

## Literatur

### Aktuell

LUKAS 2014

Dieter Lukas & Tim Clutton-Brock, *Evolution of social monogamy in primates is not consistently associated with male infanticide*. [PNAS 111 \(2014\), E1674](#).

Our analyses of data for primates provide no evidence that the evolution of monogamy in primates follows a different pattern from the evolution of monogamy in other mammals. One possible explanation for the contrasting results of Opie et al. is that their analyses underestimated the frequency of male infanticide by classifying many polygynous species as not showing male infanticide on the basis of insufficient evidence. Our results indicate that models of evolution that do not assume constant change explain transitions in infanticide better, and these reconstructions provide no support for the suggestion that the distribution of male infanticide exerted an important influence on the evolution of monogamy either in primates or in other mammals.

MARCINKOWSKA 2014

Urszula M. Marcinkowska et al., *Cross-cultural variation in men's preference for sexual dimorphism in women's faces*. [Biology Letters \(2014\), preprint, 1–4. DOI:10.1098/rsbl.2013.0850](#).

[BiolLett2014-Marcinkowska-Supplement1.doc](#), [BiolLett2014-Marcinkowska-Supplement2.doc](#)

Urszula M. Marcinkowska, Mikhail V. Kozlov, Hua Jian Cai, Jorge Contreras-Garduño, Barnaby J. Dixson, Gavita A. Oana, Gwenaël Kaminski, Norman P. Li, Minna T. Lyons, Ike E. Onyishi, Keshav Prasai, Farid Pazhoohi, Pavol Prokop, Sandra L. Rosales Cardozo, Nicolle Sydney, Jose C. Yong & Markus J. Rantala

Both attractiveness judgements and mate preferences vary considerably cross-culturally. We investigated whether men's preference for femininity in women's faces varies between 28 countries with diverse health conditions by analysing responses of 1972 heterosexual participants. Although men in all countries preferred feminized over masculinized female faces, we found substantial differences between countries in the magnitude of men's preferences. Using an average femininity preference for each country, we found men's facial femininity preferences correlated positively with the health of the nation, which explained 50.4% of the variation among countries. The weakest preferences for femininity were found in Nepal and strongest in Japan. As high femininity in women is associated with lower success in competition for resources and lower dominance, it is possible that in harsher environments, men prefer cues to resource holding potential over high fecundity.

Subject Areas: behaviour, evolution

Keywords: facial preferences, femininity, national health, other-race effect

OPIE 2014

Christopher Opie, Quentin D. Atkinson, Robin I. M. Dunbar & Susanne Shultz, *Infanticide still drives primate monogamy, Reply to Lukas and Clutton-Brock*. [PNAS 111 \(2014\), E1675](#).

The relative merits of the data and methods aside, we think there is a more obvious reason for the difference in findings. As both papers highlight, rates of monogamy in primates are much higher than in other mammals, which suggests that a different mechanism was at work in the evolution of primate mating systems. This taxonomic difference is expected: infanticide risk in primates is driven by their unusually late weaning (because of unusually large brains), which creates a reproductive strategy problem for males. This issue is unlikely to arise in other mammals with their shorter development periods, making infanticide an unlikely selection factor for monogamy. We do not disagree with Lukas and Clutton-Brock's conclusions with regard to nonprimate mammals.

#### SCHEFFER 2014

Marten Scheffer, *The forgotten half of scientific thinking*. [PNAS 111 \(2014\), 6119](#).

Should we really set time and space apart for things that distract us from our jobs? Yes we should, because many of the breakthroughs in science were made by people who were distracted.

## Amerika

#### KRAFT 2014

Kraig H. Kraft, *Multiple lines of evidence for the origin of domesticated chili pepper, *Capsicum annuum*, in Mexico*. [PNAS 111 \(2014\), 6165–6170](#).

