being an interesting observation from an isolated island ecosystem, offers a window to the future challenges facing conservation biology in its efforts to conserve imperiled species worldwide.

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A Scientific Supercourse

IN THEIR RECENT EDITORIAL "DOING MORE FOR Kate" (16 Dec., 2005, p. 1741), T. Cech and D. Kennedy describe the need to revitalize science education. They wrote, "[We need to] teach better with less struggle." In an effort to empower higher education teachers, we built a Global Health Network Supercourse library of 2500 PowerPoint lectures on public health and prevention (1). The Supercourse, funded by the National Institutes of Health, has a network of more than 32,000 volunteer scientists from 151 countries.

The realization of the Supercourse is evidence that scientists in one field can network together to share their best lectures. Judging by the many thousands of teachers and students we are drawing to our Web site, we have been highly successful in improving training, research, and collaboration in the field of public health and prevention.

The first step to expanding the system to all of science is to build a collection of the best lectures from the top scientists, such as Nobel Prize winners and members of the U.S. Institute of Medicine and National Academy of Sciences of the United States. The ultimate expansion will

be to all scientists worldwide, with a faculty of a million and 300,000 lectures available to all. If we could achieve this goal, we would reduce the time it takes for scientific information to reach the classroom from 7 years to 7 minutes. At the same time, we could improve science training for millions, which is especially needed in developing countries. A Supercourse of Science would provide a new, more efficient means of teaching.

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Reference

1. Supercourse: Epidemiology, the Internet, and Global Health (www.pitt.edu/~super1).

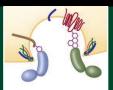
Marine Parks Need Sharks?

IN THEIR REPORT "FISHING, TROPHIC CASCADES, and the process of grazing on coral reefs" (6 Jan., p. 98), P. J. Mumby et al. showed that increased grouper biomass within the Exuma Cays Land and Sea Park (ECLSP) did not acutely impair the grazing capacity of parrotfish populations (a major prey item), alleviating concerns that marine reserves may cause trophic cascades that will impede the recovery of imperiled Caribbean coral reefs. Although Mumby et al. suggest that this finding was primarily due to coincident beneficial reserve effects for parrotfish, we suggest that the abundance of sharks in the ECLSP, due to limited shark fisheries in the Bahamas (1), may have been an important contributing factor.

Modeling suggests that sharks are important regulators of grouper biomass on Caribbean reefs (2). Thus, establishment of reserves in areas where sharks are severely overfished will release grouper from two key predators (humans and sharks), likely driving a more explosive increase in their biomass than observed in the ECLSP



Voltage-dependent proton channels



Botox receptor

540

where sharks are common. This in turn may drive an acute reduction in parrotfish biomass and grazing capacity (2).

Because many shark populations in the Atlantic are severely overfished and are unlikely to respond to protection as quickly as teleosts (3), there is an urgent need for comparative studies of trophic cascades and grazing in recently established coral reef reserves with and without healthy populations of sharks. Moreover, eco-



system-based fisheries management (4) and novel reserve designs [e.g., large, zoned reserves (5)] aimed at maintaining multiple ecosystem components, including these top predators (2, 5), are probably needed on

Caribbean coral reefs to maintain parrotfish grazing capacity and other critical ecosystem processes.

DEMIAN D. F. CHAPMAN, 1 ELLEN K. PIKITCH, 2 ELIZABETH A. BABCOCK³

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References and Notes

- 1. According to the Food and Agriculture Organization, reported shark landings in the Bahamas were <1 mt in 1999, which in part reflects a nationwide longline fishing ban.
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- 3. J. K. Baum et al., Science 299, 389 (2003).
- 4. E. K. Pikitch et al., Science 305, 346 (2004).
- 5. D. D. Chapman et al., Mar. Technol. Soc. J. 39, 42 (2005).

Response

WE DISAGREE WITH CHAPMAN ET AL.'S ASSERtion that potentially high levels of shark abundance were an important contributor to the observed increase in parrotfish grazing within the Exuma Cays Land and Sea Park (ECLSP).

