Liste erstellt am 2014-01-27

Literatur

Afrika

LaViolette 2013

Adria LaViolette, *The Swahili world.* In: Peter Mitchell & Paul Lane (Hrsg.), *The Oxford Handbook of African Archaeology.* (Oxford 2013), 901–914.

Pierron 2014

Denis Pierron et al., *Genome-wide evidence of Austronesian–Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar.* PNAS **111** (2014), 936–941.

Denis Pierron, Harilanto Razafindrazaka, Luca Pagani, François-Xavier Ricaut, Tiago Antao, Mélanie Capredon, Clément Sambo, Chantal Radimilahy, Jean-Aimé Rakotoarisoa, Roger M. Blench, Thierry Letellier & Toomas Kivisild

Linguistic and cultural evidence suggest that Madagascar was the final point of two major dispersals of Austronesian- and Bantuspeaking populations. Today, the Mikea are described as the lastknown Malagasy population reported to be still practicing a hunter-gatherer lifestyle. It is unclear, however, whether the Mikea descend from a remnant population that existed before the arrival of Austronesian and Bantu agriculturalists or whether it is only their lifestyle that separates them from the other contemporary populations of South Madagascar. To address these questions we have performed a genome-wide analysis of >700,000 SNP markers on 21 Mikea, 24 Vezo, and 24 Temoro individuals, together with 50 individuals from Bajo and Lebbo populations from Indonesia. Our analyses of these data in the context of data available from other Southeast Asian and African populations reveal that all three Malagasy populations are derived from the same admixture event involving Austronesian and Bantu sources. In contrast to the fact that most of the vocabulary of the Malagasy speakers is derived from the Barito group of the Austronesian language family, we observe that only one-third of their genetic ancestry is related to the populations of the Java-Kalimantan-Sulawesi area. Because no additional ancestry components distinctive for the Mikea were found, it is likely that they have adopted their hunter-gatherer way of life through cultural reversion, and selection signals suggest a genetic adaptation to their new lifestyle.

settlement | migration | DNA

Sinclair 2000

Paul J. J. Sinclair & Thomas Håkansson, *The Swahili city-state culture.* In: Mogens Herman Hansen (Hrsg.), *A comparative study of thirty city-state cultures, An investigation conducted by the Copenhagen Polis Centre.* (Copenhagen 2000), 463–482.

The Swahili mji were micro-states. For instance, Kilwa's core territory was confined to the island. Even including a number of settlements on the mainland, its territory is unlikely to have reached more than 1000 km2. Zanzibar, covering ca 2,500 km2, was split up into a number of states, some centred on stone towns and some perhaps on country towns. On the Lamu archipelago, towns on Lamu, Pate and Manda are so close to one another that each must have had a very small territory, even considering hinterland extensions.

These micro-states were in fact city-states each consisting of a town and its immediate hinterland dotted with a number of other settlements, the mji being the political and religious centre and an important entrepot for long-distance trade. All the mji together form a city-state culture having, notwithstanding local variations in each case, the same religion (Islam), the same language (Swahili), a common architectural tradition and material culture, and the same kinship-based political organisation, often with elected kings and a significant component of decision-making by consensus. All these mji constitute an interacting network covering ca 3,000 km of coast and with extensions to the off-shore island archipelagos of Zanzibar and the Comores and northern Madagascar. Communication was mainly by sea along the coast, but also by land especially between neighbouring communities.

Aktuell

KINTIGH 2014

Keith W. Kintigh et al., *Grand challenges for archaeology*. PNAS **111** (2014), 879–880.

