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A parabrachial hub for need-state control of enduring pain

臂旁核：持久性疼痛的稳态控制枢纽

▲ 作者：Nitsan Goldstein, Amadeus Maes et al.

▲ 链接：

<https://www.nature.com/articles/s41586-025-09602-x>

▲ 摘要：

研究者整合空间转录组学、神经调控、神经元活动记录与计算建模方法，首次证实了表达神经肽Y受体Y1的臂旁核神经元集群（Y1R神经元）在损伤后活动增强，其激活模式可准确预测功能性适应行为。

饥饿、口渴或天敌线索等生理需求状态，能通过释放神经肽Y抑制臂旁核Y1R神经元，从而广泛抑制各类损伤引发的持续性疼痛。综上，研究揭示了臂旁核Y1R神经元作为内源性镇痛枢纽，通过整合多模态需求信号来调控持续性疼痛的核心机制。

▲ Abstract：

Here we use spatial transcriptomics, neural manipulations, activity recordings and computational modelling to demonstrate that activity in an ensemble of anatomically and molecularly diverse parabrachial neurons that express the neuropeptide Y (NPY) receptor Y1 (Y1R neurons) is increased following injury and predicts functional coping behaviour. Hunger, thirst or predator cues suppressed sustained pain, regardless of the injury type, by inhibiting parabrachial Y1R neurons via the release of NPY. Together, our results demonstrate an endogenous analgesic hub at pain-responsive parabrachial Y1R neurons.

Nanobody-based recombinant antivenom for cobra, mamba and rinkhals bites

针对眼镜蛇、曼巴与唾蛇咬伤的基于纳米抗体重组抗蛇毒血清

▲ 作者：Shirin Ahmadi, Nick J. Burlet et al.

▲ 链接：

<https://www.nature.com/articles/s41586-025-09661-0>

▲ 摘要：

研究者采用18种毒蛇（含曼巴蛇、眼镜蛇与唾蛇）的毒液对羊驼和大羊驼进行免疫，构建噬菌体展示文库并筛选出高亲和力广谱中和性纳米抗体。

他们将其中8种纳米抗体配伍成精确定义的寡克隆混合物，成功研制出能中和7个毒素家族/亚家族的多价重组抗蛇毒血清。该血清在体内实验中可有效抵御17种非洲眼镜蛇科毒蛇的致死毒性，并对所有测试的细胞毒性毒液所致皮肤坏死产生显著抑制效果。

这种重组抗蛇毒血清的效能优于现行血浆源性抗蛇毒血清，有望为非洲大陆所有医学相关眼镜蛇科毒蛇咬伤提供全面防护方案。

▲ Abstract :

Here we addressed this challenge by immunizing an alpaca and a llama with the venoms of 18 different snakes, including mambas, cobras and a rinkhals, constructing phage display libraries, and identifying high-affinity broadly neutralizing nanobodies. We combined eight of these nanobodies into a defined oligoclonal mixture, resulting in an experimental polyvalent recombinant antivenom that was capable of neutralizing seven toxin families or subfamilies. This antivenom effectively prevented venom-induced lethality in vivo across 17 African elapid snake species and markedly reduced venom-induced dermonecrosis for all tested cytotoxic venoms. The recombinant antivenom performed better than a currently used plasma-derived antivenom and therefore shows considerable promise for comprehensive, continent-wide protection against snakebites by all medically relevant African elapids.

生物学Biology

Diverging fish biodiversity trends in cold and warm rivers and streams

冷暖河流与溪流中鱼类生物多样性的不同趋势

▲ 作者：Samantha L. Rumschlag, Brian Gallagher et al.

