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物理学Physics

Measurement of reactor neutrino oscillation with the first JUNO data

基于JUNO首批数据的反应堆中微子振荡测量

作者：The JUNO Collaboration

链接：

<https://www.nature.com/articles/s41586-026-10538-z>

摘要：

中微子振荡是一种能在宏观尺度显现的量子效应，其规律由轻子味混合角与中微子质量平方差决定。这两类参数是粒子物理学的基础物理量，也印证了存在超出粒子物理标准模型的新物理现象。精确测量这些参数，对于检验三味中微子理论框架的完备性、判定中微子质量排序，以及探索潜在新物理规律都至关重要。

江门中微子实验室（JUNO）搭载一台2万吨级液体闪烁体探测器，选址距离多座反应堆堆芯52.5千米，目标是以亚百分比级精度解析反应堆中微子的干涉图样。

本文基于该探测器2025年8月建成后，首批连续59.1天的观测数据，首次同步高精度测得两项中微子振荡参数。相较于此前所有联合测量结果，本次测量精度提升至原来的1.6倍。

该成果深化了人类对中微子基础特性的认知，验证了探测器设计方案的合理性，也表明江门中微子实验室已具备条件，可依托更大规模数据集破解中微子质量排序难题。仅依靠短期观测便取得突破性进展，充分展现了该实验室在高精度中微子物理领域开拓前沿的潜力，也为其后续开展各类科学研究奠定了坚实基础。

Abstract :

Neutrino oscillations, a quantum effect manifesting at macroscopic scales, are governed by lepton flavour mixing angles and neutrino mass-squared differences that are fundamental parameters of particle physics, representing phenomena beyond the Standard Model. Precision measurements of these parameters are essential for testing the completeness of the three-flavour framework, determining the mass ordering of neutrinos and probing possible new physics. The Jiangmen Underground Neutrino Observatory (JUNO) is a 20-ktonne liquid-scintillator detector located 52.5 km from multiple reactor cores, designed to resolve the interference pattern of reactor neutrinos with sub-percent precision. Here we report, using the first 59.1 days of data collected since detector completion in August 2025, the first simultaneous high-precision determination of two neutrino oscillation parameters, for the normal mass ordering scenario, improving the precision by a factor of 1.6 relative to the combination of all previous measurements. These results advance the basic understanding of neutrinos, validate the design of the detector and indicate the readiness of JUNO for resolving the neutrino mass ordering with a larger dataset. The rapid achievement with a short exposure highlights the potential of JUNO to push the frontiers of precision neutrino physics and paves the way for its broad scientific programme.

Improved quantum processor logical error rates via correction and detection

通过纠错和检测降低量子处理器的逻辑错误率

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链接：

<https://www.nature.com/articles/s41586-026-10628-y>

摘要：

要在物理和化学领域的关键问题上执行量子算法，所需的错误率远低于当前量子计算机的物理错误率。实现如此低的逻辑错误率需要量子纠错，并且物理错误率须低于某个临界阈值。

研究者通过实验，在离子阱量子电荷耦合器件（QCCD）上展示了逻辑错误率的显著降低——与多个物理线路基线（包括多量子比特上的量子计算）相比，降低了11倍到800倍。这一成果依赖于两种针对离子阱处理器优化的量子纠错码结构：一种受Knill[11]启发、编码两个量子比特的12量子比特码，以及一种编码四个量子比特的16量子比特超立方体颜色码。

这些编码结构与一种可扩展的错误检测和后选择方法相结合，从而实现了更低的逻辑错误率。我们的结果表明，当前最先进的量子器件已经能够利用容错和纠错技术，在非平凡的量子线路计算中强烈抑制错误。

Abstract：

Performing quantum algorithms for critical problems in physics and chemistry requires substantially lower error rates than the physical error rates of present quantum computers. Achieving such low logical error rates requires quantum error correction and physical error rates below a critical threshold value. We experimentally demonstrate on a trapped-ion quantum charge-coupled device (QCCD) improvements in logical error rates ranging from $11 \times$ to $800 \times$ compared with several physical circuit baselines, including quantum computation on multiple qubits. Our results hinge on two quantum error correction code constructions optimized for an ion-trap processor: a 12-qubit code encoding two qubits inspired by Knill[11] and a 16-qubit tesseract colour code encoding four qubits. These constructions are combined with a scalable method of error detection and post-selection to achieve reduced logical error rates. Our results show that state-of-the-art quantum devices are already able to make use of fault tolerance and error correction to strongly suppress errors in non-trivial quantum circuit computations.

