《科学》（20260702出版）一周论文导读

作者：writer 来源：科学网

本文原地址：https://www.iikx.com/news/progress/40751.html

《科学》（20260702出版）一周论文导读。编译李言

Science, 2 Jul 2026, VOL 393, ISSUE 6806

《科学》2026年7月2日，第393卷，6806期

地球科学Earth Science

Continental breakup – driven uplift instigated East Antarctic Ice Sheet formation

大陆裂解驱动的隆升触发了东南极冰盖的形成

▲ 作者：Thomas M. Gernon, Thea K. Hincks et al.

▲链接：

https://www.science.org/doi/10.1126/science.adz6758

▲摘要：

关于南极洲在大约3400万年前开始冰川化的原因仍存争议，因为相对温暖的气候和海水温度似乎与冰盖形成相矛盾。尽管二氧化碳浓度的大幅下降被认为是主要原因，但有证据表明其他因素也至关重要。

研究者分析了根植于侏罗纪大陆裂解和地幔—地表反馈的区域地形抬升是否促成了东南极冰盖的成核。

通过将地球动力学—地形模型与冰盖和能量平衡模型相结合，研究者表明南极东部逐步的高原隆升（包括始新世甘布里采夫山脉的抬升）在大约4500万年前，就已将地形推升至冰盖成核阈值以上。

隆升使得冰盖能够在比预期更温暖的气候下生长，形成了早期冰川作用中的半球不对称性，并调和了渐新世极地温暖与近代冰室世界开始之间的矛盾。

▲ Abstract：

Why Antarctica became glaciated ～34 million years ago (Ma) remains debated, as relatively warm climates and sea temperatures appear inconsistent with ice sheet formation. Although a critical decline in CO2 is considered primarily responsible, evidence suggests that other factors were important, too. We investigated whether regional topographic uplift, rooted in Jurassic continental breakup and mantle-surface feedbacks, enabled nucleation of the East Antarctic Ice Sheet (EAIS). By integrating geodynamic-topographic models with ice sheet and energy balance models, we show that progressive plateau growth in East Antarctica, including Eocene uplift of the Gamburtsev Mountains, pushed landscapes above the threshold for ice sheet nucleation by ～45 Ma. Uplift enabled EAIS growth under warmer-than-expected climates, producing hemispheric asymmetry in early glaciation and reconciling Oligocene polar warmth with the onset of the modern icehouse world.

生物学Biology

A Hormone Cell Atlas maps the human endocrine system at cellular resolution

激素细胞图谱以单细胞分辨率绘制人类内分泌系统

▲ 作者：Lijiang Fei, Isabel Huang-Doran et al.

▲链接：

https://www.science.org/doi/10.1126/science.aeb2672

▲摘要：

激素在组织与器官间发挥协同作用以协调生理功能。受人类细胞图谱的启发，研究者分析了一个涵盖47种人类组织、1400万个单细胞和细胞核的转录组数据集中的379个激素及受体基因的表达情况。

利用激素2细胞工具，研究者绘制了推定激素产生细胞与受体细胞类型图谱，定义了组织特异性和跨组织的内分泌特征。

研究者预测了激素表达的非常规位点，包括浆细胞样树突状细胞中的分泌素，推断了趋同的激素作用与内分泌反馈环路，并将特定细胞群体与单基因内分泌疾病相关联。

在脂肪细胞数据集的跨组织整合分析中，研究者揭示了不同脂肪库、脂肪细胞亚型内及成脂分化过程中的动态内分泌程序。综上所述，激素细胞图谱为解析激素对健康与疾病的影响提供了一个全面的框架。

▲ Abstract：

Hormones act across tissues and organs to coordinate physiological functions. Drawing inspiration from the Human Cell Atlas, we analyzed the expression of 379 hormone and receptor genes in a transcriptomic dataset comprising 14 million single cells and nuclei across 47 human tissues. Using hormone2cell, we mapped putative hormone-producing and hormone-receiving cell types, defining tissue-specific and cross-tissue endocrine signatures. We predicted nonclassical sites of hormone expression, including secretin in plasmacytoid dendritic cells, inferred convergent hormone action and endocrine feedback loops, and implicated cell populations in monogenic endocrine disorders. In a cross-tissue integration of adipocyte datasets, we uncovered dynamic endocrine programs across depots, within adipocyte subtypes and through adipogenic differentiation. Cumulatively, the Hormone Cell Atlas provides a comprehensive framework for dissecting hormonal impact on health and disease.

TranscriptFormer: A generative cell atlas across 1.5 billion years of evolution

TranscriptFormer：跨越15亿年进化的生成式细胞图谱

▲ 作者：James D. Pearce, Sara E. Simmonds, Gita Mahmoudabadi et al.

▲链接：

https://www.science.org/doi/10.1126/science.aec8514

▲摘要：

单细胞转录组学正在革新人们对细胞多样性的理解，但跨生命树比较转录程序仍然具有挑战性。研究者开发了TranscriptFormer，一个生成式基础模型族群，其训练数据涵盖12个物种、跨越15.3亿年进化历程的多达1.12亿个细胞。

研究者展示了其在细胞类型分类任务上的领先性能，即使对于进化距离超过6.85亿年的物种依然

表现卓越，并且能够零样本识别人类细胞中的疾病状态。

在TranscriptFormer的表现中，无需对相关注释进行显式训练，发育轨迹、系统发育关系和细胞层级结构便能自然涌现。这项工作为定量单细胞分析和比较细胞生物学建立了一个强大的框架，证明了细胞组织的普遍原则可以在整个生命树中被学习和预测。

▲ Abstract：

Single-cell transcriptomics is revolutionizing our understanding of cellular diversity, yet comparing transcriptional programs across the tree of life remains challenging. We developed TranscriptFormer, a family of generative foundation models trained on up to 112 million cells spanning 1.53 billion years of evolution across 12 species. We demonstrate state-of-the-art performance on cell type classification, even for species separated by over 685 million years of evolution, and zero-shot disease state identification in human cells. Developmental trajectories, phylogenetic relationships, and cellular hierarchies emerge naturally in TranscriptFormer ’ s representations without any explicit training on these annotations. This work establishes a powerful framework for quantitative single-cell analysis and comparative cellular biology, thus demonstrating that universal principles of cellular organization can be learned and predicted across the tree of life.

