

References

Aktuell

BENSON-AMRAM 2016

Sarah Benson-Amram, Ben Dantzer, Gregory Stricker, Eli M. Swanson & Kay E. Holekamp, *Brain size predicts problem-solving ability in mammalian carnivores*. [PNAS 113 \(2016\), 2532–2537](#).

[pnas113-02532-Supplement1.xlsx](#), [pnas113-02532-Supplement2.mp4](#)

Despite considerable interest in the forces shaping the relationship between brain size and cognitive abilities, it remains controversial whether larger-brained animals are, indeed, better problem-solvers. Recently, several comparative studies have revealed correlations between brain size and traits thought to require advanced cognitive abilities, such as innovation, behavioral flexibility, invasion success, and self-control. However, the general assumption that animals with larger brains have superior cognitive abilities has been heavily criticized, primarily because of the lack of experimental support for it. Here, we designed an experiment to inquire whether specific neuroanatomical or socioecological measures predict success at solving a novel technical problem among species in the mammalian order Carnivora. We presented puzzle boxes, baited with food and scaled to accommodate body size, to members of 39 carnivore species from nine families housed in multiple North American zoos. We found that species with larger brains relative to their body mass were more successful at opening the boxes. In a subset of species, we also used virtual brain endocasts to measure volumes of four gross brain regions and show that some of these regions improve model prediction of success at opening the boxes when included with total brain size and body mass. Socioecological variables, including measures of social complexity and manual dexterity, failed to predict success at opening the boxes. Our results, thus, fail to support the social brain hypothesis but provide important empirical support for the relationship between relative brain size and the ability to solve this novel technical problem.

Keywords: brain size | problem-solving | carnivore | social complexity | intelligence

Significance: Intelligence presents evolutionary biology with one of its greatest challenges. It has long been thought that species with relatively large brains for their body size are more intelligent. However, despite decades of research, the idea that brain size predicts cognitive abilities remains highly controversial; little experimental support exists for a relationship between brain size and the ability to solve novel problems. We presented 140 zoo-housed members of 39 mammalian carnivore species with a novel problem-solving task and found that the species' relative brain sizes predicted problem-solving success. Our results provide important support for the claim that brain size reflects an animal's problem-solving abilities and enhance our understanding of why larger brains evolved in some species.

CRESWELL 2016

J. David Creswell et al., *Alterations in Resting State Functional Connectivity link Mindfulness Meditation with Reduced Interleukin-6, A Randomized Controlled Trial*. [Biological Psychiatry \(2016\), preprint, 1–33. DOI:10.1016/j.biopsych.2016.01.008](#).

[BioPsych2016-Creswell-Supplement.pdf](#)

J. David Creswell, Adrienne A. Taren, Emily K. Lindsay, Carol M. Greco, Peter J. Gianaros, April Fairgrieve, Anna L. Marsland, Kirk Warren Brown, Baldwin M. Way, Rhonda K. Rosen, Jennifer L. Ferris

Background: Mindfulness meditation training interventions have been shown to improve markers of health, but the underlying neurobiological mechanisms are not known. Building on initial cross-sectional research showing that mindfulness meditation may increase default mode network (DMN) resting state functional connectivity (rsFC) with regions important in top-down executive control (dorsolateral prefrontal cortex, dlPFC), here we test whether mindfulness meditation training increases DMN-dlPFC rsFC, and whether these rsFC alterations prospectively explain improvements in interleukin-6 (IL6) in a randomized controlled trial.

Method: Stressed job-seeking unemployed community adults (N=35) were randomized to either a 3-day intensive residential mindfulness meditation or relaxation training program. Participants completed a five-minute resting state scan before and after the intervention program. Participants also provided blood samples at pre-intervention and at 4-month follow-up, which were assayed for circulating IL-6, a biomarker of systemic inflammation.