环境科学Environmental Science

Analysis of trade-offs of post-sorting plastic packaging

塑料包装后分选中的权衡分析

作者：Alexandra Schmuck, Tiago G. A. Bel é , Dani?l Withoek, Kevin M. Van Geem, Kim Ragaert Steven De Meester

链接：

<https://www.nature.com/articles/s41586-026-10606-4>

摘要：

提高回收率不仅需要更好的技术，还需要更智能地收集塑料包装废弃物。源分离——在家庭层面

将塑料和金属等材料分类——能够收集到大量废弃物，但由于误投和不参与回收，仍有相当数量的废弃物残留在家庭混合垃圾中。混合垃圾的后分选被提出作为一种单桶替代方案以提高捕获率，尽管人们担心污染物可能会降低回收质量。

研究者基于从同一个材料回收设施采集的样本表明，从目标聚合物百分比衡量的打包纯度在源分离和后分选路径中相近，但后分选打包中含有更多的污染物，包括镉和铅等被禁止的金属。后分选样本具有更高的水分和污垢含量，这可能导致复杂挥发性有机化合物的增加，并需要额外的清洗。由于非包装物品的存在，金属和卤素的浓度升高，可能损害回收质量，并进一步使机械回收和化学回收过程复杂化。尽管后分选可以作为一种有用的补充，但它不应取代源分离。

研究表明，后分选可以增加回收的原料，但它同时也成为某些污染物进入塑料包装废弃物的途径，使污染物浓度升高到典型水平以上。如果在再生料生产之前不能去除这些污染物，可能会对人类健康造成潜在风险。随着对残余垃圾进行后分选在实现循环经济目标中变得至关重要，这些发现尤其具有现实意义。

Abstract :

Increasing recycling rates requires not only better technologies but also smarter collection of plastic packaging waste. Source separation—sorting materials such as plastics and metals at the household level—captures substantial waste volumes, yet significant quantities still remain in the residual household waste fraction owing to mishthrows and non-participation. Post-sorting of mixed waste has been proposed as a one-bin alternative to boost capture, despite concerns that contamination could compromise recycling quality. Here we show, based on samples collected from one single material recovery facility, that bale purity, expressed as percent target polymer, is similar across source-separation and post-sorting pathways, but post-sorted bales contain more contaminants, including prohibited metals such as cadmium and lead. Post-sorted samples have higher moisture and dirt content⁸, which can lead to increased complex volatile organic compounds and necessitate additional washing. Concentrations of metals and halogens are elevated owing to non-packaging items, potentially compromising recycling quality and further complicating both mechanical and chemical recycling processes. Although post-sorting can be a useful supplement, it should not replace source separation. Our results demonstrate that post-sorting can increase feedstock for recycling, but it also acts as a pathway for certain contaminants to enter plastic packaging waste, raising concentrations above typical levels, with potential risks to human health if these contaminants are not removed before recycle production. As post-sorting of residual waste becomes crucial to meet circularity targets, these findings are particularly relevant.