[pnas111-06165-Supplement1.pdf](#), [pnas111-06165-Supplement2.pdf](#), [pnas111-06165-Supplement3.tif](#), [pnas111-06165-Supplement4.pdf](#), [pnas111-06165-Supplement5.png](#), [pnas111-06165-Supplement6.xls](#)

Kraig H. Kraft, Cecil H. Brown, Gary P. Nabhan, Eike Luedeling, José de Jesús Luna Ruiz, Geo Coppens d'Eeckenbrugge, Robert J. Hijmans & Paul Gepts

The study of crop origins has traditionally involved identifying geographic areas of high morphological diversity, sampling populations of wild progenitor species, and the archaeological retrieval of macroremains. Recent investigations have added identification of plant microremains (phytoliths, pollen, and starch grains), biochemical and molecular genetic approaches, and dating through <sup>14</sup>C accelerator mass spectrometry. We investigate the origin of domesticated chili pepper, *Capsicum annuum*, by combining two approaches, species distribution modeling and paleobiolinguistics, with microsatellite genetic data and archaeobotanical data. The combination of these four lines of evidence yields consensus models indicating that domestication of *C. annuum* could have occurred in one or both of two areas of Mexico: northeastern Mexico and central-east Mexico. Genetic evidence shows more support for the more northern location, but jointly all four lines of evidence support central-east Mexico, where preceramic macroremains of chili pepper have been recovered in the Valley of Tehuacán. Located just to the east of this valley is the center of phylogenetic diversity of Proto-Otomanguan, a language spoken in mid-Holocene times and the oldest protolanguage for which a word for chili pepper reconstructs based on historical linguistics. For many crops, especially those that do not have a strong archaeobotanical record or phylogeographic pattern, it is difficult to precisely identify the time and place of their origin. Our results for chili pepper show that expressing all data in similar distance terms allows for combining contrasting lines of evidence and locating the region(s) where cultivation and domestication of a crop began.

## Bibel

FAUST 2003

Avraham Faust, *Abandonment, Urbanization, Resettlement and the Formation of the Israelite State*. *Near Eastern Archaeology* **66** (2003), 147–161.

The nature of the long-term processes discussed here does not allow them to be closely related to the events described in 1-2 Samuel and 1 Kings. Moreover, it is possible that even the nature of the texts themselves, written many years after the events and loaded with additional theological and political meanings, does not permit using them to reconstruct the events that preceded the establishment of the monarchy (Edelman 1997) but rather only general processes. The following, then, is only a general outline of the biblical description of the formation of the Israelite state.

According to the Bible, the central highland population was an acephalous society composed of various groups and tribes. These groups are depicted as being in confrontation with other groups in other parts of the country, as well as among themselves. This seems to be the reality described by the books of Judges and Samuel. Although various enemies are described, it seems as if the Philistines gradually became the major threat of the highland Israelite population. Following a series of confrontations, they gained the upper hand (e.g., 1 Sam 4–5). The Philistine pressure is described as leading to the formation of the Israelite monarchy (1 Sam 8:5-10:27). Indeed, following the formation of the state, the Bible describes a more balanced picture and the Philistines were driven out of the central highlands (1 Sam 14). Later, following the battle in the Jezreel Valley, the king died and the Israelite army was defeated (1 Sam 31). David, the new king, established authority over the central hill country after a long process during which he drove out the Philistines (2 Sam 5:17-25). Later he expanded his authority over most of the country and even to other regions (2 Sam. 8; 10; 12:26-31). Solomon inherited the kingdom and organized the state. He divided it into districts, built central cities and more (1 Kgs 4; 5:1-8; 9:15).

A comparison of the archaeological evidence with this brief summary of the biblical narrative on the processes that took place in ancient Israel during the eleventh to tenth centuries BCE raises some interesting points. The biblical text describes the state formation process as taking place during the second half of the eleventh century BCE in the central highlands, a picture that the abandonment of the small villages and hamlets and the concentration of population in larger sites supports both temporally and spatially. This was, to a large extent, a result of conflict with other groups, which also correlates with the biblical traditions regarding the confrontations with the Philistines. The formation of the state was accompanied by its expansion to other regions of the country, as can be seen by the expansion of the abandonment process. The biblical description concerning the time, the place and to some extent even the motives, for the processes discussed seems, in general outlines, to match the archaeological finds.

