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The Threat to Cone Snails

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Science **302**, 391b (2003);
DOI: 10.1126/science.302.5644.391b

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LETTERS

Letters to the Editor

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The Threat to Cone Snails

AROUND 500 SPECIES OF CONE SNAILS (Conidae) inhabit tropical coral reefs and associated habitats, including mangroves. For centuries, they have been coveted for their gorgeous shells, but we are now discovering that their value as living organisms is enormous. Each species produces an estimated 50 to 100 distinct toxins to immobilize prey (*1*). These toxins are exquisitely selective in their receptor binding sites (*1*), and this is generating a biomedical research boom, with over 2600 studies published since 1980.

Among many discoveries, conotoxins have helped characterize nicotinic acetylcholine receptor subtypes in mammalian heart muscle, which mediate heart rate and contractility, as well as in skeletal muscle and brain. Many subtypes of calcium, potassium, and sodium ion channels have also been characterized using conotoxins (*2*).

In small-cell lung cancer, activation of nicotinic acetylcholine receptors and voltage-dependent calcium channels in tumor cell membranes promotes tumor cell proliferation. Conotoxins that block these activation receptors and ion channels, and that bind to antibodies that form to attack them, may be effective in early detection (*3*) and perhaps also in treatment of this devastating cancer. One synthetic conotoxin is in Stage III clinical trials for treatment of intractable pain (*4*).



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Cone snails are coming under intensive threat in the wild. Their habitats are being degraded and destroyed by coastal development, fishery overexploitation, pollution, disease epidemics, and global climate change (*5*). An estimated 26% of the planet's coral reefs have already been seriously damaged or destroyed (*6*) and 50% of the world's mangroves cleared.

The risk of global extinction is highest for species with narrow geographic distributions. We found that 20.7% of 386 cone snail species had global ranges encompassing less than 3500 km^2 of reef, equivalent to a single atoll 66 km across (*7*). People threaten reefs in more than half the ranges of 69% of species and all of the ranges of 5.8% of species (*7*).

Cone snails are intensively exploited for the ornamental trade and research, but no records are kept of numbers taken from the wild. Hundreds of tons of shells are imported into the United States and Europe annually, representing millions of individuals in trade (*8*). We estimate that researchers alone may be using hundreds of thousands of animals yearly.

Habitat loss and escalating, uncontrolled exploitation make a lethal combination that today threatens with extinction cone snails and many other species of biomedical interest. Habitat protection will require pollution mitigation and control of coastal development and destructive fishing (*5*). Coral reefs also require action at the global level to mitigate climate change. Major exporting nations currently have no effective monitoring or management. International markets can develop rapidly in the modern world, which means that wild populations can be decimated before regulatory agencies see any need to protect them. For this reason, we believe that all internationally traded organisms (whether alive or dead) must be monitored, regardless of whether they are currently listed as threatened. This would allow countries to identify emerging markets and act early enough to prevent depletion and could be achieved by extending the Convention on International Trade in Endangered Species (CITES) to cover all wild-caught species. Meanwhile, cone snails should be added to Appendix II of CITES, which would require trade monitoring and management of exploitation.

Researchers and biomedical companies need codes of conduct for responsible use of wild organisms that ensure collection is sustainable, and shareholders can hold companies to account. To reduce demand on wild sources, companies could finance development of culturing techniques and invest in early synthesis of promising compounds. They could promote sustainable collection by funding research and monitoring and supporting protected areas. Curio retailers could adopt recommendations like those developed for sustainable trade in aquarium fish (*9*).

With up to 50,000 toxins, cone snails may contain the largest and most clinically important pharmacopoeia of any genus in nature. To lose them would be a self-destructive act of unparalleled folly.

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9. See www.aquariumcouncil.org.

Coral Reef Decline in the Caribbean

THE ANALYSIS BY T. A. GARDNER *ET AL.* OF THE decade-scale trajectory of reef decline in the Caribbean ("Long-term region-wide declines in Caribbean corals," Reports, 15 Aug., p. 958) is an important contribution, providing a degree of quantification and spatiotemporal description that has been sorely needed. Several of the points implicit or explicit in the paper merit additional comment.