Decade-long warming accelerates antibiotic resistance in grassland soils

十年增温加速草地土壤抗生素耐药性

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链接：

<https://www.nature.com/articles/s41586-026-10413-x>

摘要：

土壤是抗生素抗性基因的重要储库，这些基因受到微生物相互作用和环境条件的强烈塑造，因此对扰动高度敏感。尽管气候变暖被认为是对微生物群落及其功能最显著的扰动之一，但其对土壤抗性组的影响仍知之甚少。

研究者通过综合实验与计算方法，研究了十年期实验增温对草地土壤抗生素抗性基因的影响。结果显示，增温条件下抗性基因的丰度显著增加（23.9%），尤其是糖肽类和利福平类抗性基因。增温特异地富集了放线菌门宿主（包括多种潜在植物病原菌），并增强了抗性基因的移动性。

基于大规模、前所未有的分离株表型分析也验证了增温提高了细菌对多种抗生素的耐药性。进一步的机制分析表明，增温主要通过两种方式提高抗性基因丰度：一是与适应性性状（如耐热性和氮同化能力）物理连锁的抗性基因的共选择；二是对耐热基因的正选择，而这种选择可通过水平基因转移进一步放大。综合起来，这些发现有力地证明，气候变暖在基因组、生态和进化多个层面显著加速了土壤抗生素耐药性的发展，对变暖世界中的公共健康和环境可持续性具有广泛影响。

Abstract：

Soils are critical reservoirs of antibiotic-resistance genes (ARGs), which are strongly shaped by microbial interactions and environmental conditions and are therefore highly sensitive to disturbance. Although climate warming is recognized as one of the most significant disturbances to microbial communities and their functions, its impacts on soil resistomes remain poorly understood. Here we investigated the effects of decade-long experimental warming on ARGs in grassland soils using integrated experimental and computational approaches. Our results revealed that ARG abundance substantially increased (23.9%) under warming—particularly glycopeptide- and rifamycin-resistance genes. Warming specifically enriched Actinomycetota hosts, including various potential plant pathogens, and enhanced ARG mobility. Large-scale unprecedented isolates-based phenotypic analyses also validated that warming increased bacterial resistance to multiple antibiotics. Further mechanistic analyses revealed that warming increased ARG abundance primarily through co-selection of resistance genes physically linked to adaptive traits (for example, thermal tolerance and nitrogen assimilation) and positive selection for thermal tolerance genes, which could be further amplified via horizontal gene transfer. Together, these findings convincingly demonstrate that climate warming substantially accelerates soil antibiotic resistance at genomic, ecological and evolutionary levels, with broad implications for public health and environmental sustainability in a warming world.

生命科学Life Sciences

Shared neural substrates of prosocial and parenting behaviours

亲社会行为与养育行为共享的神经基础

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链接：

摘要：

人类和其他动物能够感知其他个体的负面状态，并做出亲社会的帮助行为以改善其状况。尽管亲社会帮助行为被认为在进化上根植于对脆弱新生后代的照顾，但养育行为的神经基础是否也有助于面向成年个体的帮助行为，目前仍不清楚。

研究表明，养育水平较高的小鼠对受应激的成年个体表现出更多的亲社会性相互理毛行为。内侧视前区——一个参与养育行为的大脑区域——双向调节对受应激同类个体的相互理毛行为。相互理毛行为与养育行为共同招募了内侧视前区中部分重叠的神经元集群，两者均受内侧视前区到腹侧被盖区通路的控制，并与伏隔核中的多巴胺释放相关。通过活动依赖性标记，研究证明在养育行为中参与的内侧视前区神经元集群对于相互理毛行为在功能上是必需的；反之，在亲社会行为中激活的内侧视前区神经元对于幼崽理毛行为在功能上也是必需的。

这些发现揭示了一种亲社会帮助行为的神经环路机制，并表明养育行为与帮助行为之间存在部分共享的神经基础，提示为照顾后代而进化出的神经系统可能为成年个体之间更广泛的亲社会支持的出现提供了支架。