植物学Botany

Height does not impair the hydraulic system of the tallest tropical Dipterocarp trees

树高并不损害热带最高龙脑香树的水力系统

▲ 作者：Paulo Bittencourt, Arne Scheire et al.

▲链接：

https://www.science.org/doi/10.1126/science.aea9013

▲摘要：

森林中一半的地上生物量储存在占比极小的高大树木中。这些巨树被认为更易受干旱胁迫的损害，因为树高会损害其水力系统。研究者评估了世界最高热带树种——东南亚龙脑香科树木的水力系统是否受到树高的负面影响。

由树高引起的更负的木质部压力完全通过导管解剖结构和叶片水力性状的调整得到了补偿，并且在一次严重干旱事件中，这些树木的生长并未表现出与高度相关的损失。

因此，树高并未使世界最高热带树种的水力系统对干旱更加脆弱，且这些树木的生长速率受干旱的负面影响并不大于其较小的同类。

▲ Abstract：

Half of the aboveground biomass in forests is stored in a disproportionately small number of very tall trees. These giants are predicted to be more vulnerable to drought-induced damage because height impairs their hydraulic system. We evaluated whether the hydraulic system of world ’ s tallest tropical tree species—Southeast Asian dipterocarps—are negatively affected by their height. The more negative xylem pressures caused by tree height were fully compensated for through adjustment of vessel anatomy and leaf hydraulic traits, and the trees suffered no height-related loss in growth during a severe drought. Therefore, height does not make the hydraulic systems of the world ’ s tallest tropical tree species more vulnerable to drought, and the growth rates of these trees are not more negatively affected by drought than are their smaller counterparts.

物理学Phyasics

Observation of disorder-free localization using a (2+1)D lattice gauge theory on a quantum processor

利用量子处理器在（2+1）维格点规范理论中观测无无序局域化现象

▲ 作者：Google Quantum AI and Collaborators

▲链接：

https://www.science.org/doi/10.1126/science.adr9680

▲摘要：

量子多体系统中的无序诱导现象在相关时间和系统尺度上对解析和数值方法构成了挑战。为降低无序采样的计算成本，研究者分析了初始态为所有无序构型可调叠加的量子线路，在格点规范理论中，这种叠加态可被解释为规范扇区上的叠加态。

在实验可达的时间尺度上，研究者在一维和二维系统中观测到了无无序情况下的局域化现象：尽管演化和初始态完全无无序，扰动仍未能扩散。

然而，熵测量表明，叠加制备态与直接无序采样获得的态存在根本差异。利用叠加态，研究者提出了一种在无序构型采样中具有多项式加速的算法，这是多体局域化研究中长期存在的挑战。

▲ Abstract：

Disorder-induced phenomena in quantum many-body systems pose a challenge for analytical and numerical approaches at relevant time and system scales. To reduce the cost of disorder sampling, we investigated quantum circuits initialized in states that form tunable superpositions over all disorder configurations, which in lattice gauge theories can be interpreted as superpositions over gauge sectors. On the experimentally accessible timescales, we observed localization in the absence of disorder in one and two dimensions: Perturbations failed to diffuse despite fully disorder-free evolution and initial states. However, entropy measurements revealed that superposition-prepared states fundamentally differ from those obtained by direct disorder sampling. Leveraging superposition, we propose an algorithm with a polynomial speedup in sampling disorder configurations, a long-standing challenge in many-body localization studies.

动物学Zoology

Fruit flies actively restart their circadian clock by proactively shaping their environment

果蝇通过主动塑造环境来重启其昼夜节律钟

▲ 作者：Angelica Coculla, Luis Garcia Rodriguez et al.

▲链接：

https://www.science.org/doi/10.1126/science.adw2239

▲摘要：

昼夜节律时钟提供适应性优势，使生物能够根据地球上的每日环境变化调整其生理和行为。

研究者表明，果蝇偏好有节律组织的生活。由于光照诱导的核心昼夜节律蛋白Timeless发生降解，持续光照会使昼夜节律停止并导致运动活动节律丧失。

当果蝇在恒定光照环境中可以在黑暗与光照区域之间自由移动时，它们能够维持甚至重新获得节律性的行为模式。这些自我诱导的节律伴随着已知驱动行为节律的时钟神经元中的分子节律。

与节律丧失的果蝇相比，节律性行为与改善的睡眠质量相关，表明选择在昼夜节律控制下生活具有即时的益处。

▲ Abstract：

Circadian clocks provide adaptive advantages, enabling organisms to adjust their physiology and behavior to daily environmental changes on Earth. Here, we show that fruit flies prefer a temporally organized life. Because of light-induced degradation of the core circadian clock protein Timeless, constant illumination stops the circadian clock and leads to arrhythmic locomotor activity. When given the choice to move between dark and illuminated areas in a constant light environment, flies were able to maintain, or even regain, rhythmic behavioral patterns. These self-inflicted rhythms were accompanied by molecular rhythms in clock neurons known to drive behavioral rhythms. Behavioral rhythmicity was correlated with improved sleep quality compared with that of arrhythmic flies, demonstrating an immediate benefit of choosing to live under circadian clock control.

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