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材料科学Materials Science

Strong and brittle lithium dendrites

强而脆的锂枝晶

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▲链接：

https://www.science.org/doi/10.1126/science.adu9988

▲摘要：

锂枝晶在电解质和隔膜中的生长及渗透仍是实现高能量密度锂金属电池的关键难题。

基于学界普遍认为的锂金属的质地柔软性，采用机械强度高的电解质和隔膜一直被视为一种很有前景的策略。然而，在刚性固态电解质中，枝晶形成依然存在，这表明其具有不同的机械特性。

研究组采用无空气方案测量了单个锂枝晶的机械性能。结果意外发现，锂枝晶具有高强度和高脆性，其断裂应力超过150兆帕，这与具有延展性的块体锂金属截然不同。

低温透射电子显微镜观察和力学模型分析表明，这种行为源于固态电解质界面约束以及纳米级强化作用。这些发现为枝晶穿透和死锂形成提供了新的替代机制，并为锂金属电池的设计策略提供了指导。

▲ Abstract：

The growth and penetration of lithium dendrites through electrolytes and separators remain key challenges to realizing high – energy density lithium-metal batteries. Using mechanically strong electrolytes and separators has been considered a promising strategy based on the commonly believed softness of lithium. However, dendrite formation persists in stiff solid electrolytes, suggesting distinct mechanical behaviors. We measured the mechanical properties of individual lithium dendrites using an air-free protocol. We found that lithium dendrites are unexpectedly strong and brittle, with fracture stress greater than ~150 megapascals, unlike the ductile bulk metal. Cryo – transmission electron microscopy and mechanical modeling showed that this behavior arises from solid electrolyte interface constraints and nanoscale strengthening. These findings provide alternative mechanisms for dendrite penetration and dead lithium formation as well as guidance for design strategies for lithium-metal batteries.

环境科学Environmental Science

Rapid evolution predicts demographic recovery after extreme drought

快速进化可预测极端干旱后的种群数量复苏

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▲链接：

https://www.science.org/doi/10.1126/science.adu0995

▲摘要：

由于气候变化而出现数量减少的物种可能需要进化来维持存续。尽管进化拯救已在理论和实验室研究中得到证明，但其对于面临气候变化的自然种群的适用性仍然未知。

研究组分析了在极端干旱条件下，猩红色猴面花（Mimulus cardinalis）的快速进化及其种群动态之间的联系。对55个种群进行全基因组测序，以确定与气候相关的基因座，同时还追踪了干旱期间种群结构和等位基因频率的变化。

结果发现，在干旱期间，整个种群数量大范围下降，种群进化速度存在地理差异，种群数量的恢复情况也各不相同，而这些情况都可通过与气候相关基因座上的遗传变异程度以及该位点的快速进化来预测。

这些研究结果表明，在野外环境中存在进化拯救的可能性，即在适应性位点而非中性位点上的基因变异能够预测种群的恢复情况。

▲ Abstract：

Populations that are declining as a result of climate change may need to evolve to persist. Although evolutionary rescue has been demonstrated in theory and in the laboratory, its relevance to natural populations facing climate change remains unknown. Here we link rapid evolution and population dynamics in scarlet monkeyflower, Mimulus cardinalis, during exceptional drought. We leverage whole-genome sequencing across 55 populations to identify climate-associated loci. Simultaneously we track demography and allele frequency change throughout the drought. We establish range-wide population decline during the drought, geographically variable rapid evolution, and variable population recovery that is predictable by standing genetic variation in, and rapid evolution at, climate-associated loci. These findings demonstrate the possibility of evolutionary rescue in the wild, showing that genetic variation at adaptive, but not neutral, loci predicts population recovery.

Evolutionary adaptation to global change reduces sustainable fisheries yields

对全球变化的进化适应性降低了可持续渔业的捕捞产量

▲ 作者：TAN Koz?owski , DUSTIN J. MARSHALL AND CRAIG R. WHITE

▲链接：

https://www.science.org/doi/10.1126/science.aea1341

▲摘要：

全球变暖正在改变支撑粮食安全的渔业资源，然而对这些影响的预测通常排除了进化过程。

研究组建立了一个模型，用于预测鱼类将如何适应未来的气候状况，以及这种进化对渔业产量的影响。

他们预测，在水温较高的环境中，鱼类的生长速度虽然会加快，但其性成熟时间会提早，从而导致其最大体型变小。同时还预测，进化过程能够减缓气候变化对鱼类适应能力的影响，但会加剧其对渔业产量的负面影响——使损失加剧约50%。

排除进化因素高估了所有排放情景下的未来渔业产量，但进化的影响在最极端的情景下最为明显。所有生物的生命周期都可能因全球变化而发生相应变化——在预测生态系统及其服务功能时，应当将这种演变因素考虑在内。

▲ Abstract：

Global warming is altering the fisheries that underpin food security, but projections of these impacts generally exclude evolutionary processes. We describe a model that forecasts how fish will adapt to future climates and the consequences of that evolution for fisheries yields. We predict that fish in warmer waters will grow faster but evolve earlier maturation, decreasing their maximum size. We predict that evolution ameliorates the impacts of climate change on fish fitness but exacerbates its impacts on fisheries yields—worsening losses by ~50%. Excluding evolution overestimates future yields under all emissions scenarios, but evolution’s impacts are greatest under the most extreme scenarios. All life histories may evolve in response to global change—this evolution should be considered in projections of ecosystems and their services.