## Biologie

DOUST 2014

Andrew N. Doust, Lewis Lukens, Kenneth M. Olsen, Margarita Mauro-Herrera, Ann Meyer & Kimberly Rogers, *Beyond the single gene, How epistasis and gene-by-environment effects influence crop domestication*. *PNAS* **111** (2014), 6178–6183.

Domestication is a multifaceted evolutionary process, involving changes in individual genes, genetic interactions, and emergent phenotypes. There has been extensive discussion of the phenotypic characteristics of plant domestication, and recent research has started to identify the specific genes and mutational mechanisms that control domestication traits. However, there is an apparent disconnect between the simple genetic architecture described for many crop domestication traits, which should facilitate rapid phenotypic change under selection, and the slow rate of change reported from the archeobotanical record. A possible explanation involves the middle ground between individual genetic changes and their expression during development, where gene-by-gene (epistatic) and gene-by-environment interactions can modify the expression of phenotypes and opportunities for selection. These aspects of genetic architecture have the potential to significantly slow the speed of phenotypic evolution during crop domestication and improvement. Here we examine whether epistatic and gene-by-environment interactions have shaped how domestication traits have evolved. We review available evidence from the literature, and we analyze two domestication-related traits, shattering and flowering time, in a mapping population derived from a cross between domesticated foxtail millet and its wild progenitor. We find that compared with wild progenitor alleles, those favored during domestication often have large phenotypic effects and are relatively insensitive to genetic background and environmental effects. Consistent selection should thus be able to rapidly change traits during domestication. We conclude that if phenotypic evolution was slow during crop domestication, this is more likely due to cultural or historical factors than epistatic or environmental constraints.

QTL | genotype-by-environment interactions |  $G \times E$  | *Setaria* | domestication syndrome

#### FULLER 2014

Dorian Q. Fuller et al., *Convergent evolution and parallelism in plant domestication revealed by an expanding archaeological record*. [PNAS 111 \(2014\), 6147–6152](#).

pnas111-06147-Supplement1.docx, pnas111-06147-Supplement2.docx, pnas111-06147-Supplement3.docx, pnas111-06147-Supplement4.docx

Dorian Q. Fuller, Tim Denham, Manuel Arroyo-Kalin, Leilani Lucas, Chris J. Stevens, Ling Qin, Robin G. Allaby & Michael D. Purugganan

Recent increases in archeobotanical evidence offer insights into the processes of plant domestication and agricultural origins, which evolved in parallel in several world regions. Many different crop species underwent convergent evolution and acquired domestication syndrome traits. For a growing number of seed crop species, these traits can be quantified by proxy from archaeological evidence, providing measures of the rates of change during domestication. Among domestication traits, nonshattering cereal ears evolved more quickly in general than seed size. Nevertheless, most domestication traits show similarly slow rates of phenotypic change over several centuries to millennia, and these rates were similar across different regions of origin. Crops reproduced vegetatively, including tubers and many fruit trees, are less easily documented in terms of morphological domestication, but multiple lines of evidence outline some patterns in the development of vegicultural systems across the New World and Old World tropics. Pathways to plant domestication can also be compared in terms of the cultural and economic factors occurring at the start of the process. Whereas agricultural societies have tended to converge on higher population densities and sedentism, in some instances cultivation began among sedentary hunter-gatherers whereas more often it was initiated by mobile societies of hunter-gatherers or herder-gatherers.

archaeobotany | Neolithic | agriculture | archaeology | vegiculture

## GALVÁN 2014

Ismael Galván et al., *Chronic exposure to low-dose radiation at Chernobyl favors adaptation to oxidative stress in birds*. [Functional Ecology \(2014\), preprint, 1–46](#). DOI:10.1111/1365-2435.12283.

FuncEcol2014-Galvan-Supplement.pdf

Ismael Galván, Andrea Bonisoli-Alquati, Shanna Jenkinson, Ghanem Ghanem, Kazumasa Wakamatsu, Timothy A. Mousseau & Anders P. Møller

1. Ionizing radiation produces oxidative stress, but organisms can adapt to their exposure with physiological adaptive responses. However, the role of radioadaptive responses in wild populations remains poorly known.

