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# Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent

Marta Pereira Verdugo<sup>1\*</sup>, Victoria E. Mullin<sup>1,2</sup> †, Amelie Scheu<sup>1,3\*</sup>, Valeria Mattiangeli<sup>1</sup>, Kevin G. Daly<sup>1</sup>, Pierpaolo Maisano Delser<sup>1,4</sup>, Andrew J. Hare<sup>1</sup>, Joachim Burger<sup>3</sup>, Matthew J. Collins<sup>5,6</sup>, Ron Kehati<sup>7</sup> †, Paula Hesse<sup>8</sup>, Deirdre Fulton<sup>9</sup>, Eberhard W. Sauer<sup>10</sup>, Fatemeh A. Mohaseb<sup>11,12</sup>, Hossein Davoudi<sup>12,13,14</sup>, Roya Khazaeli<sup>12</sup>, Johanna Lhuillier<sup>15</sup>, Claude Rapin<sup>16</sup>, Saeed Ebrahimi<sup>17</sup>, Mutalib Khasanov<sup>18</sup>, S. M. Farhad Vahidi<sup>19</sup>, David E. MacHugh<sup>20,21</sup>, Okan Ertugrul<sup>22</sup>, Chaido Koukoul-Chrysanthaki<sup>23</sup>, Adamantios Sampson<sup>24</sup>, George Kazantzis<sup>25</sup>, Ioannis Kontopoulos<sup>5</sup>, Jelena Bulatovic<sup>26</sup>, Ivana Stojanovic<sup>27</sup>, Abdesalam Mikdad<sup>28</sup>, Norbert Benecke<sup>29</sup>, Jörg Linstädter<sup>30</sup>, Mikhail Sablin<sup>31</sup>, Robin Bendrey<sup>10,32</sup>, Lionel Gourichon<sup>33</sup>, Benjamin S. Arbuckle<sup>34</sup>, Marjan Mashkour<sup>11,12,13</sup>, David Orton<sup>5</sup>, Liora Kolska Horwitz<sup>35</sup>, Matthew D. Teasdale<sup>1,5</sup>, Daniel G. Bradley<sup>1</sup> ‡

Genome-wide analysis of 67 ancient Near Eastern cattle, *Bos taurus*, remains reveals regional variation that has since been obscured by admixture in modern populations. Comparisons of genomes of early domestic cattle to their aurochs progenitors identify diverse origins with separate introgressions of wild stock. A later region-wide Bronze Age shift indicates rapid and widespread introgression of zebu, *Bos indicus*, from the Indus Valley. This process was likely stimulated at the onset of the current geological age, ~4.2 thousand years ago, by a widespread multicentury drought. In contrast to genome-wide admixture, mitochondrial DNA stasis supports that this introgression was male-driven, suggesting that selection of arid-adapted zebu bulls enhanced herd survival. This human-mediated migration of zebu-derived genetics has continued through millennia, altering tropical herding on each continent.

The extinct Eurasian aurochs (*Bos primigenius*) was domesticated circa 10,500 years before present (yr B.P.) within the restricted locality of the Upper Euphrates and Tigris drainages of the Fertile Crescent (1, 2). However, the true extent and nature of interactions between humans and aurochs resulting in modern day domestic cattle are obscure.

Mitochondrial DNA (mtDNA) diversity in modern *Bos taurus* cattle suggests a highly restricted initial domestic pool of ~80 females (3–5). However, a more complex relationship with wild populations is evidenced by introgression from local aurochs into British cattle and the genomic divergence of *B. indicus* (zebu) cattle

from the Indus Valley region (6, 7). Zebu genomic influence is pervasive in modern Near Eastern herds (8). Two theories account for this: one suggests an origin from genomically intermediate Near Eastern aurochs, whereas a second hypothesizes that these Near Eastern herds resulted from an introgression of domestic zebu genomes into the region from the east, either in a discrete active process—perhaps responding to climate fluctuation—or a passive diffusion over many millennia (9).