First, a key finding of our study was that larger-bodied parrotfish species achieve an escape from grouper predation and therefore the interaction between groupers and parrotfish is surprisingly weak, reducing parrotfish grazing by only 4 to 8%. Although we cannot discount the possibility that even greater biomasses of grouper could eventually constrain grazing, current biomasses are already at least double that of other reported levels in the Caribbean.

Second, there is no empirical evidence that sharks regulate grouper biomass. In Bascompte et al. (1), the modeling of shark-grouper interactions ignores active prey selection and prey size refugia and may prove to be simplistic once studied empirically. Thus, we agree that the ecosystem functioning of sharks warrants further study.

Third, it is difficult to imagine that sharks would have a strong impact on groupers but not on parrotfishes. Indeed, Bascompte et al. (1) found that only four of 200 tritrophic relationships containing sharks, groupers, and parrotfish contained two or three strong inter-



actions. Of those four, two included direct negative impacts of sharks on parrotfish that would tend to counteract the positive indirect impact postulated by Chapman *et al.* Moreover, none of these tritrophic food chains involved the large-bodied species of parrotfishes, which undertake most of the grazing.

Even if sharks are unusually abundant in the Bahamas, their direct impacts are unlikely to differ across reserve boundaries because the shark species that most likely feed on groupers (and large parrotfish) range over large areas (2). Therefore, our results show that despite background shark predation, both groupers and parrotfish can achieve high biomasses when fishing levels are vastly reduced.

The key process driving these patterns is

Letters to the Editor

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fishing mortality. The impact of a reserve depends on both the complexities of trophic cascades within the reserve and the differential in fishing mortality across its boundaries [our Report, (3)]. Our paper and that of Bascompte *et al.* (1) show that trophic cascades can be highly complex and occasionally surprisingly weak. We also show that even minor reductions in fishing mortality can overwhelm the negative influences of weak trophic cascades. Therefore, reductions in fishing mortality within Caribbean reserves will almost always lead to a net increase in parrotfish grazing.

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A Not-So-Abrupt Departure

GIVEN R. A. KERR'S PAST RECORD OF OUTSTANDing science journalism, we were surprised by the unfortunate errors and omissions in his ScienceScope piece "Knock hockey," surrounding issues of how scientists gauge temperature over the last two millennia (10 Mar., p. 1359). The assertion that "[Michael] Mann made himself scarce throughout the proceedings, even abruptly departing as [Stephen] McIntyre stood to make a final comment" is incorrect. Mann's early departure had to do with his teaching obligations and a limited flight schedule. Mann was unaware of who may have been making comments as he departed following the official close of the presentation period, and he has been responsive to all requests made of him by the committee.



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Kerr incorrectly asserts that Mann and colleagues have "sworn off" the method used in their original work. As "sworn off" has the connotation of renouncing or conceding a flaw in past work, this is simply incorrect. Mann and colleagues have developed more sophisticated approaches, as should be expected over the decade that has passed since the original work was begun. The newer approaches yield an essentially indistinguishable result (1) but are immune to potential criticisms of the simpler, original methodology ("Estimates, uncertainties, and noise," Editors' Choice, 25 Nov. 2005, p. 1249). Kerr does make the key point that additional recent research provides "independent support for temperature trends resembling Mann's." He might also have noted that high-profile criticisms of Mann and colleagues' original work have now been shown to have been based on an incorrect implementation of their procedures (2).

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Mechanisms for Resistance in Soil

"SAMPLING THE ANTIBIOTIC RESISTOME" BY V. M. D'Costa *et al.* (Reports, 20 Jan., p. 374) presents evidence that multiple diverse mechanisms for resistance, particularly those that degrade antibacterials, are associated with microbes in different soil samples. The investigators assembled a group of 480 strains of Streptomyces and examined them for resistance to 21 different antibiotics, including all major types and targets of activity. The results were compelling; they found multiple mechanisms of resistance to both naturally occurring and synthetic antibiotics. Notably, a number of resistances were linked to enzymatic inactivation. The results of this Report indicate that there are mechanisms in soil for potentially resisting both current antibiotics and antibiotics that have yet to be developed. Analyzing soil can help determine the kinds of resistances that exist and the kinds of resistances that could eventually emerge clinically. The inactivation mechanisms for some of the older antibiotics have not yet become a clinical problem. Perhaps this type of analysis can shed light on whether they will in the future.

