<< Toward Sustainable Fisheries

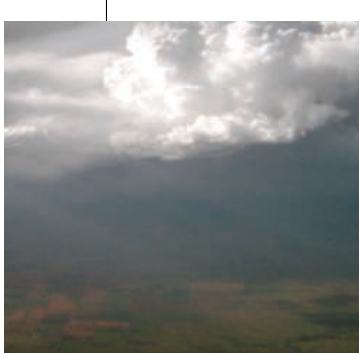
The currently observed crisis of overcapacity, overfishing, and accompanying problems of habitat destruction and bycatch, lies in competition among fishers. **Beddington *et al.*** (p. 1713) review how sustainable fisheries can be achieved if management strategies are adopted that remove subsidies and give individual fishers a right to a proportion of the total catch. By removing competition, fishers should then be prompted to act to sustain the entire fishery because, as the common fish stock improves, each individual's quota will increase. **Persson *et al.*** (p. 1743) studied fish stocks in Lake Takvatn in northern Norway, where a population of stunted Arctic charr of little worth to fisheries had replaced the mixed population of brown trout and charr. Fifteen years after the removal of 31 metric tons of fish, the size distribution of charr had shifted into a new steady state. More small fry were produced that made better prey for trout, whose population then recovered. Thus, culling of larger, slowly reproducing prey, rather than reintroductions of mature predators, might be effective in reversing an apparently collapsed fish stock.

Effective Translation

In large molecules, vibrational excitation of a particular bond often does not cause it to break because the spreading of vibrational energy across the entire framework is typically faster than bond-cleaving reactions. Smaller molecules, such as di- and triatomics, that have fewer vibrational modes are more likely to cleave particular bonds through vibrational excitation. **Yan *et al.*** (p. 1723; see the Perspective by **Crim**) have discovered that, contrary to this paradigm, when CHD_3 collides with Cl atoms to form CD_3 and HCl, translational energy promotes the reaction as effectively as selective excitation of the C–H stretch vibration. The study relied on precise control of the gas-phase collision energies, and suggests that even relatively small molecules have highly complex energy distribution dynamics.

Carbon Uptake Reconsidered

Approximately half of the CO_2 emitted by fossil fuel burning remains in the atmosphere; the rest is absorbed by the ocean or incorporated by the terrestrial biosphere in roughly equal measures. Two studies reassess the uptake of CO_2 by these sinks (see the Perspective by **Baker**). In order to understand the relative role of different parts of the terrestrial biosphere as carbon sinks, global measurements of atmospheric CO_2 concentration must be interpreted by "inversion" models to determine how uptake, emission, and transport contribute to the seasonal and regional differences. Previous studies have suggested that there must be a strong carbon sink in the Northern Hemisphere, and that the tropics are a net carbon source. **Stephens *et al.*** (p. 1732) report that global vertical distributions of CO_2 in the atmosphere are not consistent with that interpretation but are more consistent with models that show a smaller Northern Hemispheric carbon sink and possibly strong carbon uptake in the tropics. The rate of uptake of CO_2 depends on the difference between the partial pressure of CO_2 in the atmosphere and that which would exist if the ocean and the atmosphere were at equilibrium.



Le Quéré *et al.* (p. 1735, published online 17 May) report that the rate of uptake by Southern Ocean, one of the most important CO_2-absorbing regions, has slowed relative to what would be expected based solely on how fast the concentration of atmospheric CO_2 has risen since 1981. They attribute this shortfall to an increase in windiness over the Southern Ocean that increases the outgassing of natural CO_2. The increased windiness has also been ascribed to human activity, and the authors predict that this relative trend will continue.

Ferrihydrite Unfurled

The iron oxyhydroxide compound ferrihydrite, which is found in a wide range of natural sediments, is of interest for its effectiveness as a heavy metal scavenger in wastewater treatment, as well as its relation to biochemical iron sequestration motifs. However, its nanocrystalline morphology has impeded efforts to determine its precise structure. **Michel *et al.*** (p. 1726; see the Perspective by **Penn**; published online 24 May) have modeled pair distribution functions extracted from x-ray scattering data to obtain the lattice structure of the nanometer-scale particles. Their analysis supports a single hexagonal phase, with 80% of the iron ions occupying octahedral coordination sites in the ideal lattice.