Results: We tested for alterations in DMN rsFC using a posterior cingulate cortex (PCC) seed-based analysis, and found that mindfulness meditation training, and not relaxation training, increased PCC rsFC with left dlPFC ($p < .05$, corrected). These pre-post training alterations in PCC-dlPFC rsFC statistically mediated mindfulness meditation training improvements in IL-6 at 4-month follow-up. Specifically, these alterations in rsFC statistically explained 30% of the overall mindfulness meditation training effects on IL-6 at follow-up.

Conclusions: These findings provide the first evidence that mindfulness meditation training functionally couples the DMN with a region known to be important in top-down executive control at rest (left dlPFC), which in turn is associated with improvements in a marker of inflammatory disease risk.

Keywords: mindfulness meditation | functional connectivity | IL-6 | unemployment | fMRI | stress

SCOTT 2016

Andrew Scott, *Science in the shadows*. [science 351 \(2016\), 782](#).

Science was one of my passions, but the setbacks of research were beginning to grind me down, and I was realizing that actually doing science was not for me. By the time I reached the lab that day, I knew that I needed to do something different with my life than chase the “regular” job in academia or industry that I was being encouraged to prepare for.

It now occurs to me that in some ways, my life in science writing has been very similar to the lives of many science graduates who stay in research. Our driving force is a passion for what we do, but in the same way that my books are falling out of date and out of print, most research papers soon sink into the swamps of the rarely cited and the never applied. Most of us, whatever path we choose through science, must be ready to be content with a life in the shadows rather than in the limelight. But such a life, I have found, can still be fun and fulfilling.

Anthropologie

GIBBONS 2016

Ann Gibbons, *Neandertal genes linked to modern diseases*. [science 351 \(2016\), 648–649](#).

DNA inherited from our extinct cousins boosts risk of depression and other disorders.

Such examples suggest that as modern humans entered new environments that harbored new pathogens, they took an evolutionary shortcut by picking up beneficial genes from other hominins. “You just borrow diversity from another species or population that had lived there longer,” Quintana-Murci says. Neandertals had at least 200,000 years to adapt to life in the Middle East and Europe before moderns got there. But however beneficial in the Pleistocene and to people living in poor conditions today, even immune-boosting genes may have deleterious effects in the United States and Europe, where people face fewer parasites.

HSIEH 2016

PingHsun Hsieh et al., *Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies*. *Genome Research* **26** (2016), 291–300.

GenomeRes26-0291-Supplement.pdf

PingHsun Hsieh, August E. Woerner, Jeffrey D. Wall, Joseph Lachance, Sarah A. Tishkoff, Ryan N. Gutenkunst & Michael F. Hammer

Comparisons of whole-genome sequences from ancient and contemporary samples have pointed to several instances of archaic admixture through interbreeding between the ancestors of modern non-Africans and now extinct hominids such as Neanderthals and Denisovans. One implication of these findings is that some adaptive features in contemporary humans may have entered the population via gene flow with archaic forms in Eurasia. Within Africa, fossil evidence suggests that anatomically modern humans (AMH) and various archaic forms coexisted for much of the last 200,000 yr; however, the absence of ancient DNA in Africa has limited our ability to make a direct comparison between archaic and modern human genomes. Here, we use statistical inference based on high coverage whole-genome data (greater than 60×) from contemporary African Pygmy hunter-gatherers as an alternative means to study the evolutionary history of the genus *Homo*. Using whole-genome simulations that consider demographic histories that include both isolation and gene flow with neighboring farming populations, our inference method rejects the hypothesis that the ancestors of AMH were genetically isolated in Africa, thus providing the first whole genome-level evidence of African archaic admixture. Our inferences also suggest a complex human evolutionary history in Africa, which involves at least a single admixture event from an unknown archaic population into the ancestors of AMH, likely within the last 30,000 yr.