There is a strong and highly significant negative correlation between the logarithms of the number of studies reported (Y) and the percentage of coral cover observed (X)

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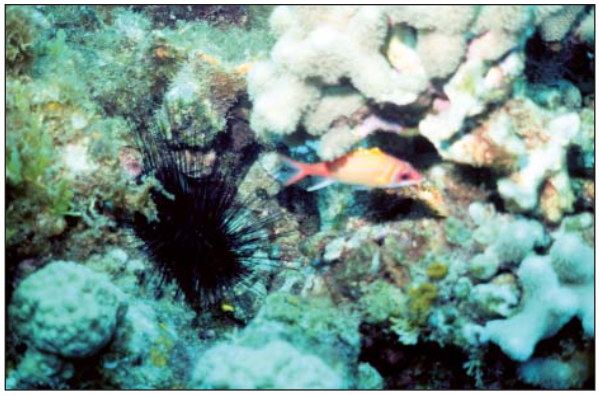
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(numbers derived from Gardner *et al.*'s Fig. 2: $\log Y = -1.53 \log X + 3.29$, $r = -0.825$, $P < 0.000001$). Although we do not suggest that research causes reef degradation, the reverse is demonstrably true; reef degradation has resulted in both motivation and resources for surveys. Because much problem-oriented funding has a specific focus that is not scientifically neutral, this has the potential to skew the sampling in either direction—either by oversampling degraded reefs or by providing incentives to seek out examples of preservation or recovery. The final decade (1992–2002) of the time period considered has major changes in the number of reports and is particularly vulnerable to such effects.

Shifts in technology may result in baseline changes; meeting presentations and anecdotal reports suggest that video transects give systematically higher cover estimates than line transects, so the apparent recent slowing of degradation could reflect an intercalibration problem.



Although we acknowledge the importance of local and regional anthropogenic pressures, we feel that climate-related factors are too casually dismissed, particularly in light of the acknowledged "partial synchrony." The Caribbean has long been recognized as a region particularly vulnerable to global change [(*1*), p. 110]. Elevated temperatures have been linked to a reduction in the reproductive potential of corals (*2*), which would contribute to net loss over time. Furthermore, the devastating diseases experienced by the region's corals have been argued to have climatic triggers or relationships (*3*, *4*).

Although we concur with the overall findings, we suggest that the possibility of recent amelioration and the inferences about the relative roles of climatic and local human factors should be viewed with caution.

ROBERT W. BUDDEMEIER[1] AND JOHN R. WARE[2]
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Response

BUDDEMEIER AND WADE SUGGEST THAT THE declines in Caribbean coral cover that we documented in our Report can be partly explained by the fact that recent increases in research activity have been biased toward already degraded reefs. We explicitly analyzed this potential bias in our paper by omitting the Florida Keys Monitoring Project, which accounted for approximately half of the data points between 1996 and 2001, i.e., part of the period highlighted by Buddemeier and Wade as being most susceptible to this bias and which focused on largely degraded reefs (*1*). This had no effect on the pattern of decline (see our fig. 2 and Supplementary Online Material). If the regression analysis of Buddemeier and Wade is repeated omitting the Florida project, the relationship between sample size and average coral cover is weaker ($\log Y = -0.32 \log X + 1.63$; $r^2 = 0.20$; $P = 0.03$). With unlogged data, it becomes marginally nonsignificant ($Y = -0.21X + 23.31$; $r^2 = 0.14$; $P = 0.06$) and accounts for only 14% of the variance. Moreover, in our survey, we included data irrespective of study purpose, thus including heavily degraded sites as well as sites that were chosen because they were as undisturbed as possible [e.g., the CARICOMP sites (*2*), a large-scale program that began in the 1990s]. Despite our unbiased approach to site selection, both the mean and, more importantly, the between-site variance in coral cover (our Fig. 2) have remained consistently low. Given that monitoring of coral reefs in the Caribbean has increased greatly and that reef condition has declined over the past three decades (*3*), degraded sites will inevitably have become more frequent in our sample in recent years; however, there is nothing in our data set to suggest that degraded sites were sampled disproportionately to their frequency at any point during the decline.