2. At Chernobyl, studies of birds and other taxa including humans show that chronic exposure to radiation depletes antioxidants and increases oxidative damage. Here we present analyses of levels of the most important intracellular antioxidant (i.e., glutathione, GSH), its redox status, DNA damage and body condition in 16 species of birds exposed to radiation at Chernobyl. We use an approach that allows considering the individual bird as the sampling unit while controlling for phylogenetic effects, thus increasing the statistical power by avoiding the use of species means as done for most previous comparative studies.

3. As a consequence, we found a pattern radically different from previous studies in wild populations, showing that GSH levels and body condition increased, and oxidative stress and DNA damage decreased, with increasing background radiation. Thus, when several species are considered, the overall pattern indicates that birds are not negatively affected by chronic exposure to radiation and may even obtain beneficial hormetic effects following an adaptive response. Analysis of the phylogenetic signal supports the existence of adaptation in the studied traits, particularly in GSH levels and DNA damage.

4. We also show that, under equal levels of radiation, the birds that produce larger amounts of the pigment pheomelanin and lower amounts of eumelanin pay a cost in terms of decreased GSH levels, increased oxidative stress and DNA damage, and poorer body condition. Radiation, however, diminished another potential cost of pheomelanin, namely its tendency to produce free radicals when exposed to radiation, because it induced a change toward the production of less pro-oxidant forms of pheomelanin with higher benzothiazole-to-benzothiazine ratios, which may have facilitated the acclimation of birds to radiation exposure.

5. Our findings represent the first evidence of adaptation to ionizing radiation in wild animals, and confirm that pheomelanin synthesis represents an evolutionary constraint under stressful environmental conditions because it requires GSH consumption.

**Keywords:** adaptation, Chernobyl, ionizing radiation, oxidative stress, pheomelanin

## GIRDLAND FLINK 2014

Linus Girdland Flink et al., *Establishing the validity of domestication genes using DNA from ancient chickens*. [PNAS 111 \(2014\), 6184–6189](#).

Linus Girdland Flink, Richard Allen, Ross Barnett, Helena Malmström, Joris Peters, Jonas Eriksson, Leif Andersson, Keith Dobney & Greger Larson

Modern domestic plants and animals are subject to human-driven selection for desired phenotypic traits and behavior. Large-scale genetic studies of modern domestic populations and their wild relatives have revealed not only the genetic mechanisms underlying specific phenotypic traits, but also allowed for the identification of candidate domestication genes. Our understanding of the importance of these genes during the initial stages of the domestication process traditionally rests on the assumption that robust inferences about the past can be made on the basis

of modern genetic datasets. A growing body of evidence from ancient DNA studies, however, has revealed that ancient and even historic populations often bear little resemblance to their modern counterparts. Here, we test the temporal context of selection on specific genetic loci known to differentiate modern domestic chickens from their extant wild ancestors. We extracted DNA from 80 ancient chickens excavated from 12 European archaeological sites, dated from  $\approx 280$  B.C. to the 18th century A.D. We targeted three unlinked genetic loci: the mitochondrial control region, a gene associated with yellow skin color ( $\beta$ -carotene dioxygenase 2), and a putative domestication gene thought to be linked to photoperiod and reproduction (thyroid-stimulating hormone receptor, TSHR). Our results reveal significant variability in both nuclear genes, suggesting that the commonality of yellow skin in Western breeds and the near fixation of TSHR in all modern chickens took place only in the past 500 y. In addition, mitochondrial variation has increased as a result of recent admixture with exotic breeds. We conclude by emphasizing the perils of inferring the past from modern genetic data alone.

selective sweep | breed formation | animal domestication | Gallus gallus | cultural history

#### MARSHALL 2014

Fiona B. Marshall, Keith Dobney, Tim Denham & José M. Capriles, *Evaluating the roles of directed breeding and gene flow in animal domestication*. [PNAS 111 \(2014\), 6153–6158](#).