PUN 2016

Anthea Pun, Susan A. J. Birch & Andrew Scott Baron, *Infants use relative numerical group size to infer social dominance*. *PNAS* **113** (2016), 2376–2381.

pnas113-02376-Supplement1.mov, pnas113-02376-Supplement2.mov, pnas113-02376-Supplement3.mov, pnas113-02376-Supplement4.mov, pnas113-02376-Supplement5.mov, pnas113-02376-Supplement6.mov, pnas113-02376-Supplement7.mov

Detecting dominance relationships, within and across species, provides a clear fitness advantage because this ability helps individuals assess their potential risk of injury before engaging in a competition. Previous research has demonstrated that 10- to 13-mo-old infants can represent the dominance relationship between two agents in terms of their physical size (larger agent = more dominant), whereas younger infants fail to do so. It is unclear whether infants younger than 10 mo fail to represent dominance relationships in general, or whether they lack sensitivity

to physical size as a cue to dominance. Two studies explored whether infants, like many species across the animal kingdom, use numerical group size to assess dominance relationships and whether this capacity emerges before their sensitivity to physical size. A third study ruled out an alternative explanation for our findings. Across these studies, we report that infants 6–12 mo of age use numerical group size to infer dominance relationships. Specifically, preverbal infants expect an agent from a numerically larger group to win in a right-of-way competition against an agent from a numerically smaller group. In addition, this is, to our knowledge, the first study to demonstrate that infants 6–9 mo of age are capable of understanding social dominance relations. These results demonstrate that infants’ understanding of social dominance relations may be based on evolutionarily relevant cues and reveal infants’ early sensitivity to an important adaptive function of social groups.

Keywords: social dominance | infancy | conflict | group size

Significance: The ability to detect dominance relationships is essential for survival because it helps individuals weigh the potential costs and benefits of engaging in a physical competition. Here we show that infants as young as 6 mo of age are capable of detecting dominance relations when provided with an ecologically relevant cue such as social group size. Furthermore, infants can infer the social dominance relationship between two competing individuals based on the size of the group to which they belong, and expect individuals from a numerically larger group to get their way. These findings reveal that infants may have an evolutionarily ancient cognitive capacity to represent social dominance relations that is shared with other species within the animal kingdom.

SIMONTI 2016

Corinne N. Simonti et al., *The phenotypic legacy of admixture between modern humans and Neandertals*. [science](#) **351** (2016), 737–741.

Corinne N. Simonti, Benjamin Vernot, Lisa Bastarache, Erwin Bottinger, David S. Carrell, Rex L. Chisholm, David R. Crosslin, Scott J. Hebring, Gail P. Jarvik, Iftikhar J. Kullo, Rongling Li, Jyotishman Pathak, Marylyn D. Ritchie, Dan M. Roden, Shefali S. Verma, Gerard Tromp, Jeffrey D. Prato, William S. Bush, Joshua M. Akey, Joshua C. Denny & John A. Capra

Many modern human genomes retain DNA inherited from interbreeding with archaic hominins, such as Neandertals, yet the influence of this admixture on human traits is largely unknown. We analyzed the contribution of common Neandertal variants to over 1000 electronic health record (EHR)–derived phenotypes in $\approx 28,000$ adults of European ancestry. We discovered and replicated associations of Neandertal alleles with neurological, psychiatric, immunological, and dermatological phenotypes. Neandertal alleles together explained a significant fraction of the variation in risk for depression and skin lesions resulting from sun exposure (actinic keratosis), and individual Neandertal alleles were significantly associated with specific human phenotypes, including hypercoagulation and tobacco use. Our results establish that archaic admixture influences disease risk in modern humans, provide hypotheses about the effects of hundreds of Neandertal haplotypes, and demonstrate the utility of EHR data in evolutionary analyses.

Bibel

NIGRO 2015

Lorenzo Nigro, *Bethlehem in the Bronze and Iron Ages in the Light of Recent Discoveries by the Palestinian Mota-Dach*. [Vicino Oriente](#) **19** (2015), 1–24.