The second message we glean from this study is that new naturally occurring antimicrobials may be overlooked because they have been inactivated, either by the producer or by other organisms. Thus, we must work to develop new

methods for finding antibiotics in soils in order to protect the antibiotics from degradation. The findings of D'Costa *et al.* are of particular interest to the Reservoirs of Antibiotic Resistance project of Alliance for the Prudent Use of Antibiotics (1), which focuses on reservoirs of antibiotic resistance genes that have the potential to affect the clinical efficacy of antimicrobials. Soil bacteria are an important source of new antibiotics; this study clearly suggests that soils offer a predictive look at drug resistance as well.

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Reference

1. Alliance for the Prudent Use of Antibiotics (www.apua.org).

IN THEIR REPORT "SAMPLING THE ANTIBIOTIC resistome" (20 Jan., p. 374), V. M. D'Costa and co-workers show that a subset of the soil microbial flora belonging to the genus Streptomyces provides a reservoir of resistance determinants (the antibiotic resistome) that have the potential to be mobilized into the microbial community. The concept of a nonmedical environmental gene pool has been recognized (1, 2). Similar studies in other environments have yielded similar results, and we caution against the perception that microbial gene transfer occurs within strict environmental compartments. Twenty years ago, resistance profiles of 2000 fecal and nonfecal bacterial isolates from lakes of differing eutrophic status were assessed (3, 4). It was shown that although a large lake directly received sewage effluent, the incidence of antibiotic resistance was higher in the bacteria isolated from the lake water than in those from the effluent. Furthermore, the incidence of antibiotic resistance in aquatic bacteria isolated from the lake was lower than in those isolated from two remote upland tarns. Although they were not totally isolated from man and other animals, the tarns did not receive sewage or other effluents and therefore the results were surprising. A possible explanation might be that increased resistance is associated with adaptation to nutrient-poor environments (3, 4). This seemingly passive resistance should be taken into account in the context of the D'Costa *et al.* study, as it would elevate the significance of the resistome. Furthermore, a recent study by Riesenfeld *et al.* (5), cited by D'Costa *et al.*, concluded that "soil bacteria are a reservoir of antibiotic resistance genes with greater genetic diversity than previously accounted for."

It is apparent that the soil environment resistome [D'Costa et al. and (5)] is a component of a global resistome. Bacteria do not abide by human-imposed boundaries, and in considering environmental antibiotic resistance, terrestrial and aquatic environments should not be perceived as separate compartments of the environment. Interaction at a microbial level is not confined to these boundaries (6, 7). We reiterate the view of D'Costa et al. and the accompanying Perspective by A. Tomasz (20 Jan., p. 342): If the extent of the resistome implied by local studies [D'Costa et al. and (3, 5)] is translated to a global scale, then we vastly underestimate the capacity of the global gene pool to respond to our use of antibiotics [D'Costa et al. and (5)].

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TECHNICAL COMMENT ABSTRACTS

COMMENT ON "Reconstructing Past Climate from Noisy Data"

Eugene R. Wahl, David M. Ritson, Caspar M. Ammann

von Storch *et al.* (Reports, 22 October 2004, p. 679) criticized the ability of the "hockey stick" climate field reconstruction method to yield realistic estimates of past variation in Northern Hemisphere temperature. However, their conclusion was based on incorrect implementation of the reconstruction procedure. Calibration was performed using detrended data, thus artificially removing a large fraction of the physical response to radiative forcing.

Full text at www.sciencemag.org/cgi/content/full/312/5773/529b

RESPONSE TO COMMENT ON "Reconstructing Past Climate from Noisy Data"

Hans von Storch, Eduardo Zorita, Julie M. Jones, Fidel González-Rouco, Simon F. B. Tett

We implemented a proxy-based method for reconstructing temperatures in the past millennium in simulations with two climate models using the pseudoproxy approach. We show results for detrended and nondetrended calibration using white-noise and red-noise pseudoproxies with realistic noise levels. In all cases, the method underestimates the low-frequency variability of the simulated Northern Hemisphere temperature.

Full text at www.sciencemag.org/cgi/content/full/312/5773/529c