For the last 150 y scholars have focused upon the roles of intentional breeding and genetic isolation as fundamental to understanding the process of animal domestication. This analysis of ethnoarchaeological, archaeological, and genetic data suggests that long-term gene flow between wild and domestic stocks was much more common than previously assumed, and that selective breeding of females was largely absent during the early phases of animal domestication. These findings challenge assumptions about severe genetic bottlenecks during domestication, expectations regarding monophyletic origins, and interpretations of multiple domestications. The findings also raise new questions regarding ways in which behavioral and phenotypic domestication traits were developed and maintained.

reproductive isolation | selected breeding | zooarchaeology | donkey | pig

#### STEUER 2014

Patrick Steuer et al., *Does body mass convey a digestive advantage for large herbivores?* [Functional Ecology \(2014\), preprint, 1–8](#). DOI:10.1111/1365-2435.12275.

FuncEcol2014-Steuer-Supplement1.pdf, FuncEcol2014-Steuer-Supplement2.docx

Patrick Steuer, Karl-Heinz Südekum, Thomas Tütken, Dennis W. H. Müller, Jacques Kaandorp, Martin Bucher, Marcus Clauss & Jürgen Hummel

1. A key concept of body mass (BM) in niche separation of large herbivores assumes that the decrease in diet quality inherent to increasing BM (due to less selective feeding behaviour) is balanced by a simultaneous increase in digestive ability (due to longer retention times), resulting in no or less-than-expected reduction in digestibility (as measured in the animal as a result of diet quality and digestive ability). However, the second part of this concept has been challenged recently due to theoretical problems and mismatch with empirical data.

2. A proxy for digestibility, such as metabolic faecal nitrogen (MFN), will comprise both information on diet quality and digestive ability in free-ranging animals. In captive animals, if diet is kept constant, such a proxy can exclusively indicate digestive ability. Comparing freeranging and captive animals under such conditions,

one would expect an increase in MFN with BM in captive animals and no relationship between these measures in free-ranging animals if BM was related to digestive ability.

3. We compared captive ungulates on a consistent grass hay diet (17 species; 30–4000 kg BM) to a sample of free-ranging East African ungulates (19 species; 12–4000 kg BM). MFN was used as the major proxy for digestibility.

4. In captive animals, there was no influence of BM on MFN ( $P = 0.466$ ); for free-ranging animals, a significant decreasing effect of body mass on MFN ( $P = 0.002$ ) and therefore diet quality was found at a scaling of  $BM^{-0.15}$ .

5. In conclusion, scenarios that assume a compensation of the evident decrease in diet quality with BM via an increased digestive ability are not supported by this study. This does not rule out other feeding-related factors in facilitating large BM, such as compensation by an increased diet intake.

**Keywords:** African ungulates, Diet quality, faecal nitrogen, feeding ecology, Jarman–Bell principle

## Energie

VON DER ASSEN 2014

Niklas von der Assen & André Bardow, *Life cycle assessment of polyols for polyurethane production using CO<sub>2</sub> as feedstock, Insights from an industrial case study*. [Green Chemistry \(2014\), preprint, 1–20.](#)  
[DOI:10.1039/C4GC00513A.](#)

[GreenChem2014-vonderAssen-Supplement.pdf](#)

Polyethercarbonate polyols from carbon dioxide (CO<sub>2</sub>) are starting to be synthesized on industrial scale. These polyols can be further processed into polyurethanes enabling CO<sub>2</sub> to be utilized in large amounts. Utilization of CO<sub>2</sub> as alternative carbon feedstock for polyols is motivated from the potential to reduce greenhouse gas (GHG) emissions and fossil resource depletion. This article presents a life cycle assessment for production of CO<sub>2</sub>-based polyethercarbonate polyols in a real industrial pilot plant. The considered cradle-to-gate system boundaries include polyol production and all upstream processes such as provision of energy and feedstocks. In particular, provision of CO<sub>2</sub> from a lignite power plant equipped with a pilot plant for CO<sub>2</sub> capture is considered. Production of polyols with 20 wt % CO<sub>2</sub> in the polymer chains causes GHG emissions of 2.65–2.86 kg CO<sub>2</sub>-eq/kg and thus, do not act as GHG sink. However, compared to production of conventional polyether polyols, production of polyols with 20 wt % CO<sub>2</sub> allows for GHG reductions of 11–19%. Relating GHG emission reductions to the amount of CO<sub>2</sub> incorporated, up to three kg CO<sub>2</sub>-eq emissions can be avoided per CO<sub>2</sub> utilized. The use of fossil resources can be reduced by 13–16%. The impacts reductions increase with further increasing the CO<sub>2</sub> content in the polyols. All other investigated environmental impacts such as eutrophication, ionizing radiation, ozone depletion, particulate matter formation, photochemical oxidant formation, and terrestrial acidification are also lowered. Therefore, synthesis of polyethercarbonate polyols from CO<sub>2</sub> is clearly favorable compared to conventional polyether polyols from an environmental point of view.