Keith W. Kintigh, Jeffrey H. Altschul, Mary C. Beaudry, Robert D. Drennan, Ann P. Kinzig, Timothy A. Kohler, W. Fredrick Limp, Herbert D. G. Maschner, William K. Michener, Timothy R. Pauketat, Peter Peregrine, Jeremy A. Sabloff, Tony J. Wilkinson, Henry T. Wright & Melinda A. Zeder

Although new archaeological field work will be needed, the greatest payoff will derive from exploiting the explosion in systematically collected archaeological data that has occurred since the mid-20th century, largely in response to laws protecting archaeological resources. Both the needed modeling and synthetic research will require far more comprehensive online access to thoroughly documented research data and to unpublished reports detailing the contextual information essential for the comparative analyses.

SARAMÄKI 2014

Jari Saramäki, E. A. Leicht, Eduardo López, Sam G. B. Roberts, Felix Reed-Tsochas & Robin I. M. Dunbar, *Persistence of social signatures in human communication*. PNAS **111** (2014), 942–947.

pnas111-00942-Supplement1.csv, pnas111-00942-Supplement2.csv

The social network maintained by a focal individual, or ego, is intrinsically dynamic and typically exhibits some turnover in membership over time as personal circumstances change. However, the consequences of such changes on the distribution of an ego's network ties are not well understood. Here we use a unique 18-mo dataset that combines mobile phone calls and survey data to track changes in the ego networks and communication patterns of students making the transition from school to university or work. Our analysis reveals that individuals display a distinctive and robust social signature, captured by how interactions are distributed across different alters. Notably, for a given ego, these social signatures tend to persist over time, despite considerable turnover in the identity of alters in the ego network. Thus, as new network members are added, some old network members either are replaced or receive fewer calls, preserving the overall distribution of calls across network members. This is likely to reflect the consequences of finite resources such as the time available for communication, the cognitive and emotional effort required to sustain close relationships, and the ability to make emotional investments.

quantitative sociology | personal relationships

WAHL 2014

Thomas Wahl, Francisco M. Calafat & Mark E. Luther, *Rapid changes in the seasonal sea level cycle along the US Gulf coast from the late 20th century*. Geophysical Research Letters (2014), preprint, 1–20. DOI:10.1002/2013GL058777.

Temporal variations of the seasonal sea level harmonics throughout the 20th and early 21st century along the United States Gulf coast are investigated. A significant amplification of the annual sea level cycle from the 1990s onwards is found, with both lower winter and higher summer sea levels in the eastern Gulf. Ancillary data are used to build a set of multiple regression models to explore the mechanisms driving the decadal variability and recent increase in the annual cycle. The results suggest that changes in the air surface temperature towards warmer summers and colder winters and changes in mean sea level pressure explain most of the amplitude increase. The changes in the seasonal sea level cycle are shown to have almost doubled the risk of hurricane induced flooding associated with sea level rise since the 1990s for the eastern and north-eastern Gulf of Mexico coastlines.

Key words Gulf of Mexico, coastal seasonal sea level, tide gauge data, atmospheric reanalysis, multiple linear regression models

ZIETSCH 2014

Brendan P. Zietsch, Ralf Kuja-Halkola, Hasse Walum & Karin J. H. Verweij, *Perfect genetic correlation between number of offspring and grandoffspring in an industrialized human population*. PNAS **111** (2014), 1032–1036.

Reproductive success is widely used as a measure of fitness. However, offspring quantity may not reflect the genetic contribution to subsequent generations if there is nonrandom variation in offspring quality. Offspring quality is likely to be an important component of human fitness, and tradeoffs between offspring quantity and quality have been reported. As such, studies using offspring quantity as a proxy for fitness may yield erroneous projections of evolutionary change, for example if there is little or no genetic variance in number of grandoffspring or if its genetic variance is to some extent independent of the genetic variance in number of offspring. To address this, we performed a quantitative genetic analysis on the reproductive history of 16,268 Swedish twins born between 1915 and 1929 and their offspring. There was significant sex limitation in the sources of familial variation, but the magnitudes of the genetic and environmental effects were the same in males and females. We found significant genetic variation in number of offspring and grandoffspring (heritability = 24 % and 16 %, respectively), and genetic variation in the two variables completely overlapped—i.e., there was a perfect genetic correlation between number of offspring and grandoffspring. Shared environment played a smaller but significant role in number of offspring and grandoffspring; again, there was a perfect shared environmental correlation between the two variables. These findings support the use of lifetime reproductive success as a proxy for fitness in populations like the one used here, but we caution against generalizing this conclusion to other kinds of human societies.