▲ 链接：

<https://www.nature.com/articles/s41586-025-09556-0>

▲ 摘要：

研究者整合了涵盖27年间2992个站点、389个鱼类物种的美国联邦生物监测数据集，以分析鱼类生物多样性变化趋势。在冷水溪流（历史夏季水温低于15.4 °C）中，鱼类丰度与丰富度在27年间分别下降53.4%和32%，群落独特性则有所提升。

周期性鱼类（体型大、成熟晚）数量增加，机会型鱼类（体型小、世代周期短、属于r-选择策略者）减少，这可能源于本土或引入游钓鱼类的增殖。在暖水溪流（水温高于23.8 °C）中，鱼类丰度与丰富度分别上升70.5%和15.6%，群落呈现同质化趋势。

小型机会主义鱼类取代了大型周期性鱼类。而代表一般状况的温水溪流（水温15.4—23.8 °C）中，鱼类生物多样性随时间变化极小。水温上升与鱼类引入的交互作用，加速了当地鱼类生物多样性的退化。

鉴于这些变化在较短时间内达到的严重程度，亟需遏制由鱼类引入和水温上升导致的鱼类生物多样性退化。

▲ Abstract :

Here we harmonized US federal biomonitoring datasets with 389 species spanning 27 years (1993 – 2019) and 2,992 sites to analyse trends in fish biodiversity. In cold streams (past summer stream temperatures below 15.4 ° C), fish abundance and richness declined by 53.4% and 32% over 27 years, respectively, and uniqueness increased. Periodic (large-bodied, late-maturing) fishes increased, and opportunists (small-bodied, short generation time, ' r-selected ') decreased, possibly due to proliferation of native or introduced game fishes. In warm streams (stream temperatures greater than 23.8 ° C), fish abundance and richness increased by 70.5% and 15.6% over 27 years, respectively, and communities homogenized. Small opportunistic fishes replaced large periodic fishes. Intermediate streams (stream temperatures 15.4 – 23.8 ° C), representing the average stream, had minimal changes in fish biodiversity through time. Interactions between warming and introduced fish were associated with increased rates of degradation to local fish biodiversity. Given the magnitude of these changes in a relatively short time span, there is an urgent need to curb degradation of fish biodiversity caused by fish introductions and warming water temperatures.

The oldest known lepidosaur and origins of lepidosaur feeding adaptations

已知最古老的鳞龙与鳞龙摄食适应机制的起源

▲ 作者 : Daniel Marke, David I. Whiteside et al.

▲ 链接 :

<https://www.nature.com/articles/s41586-025-09496-9>

▲ 摘要 :

研究者在英国德文郡的中三叠世（阿尼西期）赫尔斯比砂岩组发现了一具保存较为完整的原始喙头类颅骨及骨架标本，其年代较现存最古老鳞龙化石早约300—700万年。

该新物种特征符合预期：颅骨固定不动，但具有开放式下颞弓且缺乏大型腭齿，表明其为专性食虫动物。

这一标本为理解鳞龙类在三叠纪革命时期的早期分化提供了关键证据，该时期正是现代陆生生态系统形成的重要阶段。

▲ Abstract :

Here we report a reasonably complete skull and skeleton of a definitive rhynchocephalian from the Middle Triassic (Anisian) Helsby Sandstone Formation of Devon, UK that is around 3 – 7 million years older than the oldest currently known lepidosaur. The new species shows, as predicted, a non-mobile skull but an open lower temporal bar and no large palatine teeth, and it seems to have been a specialized feeder on insects. This specimen helps us understand the initial diversification of Lepidosauria as part of the Triassic Revolution, when modern-style terrestrial ecosystems emerged.

Mosaic anatomy in an early fossil squamate

早期有鳞类化石中发现的镶嵌式解剖结构

▲ 作者：Roger B. J. Benson, Stig A. Walsh et al.