To analyze now-obscured early cattle genome strata from the region of *B. taurus* domestication, we retrieved genome-wide data from 67 ancient bovines (including six aurochs). These

date from Mesolithic to early Islamic periods, and despite poor preservation, which is typical of the region, we obtained an average genome coverage of 0.9× (table S1).

The pattern of genetic variation in extant cattle is well established. European *B. taurus*, West African *B. taurus*, and *B. indicus* of South Asian origin represent three distinct apices in plotted principal components (PCs) (Fig. 1A). Geographically intermediate populations, such as Near Eastern and East African animals, fall in genetically intermediate positions (7, 8, 10). Projecting ancient cattle genomes (provenance shown in Fig. 1B) against this genetic landscape (Fig. 1A), we observe that to the left of PC1, earlier (Neolithic and Bronze Age) genomes fall in three geographical clusters (a, Balkans; b, Anatolia/Iran; and c, southern Levant) along with modern European and African *B. taurus*, whereas *B. indicus* breeds are separated and represented on the far right of the PC plot (Fig. 1A). This suggests that cattle origins included two divergent aurochs populations that formed the basis of the *B. indicus*–*B. taurus* divide.

Six ancient aurochs genomes, including four from the greater Near East, provide additional context: two ~9000-year-old samples from the Levantine Aceramic village of Abu Ghosh (Abu1 and Abu2), a 7500-year-old sample from the early Anatolian settlement Çatalhöyük (Ch22), and a 7000-year-old Armenian aurochs (Gyu2) (11). These four genomes fall close to the Anatolia and Iran ancient domestic cattle cluster (Fig. 1A, cluster b) and reveal this as the oldest ancestral stratum of *B. taurus*. The genomic signature of this earliest population has been obscured in modern Near Eastern cattle by later admixture. From this group, we sequenced a well-preserved 8000-year-old Anatolian genome (Sub1) (11) to 13.5× coverage and use this in D statistics testing for zebu introgression in other ancient individuals (Fig. 2).

*B. indicus* cattle are adapted to, and predominate in, modern arid and tropical regions of the world (11). Zebu cattle originated circa 8000 yr B.P. (12). However, despite archaeological evidence for contact between civilizations of the Fertile Crescent region and the Indus Valley (9), the influence of the zebu genome is