fertility | fecundity | children | grandchildren | selection

Amerika

DULIK 2012

Matthew C. Dulik et al., *Mitochondrial DNA and Y Chromosome Variation Provides Evidence for a Recent Common Ancestry between*

Native Americans and Indigenous Altaians. Journal of Human Genetics **90** (2012), 229–246.
JHumGen90-0229-Supplement.pdf
Matthew C. Dulik, Sergey I. Zhadanov, Ludmila P. Osipova, Ayken Askapuli, Lydia Gau, Omer Gokcumen, Samara Rubinstein & Theodore G. Schurr
The Altai region of southern Siberia has played a critical role in the peopling of northern Asia as an entry point into Siberia and a possible homeland for ancestral Native Americans. It has an old and rich history because humans have inhabited this area since the Paleolithic. Today, the Altai region is home to numerous Turkic-speaking ethnic groups, which have been divided into northern and southern clusters based on linguistic, cultural, and anthropological traits. To untangle Altaian genetic histories, we analyzed mtDNA and Y chromosome variation in northern and southern Altaian populations. All mtDNAs were assayed by PCR-RFLP analysis and control region sequencing, and the nonrecombining portion of the Y chromosome was scored for more than 100 biallelic markers and 17 Y-STRs. Based on these data, we noted differences in the origin and population history of Altaian ethnic groups, with northern Altaians appearing more like Yeniseian, Ugric, and Samoyedic speakers to the north, and southern Altaians having greater affinities to other Turkic speaking populations of southern Siberia and Central Asia. Moreover, high-resolution analysis of Y chromosome haplogroup Q has allowed us to reshape the phylogeny of this branch, making connections between populations of the New World and Old World more apparent and demonstrating that southern Altaians and Native Americans share a recent common ancestor. These results greatly enhance our understanding of the peopling of Siberia and the Americas.

Anthropologie

KIMBEL 2014

William H. Kimbel, Gen Suwa, Berhane Asfaw, Yoel Rak & Tim D. White, *Ardipithecus ramidus and the evolution of the human cranial base.* PNAS **111** (2014), 948–953.
pnas111-00948-Supplement1.xlsx, pnas111-00948-Supplement2.xlsx
The early Pliocene African hominoid Ardipithecus ramidus was diagnosed as a having a unique phylogenetic relationship with the Australopithecus + Homo clade based on nonhoning canine teeth, a foreshortened cranial base, and postcranial characters related to facultative bipedality. However, pedal and pelvic traits indicating substantial arboreality have raised arguments that this taxon may instead be an example of parallel evolution of human-like traits among apes around the time of the chimpanzee–human split. Here we investigated the basicranial morphology of Ar. ramidus for additional clues to its phylogenetic position with reference to African apes, humans, and Australopithecus. Besides a relatively anterior foramen magnum, humans differ from apes in the lateral shift of the carotid foramina, mediolateral abbreviation of the lateral tympanic, and a shortened, trapezoidal basioccipital element. These traits reflect a relative broadening of the central basicranium, a derived condition associated with changes in tympanic shape and the extent of its contact with the petrous. Ar. ramidus shares with Australopithecus each of these human-like modifications. We used the preserved morphology of ARA-VP 1/500 to estimate the missing basicranial length, drawing on consistent proportional relationships in apes and humans. Ar. ramidus is confirmed to have a relatively short basicranium, as in Australopithecus and Homo. Reorganization of the central cranial base is among the earliest morphological markers of the Ardipithecus + Australopithecus + Homo clade.

human origins | fossil record | skull | occipital bone | temporal bone

Meyer 2014

Matthias Meyer et al., *A mitochondrial genome sequence of a hominin from Sima de los Huesos*. nature **505** (2014), 403–406.

