ARCHON CONFERENCE PATHWAYS TO THE PRESENT

JUNE 3, 2022

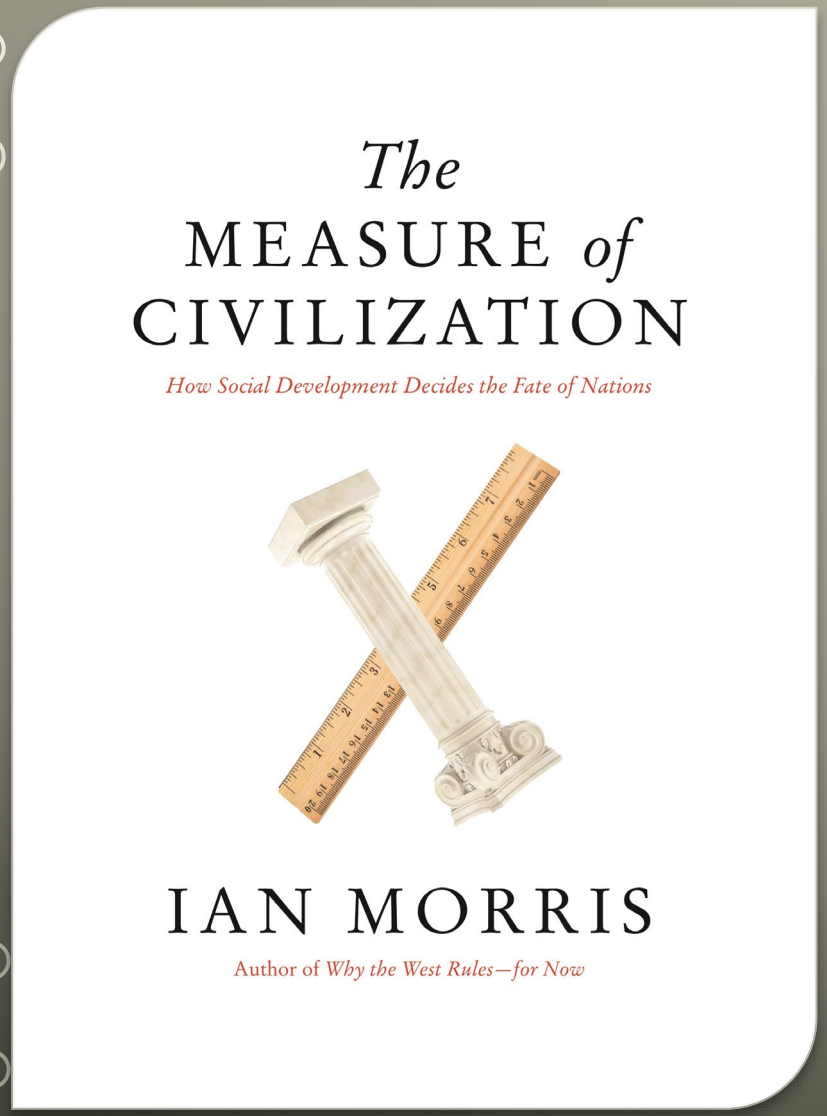
IDENTITY AND BELONGING

LEONARD RUTGERS

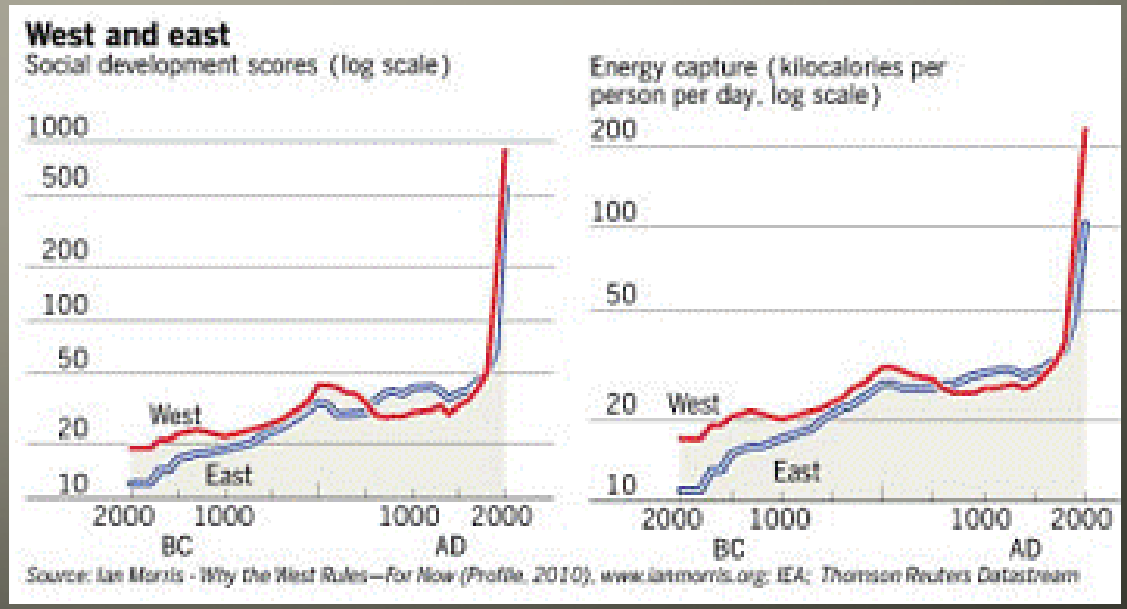
Universiteit Utrecht

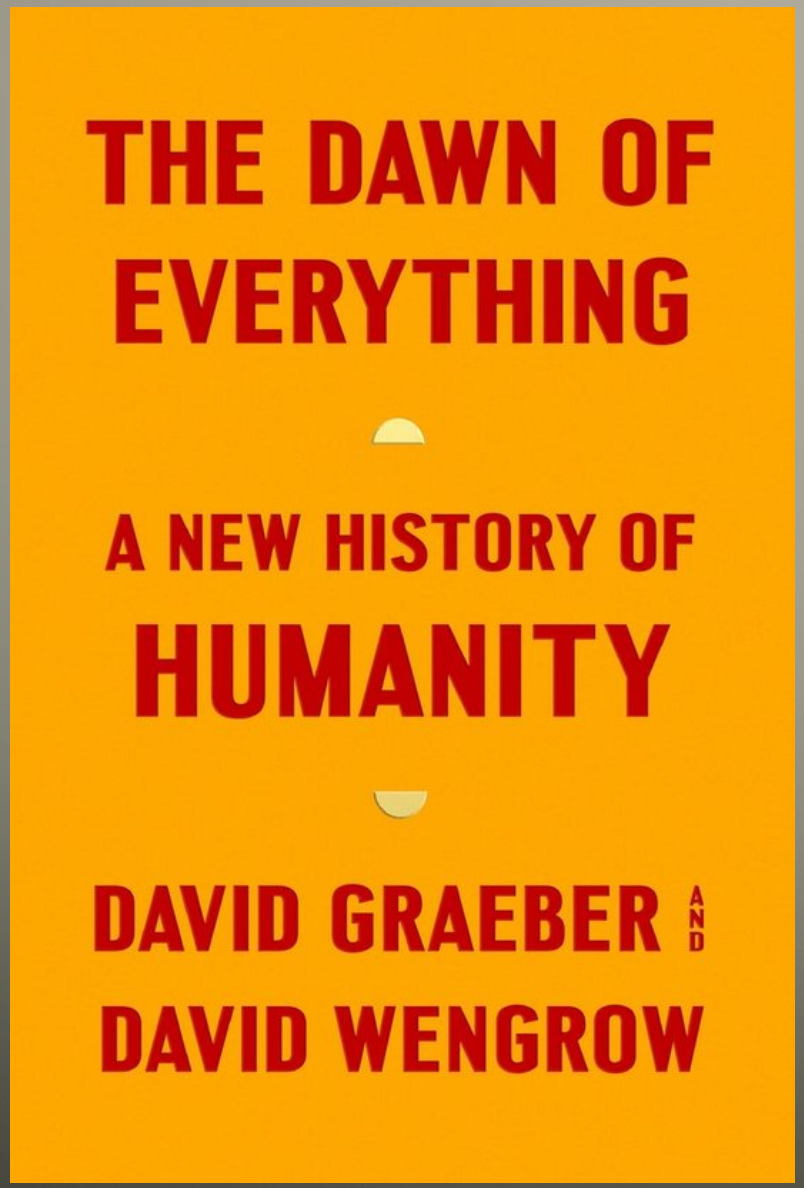
MIGRATION

Migrants at Mellila Golf Course - Spain/Morocco

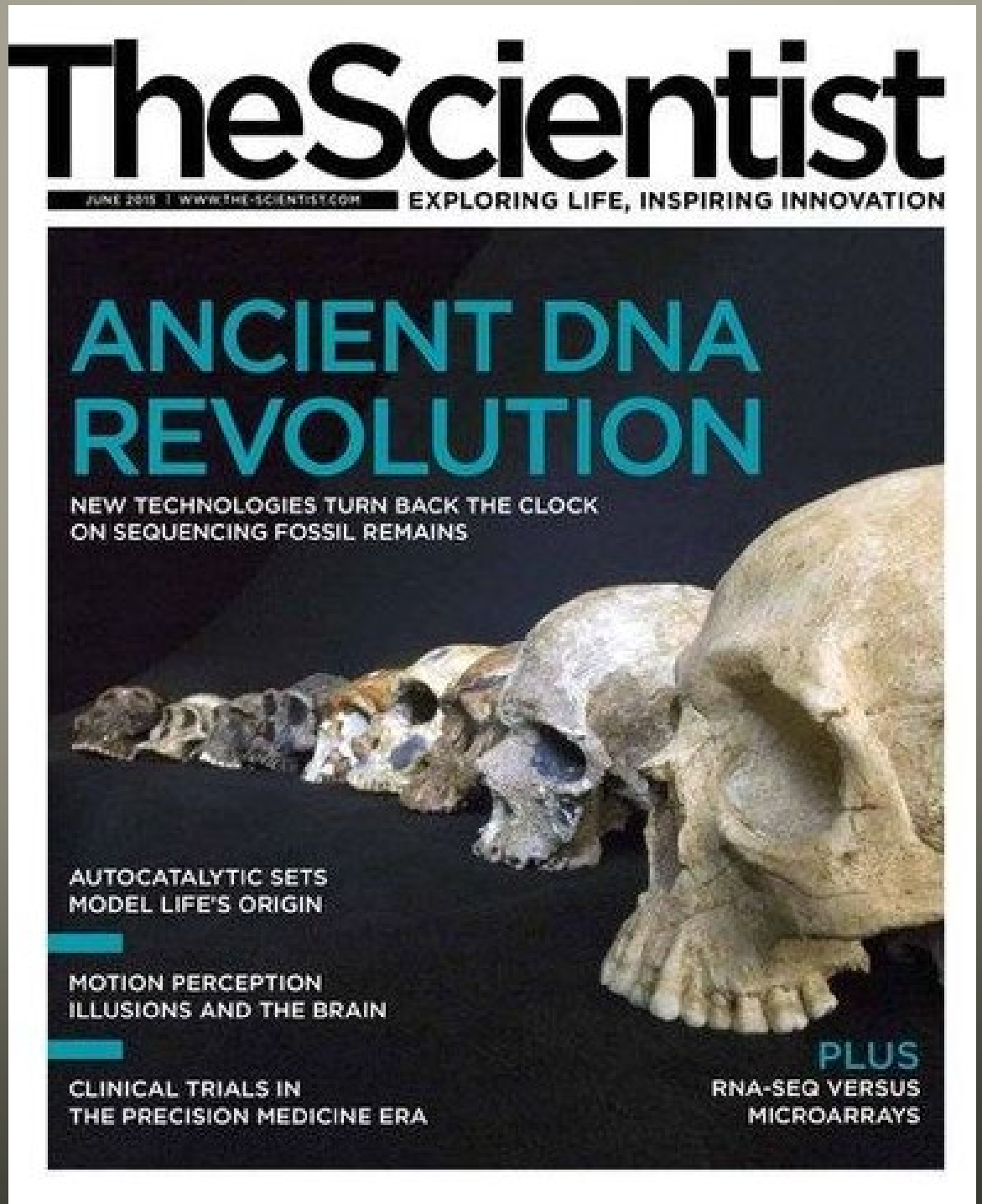


ARCHAEOLOGISTS LOOKING FOR PATTERNS




THE DAWN OF EVERYTHING
A NEW HISTORY OF HUMANITY
DAVID GRAEBER AND DAVID WENGROW


BELONGING
friendship
factions
class
treaty
religion
alienation
culture
isolation
conventions
disaffection
inclusion
exclusion
unity
family
nationality
community
bullying
alliance
comradeship
estrangement
traditions
customs
brotherhood
ethnicity
separation


TheScientist
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EXPLORING LIFE, INSPIRING INNOVATION
ANCIENT DNA REVOLUTION