<sup>1</sup> Smurfit Institute of Genetics, Trinity College Dublin, Dublin D02 PN40, Ireland. <sup>2</sup> Department of Earth Sciences, Natural History Museum, London SW7 5BD, UK. <sup>3</sup> Palaeogenetics Group, Institute of Organismic and Molecular Evolution (iOME), Johannes Gutenberg-University Mainz, 55099 Mainz, Germany. <sup>4</sup> Department of Zoology, University of Cambridge, Cambridge CB2 3EJ, UK. <sup>5</sup> BioArCh, University of York, York YO10 5DD, UK. <sup>6</sup> Museum of Natural History, University of Copenhagen, Copenhagen, Denmark. <sup>7</sup> 448 Shvil Hachalav Street, Nir Banim 7952500, Israel. <sup>8</sup> Jewish Studies Program, Department of Classics and Ancient Mediterranean Studies, The Pennsylvania State University, University Park, PA 16802, USA. <sup>9</sup> Department of Religion, Baylor University, Waco, TX 76798, USA. <sup>10</sup> School of History, Classics and Archaeology, University of Edinburgh, Edinburgh EH8 9AG, UK. <sup>11</sup> Archéozoologie et Archéobotanique (UMR 7209), CNRS, MNHN, UPMC, Sorbonne Universités, Paris, France. <sup>12</sup> Bioarchaeology Laboratory, Central Laboratory, University of Tehran, 1417634934 Tehran, Iran. <sup>13</sup> Osteology Department, National Museum of Iran, 1136918111 Tehran, Iran. <sup>14</sup> Department of Archaeology, Faculty of Humanities, Tarbiat Modares University, 111-14115 Tehran, Iran. <sup>15</sup> Archéorient Université Lyon 2, CNRS UMR 5133, Maison de Orient et de la Méditerranée, 69365 Lyon, France. <sup>16</sup> Archéologie d'Orient et d'Occident (AOROC, UMR 8546, CNRS ENS), Centre d'archéologie, 75005 Paris, France. <sup>17</sup> Faculty of Literature and Humanities, Islamic Azad University, 1711734353 Tehran, Iran. <sup>18</sup> Uzbekistan Institute of Archaeology of the Academy of Sciences of the Republic of Uzbekistan, 703051 Samarkand, Uzbekistan. <sup>19</sup> Agricultural Biotechnology Research Institute of Iran-North branch (ABRII), Agricultural Research, Education and Extension Organization, 4188958883 Rasht, Iran. <sup>20</sup> Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Dublin D04 V1W8, Ireland. <sup>21</sup> UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin D04 V1W8, Ireland. <sup>22</sup> Veterinary Faculty, Ankara University, 06110 Ankara, Turkey. <sup>23</sup> Hellenic Ministry of Culture and Sports, Department of Prehistoric and Classical Antiquities, and Museums, Serres 62 122, Greece. <sup>24</sup> Department of Mediterranean Studies, University of the Aegean, 85132 Rhodes, Greece. <sup>25</sup> Archaeological Museum of Aeani, 500 04, Kozani, Western Macedonia, Greece. <sup>26</sup> Laboratory for Bioarchaeology, Department of Archaeology, University of Belgrade, 11000 Belgrade, Serbia. <sup>27</sup> Institute of Archaeology, 11000 Belgrade, Serbia. <sup>28</sup> Institut National des Sciences de l'Archéologie et du Patrimoine de Maroc (INSAP) Hay Riad, Madinat al Ifrane, Rabat Instituts, 10000 Rabat, Morocco. <sup>29</sup> Department of Natural Sciences, German Archaeological Institute, 14195 Berlin, Germany. <sup>30</sup> Deutsches Archäologisches Institut, Kommission für Archäologie Außereuropäischer Kulturen (KAAK), 53173 Bonn, Germany. <sup>31</sup> Zoological Institute of the Russian Academy of Sciences, 199034 St Petersburg, Russia. <sup>32</sup> Department of Archaeology, University of Reading, Reading RG6 6AB, UK. <sup>33</sup> Université Côte d'Azur, CNRS, CEPAM (UMR 7264), 06357 Nice, France. <sup>34</sup> Department of Anthropology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA. <sup>35</sup> National Natural History Collections, Faculty of Life Sciences, The Hebrew University, 9190401 Jerusalem, Israel.

\*These authors contributed equally to this work. †Independent researcher

‡Corresponding author. Email: dbradley@tcd.ie

detectable in ancient Southwest Asian cattle only 4000 years later (Fig. 2). However, after ~4000 yr B.P., hybrid animals (median 35% indicine ancestry) are found across the Near East, from Central Asia and Iran to the Caucasus and Mediterranean shores of the southern Levant (table S2 and fig. S1). During this period, depictions and osteological evidence for *B. indicus* also appear in the region (9,13). In contrast to autosomal data, but similar to earlier work (14), we find persistence of *B. taurus* mitochondria, suggesting introgression may have been mediated by bulls (Fig. 2).

This sharp influx may have been stimulated by the onset of a period of increased aridity known as the 4.2-thousand-year abrupt climate

change event (9,15–17). This multicentury drought coincided with empire collapse in both Mesopotamia and Egypt as well as a decline in the Indus civilization and has been accepted as the boundary defining the onset of our current geological age, the Meghalayan (18).

Three features of this zebu influx after ~4000 yr B.P. attest that the influx was likely driven by adaptation and/or human agency rather than passive diffusion. First, the extent of indicine introgression does not follow a simple east-to-west gradient; for example, it is pronounced in Levantine genomes from the western edge of the Near East. Second, the introgression was widespread and took place in a relatively restricted time interval after four millennia of barely de-

tectable *B. indicus* influence. Third, it was plausibly driven by bull choice, as we observe up to ~70% autosomal genome change but a retained substratum of *B. taurus* mtDNA haplotypes (Fig. 2 and table S3). Hybrid *B. taurus*–*B. indicus* herds may have enabled the survival of communities under stress and perhaps facilitated expansion of herding into more-peripheral regions. Restocking after herd decline may have also been a factor. Westward human migration has been documented around this time (19,20) along with archaeological evidence for the appearance of other South Asian taxa such as water buffalo and Asian elephants in the Near East (21), suggesting the movement of large animals by people.