## Grundlagen

GERBAULT 2014

Pascale Gerbault et al., *Storytelling and story testing in domestication*. [PNAS 111 \(2014\), 6159–6164.](#)

Pascale Gerbault, Robin G. Allaby, Nicole Boivin, Anna Rudzinski, Ilaria M. Grimaldi, J. Chris Pires, Cynthia Climer Vigueira, Keith Dobney, Kristen J. Gremillion, Loukas Barton, Manuel Arroyo-Kalin, Michael D. Purugganan, Rafael Rubio de Casas, Ruth Bollongino, Joachim Burger, Dorian Q. Fuller, Daniel G. Bradley, David J. Balding, Peter J. Richerson, M. Thomas P. Gilbert, Greger Larson & Mark G. Thomas

The domestication of plants and animals marks one of the most significant transitions in human, and indeed global, history. Traditionally, study of the domestication process was the exclusive domain of archaeologists and agricultural scientists; today it is an increasingly multidisciplinary enterprise that has come to involve the skills of evolutionary biologists and geneticists. Although the application of new information sources and methodologies has dramatically transformed our ability to study and understand domestication, it has also generated increasingly large and complex datasets, the interpretation of which is not straightforward. In particular, challenges of equifinality, evolutionary variance, and emergence of unexpected or counter-intuitive patterns all face researchers attempting to infer past processes directly from patterns in data. We argue that explicit modeling approaches, drawing upon emerging methodologies in statistics and population genetics, provide a powerful means of addressing these limitations. Modeling also offers an approach to analyzing datasets that avoids conclusions steered by implicit biases, and makes possible the formal integration of different data types. Here we outline some of the modeling approaches most relevant to current problems in domestication research, and demonstrate the ways in which simulation modeling is beginning to reshape our understanding of the domestication process.

model | inference | evolution | agriculture | Neolithic

#### GREMILLION 2014

Kristen J. Gremillion, Loukas Barton & Dolores R. Piperno, *Particularism and the retreat from theory in the archaeology of agricultural origins*. [PNAS 111 \(2014\), 6171–6177](#).

The introduction of new analytic methods and expansion of research into previously untapped regions have greatly increased the scale and resolution of data relevant to the origins of agriculture (OA). As a result, the recognition of varied historical pathways to agriculture and the continuum of management strategies have complicated the search for general explanations for the transition to food production. In this environment, higher-level theoretical frameworks are sometimes rejected on the grounds that they force conclusions that are incompatible with real-world variability. Some of those who take this position argue instead that OA should be explained in terms of local and historically contingent factors. This retreat from theory in favor of particularism is based on the faulty beliefs that complex phenomena such as agricultural origins demand equally complex explanations and that explanation is possible in the absence of theoretically based assumptions. The same scholars who are suspicious of generalization are reluctant to embrace evolutionary approaches to human behavior on the grounds that they are ahistorical, overly simplistic, and dismissive of agency and intent. We argue that these criticisms are misplaced and explain why a coherent theory of human behavior that acknowledges its evolutionary history is essential to advancing understanding of OA. Continued progress depends on the integration of human behavior and culture into the emerging synthesis of evolutionary developmental biology that informs contemporary research into plant and animal domestication.

evolutionary theory | behavioral ecology

## LARSON 2014

Greger Larson et al., *Current perspectives and the future of domestication studies*. [PNAS 111 \(2014\), 6139–6146](#).