NEW TECHNOLOGIES TURN BACK THE CLOCK ON SEQUENCING FOSSIL REMAINS
AUTOCATALYTIC SETS MODEL LIFE'S ORIGIN
MOTION PERCEPTION ILLUSIONS AND THE BRAIN
CLINICAL TRIALS IN THE PRECISION MEDICINE ERA
PLUS
RNA-SEQ VERSUS MICROARRAYS

EXAMPLES

The mixed genetic origin of the first farmers of Europe

Nina Marchi, Laura Winkelbach, Ilektra Schulz, Maxime Brami, Zuzana Hofmanová, Jens Blöcher, Carlos S. Reyna-Blanco, Yoan Diekmann, Alexandre Thiéry, Adamandia Kapopoulou, Vivian Link, Valérie Piuz, Susanne Kreutzer, Sylwia M. Figarska, Elisavet Ganiatsou, Albert Pukaj, Necmi Karul, Fokke Gerritsen, Joachim Pechtl, Joris Peters, Andrea Zeeb-Lanz, Eva Lenneis, Maria Teschler-Nicola, Sevasti Triantaphyllou, Sofija Stefanović, Christina Papageorgopoulou, Daniel Wegmann, Joachim Burger, Laurent Excoffier

doi: https://doi.org/10.1101/2020.11.23.394502

ANTHROPOLOGY

The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect

Cosimo Posth[1,2,3]*, Valentina Zaro[1,4†], Maria A. Spyrou[1,2†], Stefania Vai[4], Guido A. Gnecchi-Ruscone[1], Alessandra Modi[4], Alexander Peltzer[1], Angela Mötsch[1], Kathrin Nägele[1], Åshild J. Vågene[1,5], Elizabeth A. Nelson[1,6], Rita Radzevičiūtė[1], Cäcilia Freund[1], Lorenzo M. Bondioli[7], Luca Cappuccini[8], Hannah Frenzel[9], Elsa Pacciani[10], Francesco Boschin[11], Giulia Capecchi[11], Ivan Martini[12], Adriana Moroni[11], Stefano Ricci[11], Alessandra Sperduti[13,14], Maria Angela Turchetti[15], Alessandro Riga[4], Monica Zavattaro[16], Andrea Zifferero[17], Henrike O. Heyne[18,19], Eva Fernández-Domínguez[20], Guus J. Kroonen[21,22], Michael McCormick[23], Wolfgang Haak[1], Martina Lari[4], Guido Barbujani[24], Luca Bondioli[13,25], Kirsten I. Bos[1], David Caramelli[4]*, Johannes Krause[1,26]*