Before zebu admixture, ancient southern Levantine animals occupy a distinctive space within the PC plot (Fig. 1A, cluster c), toward modern African cattle and adjacent to a 9000-yr-B.P. Epipalaeolithic Moroccan aurochs (Th7). A 7000-yr-B.P. Mesolithic British aurochs genome (CPC98) (6) also plots away from the core Anatolia/Iran ancestral Near Eastern cluster and close to Neolithic Balkan (cluster a) and modern European cattle. These genetic affinities in ancient cattle suggest an early secondary recruitment from diverse wild populations.

Concordantly, D statistic tests of allele sharing by cattle population pairs with three divergent aurochs confirm that early cattle exhibit asymmetric relationships with different wild populations (Fig. 3). The most extreme deviations are found in comparisons featuring the *B. taurus* Levantine population (Fig. 1, cluster c); these share the least affinity with the British and Armenian aurochs ( $z$ -score  $> 5.67$ ;  $P < 10^{-5}$ ) but more with the Moroccan Epipalaeolithic sample. We infer that a distinct strain of aurochs, probably from the Levant and similar to those ranging across North Africa, had considerable input into early cattle in the southern Levant. The Mesolithic British aurochs also shows asymmetric affinity with the Neolithic Balkans samples, implying that the hybridization of European aurochs (6) was initiated more than 7000 years ago, close to the onset of human herding of cattle in Europe. These findings are supported by a qpgraph analysis (figs. S2 and S3) and cannot be explained by cattle-into-aurochs admixture, as both the British and Moroccan aurochs have securely predomestic dates. Although each of these three aurochs have divergent mtDNA haplotypes falling outside normal *B. taurus* variation, ancient domesticates display typical modern domestic haplotypes (fig. S4). This points toward common matrilineal origins for domestic taurine cattle and away from an archaeologically less parsimonious interpretation that our observed ancient genetic structure may have arisen from separate domestications; it also suggests that introgression may have been via mating with wild males. Sexually mature bulls, because of size and aggression, were likely the most dangerous stock in Neolithic villages, and thus unsupervised field insemination by aurochs bulls may have played a role in early herd management (22).