Matthias Meyer, Qiaomei Fu, Ayinuer Aximu-Petri, Isabelle Glocke, Birgit Nickel, Juan-Luis Arsuaga, Ignacio Martínez, Ana Gracia, José María Bermúdez de Castro, Eudald Carbonell & Svante Pääbo

Excavations of a complex of caves in the Sierra de Atapuerca in northern Spain have unearthed hominin fossils that range in age from the early Pleistocene to the Holocene1. One of these sites, the 'Sima de los Huesos' ('pit of bones'), has yielded the world's largest assemblage of Middle Pleistocene hominin fossils2,3, consisting of at least 28 individuals4 dated to over 300,000 years ago5. The skeletal remains share a number of morphological features with fossils classified as Homoheidelbergensisand also display distinct Neanderthalderived traits6–8. Here we determine an almost complete mitochondrial genome sequence of a hominin from Sima de los Huesos and show that it is closely related to the lineage leading to mitochondrial genomes of Denisovans9,10, an eastern Eurasian sister group to Neanderthals. Our results pave the way for DNA research on hominins from the Middle Pleistocene.

Biologie

Boulanger 2014

Matthew T. Boulanger & R. Lee Lyman, *Northeastern North American Pleistocene megafauna chronologically overlapped minimally with Paleoindians*. Quaternary Science Reviews **85** (2014), 35–46.

qsr085-0035-Supplement1.xlsx, qsr085-0035-Supplement2.xlsx, qsr085-0035-Supplement3.xlsx, qsr085-0035-Supplement4.xlsx

It has long been argued that specialized big-game-hunting Paleoindians were responsible for the extinction of three dozen large-bodied mammalian genera in North America. In northeastern North America, the overkill hypothesis cannot be tested on the basis of associations of Paleoindian artifacts and remains of extinct mammals because no unequivocal associations are known. The overkill hypothesis requires Paleoindians to be contemporaneous with extinct mammalian taxa and this provides a means to evaluate the hypothesis, but contemporaneity does not confirm overkill. Blitzkrieg may produce evidence of contemporaneity but it may not, rendering it difficult to test. Overkill and Blitzkrieg both require large megafaunal populations. Chronological data, Sporormiella abundance, genetics, and paleoclimatic data suggest megafauna populations declined prior to human colonization and people were only briefly contemporaneous with megafauna. Local Paleoindians may have only delivered the coup de grace to small scattered and isolated populations of megafauna.

Keywords: Extinction | Megafauna | North America | Paleoindian | Radiocarbon

Ričánková 2014

Věra Pavelková Ričánková, Jan Robovský & Jan Riegert, *Ecological Structure of Recent and Last Glacial Mammalian Faunas in Northern Eurasia, The Case of Altai-Sayan Refugium*. PLoS ONE **9** (2014), e85056. DOI:10.1371/journal.pone.0085056.

Pleistocene mammalian communities display unique features which differ from present-day faunas. The paleocommunities were characterized by the extraordinarily large body size of herbivores and predators and by their unique structure consisting of species now inhabiting geographically and ecologically distinct natural zones. These features were probably the result of the unique environmental conditions of ice age ecosystems. To analyze the ecological structure of Last Glacial and Recent mammal communities we classified the species into biome and trophic-size categories, using Principal Component analysis. We found a marked similarity in ecological structure between Recent eastern Altai-Sayan mammalian assemblages and comparable Pleistocene faunas. The composition of Last Glacial and Recent eastern Altai-Sayan assemblages were characterized by the occurrence of large herbivore and predator species associated with steppe, desert and alpine biomes. These three modern biomes harbor most of the surviving Pleistocene mammals. None of the analyzed Palearctic Last Glacial faunas showed affinity to the temperate forest, taiga, or tundra biome. The Eastern part of the AltaiSayan region could be considered a refugium of the Last Glacial-like mammalian assemblages. Glacial fauna seems to persist up to present in those areas where the forest belt does not separate alpine vegetation from the steppes and deserts.