The origin, development, and legacy of the enigmatic Etruscan civilization from the central region of the Italian peninsula known as Etruria have been debated for centuries. Here we report a genomic time transect of 82 individuals spanning almost two millennia (800 BCE to 1000 CE) across Etruria and southern Italy. During the Iron Age, we detect a component of Indo-European–associated steppe ancestry and the lack of recent Anatolian-related admixture among the putative non–Indo-European–speaking Etruscans. Despite comprising diverse individuals of central European, northern African, and Near Eastern ancestry, the local gene pool is largely maintained across the first millennium BCE. This drastically changes during the Roman Imperial period where we report an abrupt population-wide shift to ~50% admixture with eastern Mediterranean ancestry. Last, we identify

RESEARCH ARTICLE

ANCIENT GENOMICS

Ancient Rome: A genetic crossroads of Europe and the Mediterranean

Margaret L. Antonio[1]*, Ziyue Gao[2,3]*, Hannah M. Moots[4]*, Michaela Lucci[5], Francesca Candilio[6,7], Susanna Sawyer[8], Victoria Oberreiter[8], Diego Calderon[1], Katharina Devitofranceschi[8], Rachael C. Aikens[1], Serena Aneli[9], Fulvio Bartoli[10], Alessandro Bedini[11], Olivia Cheronet[8], Daniel J. Cotter[3], Daniel M. Fernandes[8,12], Gabriella Gasperetti[13], Renata Grifoni[14], Alessandro Guidi[15], Francesco La Pastina[7], Ersilia Loreti[16], Daniele Manacorda[17], Giuseppe Matullo[9], Simona Morretta[18], Alessia Nava[5,19], Vincenzo Fiocchi Nicolai[20], Federico Nomi[15], Carlo Pavolini[21], Massimo Pentiricci[16], Philippe Pergola[22], Marina Piranomonte[23], Ryan Schmidt[24], Giandomenico Spinola[25], Alessandra Sperduti[19,26], Mauro Rubini[27,28], Luca Bondioli[19], Alfredo Coppa[7]†, Ron Pinhasi[8]†‡, Jonathan K. Pritchard[2,3,29]†‡

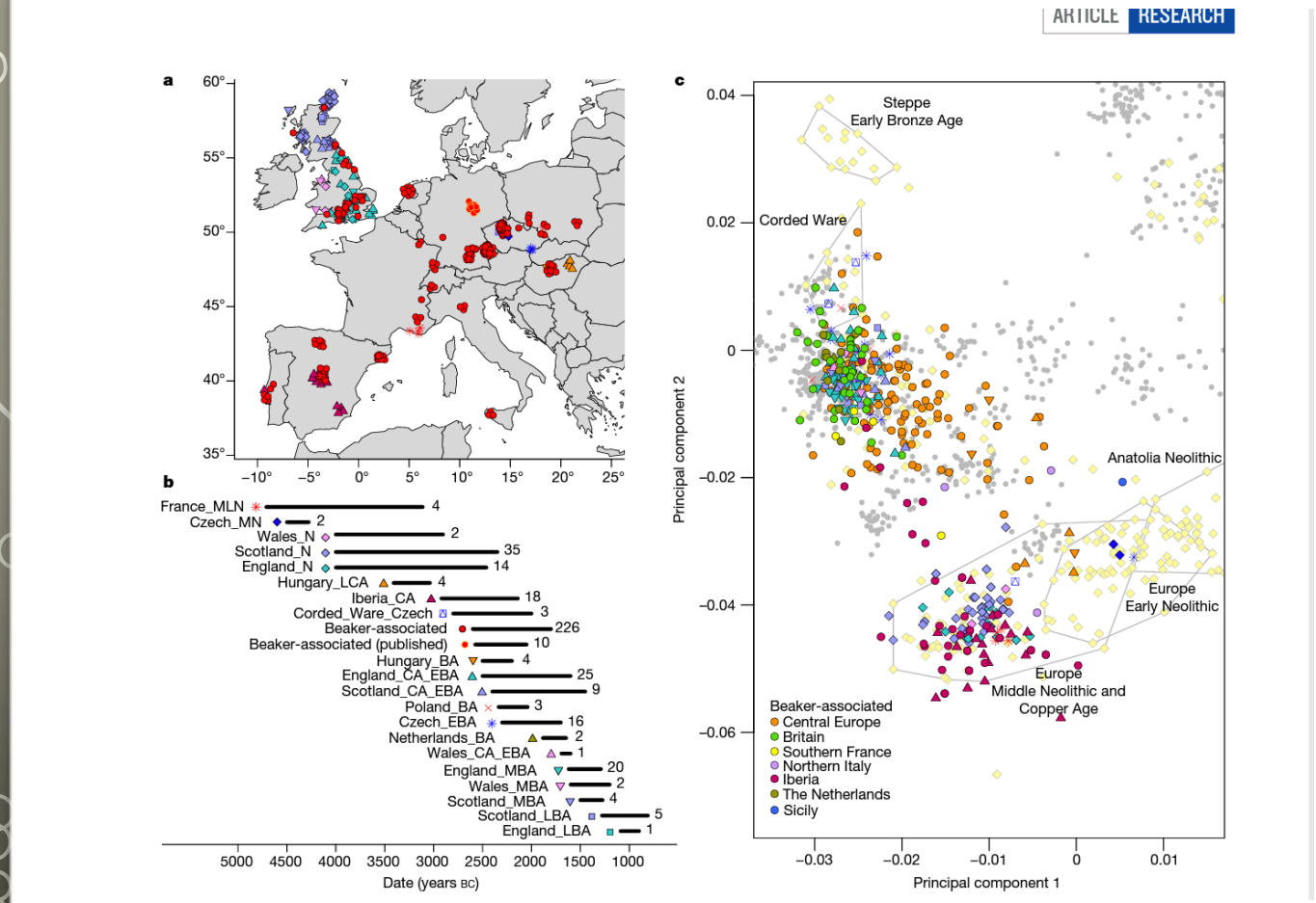
Ancient Rome was the capital of an empire of ~70 million inhabitants, but little is known about the genetics of ancient Romans. Here we present 127 genomes from 29 archaeological sites in and around Rome, spanning the past 12,000 years. We observe two major prehistoric ancestry transitions: one with the introduction of farming and another prior to the Iron Age. By the founding of Rome, the genetic composition of the region approximated that of modern Mediterranean populations. During the Imperial period, Rome's population received net immigration from the Near East, followed by an increase in genetic contributions from Europe. These ancestry shifts mirrored the geopolitical affiliations of Rome and were accompanied by marked interindividual diversity, reflecting gene flow from across the Mediterranean, Europe, and North Africa.