Regarding the potential for temporal changes in survey methods to cause the observed pattern of decline, once again we explored this in our Report (see Supplementary Online Material) and found that overall rates of coral cover decline did not differ among survey methods. This result has been upheld in a separate field study that showed that different methods generated similar estimates of hard coral cover (*4*). The

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apparent slowing of degradation in some subregions is likely to be due to the earlier loss of more susceptible species [e.g., (*5*)], although we emphasize that there is no clear abatement in the overall rate of loss in the 1990s (our fig. 3C).

We agree with Buddemeier and Wade that climate change is a threat to coral reefs. However, although factors directly related to climate change (e.g., bleaching) have affected Caribbean corals at subregional scales [e.g., (*6*)], their role in contributing to observed coral declines across the entire region is not yet detectable, at least to the extent that it is for other regions of the world (*7*). In highlighting the potential for synergy between climate change and other threats, such as chronic overfishing and pollution, we stressed utmost caution in dismissing the importance of the potential indirect effects suggested by Buddemeier and Wade. Furthermore, we emphasized that the ability of Caribbean coral reefs to cope with the threat of future climate change may be irretrievably compromised.

TOBY A. GARDNER,[1,3] ISABELLE M. CÔTÉ,[1] JENNIFER A. GILL,[1,2,3] ALASTAIR GRANT,[2] ANDREW R. WATKINSON[1,2,3]

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CORRECTIONS AND CLARIFICATIONS

Perspective: "It's never too late" by J. W. Vaupel *et al.* (19 Sept., p. 1679). In the figure, the maximum value of the *y* axis (annual probability of death) should read 0.50, and not 0.05, as printed.

TECHNICAL COMMENT ABSTRACTS

COMMENT ON "'Stemness': Transcriptional Profiling of Embryonic and Adult Stem Cells" and "A Stem Cell Molecular Signature" (I)

Nicolas O. Fortunel,* Hasan H. Otu,* Huck-Hui Ng,* Jinhui Chen, Xiuqian Mu, Timothy Chevassut, Xiaoyu Li, Marie Joseph, Charles Bailey, Jacques A. Hatzfeld, Antoinette Hatzfeld, Fatih Usta, Vinsensius B. Vega, Philip M. Long, Towia A. Libermann, Bing Lim

Ramalho-Santos *et al.* (Reports, 18 Oct. 2002, p. 597) and Ivanova *et al.* (Reports, 18 Oct. 2002, p. 601) proposed that universal "stemness" genes may confer the common characteristics of stem cells. We have generated a third list of putative "stemness" genes. Although the overlap among the three studies of genes for individual stem cell types was significant, overlap of general "stemness" genes encompassing different stem cell types appeared minimal. We suggest and discuss reasons for this marked discrepancy.

*These authors contributed equally to this work.

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COMMENT ON "'Stemness': Transcriptional Profiling of Embryonic and Adult Stem Cells" and "A Stem Cell Molecular Signature" (II)

Alexei V. Evsikov and Davor Solter

Ramalho-Santos *et al.* and Ivanova *et al.* compared several types of stem cells using DNA arrays and claimed to identify a common set of "stemness" genes. There is, however, negligible overlap between the lists of "stemness" genes reported from two different laboratories, which indicates that this approach, though theoretically useful, is far from foolproof.

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RESPONSE TO COMMENTS ON "'Stemness': Transcriptional Profiling of Embryonic and Adult Stem Cells" and "A Stem Cell Molecular Signature"

Natalia B. Ivanova, John T. Dimos, Christoph Schaniel, Jason A. Hackney, Kateri A. Moore, Miguel Ramalho-Santos, Soonsang Yoon, Yumi Matsuzaki, Richard C. Mulligan, Douglas A. Melton, Ihor R. Lemischka

Global gene expression analyses in stem cells are providing much information. To interpret this information, it is crucial to precisely define the biological properties of the candidate stem cell populations. Constructive integration of independent data sets will be necessary to identify core components and architectures of stem cell regulatory networks.

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