The discovery of the necropolis of Khalet al-Jam'a, around 2.2 km south-east of Bethlehem (Nigro et al. in this volume), provides new data on the Bronze and Iron Age town which controlled the main route connecting Jerusalem to Hebron, and the access to the wadiat crossing the southern Judean desert and leading to the coastal plain. Intermediate Bronze Age/Early Bronze IV, Middle Bronze shaft tombs, and at least two major Iron II burial caves (Tomb A7 and the Barmil's Tomb) excavated by the Palestinian MOTA-DACH in an Iron Age cemetery allow to draw up a renewed picture of Bethlehem and its environs and give the opportunity to re-appraise its long history.

Keywords: Bethlehem | Bronze Age | necropolis | Iron Age | David

Klima

BELLPRAT 2016

Omar Bellprat & Francisco Doblas-Reyes, *Unreliable climate simulations overestimate attributable risk of extreme weather and climate events*. [Geophysical Research Letters \(2016\), preprint, 1–22.](#) DOI:10.1002/2015GL067189.

GeoResLet2016-Bellprat-Supplement1.pdf, GeoResLet2016-Bellprat-Supplement2.pdf, GeoResLet2016-Bellprat-Supplement3.pdf, GeoResLet2016-Bellprat-Supplement4.pdf, GeoResLet2016-Bellprat-Supplement5.pdf, GeoResLet2016-Bellprat-Supplement6.docx

Event attribution aims to estimate the role of an external driver after the occurrence of an extreme weather and climate event by comparing the probability that the event occurs in two counterfactual worlds. These probabilities are typically computed using ensembles of climate simulations whose simulated probabilities are known to be imperfect. The implications of using imperfect models in this context are largely unknown, limited by the number of observed extreme events in the past to conduct a robust evaluation. Using an idealized framework, this model limitation is studied by generating large number of simulations with variable reliability in simulated probability. The framework illustrates that unreliable climate simulations are prone to overestimate the attributable risk to climate change. Climate model ensembles tend to be overconfident in their representation of the climate variability which leads to systematic increase in the attributable risk to an extreme event. Our results suggest that event attribution approaches comprising of a single climate model would benefit from ensemble calibration in order to account for model inadequacies similarly as operational forecasting systems.

YOKOYAMA 2016

Yusuke Yokoyama et al., *Widespread collapse of the Ross Ice Shelf during the late Holocene*. [PNAS 113 \(2016\), 2354–2359](#).

Yusuke Yokoyama, John B. Anderson, Masako Yamane, Lauren M. Simkins, Yosuke Miyairi, Takahiro Yamazaki, Mamito Koizumi, Hisami Suga, Kazuya Kushihara, Lindsay Prothro, Hiroyasu Hasumi, John R. Southon & Naohiko Ohkouchi

The stability of modern ice shelves is threatened by atmospheric and oceanic warming. The geologic record of formerly glaciated continental shelves provides a window into the past of how ice shelves responded to a warming climate. Fields of deep (560 m), linear iceberg furrows on the outer, western Ross Sea continental shelf record an early post-Last Glacial Maximum episode of ice-shelf collapse that was followed by continuous retreat of the grounding line for ≈ 200 km. Runaway grounding line conditions culminated once the ice became pinned on shallow banks in the western Ross Sea. This early episode of ice-shelf collapse is not observed in

the eastern Ross Sea, where more episodic grounding line retreat took place. More widespread ($\approx 280,000 \text{ km}^2$) retreat of the ancestral Ross Ice Shelf occurred during the late Holocene. This event is recorded in sediment cores by a shift from terrigenous glaci-marine mud to diatomaceous open-marine sediment as well as an increase in radiogenic beryllium (^{10}Be) concentrations. The timing of ice-shelf breakup is constrained by compound specific radiocarbon ages, the first application of this technique systematically applied to Antarctic marine sediments. Breakup initiated around 5 ka, with the ice shelf reaching its current configuration ≈ 1.5 ka. In the eastern Ross Sea, the ice shelf retreated up to 100 km in about a thousand years. Three-dimensional thermodynamic ice-shelf/ocean modeling results and comparison with ice-core records indicate that ice-shelf breakup resulted from combined atmospheric warming and warm ocean currents impinging onto the continental shelf.