Greger Larson, Dolores R. Piperno, Robin G. Allaby, Michael D. Purugganan, Leif Andersson, Manuel Arroyo-Kalin, Loukas Barton, Cynthia Climer Vigueira, Tim Denham, Keith Dobney, Andrew N. Doust, Paul Gepts, M. Thomas P. Gilbert, Kristen J. Gremillion, Leilani Lucas, Lewis Lukens, Fiona B. Marshall, Kenneth M. Olsen, J. Chris Pires, Peter J. Richerson, Rafael Rubio de Casas, Oris I. Sanjur, Mark G. Thomas & Dorian Q. Fuller

It is difficult to overstate the cultural and biological impacts that the domestication of plants and animals has had on our species. Fundamental questions regarding where, when, and how many times domestication took place have been of primary interest within a wide range of academic disciplines. Within the last two decades, the advent of new archaeological and genetic techniques has revolutionized our understanding of the pattern and process of domestication and agricultural origins that led to our modern way of life. In the spring of 2011, 25 scholars with a central interest in domestication representing the fields of genetics, archaeobotany, zooarchaeology, geoarchaeology, and archaeology met at the National Evolutionary Synthesis Center to discuss recent domestication research progress and identify challenges for the future. In this introduction to the resulting Special Feature, we present the state of the art in the field by discussing what is known about the spatial and temporal patterns of domestication, and controversies surrounding the speed, intentionality, and evolutionary aspects of the domestication process. We then highlight three key challenges for future research. We conclude by arguing that although recent progress has been impressive, the next decade will yield even more substantial insights not only into how domestication took place, but also when and where it did, and where and why it did not.

evolution | selection | agriculture | human ecology | human history

## Klima

### FAUST 2007

Avraham Faust & Yosef Ashkenazy, *Excess in precipitation as a cause for settlement decline along the Israeli coastal plain during the third millennium BC*. [Quaternary Research 68 \(2007\), 37–44](#).

Although the relations between climate and settlement are not straightforward, there is a general agreement that arid conditions are less favorable for human settlement in the semiarid Near East than humid conditions. Here we show that humid conditions resulted in the abandonment of settlements along the Israeli coastal plain. We first present archaeological evidence for a drastic decline in settlement along the Israeli coast during most of the third millennium BC (Early Bronze Age II–III). Then, based on archaeological and climatic evidence, we link this decline to an environmental change occurring at that time. We propose that increased precipitation intensified the already existing drainage problems and resulted in flooding, which led to the transformation of arable land into marshes and to the spread of diseases, gradually causing settlement decline and abandonment.

Keywords: Early Bronze; Archaeology; Environment; Israel; Coast; Settlement; Precipitation

## Mesolithikum

CZIESLA 1992

Erwin Cziesla, *Jäger und Sammler, Die mittlere Steinzeit im Landkreis Pirmasens*. (Brühl 1992), 142–290. Kapitel 7: Die mittlere Steinzeit; 8: Kulturgeschichte.

Im folgenden sollen die Umwelt- und Lebensverhältnisse während der mittleren Steinzeit, der Epoche der letzten europäischen Jäger- und Sammler-Gruppen, ausführlich beleuchtet werden. Der rote Faden soll die Frage nach der Lebensqualität sein. Diese ist zwar aus einem Abstand von mehr als acht Jahrtausenden und damit über 300 Generationen kaum noch abzuschätzen, trotzdem gibt es mittlerweile (ausreichend) viele Anhaltspunkte, die dieses auf den ersten Blick unmögliche Unterfangen dennoch gestatten. Zahlreiche Daten klimatologischer, biologischer und archäologischer Natur liegen vor, so daß eine Zusammenschau lohnenswert erscheint.

## Mittelpaläolithikum

VILLA 2014

Paola Villa & Wil Roebroeks, *Neandertal Demise, An Archaeological Analysis of the Modern Human Superiority Complex*. [PLoS ONE 9 \(2014\), e96424](#). DOI:10.1371/journal.pone.0096424.