age (range 0.4 to 4.0×; table S2) and analyzed the data jointly with published ancient and modern genomes using principal component analysis (PCA), ADMIXTURE (*8*), *f*-statistics (*9*), and *qpAdm* admixture modeling (*10*) on pseudo-haploid genotypes; and ChromoPainter (*11*) on imputed diploid genotypes.

Individuals in this time series fall into three distinct genetic clusters according to chronology, as illustrated by PCA and ADMIXTURE (Fig. 2): (i) Mesolithic hunter-gatherers; (ii) early farmers (Neolithic and Copper Age individuals); and (iii) a broad historic cluster encompassing individuals from the Iron Age to the present. The historic individuals approximate modern Mediterranean and European populations in PCA space. However, there are highly variable ancestries among the historic individuals, both within and across time periods (Figs. 2 and 3).

The Mesolithic

The oldest genomes in our dataset are from three Mesolithic hunter-gatherers (10,000 to 7,000 BCE) from Grotta Continenza, a cave in the Apennine Mountains. In PCA, these individuals project close to Western hunter-gatherers (WHG) from elsewhere in Europe, including those from the Villabruna cave in northern Italy and from Grotta d'Oriente in Sicily (*12*–*15*)



BELL BEAKER CULTURE STUDY

NATURE **VOLUME 555,**

PAGES190–196

(2018)

MAX PLANCK INSTITUTE
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Curriculum Vitae
Publications

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Ancient DNA, Biology, and Disease

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Photo by Kayana Szymczak / The New York Times

OCT. 2021 RELEASE – Compendium of published ancient DNA data

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Apply for a post-doc to study human history with DNA

