

References

Aktuell

AMIGO 2016

Ignacio Amigo, *Science made me a better parent*. [science 350 \(2015\), 1286](#).

Chefs can cook delightful meals for their families. Musicians can enliven social gatherings with friends. And having medical doctors, mechanics, or lawyers on call can be a great help if you get into trouble. As a biochemist with a Ph.D. in molecular biology, however, I always felt that my professional skills were of little value outside the lab. Let's face it: As fun as they can be, cutting and pasting DNA and growing cells are not things that you do very often when you're home or out with friends. Until recently, I didn't think anything I had learned in the lab could be used in the rest of my life. Since I became a father, though, my view has been steadily changing.

KINTISCH 2016

Eli Kintisch, *Born to rewild*. [science 350 \(2015\), 1148–1151](#).

A father and son's quixotic quest to bring back a lost ecosystem—and save the world.

MOORAD 2016

Jacob A. Moorad & Daniel H. Nusse, *Evolution of maternal effect senescence*. [PNAS 113 \(2016\), 362–367](#).

Increased maternal age at reproduction is often associated with decreased offspring performance in numerous species of plants and animals (including humans). Current evolutionary theory considers such maternal effect senescence as part of a unified process of reproductive senescence, which is under identical age-specific selective pressures to fertility. We offer a novel theoretical perspective by combining William Hamilton's evolutionary model for aging with a quantitative genetic model of indirect genetic effects. We demonstrate that fertility and maternal effect senescence are likely to experience different patterns of age-specific selection and thus can evolve to take divergent forms. Applied to neonatal survival, we find that selection for maternal effects is the product of age-specific fertility and Hamilton's age-specific force of selection for fertility. Population genetic models show that senescence for these maternal effects can evolve in the absence of reproductive or actuarial senescence; this implies that maternal effect aging is a fundamentally distinct demographic manifestation of the evolution of aging. However, brief periods of increasingly beneficial maternal effects can evolve when fertility increases with age faster than cumulative survival declines. This is most likely to occur early in life. Our integration of theory provides a general framework with which to model, measure, and compare the evolutionary determinants of the social manifestations of aging. Extension of our maternal effects model to other ecological and social contexts could provide important insights into the drivers of the astonishing diversity of lifespans and aging patterns observed among species.

Keywords: aging | demography | indirect genetic effects | selection | social

Significance: Evolutionary theory underpins our understanding of the aging process. The many aspects of reproduction that decline with maternal age in

animals include number of offspring born, offspring size, and neonatal survival. Current theories of aging ignore potential differences in the evolutionary pressures on these traits. Here, we combine two important branches of evolutionary theory to allow consideration of age-dependent selection at both offspring and maternal levels. We show that we should actually expect the rates of age-related decline in female fertility and offspring performance to diverge under selection. Our model has the potential to significantly improve our understanding of the evolution of reproductive senescence and, more generally, the variability of aging patterns in nature.

STOKSTAD 2016

Erik Stokstad, *Bringing back the aurochs*. *science* **350** (2015), 1144–1147.

By conjuring the extinct ancestor of modern cattle, breeders are making Europe just a little wilder.

WIXTED 2016

John T. Wixted, Laura Mickes, John C. Dunn, Steven E. Clark & William Wells, *Estimating the reliability of eyewitness identifications from police lineups*. *PNAS* **113** (2016), 304–309.

Laboratory-based mock crime studies have often been interpreted to mean that (i) eyewitness confidence in an identification made from a lineup is a weak indicator of accuracy and (ii) sequential lineups are diagnostically superior to traditional simultaneous lineups. Largely as a result, juries are increasingly encouraged to disregard eyewitness confidence, and up to 30% of law enforcement agencies in the United States have adopted the sequential procedure. We conducted a field study of actual eyewitnesses who were assigned to simultaneous or sequential photo lineups in the Houston Police Department over a 1-y period. Identifications were made using a three-point confidence scale, and a signal detection model was used to analyze and interpret the results. Our findings suggest that (i) confidence in an eyewitness identification from a fair lineup is a highly reliable indicator of accuracy and (ii) if there is any difference in diagnostic accuracy between the two lineup formats, it likely favors the simultaneous procedure.

Keywords: eyewitness identification | confidence–accuracy relationship | simultaneous vs. sequential lineups

Significance: In contrast to prior research, recent studies of simulated crimes have reported that (i) eyewitness confidence can be a strong indicator of accuracy and (ii) traditional simultaneous lineups may be diagnostically superior to sequential lineups. The significance of our study is that these issues were investigated using actual eyewitnesses to a crime. Recent laboratory trends were confirmed: Eyewitness confidence was strongly related to accuracy, and simultaneous lineups were, if anything, diagnostically superior to sequential lineups. These results suggest that recent reforms in the legal system, which were based on the results of older research, may need to be reevaluated.