动物学Zoology

Seal and sea lion brains have evolved to support volitional control of vocal behavior and learning

海豹和海狮的大脑已进化出支持自主发声控制以及发声学习的能力

▲ 作者：PETER F. COOK, ANDREW A. ROUSE, EVA SAWYER, KARLA MILLER AND GREGORY BERNS

▲链接：

https://www.science.org/doi/10.1126/science.adx9367

▲摘要：

海豹和海狮具有高度发达的自主呼吸控制能力，而海豹科还在此基础上进化出包括模仿在内的发

声学习。

在这项工作中，研究组通过组织学分析和体外扩散磁共振成像追踪技术，为支持鳍足动物自主发声控制方面的累积神经适应的系统发育谱提供了证据。海狮科和海豹科动物（并非郊狼）的发声运动皮层与发声脑干核团之间存在直接联系。

海豹的丘脑前腹外侧与发声前运动皮层之间存在增生性连接——这是与鸟类发声学习以及人类和鹦鹉模仿能力相关的前脑回路的一部分。研究组证明，海豹科具有与发育阶段的发声学习相关的听觉-前运动通路。

▲ Abstract：

Seals and sea lions have highly developed volitional breathing control, to which the phocid seals add vocal production learning, including mimicry. In this work, using histology and ex vivo diffusion magnetic resonance imaging tractography, we provide evidence for a phylogenetic spectrum of accumulative neural adaptations supporting aspects of volitional vocal control across pinnipeds. Otariids and phocid seals, but not coyotes, have a direct connection between the vocal motor cortex and phonatory brainstem nuclei. Harbor seals showed hypertrophic connectivity between the anterior ventrolateral thalamus and the vocal premotor cortex—part of a forebrain circuit related to vocal learning in birds and mimicry in humans and parrots. We demonstrate that phocid seals have auditory-premotor pathways potentially related to developmental call learning.

Ravens anticipate wolf kill sites across broad scales

乌鸦预测大规模的狼群捕杀地点

▲ 作者：MATTHIAS-CLAUDIO LORETTO, KRISTINA B. BECK, DOUGLAS W. SMITH, DANIEL R. STAHLER, LAUREN E. WALKER, MARTIN WIKELSKI, ET AL.

▲链接：

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▲摘要：

食腐动物通常依赖分布零散且难以预测的腐肉为食。长期以来有一种假设认为，食腐乌鸦通过直接追踪大型食肉动物前往其捕猎点来可靠地定位这些食物。

然而，通过对黄石国家公园内69只乌鸦、20只狼和11只美洲狮进行卫星追踪，研究组发现乌鸦很少会远距离跟随捕食者。相反，乌鸦通常会再次重访狼群经常捕杀猎物的地点，它们会从远至155千米外返回来寻找腐肉。

就像导航至永久性的人为补给站一样，乌鸦似乎能够记住先前与狼或其猎物接触所形成的潜在腐肉来源。这些发现表明，在寻找短暂性资源的过程中，空间记忆和导航能力在食腐动物（以及可能在其他广泛物种中）的发挥作用要远大于此前假设。

▲ Abstract：

Scavengers generally rely on patchily distributed, unpredictable carrion. A long-standing hypothesis suggests scavenging ravens reliably locate such food by directly following large carnivores to their kills. However, by satellite tracking 69 ravens, 20 wolves, and 11 cougars in Yellowstone National Park, we found that following of predators over large distances rarely occurred. Instead, ravens routinely revisited sites where wolf kills were common—returning from distances of up to 155 kilometers to find carrion. Much like navigating to permanent anthropogenic subsidies, ravens appear to remember potential sources of carrion shaped by previous encounters with wolves or their kills. These findings suggest that spatial memory and navigation play a considerably greater role than previously assumed among scavengers, and possibly other wide-ranging species, in search of ephemeral resources.

公共卫生Public Health

Polymerase trapping as the mechanism of H5 highly pathogenic avian influenza virus genesis

聚合酶捕获导致H5高致病性禽流感病毒产生

▲ 作者：MATHIS FUNK, MONIQUE I. SPRONKEN , ROY M. HUTCHINSON, BENOIT ARRAGAIN, PAULINE JUYOUX, THEO M. BESTEBROER, ET AL.

▲链接：

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▲摘要：

高致病性禽流感病毒（HPAIV）源于H5和H7型低致病性禽流感病毒（LPAIV）。尽管几十年前学界就已确定，在血凝素基因中插入可被蛋白酶切割的多碱基切割位点（MBCS）是LPAIV向HPAIV转变的遗传基础，但这种插入事件的机制尚不清楚。

研究组展示了瞬时H5 RNA结构，预测将流感病毒聚合酶捕获在富含嘌呤的序列上，驱动核苷酸插入，为RNA结构参与MBCS获取提供了经验证据。将H5样序列和结构引入H6血凝素中，导致MBCS生成插入突变。

该研究结果表明，H5 HPAIV出现的核苷酸插入源于RNA结构驱动的多样性生成机制，该机制也可能发生在其他RNA病毒中。

▲ Abstract：

Highly pathogenic avian influenza viruses (HPAIVs) derive from H5 and H7 low pathogenic avian influenza viruses (LPAIVs). Although insertion of a furin-cleavable multibasic cleavage site (MBCS) in the hemagglutinin gene was identified decades ago as the genetic basis for the LPAIV-to-HPAIV transition, the mechanisms underlying the occurrence of insertion are unknown. Here, we show that transient H5 RNA

structures, predicted to trap the influenza virus polymerase on purine-rich sequences, drive nucleotide insertions, providing empirical evidence of RNA structure involvement in MBCS acquisition. Introduction of H5-like sequences and structures into an H6 hemagglutinin resulted in MBCS-yielding insertions. Our results show that nucleotide insertions that underlie H5 HPAIV emergence result from an RNA structure – driven diversity-generating mechanism, which could also occur in other RNA viruses.

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