Klima

LUPASCU 2014

M. Lupascu, J. M.Welker, U. Seibt, K. Maseyk, X. Xu & C. I. Czimczik, *High Arctic wetting reduces permafrost carbon feedbacks to climate warming*. nature climate change **4** (2014), 51–55.

NatClimCh04-051-Supplement.pdf

The carbon (C) balance of permafrost regions is predicted to be extremely sensitive to climatic changes1-3. Major uncertainties exist in the rate of permafrost thaw and associated C emissions (33-508 Pg C or 0.04-1.69 C by 2100; refs 2,3) and plant C uptake. In the High Arctic, semideserts retain unique soil-plant-permafrost interactions4,5 and heterogeneous soil C pools6 (>12 Pg C; ref. 7). Owing to its coastal proximity, marked changes are expected for High Arctic tundra8. With declining summer sea-ice cover9, these systems are simultaneously exposed to rising temperatures9, increases in precipitation10 and permafrost degradation11. Here we show, using measurements of tundra-atmosphere C fluxes and soil C sources (14C) at a long-term climate change experiment in northwest Greenland, that warming decreased the summer CO2 sink strength of semi-deserts by up to 55 %. In contrast, warming combined with wetting increased the CO2 sink strength by an order of magnitude. Further, wetting while relocating recently assimilated plant C into the deep soil decreased old C loss compared with the warming-only treatment. Consequently, the High Arctic has the potential to remain a strong C sink even as the rest of the permafrost region transitions to a net C source as a result of future global warming.

Methoden

KIRMANI 2014

Ahmed Kirmani, Dheera Venkatraman, Dongeek Shin, Andrea Colaço, Franco N. C. Wong, Jeffrey H. Shapiro & Vivek K. Goyal, *First-Photon Imaging*. science **343** (2014), 58–61.

s343-0058-Supplement.pdf, s343-0058-Supplement1.mov, s343-0058-Supplement2.mov

Imagers that use their own illumination can capture three-dimensional (3D) structure and reflectivity information. With photon-counting detectors, images can be acquired at extremely low photon fluxes. To suppress the Poisson noise inherent in low-flux operation, such imagers typically require hundreds of detected photons per pixel for accurate range and reflectivity determination. We introduce a low-flux imaging technique, called first-photon imaging, which is a computational imager that exploits spatial correlations found in real-world scenes and the physics of low-flux measurements. Our technique recovers 3D structure and reflectivity from the first detected photon at each pixel. We demonstrate simultaneous acquisition of sub–pulse duration range and 4-bit reflectivity information in the presence of high background noise. First-photon imaging may be of considerable value to both microscopy and remote sensing.

MATTICK 2012

John S. Mattick, *Rocking the foundations of molecular genetics*. PNAS **109** (2012), 16400–16401.

The available evidence not only suggests an intimate interplay between genetic and epigenetic inheritance, but also that this interplay may involve communication between the soma and the germline. This idea contravenes the so-called Weismann barrier, sometimes referred to as Biology's Second Law, which is based on flimsy evidence and a desire to distance Darwinian evolution from Lamarckian inheritance at the time of the Modern Evolutionary Synthesis. However, the belief that the soma and germline do not communicate is patently incorrect—as demonstrated by the multigenerational inheritance of RNAi-mediated phenotypes delivered to somatic cells in Caenorhabditis elegans.

Thus, if RNA editing can alter hardwired genetic information in a context-dependent manner, and thereby alter epigenetic memory, it is feasible that not only allelic but also environmental history may shape phenotype, and provide a far more plastic and dynamic inheritance platform than envisaged by the genetic orthodoxy of the past century.

