



Communities Under Climate Change

David Nogués-Bravo, et al. Science **334**, 1070 (2011); DOI: 10.1126/science.1214833

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degradation of paternal mitochondria.

The findings of Sato and Sato and Al Rawi *et al.* help to explain how paternal mitochondria and mtDNA are destroyed, but why they are destroyed remains a mystery. Is heteroplasmy, the occurrence of more than one mtDNA genotype, dangerous for the developing embryo? Or is the degradation of paternal mitochondria merely a primitive defense in which the fertilized oocyte views the paternal mitochondria as a potentially dangerous intruder that must be destroyed? In this scenario, the degradation of paternal mitochondria by selective autophagy may parallel the use of this pathway by somatic cells to defend themselves against

invasive bacteria. It also may be that paternally derived mitochondrial factors, rather than heteroplasmy per se, are detrimental to the developing embryo. Sato an Sato found that 95% of animals lacking *lgg-1* die at or before the L1 larval stage, suggesting that persisting paternal mitochondria may harm development during embryogenesis. However, this lethality may be due to other zygotic effects of loss of LGG-1.

The results of Sato and Sato and Al Rawi et al. in C. elegans should help guide investigation into how, and perhaps even why, mammalian mitochondrial DNA comes mainly from mothers. Such an understanding will have far-reaching implications for human

developmental biology and for unraveling the pathogenesis of mitochondrial diseases.

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ECOLOGY

Communities Under Climate Change

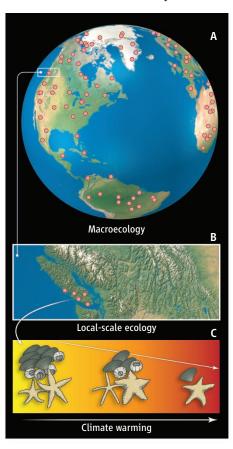
David Nogués-Bravo and Carsten Rahbek

The distribution of species on Earth and the interactions among them are tightly linked to historical and contemporary climate, so that global climate change will transform the world in which we live. Biological models can now credibly link recent decadal trends in field data to climate change, but predicting future impacts on biological communities is a major challenge. Attempts to move beyond general macroecological predictions of climate change impact on one hand, and observations from specific, local-scale cases, small-scale experiments, or studies of a few species on the other, raise a plethora of unanswered questions. On page 1124 of this issue, Harley (1) reports results that cast new light on how biodiversity, across different trophic levels, responds to climate change.

Some species are already moving toward the poles (2) or to higher elevations (3) as a result of climate change, but shifts to lower elevations are also known (4). Other species will cope with climate change in situ or perish. But how can we predict how particular species will react? Species interactions shape communities and ecosystem functions, but how will these interactions change as species evolve, migrate, or become extinct when the climate changes? The mechanistic links

Center for Macroecology, Evolution and Climate, University of Copenhagen, Copenhagen, Denmark. E-mail: dnogues@bio.ku.dk

between climate and the ecological processes that determine species diversity across spatial and temporal scales remain poorly understood. Neither do we fully understand



An interdisciplinary study shows how animal communities respond to climate change.

the consequences of those changes for the structure and dynamics of food webs and the extent to which they matter for humans.

Understanding of community composition and dynamics has traditionally come from two sources. The community ecology approach usually relies on local, smallscale studies and on manipulative experiments, with typical plot sizes of 1 m² to 1 ha, across small environmental gradients. This approach has yielded important insights into small-scale population and community dynamics (5, 6) and more recently into the functions of species within complex ecological networks, including the coevolution and extinctions of species across such networks (7, 8). In contrast, macroecological studies have usually focused on patterns along global environmental or geographical gradients, with typical sample size ranging from 25 to 40,000 km². This approach has unveiled the role of regional species pools, some major determinants of species diversity at specific spatial scales, and the effects of large-scale processes on local species assemblies (9, 10), including the footprints of Late-Pleistocene extinctions (50,000 to 11,700 years ago) (11, 12).

Biological effects of climate change. Studying species interactions at the local scale along their climatic niche gradient within a region (**B**) and across different biogeographic regions (**A**) will better predict biodiversity responses to climate change (**C**).

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Harley examines how species-specific climatic tolerances, climatic niches, and species interactions drive species distributions, abundances, and species richness. Focusing on a predator (sea stars) and its prey (mussels and barnacles), he integrates information on changes in the prey and predator distribution between 1957 and 2010, a period during which the local climate warmed by almost 1°C. The author also analyzes predator removal experiments to elucidate species responses across a whole community.