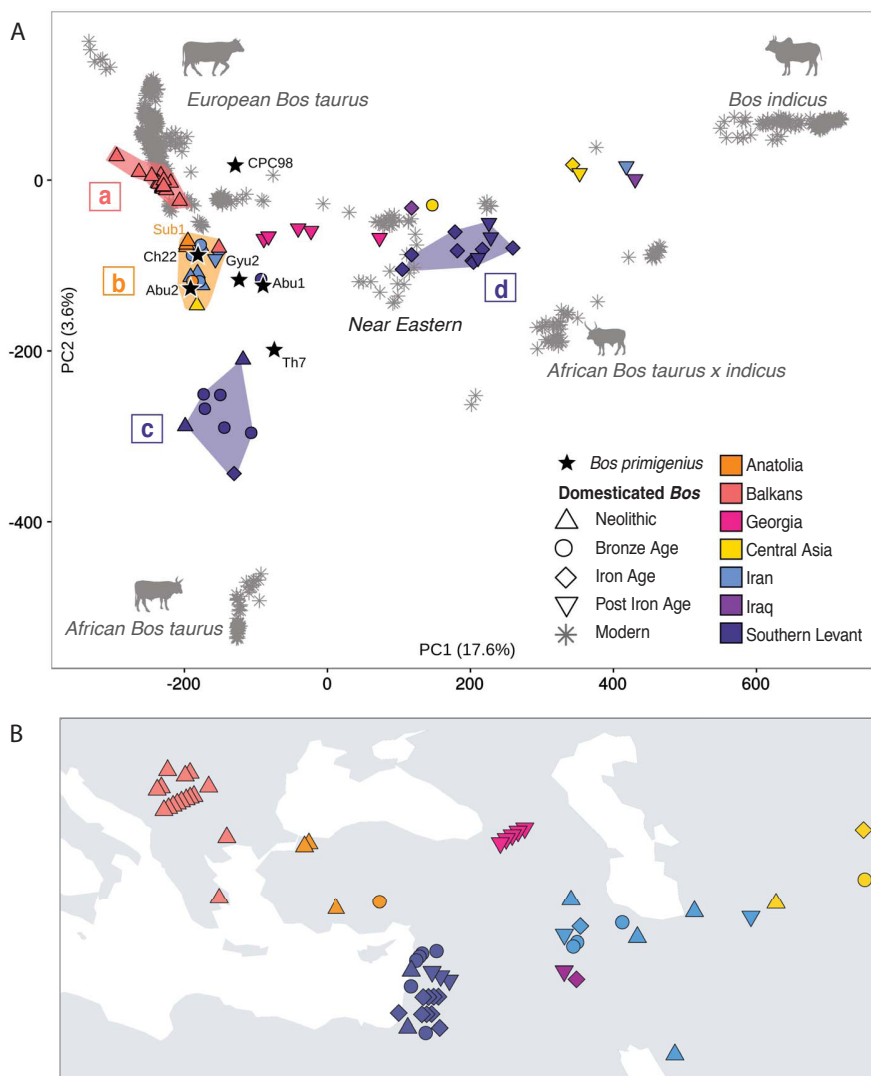


Fig. 1. Procrustes projection principal components analysis of ancient cattle. (A) Ancient animals are projected on modern 770K Bovine single-nucleotide polymorphism (SNP) genotypes, shown as background gray asterisks (figs. S1 and S2). Four clusters are highlighted: Neolithic Balkans, which plot with modern Europeans (a); a group of mainly Anatolian and Iranian cattle close to four aurochs from the Near East (b); and Levantine cattle that fall into two groups, a cluster of earlier samples (c) and a cluster of later samples (d) close to contemporary Near Eastern cattle with *B. indicus* admixture. (B) Approximate geographical distribution of ancient sample sites.

Fig. 2. Zebu introgression through time in the greater Near East. Whole genome  $D$  statistic calculations with a gaur (*B. gaurus*) as an outgroup and the Neolithic Anatolian domestic genome Sub1 as a representative nonadmixed individual (see inset). Lower coverage samples with <200 informative sites were excluded. A step change in zebu introgression is apparent circa 4000 yr B.P. MtDNA counts of taurine (gray) and the single zebu (black) mtDNA in ancient domestic cattle are graphed (bottom, with a shared time axis) in 250-year intervals.

