

the exploration of macroscopic quantum mechanics.

Although quantum mechanics is often regarded as a theory of the microscopic world, its postulates do not indicate any particular scale at which they should cease to play a dominant role. Quantum properties like the superposition principle have thus far been observed for systems of up to some thousands of atoms (7). Thus, the range of applicability of quantum mechanics remains a matter of scientific debate. The answer to this puzzle should ultimately come from an experiment, and the field of levitodynamics (8) suggests that nanoparticles levitated in vacuum might be the right platform for testing this unseen boundary of where the quantum “rules” apparently become weak (9–11).

Future research efforts may look to combine the tunable optical binding demonstrated by Rieser *et al.* with the already established ground-state cooling of a levitated nanoparticle (12). In doing so, this type of experiment would usher in the regime of quantum coherent interactions between levitated nanoparticles, opening the door for the generation of entanglement between them (13, 14). One can imagine the possibilities offered by a programmable, many-body platform, where particles are solids with rotational degrees of freedom and masses that allow them to interact gravitationally with each other and with the environment. In just one decade, the field of levitated optomechanics has gone from being proposed as a theory for the cooling of a levitated nanoparticle to its experimental demonstration. Rieser *et al.* added a technique to the toolbox of this nascent field and may be regarded as a milestone on the path toward realizing the once niche theoretical endeavor in applications. ■

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#### EVOLUTION

## Ancient genomes and West Eurasian history

Storytelling with ancient DNA reveals challenges and potential for writing new histories

By Benjamin S. Arbuckle and Zoe Schwandt

Innovations in the sequencing of ancient (>100 years old) DNA have provided a new source of historical information that is complementary to ancient texts, oral traditions, and the archaeological record. The geographic application of this new technology has been uneven, focusing largely on Western and Northern Europe. On pages 939, 940, and 982 of this issue, Lazaridis *et al.* (1–3) report leveraging newly sequenced ancient DNA from the remains of 777 humans from across West Eurasia. They describe the genomic history of the “Southern Arc,” the region surrounding the Black Sea and including Southeastern and Eastern Europe, the Anatolian peninsula, the Pontic steppe, and the Caucasus. Focusing on the relative contributions of five ancestral West Eurasian populations, they reveal shifting proportions of these lineages, which are used to reconstruct population movements extending from

the Neolithic (10,000 BCE) to the Ottoman (~1700 CE) periods and representing the demographic foundations of the modern West Eurasian world.

Once thought to represent a revolution emanating from a single “hearth” in the Euphrates river valley, Lazaridis *et al.* analyze ancient genomes from five populations (ancient Anatolian and Levantine farmers and Eastern, Balkan, and Caucasus hunter-gatherers) and show that the origins of farming in the Neolithic instead involved complex networks of communication and reproduction that connected populations in Anatolia, the Levant, Mesopotamia, and Iran (1–3). They also focus their powerful analytical tools on genomes associated with the expansionary Yamnaya archaeological culture emanating from the Pontic steppe in the Bronze Age (third millennium BCE) (4). Associating the Yamnaya with distinctive Eastern hunter-gatherer ancestry and the spread of Indo-European languages, Lazaridis *et al.* explore details of the expansion of steppe populations into Southeastern Europe and Armenia, two regions with ancient Indo-European lan-

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The Crater of Warriors terracotta vase from Mycenae, an archaeological site in Greece, is dated to ~1200 BCE. It depicts Mycenaean warriors on the march.

guages (1–3). In Southeastern Europe, they show that steppe ancestry is associated with some but not all individuals from high-status tombs in Mycenaean Greece, indicating complex cultural (and biological) dynamics between the local Minoan population and incoming steppe migrants. They also use genomic evidence to evaluate events described in ancient texts. They highlight the variable patterns of ancient Greek colonization, discover that Anatolian migrants transformed the demographic composition of Imperial Rome, and show that ancient DNA can identify the expansion of Slavic and Turkic speakers into Eastern Europe and Anatolia in the medieval period (~500 to 1100 CE).

Although Lazaridis *et al.* address an extraordinarily wide range of topics and provide insights into the Eurasian past (1–3), several issues common to ancient DNA research are evident in the framing of the data, especially with regard to the stories that are chosen (or not) for explication. In ancient genome research, DNA sequences are often presented as revealing a “true” history of humanity in contrast to historical and archaeological records that are prone to untruthfulness and imprecision. Although base pairs do not lie or exaggerate (though they do decay), neither do they tell stories, and storytelling that is used to interpret ancient genome analyses inevitably projects specific worldviews (5).