Mittelpaläolithikum

HUBLIN 2009

Jean-Jacques Hublin, Wil Roebroeks, *Ebb and flow or regional extinctions? On the character of Neandertal occupation of northern environments*. Comptes Rendus Palevol **8** (2009), 503–509.

In the course of the last 500,000 years, the Neandertal lineage was the first human group to extensively colonize the middle latitudes of western Eurasia up to 55° N. Although Neandertals were able to adapt to a variety of environments, their ability to cope with extreme glacial environments seems to have been very limited. Depending on the climatic cycles, their presence in the northern environments was essentially discontinuous. The periodical abandonment of some areas is generally interpreted as resulting in a movement of northern populations into southern refuges and a subsequent recolonisation of the northern regions. Here, we argue that the current palaeo-ecological, archaeological and palaeogenetic evidence supports a model of local extinctions rather than a habitat tracking model.

Keywords: Neandertal; Climate; Demography; Mousterian; Glaciation; Interglacial; Refuge

Neolithikum

BALTER 2014

Michael Balter, *Monumental Roots*. science **343** (2014), 18–23.

The great stone monuments of prehistoric Britain, including Stonehenge, were born in a wave of innovation that apparently began on a remote Scottish island. Although cereal cultivation arrived in Britain around 4000 B.C.E., it was quickly supplanted in most of the region by herds of cattle, sheep, and pigs, according to work published last year in Antiquity by archaeologists Chris Stevens of Wessex Archaeology in the United Kingdom and Dorian Fuller of UCL. But Orkney and other Scottish islands were a major exception. For example, the recently excavated settlement called Ha'Breck, on the tiny island of Wyre northeast of Mainland, yielded tens of thousands of charred barley grains, more than any other Neolithic site in Britain. There was “a significant divergence in terms of subsistence practice between the mainland and the islands,” Stevens says.

One controversial idea is that northern Scotland (including the Orkney Islands) and England were colonized by different groups of European farmers, and that Orkney might even have been colonized twice. But were these supposed European newcomers responsible for the cultural innovations on Orkney? Yes, some researchers suggest, citing the common vole, Microtus arvalis. This grass-eating rodent lives all over continental Europe but is completely absent from the British Isles except for one place: the Orkney Islands. The so-called Orkney vole has long been a source of mystery, and its tiny bones have been found at many Neolithic sites on the islands.

GUBA 2011

Zsuzsanna Guba, Éva Hadadi, Ágnes Major, Tünde Furka, Emese Juhász, Judit Koós, Károly Nagy & Tamás Zeke, *HVS-I polymorphism screening of ancient human mitochondrial DNA provides evidence for N9a discontinuity and East Asian haplogroups in the Neolithic Hungary.* Journal of Human Genetics **56** (2011), 784–796.

JHumGen56-0784-Supplement1.ppt, JHumGen56-0784-Supplement2.ppt, JHumGen56-0784-Supplement3.doc, JHumGen56-0784-Supplement4.doc, JHumGen56-0784-Comment.pdf, JHumGen56-0784-Reply.pdf

Analysis of mitochondrial mutations in the HVS-I region is an effective method for ancient human populational studies. Discontinuous haplotype data between the first farmers and contemporary Europeans has been described before. Our contribution is based on a survey initiated on the Neolithic skeletons from Hungarian archaeological sites in the Alföld. This Lowland, the Hungarian Plain, is well excavated as an important region for spread of Neolithic culture from Near East and Balkans toward Central and Western Europe, started circa 8000 years ago. HVS-I sequences from nt15977 to nt16430 of 11 such specimens with sufficient mitochondrial DNA preservation among an extended Neolithic collection were analysed for polymorphisms, identifying 23 different ones. After assigning all single-nucleotide polymorphisms, a novel, N9a, N1a, C5, D1/G1a, M/R24 haplogroups were determined. On mitochondrial control mutations at nt16257 and nt16261, polymorphic PCRs were carried out to assess their distribution in remains. Neolithic data set was compared with contemporary Vác samples and references, resulting in higher frequency of N9a in Alföld as a remarkable genetic discontinuity. Our investigation is the first to study mutations form Neolithic of Hungary, resulting in an outcome of Far Eastern haplogroups in the Carpathian Basin. It is worth further investigation as a non-descendant theory, instead of a continuous population history, supporting genetic gaps between ancient and recent human populations.