[pone09-e96424-Supplement1.pdf](#), [pone09-e96424-Supplement2.pdf](#), [pone09-e96424-Supplement3.pdf](#)

Neandertals are the best-studied of all extinct hominins, with a rich fossil record sampling hundreds of individuals, roughly dating from between 350,000 and 40,000 years ago. Their distinct fossil remains have been retrieved from Portugal in the west to the Altai area in central Asia in the east and from below the waters of the North Sea in the north to a series of caves in Israel in the south. Having thrived in Eurasia for more than 300,000 years, Neandertals vanished from the record around 40,000 years ago, when modern humans entered Europe. Modern humans are usually seen as superior in a wide range of domains, including weaponry and subsistence strategies, which would have led to the demise of Neandertals. This systematic review of the archaeological records of Neandertals and their modern human contemporaries finds no support for such interpretations, as the Neandertal archaeological record is not different enough to explain the demise in terms of inferiority in archaeologically visible domains. Instead, current genetic data suggest that complex processes of interbreeding and assimilation may have been responsible for the disappearance of the specific Neandertal morphology from the fossil record.

WADLEY 2014

Lyn Wadley & Linda C. Prinsloo, *Experimental heat treatment of silcrete implies analogical reasoning in the Middle Stone Age*. [Journal of Human Evolution 70 \(2014\), 49–60](#).

Siliceous rocks that were not heated to high temperatures during their geological formation display improved knapping qualities when they are subjected to controlled heating. Experimental heat treatment of South African silcrete, using open fires of the kind used during the Middle Stone Age, shows that the process needed careful management, notwithstanding recent arguments to the contrary. Silcrete blocks fractured when heated on the surface of open fires or on coal beds, but were

heated without mishap when buried in sand below a fire. Three silcrete samples, a control, a block heated underground with maximum temperature between 400 and 500 °C and a block heated in an open fire with maximum temperature between 700 and 800 °C, were analysed with X-ray powder diffraction (XRD), X-ray fluorescence (XRF), optical microscopy, and both Fourier transform infrared (FTIR) and Raman spectroscopy. The results show that the volume expansion during the thermally induced  $\alpha$ - to  $\beta$ -quartz phase transformation and the volume contraction during cooling play a major role in the heat treatment of silcrete. Rapid heating or cooling through the phase transformation at 573 °C will cause fracture of the silcrete. Successful heat treatment requires controlling surface fire temperatures in order to obtain the appropriate underground temperatures to stay below the quartz inversion temperature. Heat treatment of rocks is a transformative technology that requires skilled use of fire. This process involves analogical reasoning, which is an attribute of complex cognition.

**Keywords:** Silcrete |  $\alpha$ - to  $\beta$ -quartz phase transformation | Controlled heating | Transformative technology | Complex cognition | Homo sapiens | South Africa

## Ostasien

### GROSS 2014

Briana L. Gross & Zhijun Zhao, *Archaeological and genetic insights into the origins of domesticated rice*. [PNAS 111 \(2014\), 6190–6197](#).

Rice (*Oryza sativa*) is one of the most important cereal grains in the world today and serves as a staple food source for more than half of the world's population. Research into when, where, and how rice was brought into cultivation and eventually domesticated, along with its development into a staple food source, is thus essential. These questions have been a point of nearly continuous research in both archaeology and genetics, and new information has continually come to light as theory, data acquisition, and analytical techniques have advanced over time. Here, we review the broad history of our scientific understanding of the rice domestication process from both an archaeological and genetic perspective and examine in detail the information that has come to light in both of these fields in the last 10 y. Current findings from genetics and archaeology are consistent with the domestication of *O. sativa japonica* in the Yangtze River valley of southern China. Interestingly, although it appears rice was cultivated in the area by as early as 8000 BP, the key domestication trait of nonshattering was not fixed for another 1,000 y or perhaps longer. Rice was also cultivated in India as early as 5000 BP, but the domesticated *indica* subspecies currently appears to be a product of the introgression of favorable alleles from *japonica*. These findings are reshaping our understanding of rice domestication and also have implications for understanding the complex evolutionary process of plant domestication.

*Oryza rufipogon* | *Oryza nivara* | domestication gene