Previous studies have either focused on specific taxa, localities, or period of time, or have been so general that many relevant macroecological details remained implicit. Harley overcomes many of these limitations by using a more comprehensive toolbox borrowed from both community ecology and macroecology. By analyzing the change in the amount of suitable habitat for mussels and barnacles due to climate change since 1957, combined with the experimental removal of the predator, Harley identifies responses of intertidal communities, including local extinctions, to different stress factors such as temperature increase and predator pressure. He further demonstrates that those changes have a substantial impact on the composition and richness of communities of up to 37 intertidal species, which depend on the cool and moist conditions created by mussel beds, that is, on the microclimate induced by a dominant species in the community.

Imagine community ecologists moving away from small-scale, single-locality research and beginning to use Harleyinspired study designs at macroecological scales, with thousands of sites in different biomes across biogeographical regions (see the figure). If the resulting ecological data are combined with physiological and genetic data, such a framework could answer highly relevant questions on the physiological limits of populations and on the extant plasticity and genetic variation, helping to predict which species can adapt to a changing climate. Such research designs would further benefit from manipulative climate-change experiments across trophic levels. Imagine also macroecologists incorporating these insights into their models to move beyond statistical correlations (13) toward explaining biodiversity patterns by a mechanistic evaluation of processes across spatial and temporal scales (14). Such large-scale, interdisciplinary, and cross-scale approaches are needed to predict more accurately and precisely how biodiversity will respond to ongoing global climate change.

Such a change from the traditional research and funding structure in ecological disciplines, from small individual grants to large global consortia, is by no means trivial. It would require substantial, if not dramatic, changes in the distribution of funds, the criteria by which they are awarded, how researchers collaborate, and (not least) how scientific credit is partitioned between groups and individuals. It is time for ecologists to discuss the pros and cons of such changes, because moving in this direction will allow us to better cope with the research challenges of our changing world.

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ASTRONOMY

Cosmic-Ray Origins

W. Robert Binns

The detection of distributed, high-energy gamma-ray emission points to cosmic-ray acceleration in a superbubble.

The origin of cosmic rays has been a mystery since it was conclusively shown by Victor Hess (1) that ionizing radiation impinges on Earth from space, and subsequently shown by Arthur Compton (2) that this cosmic radiation is primarily composed of charged particles. Since that time, there has been great interest in understanding the origin of these cosmic nuclei accelerated to nearly the speed of light—identifying the source of the material that is accelerated, the nature of the accelerator, and the mechanism by which the source material is injected into the accelerator. On page 1103 of this issue, Ackermann et al. (3) report observations with NASA's Fermi Large Area Telescope that are directly related to the origin of cosmic rays. They identified distributed emission of gamma-rays over the energy range of 1 to 100 GeV in the Cygnus X region of the sky with a "cocoon" of freshly accelerated cosmic rays.

The direct measurement of cosmic rays—their elemental and isotopic composition, and their energy spectra—has also provided important clues to the origin of cosmic rays since they bear the direct imprint of

Department of Physics and the McDonnell Center for the Space Sciences, Washington University, St Louis, MO 63130, USA. E-mail: wrb@wustl.edu

their nucleosynthesis, injection, and acceleration. However, because our galaxy and all of space is riddled with magnetic fields, and because cosmic rays are charged particles, their arrival directions at Earth do not usually point back to their sources. By contrast, instruments that detect gamma rays do point back to the source where they are produced. Gamma-ray measurements can therefore indicate specific sites of acceleration, and in some cases can distinguish between electron and hadron acceleration processes.

The cocoon identified by Ackermann et al. extends ~50 parsec from the Cygnus OB2 association—a very large cluster of more than 500 stars, each with mass greater than 10 solar masses (M_{\odot}) (3) (called types O and B stars)—to γ Cygni, a young (age ~7000 years) supernova (4). Near γ Cygni is NGC 6910, an open cluster containing ~75 massive stars. The gamma-ray emission is most intense in Cygnus OB2 and γ Cygni. After subtraction of a modeled background emission spectrum, including the point source emission from γ Cygni, most of the remaining distributed emission extends along a line from Cygnus OB2 to NGC 6910, with peak emission coming from those stellar clusters. The morphology of the enhanced emission region is bounded by regions of 8 μm