Many of the narratives explored in the studies of Lazaridis *et al.* reflect a Eurocentric worldview. For example, the naming of the Southern Arc conjures a map projection that centers on the western tip of Eurasia rather than the Anatolian peninsula—a more intuitive geographic center of the research area. Moreover, in terms of scale, narratives based on genomes often project a high-altitude view of history (6), mostly devoid of individuals despite being derived from its most personal components. Neolithic farmer or steppe Yamnaya genetic material moves abstractly on its way from central Anatolia to the Balkans or from the Don to the Danube and the Peloponnese.

This approach to history-making offers a sanitized version of the past that avoids engaging with bodily experiences, including sexual violence, which was probably involved in the movement of genetic material through time and space (7). Sexual reproduction itself is reduced to a process motivated by competition and survival and carried out primarily by men. Thus, with this approach, history is made through vague processes of migration

and admixture, but the social mechanisms remain uncharted (8).

In constructing the history of the Southern Arc, Lazaridis *et al.* focus on Y chromosome lineages, especially to link populations in Southeastern Europe, the Aegean, and the southern Caucasus to the Bronze Age Yamnaya through shared patrilineal lines (1–3). Ostensibly, there are technical reasons for this—Y chromosomes allow for precise reconstructions of lineages and divergence times. However, the resulting emphasis on patrilineal descent and the absence of discussions of parallel networks of matrilineal (or of XX chromosome humans at all) creates a strong sense that the events of history are carried forward by “great men”—especially those bearing Eastern hunter-gatherer ancestry and buried under mounds of earth and stone. This emphasis on Y chromosome networks inadvertently projects gender stereotypes into the past, perpetuating an androcentric narrative of dominance and competition that equates chromosomes to gender and gender to behavior. Conversely, approaches that explore maternal markers and sex-neutral kinship coefficients have recently been used, showing that alternate methods that overcome sex biases are possible (9, 10).

Lazaridis *et al.* also present a dataset that estimates the phenotype, in terms of hair, eye, and skin pigmentation, for humans in the Southern Arc and Europe over the past 15,000 years (1–3). They show that brown hair and eyes and “intermediate” skin pigmentation was the most common phenotype in the region through time and that, despite common stereotypes, Bronze Age steppe populations were not dominated by blonde and blue-eyed individuals. They also document an increase in “light” pigmentation over time in West Eurasia, although potential reasons for selection of these traits are not addressed.

Despite the authors’ intention of dispelling stereotypes, this brief presentation of phenotypes instead amplifies a Eurocentric worldview that highlights light pigmentation (5). Genomics scholars should think carefully about the political ramifications of presenting sensitive data such as these because they are consumed by a wide audience, and some may repurpose them (11). Other ways of presenting the data are possible. For example, it is equally interesting that southern Mesopotamians sometimes called themselves the “black-headed people,” perhaps to contrast their own phenotype with the abundance of brown hair in adjacent regions (12).

Lazaridis *et al.* have produced an astounding dataset, unimaginable in its scale just a decade ago (1–3). It is important to

acknowledge that the narrative scaffolding used to interpret these data inevitably represents worldviews that center certain people and places (13). Other narratives and scales of inquiry are also possible. For example, one of the most interesting alternative interpretations emerging from the studies of Lazaridis *et al.* is the resilience of hunter-gatherer genomes in regions outside the Fertile Crescent region of Southwest Asia, where farming first emerged. In particular, and despite documenting large-scale incursions of exogenous populations into the Balkans in the Neolithic and Bronze Age, the authors show the surprising resilience of local Balkan hunter-gatherer ancestry in the region that continues to the present day. This finding complicates previous narratives of linear population replacements and further highlights the need to explore the complex social interactions associated with ancient population movements.

Moving forward, the growing corpus of ancient genomic data will continue to transform views of human history. This work can be particularly effective if researchers recognize their lack of neutrality and embrace their role in constructing narratives while allowing room for diverse perspectives that shine light onto people and places whose histories are less well known. Lazaridis *et al.* do an excellent job of this, for example, by exploring the genomic diversity of the poorly known kingdom of Biainili (known as Urartu to their Assyrian neighbors) in the mountains of Transcaucasia (1–3). Rather than presenting history from a traditional top-down view, genomic scholars can leverage the high resolution of their data to pivot between different scales—from the continental to the individual—and can address historical networks of interaction involving both patrilineal and matrilineal. The studies by Lazaridis *et al.* represent an important milestone for ancient genomic research, providing a rich dataset and diverse observations that will drive the next iteration of interpretations of the human history of West Eurasia. ■

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