Tropical Disease Vector Genome

The mosquito *Aedes aegypti* is responsible for the transmission of dengue and yellow fever, which together affect more than 50 million people each year. **Nene *et al.*** (p. 1718, see the cover and see the Perspective by **Chadee *et al.***) present the genome sequence for *Ae. aegypti*, which reveals extensive gene conservation with the malaria vector mosquito, *Anopheles gambiae*.

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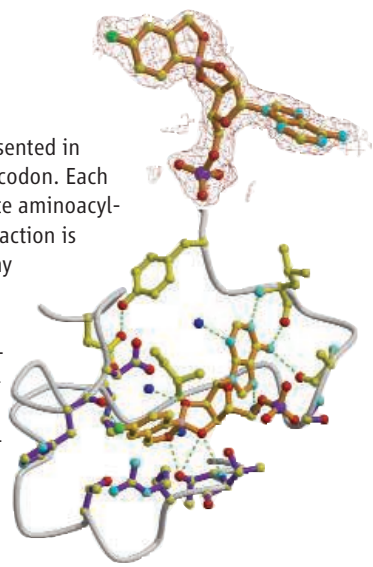
As representatives of the two major mosquito subfamilies, the differences observed should underlie inherent biological traits including blood-feeding preferences, host-seeking behavior, and the ability to transmit specific pathogens. **Waterhouse *et al***. (p. 1738) examined the evolution of innate immunity by comparing the genome of *Ae. aegypti* with the malaria mosquito, *An. gambiae*, and the fruit fly, *Drosophila melanogaster*, which represents a genetic outgroup. Different phases of immune signaling (recognition, modulation, signal transduction, transcriptional activation, and effector production) revealed different evolutionary dynamics.

In Support of Darwin

Darwin suggested that closely related species are less likely to coexist in communities because of shared resource requirements. Using a model plant-mycorrhizal system, **Maherali and Klironomos** (p. 1746) examined the effect of phylogenetic relatedness of mycorrhizae on roots of *Plantago* on the species richness that persisted 1 year after inoculation, on mycorrhizal production, and on productivity of the host plant. As predicted, community biodiversity was greatest when fungal species were more distantly related. Moreover, these species-rich communities had higher productivity than species-poor communities consisting of closely related taxa.

Boron Boost to Antifungal Agents



Transfer RNAs (tRNAs) recognize the genetic code represented in messenger RNAs, with tRNAs specific for each different codon. Each tRNA is charged with the correct amino acid by a cognate aminoacyl-tRNA synthetase (AARS). Because the accuracy of this reaction is vital in maintaining the fidelity of the genetic code many AARSs have evolved the ability to hydrolyze tRNAs aminoacylated with the incorrect amino acid, so-called "editing." **Rock *et al***. (p. 1759) show that a benzoxaborole antifungal drug can inhibit yeast LeuRS by interfering specifically with the editing reaction. The boron atom in the oxaborole ring is critical for this effect, suggesting that incorporating boron into small molecule antifungals may lead to the production of additional classes of therapeutic agents.

Actin to Safeguard Transcription

Besides its well-characterized function as a cytoskeletal component, actin has emerged as a regulator of nuclear processes, including transcription. MAL, a coactivator of the transcription factor serum response factor (SRF), directly binds to and senses cellular levels of monomeric G-actin. MAL responds to serum-induced depletion of cellular G-actin with nuclear accumulation and SRF activation. **Vartiainen *et al***. (p. 1749; see the Perspective by **Wu and Crabtree**) report that MAL rapidly shuttles between the nucleus and cytoplasm in resting cells. Actin binding in the nucleus targets MAL for efficient nuclear export and, furthermore, prevents activation of SRF during the short time that MAL spends in the nucleus. When growth factor stimulation interferes with actin binding, this lock on MAL activity is released.

Resurrecting Infections Past

Our genomes contain endogenous retroviruses that can be regarded as an archaeological record of past infections. **Kaiser *et al***. (p. 1756) undertook a genetic excavation to explore why chimpanzee and gorilla genomes, but not those of humans, contain hundreds of copies of a particular endogenous retrovirus. They revived the virus's core protein from the chimp genome and found that infection of cells with chimeric viruses containing this protein could be inhibited by the human antiviral factor, TRIM5α. However, the same protein had relatively poor activity against human immunodeficiency virus type 1 (HIV-1), contrasting with the efficiency primate TRIM5α against both viruses. It seems that by acquiring resistance to one ancient virus, humans became more susceptible to HIV-1.

CREDITS: ROCK *ET AL.*

Published by AAAS