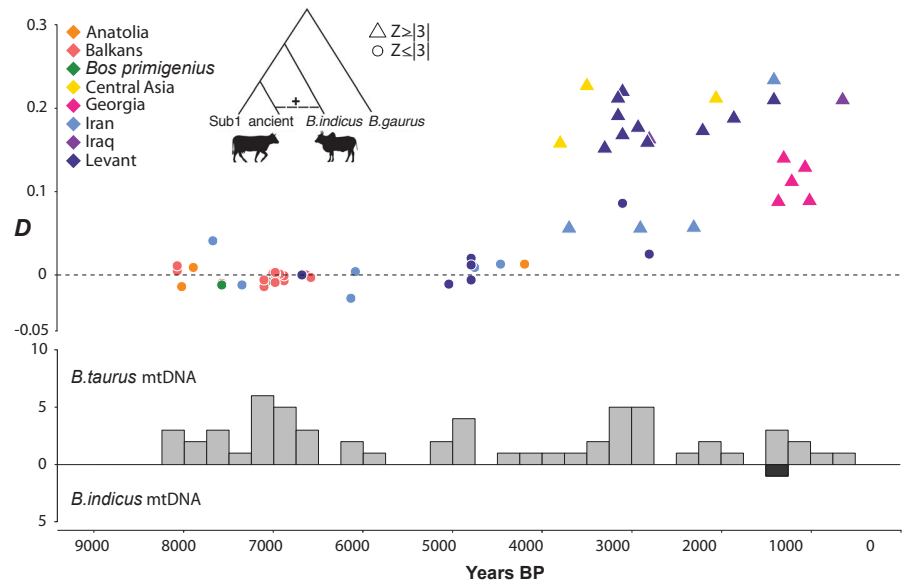
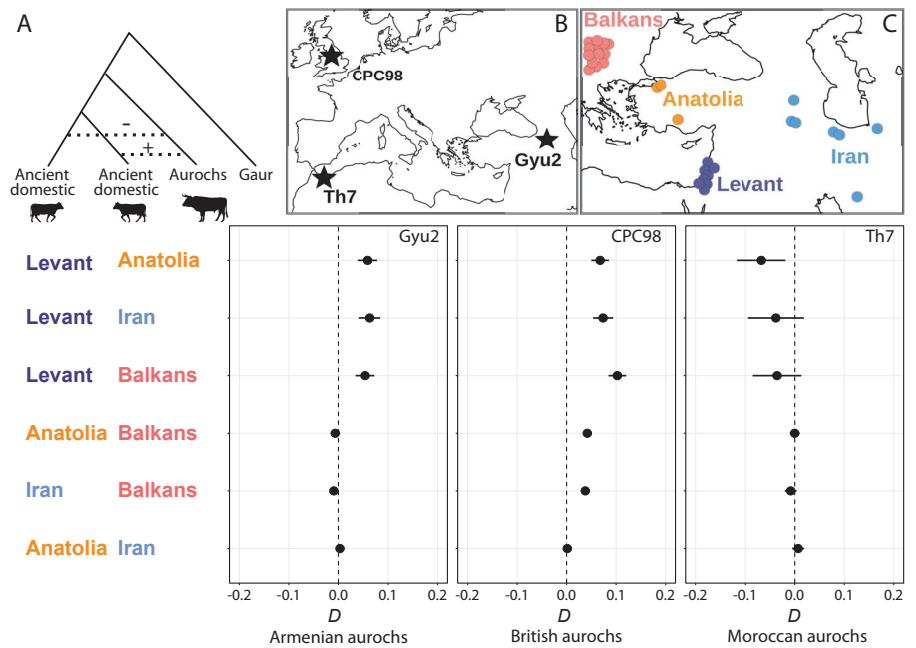


Fig. 3. Clade integrity of ancient population pairs with respect to aurochs introgression. (A) The test  $D$ (gaur, aurochs; ancient group1, ancient group2) reveals asymmetric affinities of aurochs genomes with pre-4000-yr-B.P. cattle populations. Levantine cattle show reduced allele sharing relative to other populations with the Armenian (Gyu2) and British (CPC98) aurochs but more with the Moroccan aurochs (Th7). Balkan cattle show asymmetric affinities with the British aurochs. Bars denote two standard errors. (B) Geographical location of aurochs tested. (C) Distribution of ancient domestic cattle groups tested; post-4000-yr-B.P. Near Eastern samples were excluded because of their zebu admixture.



Distinct genotypes and phenotypes in *B. taurus* cattle native to Africa, such as tolerance of tropical infections, have been attributed to either local domestication or introgression from African aurochs (10, 23). However, ancient Levantine genome affinity with North African aurochs hints that this distinctiveness may have origins in the southern Fertile Crescent. Supporting this, the *B. taurus* mtDNA haplogroup (T1), which is almost fixed in African cattle populations (24), is the most frequent in the southern Levant, including earliest samples, but was not found among other ancient domesticates (table S3).

*B. taurus* were initially derived from a restricted northern Fertile Crescent genetic background, but early domestic cattle outside this

region gained heterogeneous inputs from diverse aurochs strains, including contributions specific to European and African cattle ancestors. After ~4200 yr B.P., gross genome turnover reflecting the spread of *B. indicus*, and likely associated with climate change, was effected by cattle herders throughout southwest and central Asia, representing the start of a global *B. indicus* genome diaspora (25) that continues today.

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#### SUPPLEMENTARY MATERIALS

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