Abstract：

Humans and other animals can sense the negative states of other individuals and respond with prosocial helping behaviour to improve their conditions. Although prosocial helping behaviour is proposed to have an evolutionary root in caring for vulnerable newborn offspring, whether the neural substrates underlying parenting may contribute to adult-directed helping behaviours remains largely unclear. Here we show that mice with higher levels of parenting show more prosocial allogrooming towards stressed adults. The medial preoptic area (MPOA), a brain area involved in parenting behaviour, bidirectionally regulates allogrooming towards stressed conspecifics. Allogrooming and parenting behaviours recruit a partially overlapping neuronal ensemble in the MPOA, are both controlled by an MPOA-to-ventral tegmental area pathway and are associated with dopamine release in the nucleus accumbens. Using activity-dependent labelling, we demonstrate that MPOA neuronal ensembles engaged during parenting behaviours are functionally required for allogrooming. Conversely, MPOA neurons activated during prosocial behaviour are functionally required for pup grooming. Collectively, these findings uncover a neural circuit mechanism of prosocial helping behaviour and reveal partially shared neural substrates between parenting and helping behaviours, suggesting that the neural systems evolved for offspring care may have provided a scaffold for the emergence of broader prosocial support between adults.

Dopamine drives persistent remodelling of the maternal brain

多巴胺驱动母性大脑的持续重塑

作者：Jennifer C. O' Chan, Giuseppina Di Salvo, Ashley M. Cunningham, Sohini Dutta, Elizabeth Brindley, Benjamin H. Weekley, Winnie Chen, Rasika R. Iyer, Ethan Wan, Cindy Zhang, Naguib Mechawar, Gustavo Turecki Ian Maze

链接：

摘要：

妊娠和产后经历代表着一种生理状态上的深刻转变，对母体的身体和大脑施加了持久的需求，从而引发终生的神经适应。然而，驱动这些持续改变的确切分子机制仍不清楚。本研究利用全脑转录组图谱分析，定义了生殖经历所诱导的神经可塑性的分子景观，并发现背侧海马结构是转录重塑的关键位点。

结合单细胞RNA测序与母亲—幼崽分离范式，研究者还发现慢性产后应激通过改变多巴胺动态，显著干扰了背侧海马结构的适应过程，导致多巴胺依赖性的组蛋白翻译后修饰——H3多巴胺化发生改变，进而因果性地介导了下游的基因表达和行为变化。

在人类背侧下托（背侧海马结构内的一个脑区）中，他们发现了依赖于产次数的H3多巴胺化和转录改变的保守模式。通过化学遗传学手段抑制多巴胺向背侧海马结构的释放，我们进一步证实了多巴胺调控在调节这些适应过程中的充分性，并在未交配的雌性小鼠中重现了生殖经历的关键表观基因组和行为特征。

此次发现确立了多巴胺作为产次诱导的神经适应（在人类和小鼠中）的核心调节因子，揭示了一种基本的转录机制，雌性哺乳动物通过该机制重塑大脑以维持长期的行为适应。

Abstract：

Pregnancy and postpartum experiences represent transformative physiological states that impose lasting demands on the maternal body and brain, resulting in lifelong neural adaptations. However, the precise molecular mechanisms that drive these persistent alterations remain poorly understood. Here we used brain-wide transcriptomic profiling to define the molecular landscape of neuroplasticity induced by reproductive experience, identifying the dorsal hippocampal formation (dHF) as a key site of transcriptional remodelling. Combining single-cell RNA sequencing with a maternal – pup separation paradigm, we additionally found that chronic postpartum stress significantly disrupts dHF adaptations by altering dopamine dynamics, leading to changes in the dopamine-dependent histone post-translational modification, H3 dopaminylation, which causally mediates downstream alterations in gene expression and behaviour. In human dorsal subiculum, a brain structure within the dHF, we uncovered conserved patterns of parity-dependent alterations in H3 dopaminylation and transcription. We further established the sufficiency of dopamine modulation in regulating these adaptations via chemogenetic suppression of dopamine release into the dHF, which recapitulated key epigenomic and behavioural features of reproductive experience in virgin female mice. In sum, our findings establish dopamine as a central regulator of parity-induced neuroadaptations in humans and mice, revealing a fundamental transcriptional mechanism by which female reproductive experience remodels the brain to sustain long-term behavioural adaptations.

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