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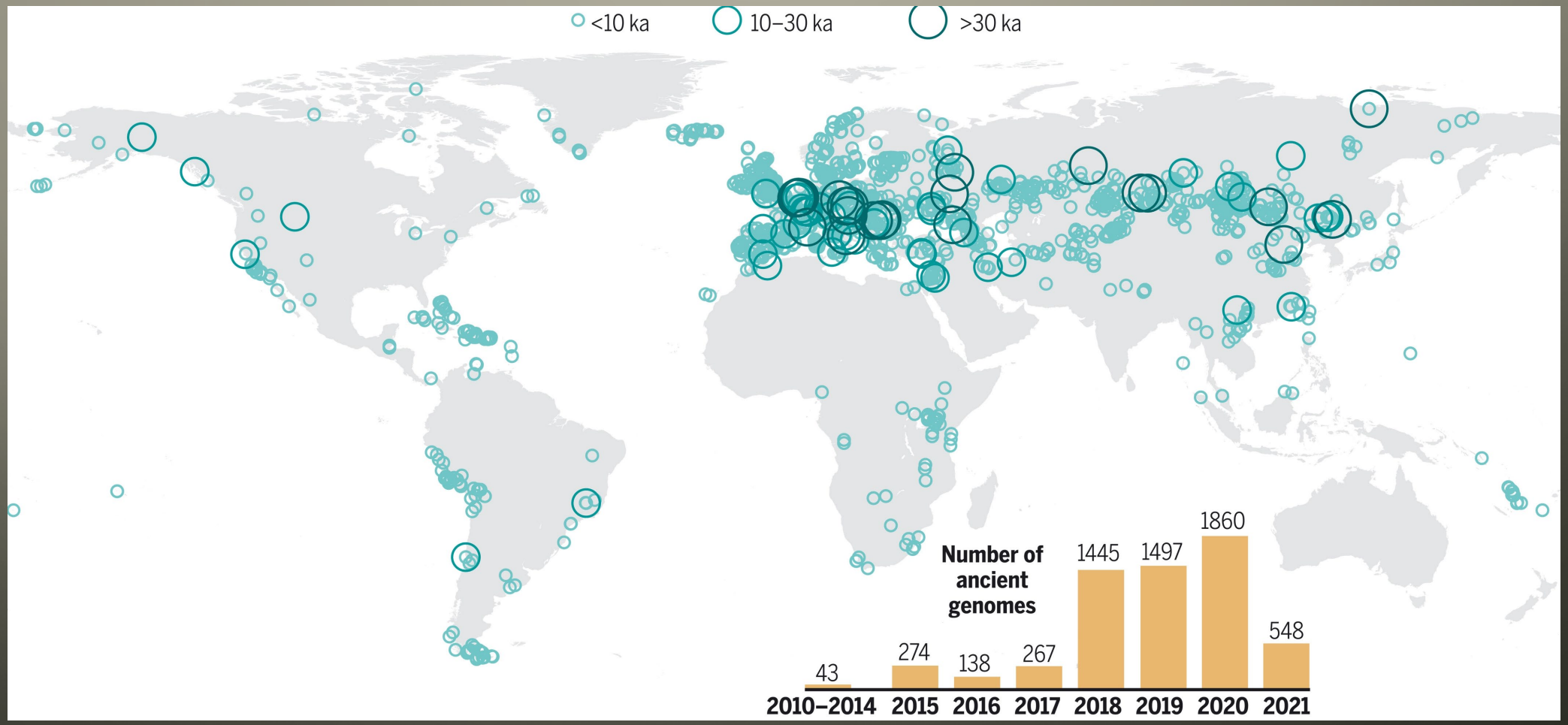
Genome-wide data from medieval German Jews show that the Ashkenazi founder event pre-dated the 14th century

Shamam Waldman, Daniel Backenroth, Éadaoin Harney, Stefan Flohr, Nadia C. Neff, Gina M. Buckley, Hila Fridman, Ali Akbari, Nadin Rohland, Swapan Mallick, Jorge Cano Nistal, Jin Yu, Nir Barzilai, Inga Peter, Gil Atzmon, Harry Ostrer, Todd Lencz, Yosef E. Maruvka, Maike Lämmerhirt, Leonard V. Rutgers, Virginie Renson, Keith M. Prufer, Stephan Schiffels, Harald Ringbauer, Karin Sczech, Shai Carmi, David Reich