Archäologie

CASSIDY 2016

Lara M. Cassidy et al., *Neolithic and Bronze Age migration to Ireland and establishment of the insular Atlantic genome*. *PNAS* **113** (2016), 368–373.

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Lara M. Cassidy, Rui Martiniano, Eileen M. Murphy, Matthew D. Teasdale, James Mallory, Barrie Hartwell & Daniel G. Bradley

The Neolithic and Bronze Age transitions were profound cultural shifts catalyzed in parts of Europe by migrations, first of early farmers from the Near East and then Bronze Age herders from the Pontic Steppe. However, a decades-long, unresolved controversy is whether population change or cultural adoption occurred at the Atlantic edge, within the British Isles. We address this issue by using the first whole genome data from prehistoric Irish individuals. A Neolithic woman (3343–3020 cal BC) from a megalithic burial (10.3× coverage) possessed a genome of predominantly Near Eastern origin. She had some hunter–gatherer ancestry but belonged to a population of large effective size, suggesting a substantial influx of early farmers to the island. Three Bronze Age individuals from Rathlin Island (2026–1534 cal BC), including one high coverage (10.5×) genome, showed substantial Steppe genetic heritage indicating that the European population upheavals of the third millennium manifested all of the way from southern Siberia to the western ocean. This turnover invites the possibility of accompanying introduction of Indo-European, perhaps early Celtic, language. Irish Bronze Age haplotypic similarity is strongest within modern Irish, Scottish, and Welsh populations, and several important genetic variants that today show maximal or very high frequencies in Ireland appear at this horizon. These include those coding for lactase persistence, blue eye color, Y chromosome R1b haplotypes, and the hemochromatosis C282Y allele; to our knowledge, the first detection of a known Mendelian disease variant in prehistory. These findings together suggest the establishment of central attributes of the Irish genome 4,000 y ago.

Keywords: ancient DNA | genomics | population genetics

Significance: Modern Europe has been shaped by two episodes in prehistory, the advent of agriculture and later metallurgy. These innovations brought not only massive cultural change but also, in certain parts of the continent, a change in genetic structure. The manner in which these transitions affected the islands of Ireland and Britain on the northwestern edge of the continent remains the subject of debate. The first ancient whole genomes from Ireland, including two at high coverage, demonstrate that large-scale genetic shifts accompanied both transitions. We also observe a strong signal of continuity between modern day Irish populations and the Bronze Age individuals, one of whom is a carrier for the C282Y hemochromatosis mutation, which has its highest frequencies in Ireland today.

Methoden

DIAMOND 2016

Jared Diamond, *Sources of Chaco wood*. [nature 529 \(2016\), 31–33](#).

Tree rings can pinpoint the source of wood as well as how old it is. This method has now been used to identify the sources of timber used by the Native Americans who constructed the pre-Columbian ‘great houses’ of Chaco Canyon.

Neolithikum

COIA 2016

V. Coia et al., *Whole mitochondrial DNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman*. [Scientific Reports 6 \(2016\), 18932](#). DOI:10.1038/srep18932.

The Tyrolean Iceman is an extraordinarily well-preserved natural mummy that lived south of the Alpine ridge $\approx 5,200$ years before present (ybp), during the Copper Age. Despite studies that have investigated his genetic profile, the relation of the Iceman's maternal lineage with present-day mitochondrial variation remains elusive. Studies of the Iceman have shown that his mitochondrial DNA (mtDNA) belongs to a novel lineage of haplogroup K1 (K1f) not found in extant populations. We analyzed the complete mtDNA sequences of 42 haplogroup K bearing individuals from populations of the Eastern Italian Alps—putatively in genetic continuity with the Tyrolean Iceman—and compared his mitogenome with a large dataset of worldwide K1 sequences. Our results allow a re-definition of the K1 phylogeny, and indicate that the K1f haplogroup is absent or rare in present-day populations. We suggest that mtDNA Iceman's lineage could have disappeared during demographic events starting in Europe from $\approx 5,000$ ybp. Based on the comparison of our results with published data, we propose a scenario that could explain the apparent contrast between the phylogeographic features of maternal and paternal lineages of the Tyrolean Iceman within the context of the demographic dynamics happening in Europe from 8,000 ybp.