Keywords: ancient DNA; mitochondrial control mutation; N9a haplogroup; neolithisation; polymorphic PCR

Humphrey 2014

Louise T. Humphrey et al., *Earliest evidence for caries and exploitation of starchy plant foods in Pleistocene hunter-gatherers from Morocco.* PNAS **111** (2014), 954–959.

Louise T. Humphrey, Isabelle De Groote, Jacob Morales, Nick Barton, Simon Collcutt, Christopher Bronk Ramsey & Abdeljalil Bouzouggar

Dental caries is an infectious disease that causes tooth decay. The high prevalence of dental caries in recent humans is attributed to more frequent consumption of plant foods rich in fermentable carbohydrates in food-producing societies. The transition from hunting and gathering to food production is associated with a change in the composition of the oral microbiota and broadly coincides with the estimated timing of a demographic expansion in Streptococcus mutans, a causative agent of human dental caries. Here we present evidence linking a high prevalence of caries to reliance on highly cariogenic wild plant foods in Pleistocene hunter-gatherers from North Africa, predating other high caries populations and the first signs of food production by several thousand years. Archaeological deposits at Grotte des Pigeons in Morocco document extensive evidence for human occupation during the Middle Stone Age and Later Stone Age (Iberomaurusian), and incorporate numerous human burials representing the earliest known cemetery in the Maghreb. Macrobotanical remains from occupational deposits dated between 15,000 and 13,700 cal B.P. provide evidence for systematic harvesting and processing of edible wild plants, including acorns and pine nuts. Analysis of oral pathology reveals an exceptionally high prevalence of caries (51.2 % of teeth in adult dentitions), comparable to modern industrialized populations with a diet high in refined sugars and processed cereals. We infer that increased reliance on wild plants rich in fermentable carbohydrates and changes in food processing caused an early shift toward a disease-associated oral microbiota in this population.

Larson 2005

Greger Larson et al., *Worldwide Phylogeography of Wild Boar Reveals Multiple Centers of Pig Domestication.* science **307** (2005), 1618–1621.

s307-1618-Supplement.pdf

Greger Larson, Keith Dobney, Umberto Albarella, Meiying Fang, Elizabeth Matisoo-Smith, Judith Robins, Stewart Lowden, Heather Finlayson, Tina Brand, Eske Willerslev, Peter Rowley-Conwy, Leif Andersson & Alan Cooper

Mitochondrial DNA (mtDNA) sequences from 686 wild and domestic pig specimens place the origin of wild boar in island Southeast Asia (ISEA), where they dispersed across Eurasia. Previous morphological and genetic evidence suggested pig domestication took place in a limited number of locations (principally the Near East and Far East). In contrast, new genetic data reveal multiple centers of domestication across Eurasia and that European, rather than Near Eastern, wild boar are the principal source of modern European domestic pigs.

Martínková 2013

Natália Martínková et al., *Divergent evolutionary processes associated with colonization of offshore islands.* Molecular Ecology **22** (2013), 5205–5220.