doi: https://doi.org/10.1101/2022.05.13.491805

THE GREAT GAME

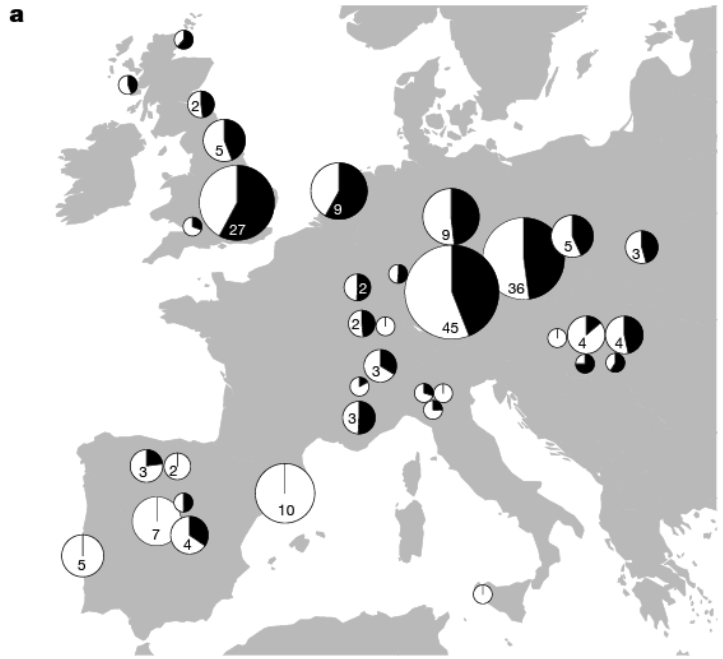


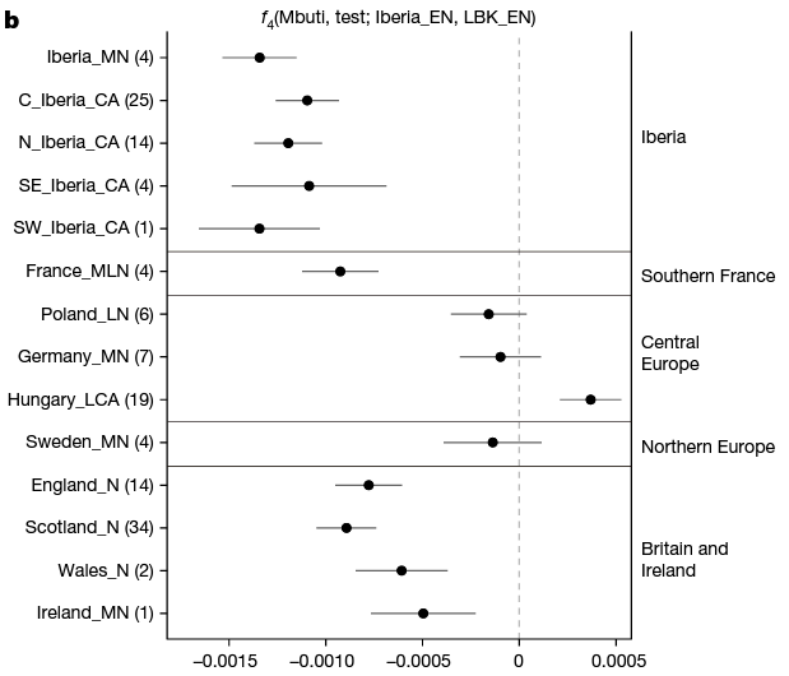
STEVENS AND PLETS

WHO'S IN THE DRIVER'S SEAT?

BELL BEAKER: CULTURAL VERSUS ETHNIC IDENTITY

RESEARCH ARTICLE





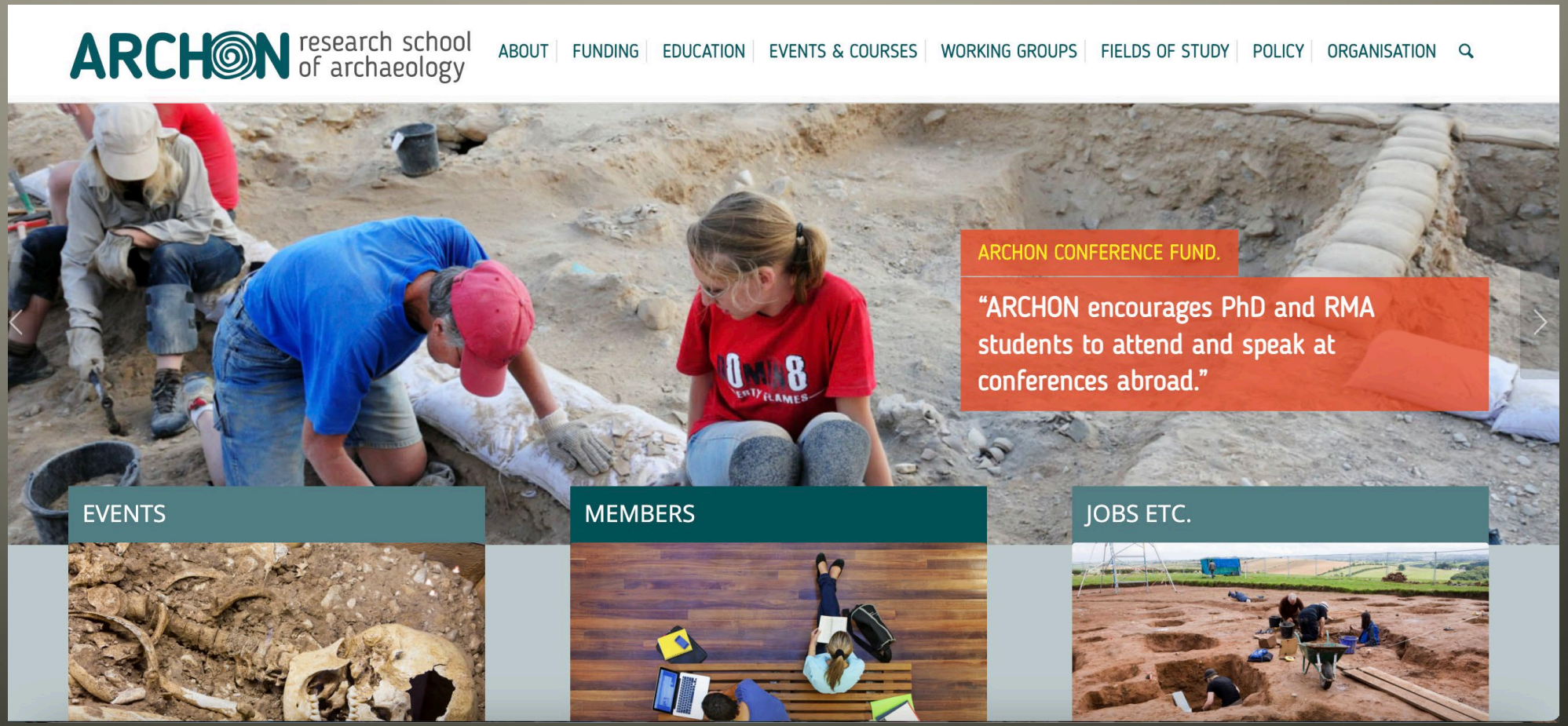
c

		Neolithic/Copper Age source population									
		Iberia_MN	C_Iberia_CA	N_Iberia_CA	SE_Iberia_CA	SW_Iberia_CA	Germany_MN	Poland_LN	Hungary_LCA	Sweden_MN	France_MLN
Test population	Beaker complex Iberia combined	1.66×10^{-1}*	7.23×10^{-1}*	1.76×10^{-5}	1.15×10^{-1}*	6.11×10^{-1}*	8.17×10^{-11}	3.36×10^{-6}	2.72×10^{-59}	6.28×10^{-3}	4.53×10^{-2}
	Beaker complex outside Iberia combined	1.11×10^{-12}	7.48×10^{-10}	2.18×10^{-10}	9.93×10^{-3}	1.04×10^{-2}	2.51×10^{-13}	1.84×10^{-1}*	6.05×10^{-55}	2.45×10^{-1}*	4.61×10^{-4}