Keywords: ice shelf | Antarctica | radiocarbon | Ross Sea | ice sheet

Significance: The Ross Sea is a major drainage basin for the Antarctic Ice Sheet and contains the world's largest ice shelf. Newly acquired swath bathymetry data and sediment cores provide evidence for two episodes of ice-shelf collapse. Two novel geochemical proxies, compound specific radiocarbon dating and radiogenic beryllium (^{10}Be), constrain the timing of the most recent and widespread ($\approx 280,000 \text{ km}^2$) breakup as having occurred in the late Holocene. Three-dimensional ice-shelf/ocean modeling results and comparison with ice-core records indicate that oceanic and atmospheric warming caused ice-shelf collapse.

Klima Biologie

NELSEN 2016

Matthew P. Nelsen, William A. DiMichele, Shanan E. Peters & C. Kevin Boyce, *Delayed fungal evolution did not cause the Paleozoic peak in coal production*. [PNAS 113 \(2016\), 2442–2447](#).

[pnas113-02442-Supplement.xls](#)

Organic carbon burial plays a critical role in Earth systems, influencing atmospheric O_2 and CO_2 concentrations and, thereby, climate. The Carboniferous Period of the Paleozoic is so named for massive, widespread coal deposits. A widely accepted explanation for this peak in coal production is a temporal lag between the evolution of abundant lignin production in woody plants and the subsequent evolution of lignin-degrading Agaricomycetes fungi, resulting in a period when vast amounts of lignin-rich plant material accumulated. Here, we reject this evolutionary lag hypothesis, based on assessment of phylogenomic, geochemical, paleontological, and stratigraphic evidence. Lignin-degrading Agaricomycetes may have been present before the Carboniferous, and lignin degradation was likely never restricted to them and their class II peroxidases, because lignin modification is known to occur via other enzymatic mechanisms in other fungal and bacterial lineages. Furthermore, a large proportion of Carboniferous coal horizons are dominated by unligified lycopsid periderm with equivalent coal accumulation rates continuing through several transitions between floral dominance by lignin-poor lycopsids and lignin-rich tree ferns and seed plants. Thus, biochemical composition had little relevance to coal accumulation. Throughout the fossil record, evidence of decay is pervasive in all organic matter exposed subaerially during deposition, and high coal accumulation rates have continued to the present wherever environmental conditions permit. Rather than a consequence of a temporal decoupling of evolutionary innovations between fungi and plants, Paleozoic coal abundance was likely the result of a unique combination of everwet tropical conditions and extensive depositional systems during the assembly of Pangea.

Keywords: lignin | carbon cycle | wood rot | fungi | lignin degradation

Significance: The Carboniferous-Permian marks the greatest coal-forming interval in Earth's history, contributing to glaciation and uniquely high oxygen concentrations at the time and fueling the modern Industrial Revolution. This peak in coal deposition is frequently attributed to an evolutionary lag between plant synthesis of the recalcitrant biopolymer lignin and fungal capacities for lignin degradation, resulting in massive accumulation of plant debris. Here, we demonstrate that lignin was of secondary importance in many floras and that shifts in lignin abundance had no obvious impact on coal formation. Evidence for lignin degradation—including fungal—was ubiquitous, and absence of lignin decay would have profoundly disrupted the carbon cycle. Instead, coal accumulation patterns implicate a unique combination of climate and tectonics during Pangea formation.

Metallzeiten

SERJEANTSON 2007

Dale Serjeantson, *Intensification of animal husbandry in the Late Bronze Age? The contribution of sheep and pigs*. In: COLIN HASELGROVE & RACHEL POPE (Hrsg.), *The Earlier Iron Age in Britain and the Near Continent*. (Oxford 2007), 80–93.

