Père David's deer (*Elaphurus davidianus*) remain at risk after rewilding.

**LETTERS**

PHOTO: ZHENYU ZHONG

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# Reversing extinction in China's Père David's deer

Père David's deer (*Elaphurus davidianus*) became extinct in the wild in China in the late 19th century (*1*), but after reintroduction three decades ago, the population has grown to more than 8000 individuals, with at least 2420 living in the wild in China (*2, 3*). This species reintroduction is considered one of the most successful stories in the world (*4*); it provides a watershed example of biodiversity conservation best practices for the upcoming UN Decade on Ecosystem Restoration. However, the species needs continued support to thrive.

Heavily endangered as a result of overhunting and habitat loss (*1*), the last of China's Père David's deer had been pillaged by Europeans and sent to zoos across Europe before the Qing Dynasty fell in 1912 (*1*). In 1985, nearly a century later, 38 deer were donated back to China for re-wilding (*5*). After the reintroduction of an additional 39 deer from zoos in England in 1986 (*6*), the population in Dafeng Milu National Nature Reserve grew to 5681 individuals (*2*). Père David's deer populations now cover all habitats in which they lived before the species' extinction in the wild.

The conservation of Père David's deer, however, faces ongoing challenges. The populations within China lack genetic diversity and are therefore susceptible to multiple risks, such as high miscarriage rates, reduced life span, and diseases (*4*). Wild populations are also limited by environmental constraints, keeping population numbers low and hindering stability. Moreover, there is no master plan for Père David's deer conservation at the national level and thus no coordinated monitoring platform or guidelines for overcoming inbreeding and environmental obstacles. Finally, there is a lack of international cooperation between researchers in China and abroad. National and international cooperation to strengthen monitoring of Père David's deer populations and to develop a shared database and germplasm databank between all countries with wild populations would be a major step forward for securing the long-term conservation of this species.

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# A marine biodiversity plan for China and beyond

Although China has taken important steps to protect biodiversity, including a 10-year fishing ban in inland waters (*1*) and a summer fishing moratorium in oceans (*2*), the country's marine biodiversity protection needs a plan to better ameliorate the threats to marine life, including the deterioration of ecosystems and loss of biodiversity (*3*). By 2019, China had established 271 protected areas that include oceans (*4, 5*). They cover 12.4 million hectares of ocean but represent only 4.1% of China's maritime area (*4, 5*), far below the 10% goal set by Aichi Target 11 (*6*). In contrast, China has established protected areas covering 18% of its total terrestrial habitats and inland waters, more than the 17% goal of Aichi Target 11 (*6, 7*). Nearly all of China's marine protected areas (MPAs) are in coastal and continental-shelf regions (*5*), and their ability to protect migratory fishes and mammals is likely hindered by their fragmentation (*4*). The current MPA system cannot keep up with the demand for effective marine biodiversity protection. China needs to accelerate the optimization and integration of existing MPAs and establish new MPAs that use the national parks model (*8*) to strengthen the protection of marine biodiversity.

Given the connectivity of the ocean and the migratory ability of animals, MPAs should target protection of their key habitats such as breeding or spawning sites. Because shortfalls in effective management can diminish protected areas' ability to stem biodiversity loss (*9*, *10*), MPA policies such as fishing intensity limits and seasonal fishing moratoriums need to be better enforced. In China's protected areas management system, the national park model emphasizes the integrity of the ecosystem and prioritizes the integration of one or more complete ecosystems. Designating areas as national parks can break through administrative obstacles. The current MPA system should be expanded to add more and larger national parks in key ecosystems as determined by scientific data (*8*). These areas likely include the Changshan islands, the Nanji and Beiji islands, the estuaries of the Yangtze and Yellow rivers, the Beibu Gulf, Nanpeng islands, and the coral reef islands in the South China Sea.

Scientists are calling for 30% of the world's oceans to be fully protected by 2030 (*11*). However, 61% of the world's oceans are high seas, which hold the largest global biodiversity richness. In order to protect marine biodiversity in international waters, countries will have to cooperate (*11*). In April 2019, Chinese President Xi Jinping proposed that the international community work together to ensure a shared future for the world's oceans (*12*). To achieve this goal, greater efforts are required by China and all countries.

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# Worst climate outcomes are still possible

In his news item "Global warming forecasts sharpen" in the Breakthrough of the Year news package (18 December, http://scim.ag/BOTYwarming), P. Voosen wrote that new research on climate sensitivity "rule[s] out" the most dire climate scenarios. Although this work is a major advance, its scope is insufficient to eliminate the worst possible outcomes.

The research to which Voosen refers constrains "climate sensitivity"—the warming response to a given increase in the atmospheric $CO_2$ concentration (*1*). However, climate sensitivity does not account for the complex relationship between human $CO_2$ emissions and changes in atmospheric $CO_2$. That relationship depends on carbon cycle feedbacks, which currently act to stabilize climate but could weaken or reverse as warming progresses (*2*, *3*). Even uncontrolled warming is potentially possible (*4*); paleoclimate evidence suggests that carbon cycle feedbacks may have amplified past natural warming trends (*5*–*7*). Of particular concern are greenhouse gas emissions from thawing permafrost, which are substantial now and will only increase as warming progresses (*8*).

Because of limited scientific understanding, carbon cycle feedbacks are incompletely represented in many climate models, including those used in the recent Intergovernmental Panel on Climate Change special report, "Global warming of 1.5°C" (*9*). Every ton of carbon emitted by permafrost is one less ton that humans can emit while limiting warming to 1.5° or 2°C. Thus, unaccounted-for carbon cycle feedbacks increase the challenge of meeting any top-line climate goal.

The new constraints on climate sensitivity that Voosen highlights are welcome, but they must be carefully interpreted to avoid creating a false sense of security about the possible severity of the warming response to human emissions of greenhouse gases. Even with perfect knowledge of climate sensitivity, we would still need better understanding of carbon cycle feedbacks to determine how much humans can emit and still meet top-line climate policy goals of limiting global warming to 1.5° or 2°C —a question of fundamental importance to our collective future.

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## TECHNICAL COMMENT ABSTRACTS

### Comment on "Structural evidence for a dynamic metallocofactor during $N_2$ reduction by Mo-nitrogenase"

**John W. Peters, Oliver Einsle, Dennis R. Dean, Serena DeBeer, Brian M. Hoffman, Patrick L. Holland, Lance C. Seefeldt**

Kang *et al*. (Reports, 19 June 2020, p. 1381) report a structure of the nitrogenase MoFe protein that is interpreted to indicate binding of $N_2$ or an $N_2$-derived species to the active-site FeMo cofactor. Independent refinement of the structure and consideration of biochemical evidence do not support this claim.

**Full text:** dx.doi.org/10.1126/science.abe5481

### Response to Comment on "Structural evidence for a dynamic metallocofactor during $N_2$ reduction by Mo-nitrogenase"

**Wonchull Kang, Chi Chung Lee, Andrew J. Jasniewski, Markus W. Ribbe, Yilin Hu**

Peters *et al*. comment on our report of the dynamic structure of the nitrogenase metallocofactor during $N_2$ reduction. Their claim that their independent structural refinement and consideration of biochemical data contradict our finding is incorrect and is strongly refuted by our biochemical and structural data that collectively and conclusively point to the binding of dinitrogen species to the nitrogenase cofactor.

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