Figure 2 | Investigating the genetic makeup of Beaker-complex-associated individuals. a, Proportion of steppe-related ancestry (in black)

LBK_EN) computed for European populations (number of individuals for each group is given in parentheses) before the emergence of the Beaker

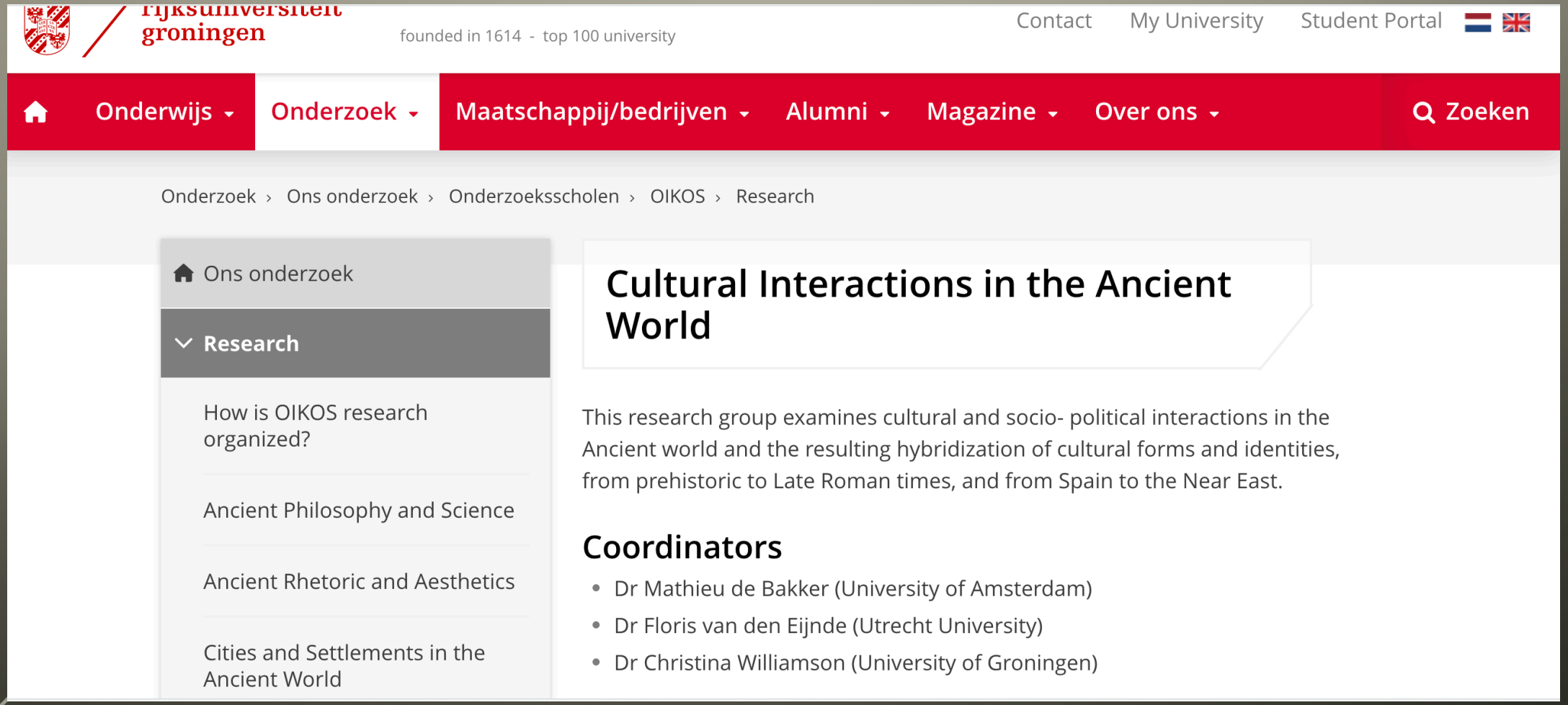
ARCHON AS OUR NATIONAL PLATFORM



IDENTITY FORMATION IN A GLOBAL AND GLOCAL WORLD

“MESOLITHIC SKELETON KNOWN AS ‘CHEDDAR MAN’ SHARES THE SAME DNA WITH ENGLISH TEACHER OF HISTORY!”

CROSS-FERTILIZATIONS



SUMMARY

1. Make full use of the DNA revolution while working on issues of identity and belonging
2. Work as a collective through ARCHON
3. Relate research to current societal issues
4. Train the next generation