▲ 链接：

<https://www.nature.com/articles/s41586-025-09566-y>

▲ 摘要：

研究者基于在苏格兰中侏罗世（约1.67亿年前）地层中发现的一具新型骨架化石，建立了新属新种——*Breugnathair elgolensis* gen. et sp. nov.。该标本是迄今发现最完整的早期有鳞类化石之一。

*Breugnathair*被归入新建立的小盗龙科（*Parviraptoridae*），这个神秘类群对揭示蛇类起源具有重要潜在价值，此前仅通过极度残缺的化石材料为人所知。该物种呈现出独特的解剖特征镶嵌现象：其头身比例近似巨蜥，牙齿与颌部却具有蛇类特征，同时保留了与壁虎等早期分化类群共有的原始性状。

基于多数据集的系统发育分析得出矛盾结论——小盗龙科可能属于早期毒蜥类（或是潜在的基干蛇类），也可能是通过趋同演化出与食性相关的蛇型齿颌特征的基干有鳞类。

这些发现揭示了有鳞类在早期辐射演化阶段存在显著的同塑性与形态创新实验，同时表明在深时演化分歧过程中，趋同形态变革可能具有关键意义。

▲ Abstract：

Here we present *Breugnathair elgolensis* gen. et sp. nov., based on a new skeleton from the Middle Jurassic epoch (167?million years ago) of Scotland, which is among the oldest relatively complete fossil squamates. *Breugnathair* is placed in a new family, *Parviraptoridae*, an enigmatic group with potential importance for snake origins, that was previously known from very incomplete remains. It displays a mosaic of anatomical traits that is not present in living groups, with head and body proportions similar to varanids (monitor lizards) and snake-like features of the teeth and jaws, alongside primitive traits shared with early-diverging groups such as gekkotans. Phylogenetic analyses of multiple datasets return conflicting results, with parviraptorids either as early toxicoferans (and potentially stem snakes) or as stem squamates that convergently evolved snake-like dental and mandibular traits related to feeding. These findings indicate high levels of homoplasy and experimentation during the initial radiation of squamates and highlight the potential importance of convergent morphological transformations during deep evolutionary divergences.

农业Agriculture

A haplotype-based evolutionary history of barley domestication

基于单倍型的大麦驯化演化史研究

▲ 作者：Yu Guo, Murukarthick Jayakodi et al.

▲ 链接：

<https://www.nature.com/articles/s41586-025-09533-7>

▲ 摘要：

大麦是最古老的栽培作物之一，其演化与驯化历史极为复杂。早期研究已否定单次起源假说，转而支持基因组镶嵌起源模型。

随着基因组数据日益完善，我们需要探究的是：构成这一基因组镶嵌的基本单元——单倍型——究竟源自何处？所有栽培大麦是否共享同一野生祖先，抑或特定野生种群对某些栽培谱系存在更显著的基因贡献？

为解决这些问题，我们采用单倍型分析方法，系统研究了野生与栽培大麦的遗传多样性及种群结构。通过分析682份种质库样本与23份考古样本的全基因组数据，研究者们成功追溯了单倍型的时空起源，并识别出在驯化过程及后期基因流事件中发挥重要作用的野生种群。

古DNA证据有力佐证了基于现代样本的全基因组研究结果。研究表明，奠基性栽培种群最早出现于新月沃地，经历了漫长的预驯化栽培阶段。一个关键实践发现是：大麦种群间显著的单倍型分化（无论源于独立产生还是叠加于选择之上）为定位适应性基因座带来了挑战。

▲ Abstract：

Barley is one of the oldest cultivated crops, with a complex evolutionary and domestication history. Previous studies have rejected the idea of a single origin and instead support a model of mosaic genomic ancestry. With increasingly comprehensive genome data, we now ask where the haplotypes — the building blocks of this mosaic — originate, and whether all domesticated barleys share the same wild progenitors or whether certain wild populations contribute more heavily to specific lineages. To address these questions, we apply a haplotype-based approach to investigate the genetic diversity and population structure of wild and domesticated barley. We analyse whole-genome sequences from 682 genebank accessions and 23 archaeological specimens, tracing the spatiotemporal origins of haplotypes and identifying wild contributors during domestication and later gene flow events. Ancient DNA supports our genome-wide findings from modern samples. Our results suggest that a founding domesticated population emerged in the Fertile Crescent during a prolonged period of pre-domestication cultivation. A key practical insight is that the high haplotype differentiation among barley populations — arising independently, or layered on top, of selection — poses challenges for mapping adaptive loci.

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