MolEcol22-5205-Supplement.pdf

Natália Martínková, Ross Barnett, Thomas Cucchi, Rahel Struchen, Marine Pascal, Michel Pascal, Martin C. Fischer, Thomas Higham, Selina Brace, Simon Y. W. Ho, Jean-Pierre Quéré, Paul O' Higgins, Laurent Excoffier, Gerald Heckel, A. Rus Hoelzel, Keith M. Dobney & Jeremy B. Searle

Oceanic islands have been a test ground for evolutionary theory, but here, we focus on the possibilities for evolutionary study created by offshore islands. These can be colonized through various means and by a wide range of species, including those with low dispersal capabilities. We use morphology, modern and ancient sequences of cytochrome b (cytb) and microsatellite genotypes to examine colonization history and evolutionary change associated with occupation of the Orkney archipelago by the common vole (Microtus arvalis), a species found in continental Europe but not in Britain. Among possible colonization scenarios, our results are most consistent with human introduction at least 5100 BP (confirmed by radiocarbon dating). We used approximate Bayesian computation of population history to infer the coast of Belgium as the possible source and estimated the evolutionary timescale using a Bayesian coalescent approach. We showed substantial morphological divergence of the island populations, including a size increase presumably driven by selection and reduced microsatellite variation likely reflecting founder events and genetic drift. More surprisingly, our results suggest that a recent and widespread cytb replacement event in the continental source area purged cytb variation there, whereas the ancestral diversity is largely retained in the colonized islands as a genetic ‘ark’. The replacement event in the continental M. arvalis was probably triggered by anthropogenic causes (land-use change). Our studies illustrate that small offshore islands can act as field laboratories for studying various evolutionary processes over relatively short timescales, informing about the mainland source area as well as the island.

Keywords: demographic analysis, genetic replacement, island colonization, Microtus arvalis, phylogeography

NIKITIN 2012

Alexey G. Nikitin, Jeremy R. Newton & Inna D. Potekhina, *Mitochondrial haplogroup C in ancient mitochondrial DNA from Ukraine extends the presence of East Eurasian genetic lineages in Neolithic Central and Eastern Europe*. Journal of Human Genetics **57** (2012), 610–612.

Recent studies of ancient mitochondrial DNA (mtDNA) lineages have revealed the presence of East Eurasian mtDNA haplogroups in the Central European Neolithic. Here we report the finding of East Eurasian lineages in ancient mtDNA from two Neolithic cemeteries of the North Pontic Region (NPR) in Ukraine. In our study, comprehensive haplotyping information was obtained for 7 out of 18 specimens. Although the majority of identified mtDNA haplogroups belonged to the traditional West Eurasian lineages of H and U, three specimens were determined to belong to the lineages of mtDNA haplogroup C. This find extends the presence of East Eurasian lineages in Neolithic Europe from the Carpathian Mountains to the northern shores of the Black Sea and provides the first genetic account of Neolithic mtDNA lineages from the NPR.

Keywords: archeogenetics; Dnieper-Donets Culture complex; mitochondrial DNA (mtDNA) haplogroups; Neolithic; North Pontic Region

Physik

BERGER 1955

Walter Berger, *Zum Durchgang langsamer Elektronen durch Metallfolien*. Annalen der Physik **450** (1955), 394–405. vormals: 6. Folge, Band 15.

In Anlehnung an Arbeiten von Katz wird die Durchlässigkeit chemisch niedergeschlagener Silberfolien für langsame Elektronen von 0 bis 200 eV untersucht, wobei es gelingt, durch weitgehende Ausschaltung systematischer Fehler zuverlässige, auch an verschiedenen Folien reproduzierbare Meßwerte zu erhalten.

Die Ursache der Durchlässigkeit wird mit dem Elektronenmikroskop ermittelt. Entgegen den bisherigen Anschauungen ergibt sich, daß die durchgelassenen Elektronen nicht durch eine homogene Folienfläche, sondern durch gleichmäßig uber die gesamte Folie verstreute kleine Löcher von etwa 1000 Å Durchmesser gegangen sind.

Es wird gezeigt, daß sehr wahrscheinlich auch bei früheren Untersuchungen die gleiche Ursache fur die Durchlässigkeit der Folien vorgelegen hat, die aber ohne Elektronenmikroskop nicht erkannt werden konnte.