Much has been written about husbandry in Iron Age Britain, but there has been little discussion of how the patterns seen in the Iron Age were prefigured in the centuries before 600 BC. In this paper, I have analysed the particular character of sheep and pig keeping at the end of the Bronze Age in the south of Britain. There are some strong contrasts between sites even within one region, with pigs being found at a few sites in unusually high numbers. Earlier work has shown that at some sites, cattle were kept mainly for milk. Here, using the same arguments, I have shown that sheep were maintained in a manner which suggests that they too were specialised for the production of milk at some settlements, a possibility that prehistorians have not seriously taken into account. The ability to specialise, and to keep contrasting herds and flocks, must reflect the diverse social and economic links that characterised Bronze Age societies.

The transformation of Bronze Age to Iron Age economies in Britain seems in part at least to have been brought about by a collapse of the prevailing bronze standard (Needham this volume), a collapse which can also be seen in animal husbandry. Settlements could no longer support pig keeping on any scale, as each one became more self-sufficient, although the intensive management of herds and flocks continued. The more fragmented societies and deteriorating climate of the early first millennium BC provided less freedom for communities to specialise at different settlements.

Neolithikum

LARSON 2014

Greger Larson & Dorian Q. Fuller, *The Evolution of Animal Domestication*. *Annual Review of Ecology, Evolution, and Systematics* 45 (2014), 115–136.

The domestication of plants and animals over the past 11,500 years has had a significant effect not just on the domesticated taxa but also on human evolution and on the biosphere as a whole. Decades of research into the geographical and chronological origins of domestic animals have led to a general understanding of

the pattern and process of domestication, though a number of significant questions remain unresolved. Here, building upon recent theoretical advances regarding the different pathways animals followed to become domesticated, we present a large-scale synthesis that addresses the global pattern of animal domestication alongside a discussion of the differential evolutionary processes that have shaped domestic animal populations. More specifically, we present a framework for understanding how unconscious selection characterized the earliest steps of animal domestication and the role of introgression and the importance of relaxed and positive selection in shaping modern domestic phenotypes and genomes.

Keywords: archaeology | genetics | livestock | introgression | selection | agriculture

ÖZDOĞAN 2014

Mehmet Özdoğan, *The Neolithic Collapse, or the Transition from the Pre-Pottery Neolithic to the Pottery Neolithic*. In: B. FINLAYSON & C. MAKAREWICZ (Hrsg.), *Settlement, Survey and Stone, Essays on Near Eastern Prehistory in Honour of Gary Rollefson*. (Berlin 2014), 169–175.

The final stages of the Pre-Pottery Neolithic, just before the onset of the Pottery Neolithic, is marked by substantial changes that can be observed in every aspect of the socio-cultural structure throughout the region; this process is occasionally defined as the Neolithic collapse. Whether due to climatic fluctuations, deterioration of the habitat, social turbulence, or demographic stress, this change had far-reaching consequences on a supra-regional level, as it coincides temporally with the rapid expansion of the Neolithic from the primary core area in the Near East to other regions. As it has generally been customary to base assessment on the evidence from the southern Levant, this paper will note relevant evidence from southeastern Turkey and present a conspectus on some of the implications of this collapse event.

SIKLÓSI 2013

Zsuzsanna Siklósi, *Traces of Social Inequality during the Late Neolithic in the Eastern Carpathian Basin*. *Dissertationes Pannonicae IV 3* (Budapest 2013).

All these phenomena clearly indicate social inequality within a given community and settlement, and the competition among smaller-scale social groups (e.g. families, lineages) in the Late Neolithic Eastern Hungary. Competition appearing on various levels, and emphasizing the significance of children's graves rather reflects social uncertainty. It also means that although people attempted to transmit acquired rank, a socially accepted system supporting this could not be established. However, our data do not have implications of consolidated hereditary social rank, and the establishment of a social elite, which would have restricted the access not only to prestige goods but also to the basic subsistence resources for other members of the community.