

CROP DOMESTICATION

Corn in the USA

Sequencing ancient DNA from archaeological samples reveals both how maize was transported through North America, and the shifting genomic patterns in response to selection for drought tolerance and sugar content.

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Civilization exists on a foundation of domestic plants and animals. From the emergence of our species approximately 200,000 years ago, hunting and gathering strategies allowed humans to spread across six continents. Our global population size never climbed beyond a few million, however, until the development of settled agricultural economies based upon the production of crop staples and the management of captive animals (beginning about 10,000 years ago) allowed the human population to climb past seven billion¹. Maize is arguably the most important staple crop domesticated in North America. In this issue of *Nature Plants*, da Fonseca *et al.*² report how they have applied next-generation sequencing techniques to DNA extracts obtained from 32 well-dated ancient maize remains dating from as long ago as 6,000 years up until less than 700 years ago (Fig. 1) to investigate its geographic and evolutionary history. This has given them the unique opportunity to observe the genomic effects of the evolutionary and demographic shifts that have occurred during the history of maize's association with humans.

Ancient human populations carried their domestic crops and animals with them on a multitude of migration trajectories, while at the same time placing significant selective pressure on them, allowing for increased production in regions where environmental conditions were often radically different than those in the native regions of the organisms' wild ancestors. Understanding the origins, migration routes, and histories of selection for each of our domestic partners therefore provides us with an understanding of the history of our own species. It also demonstrates the power of selection to shape genomes and morphologies over short evolutionary timescales.

It is difficult to overstate the increase in observational and explanatory power that has resulted from fusing archaeology's temporal depth with the resolution now provided by high-throughput sequencing of billions of nucleotides. In this case, da Fonseca *et al.* were first able to settle a longstanding conflict regarding whether



Figure 1 | Growing corn. Morphological variation in maize cobs from Tehuacan, Mexico; in the Collections of the R. S. Peabody Museum. Age of cobs from left to right (calibrated calendar years intercept): 5,310 BP; 5,280 BP; 1,330 BP; 1,220 BP. The second cob from the left was used by da Fonseca *et al.* Photo by Donald E. Hurlbert, Smithsonian Institution.

the dispersal of maize from Mexico into the Southwestern US proceeded along coastal³ or highland⁴ routes. The increased resolving power of their approach, along with the 348 genes analysed, provided da Fonseca and colleagues with the means to assess temporal and geographic patterns of admixture, and the interbreeding between previously diverged populations, to reveal a more complex and satisfying chronology that combines elements of both competing hypotheses. They propose a narrative in which maize entered the Southwestern US by a route through the highlands about 4,000 years ago, and that gene flow between this recently arrived population and maize located along the Pacific coast began about 2,000 years ago.

Not content with settling this classic archaeological debate, da Fonseca *et al.* have built on pioneering work³ that evaluated the selection pressures placed on genes during different stages of the domestication process. By comparing wild teosinte populations with maize dated to around 2,000 years ago, they uncovered signatures of selection during the early phases of evolution on genes including those previously implicated in domestication, control of seed shattering and flowering,

as well as several loci that allowed maize to survive the arid conditions in the Southwestern US. More recently (between 2,000 and 750 years ago) subsequent human selection pressure led to a 60% reduction in diversity around the *sugary1* locus responsible for replacing starch with sugar and thus producing sweetcorn.

These twin conclusions related to migratory trajectories and temporal patterns of environmental and cultural selection demonstrate the state-of-the-art in palaeo-population genomics. In addition, this study reveals the power of these techniques to resolve paradoxes and expose complex patterns of human-assisted migration and admixture in multiple, geographically and genetically distinct populations. In short, when applied to other species, these approaches will not only resolve outstanding conundrums, they will also reveal why the questions were so intractable in the first place.

More generally, these results add to a growing body of literature that increasingly identifies the important, perhaps even dominant, role that admixture has played during the histories of domestic animals and plants including maize⁶. Earlier studies were limited to the non-recombining components of plant and animal genomes, such as mitochondrial or plastid DNA, and so tended to interpret patterns of domestication through the lens of bifurcating phylogenetic trees. These approaches lacked the capacity to account for the interweaving branches that result from admixture, leaving them unable to effectively either address or quantify gene flow between populations through time. The resulting narratives were therefore overly simplistic and often contradictory.

As genomic and palaeo-genomic studies have become more common, it has become increasingly clear that virtually every domestic plant and animal has incorporated genomes of numerous populations, including many that were not involved in the original domestication process⁷. For example, although grapes⁸, apples⁹ and pigs⁷ were domesticated outside of Europe, admixture with native wild

European species has been so significant as to obscure the geographic origins of the modern domestic populations. By directly assessing the genomes of ancient populations through time as demonstrated by da Fonseca and colleagues, it becomes possible to shed the biased assumptions of previous approaches, and to reach far more satisfying (and truthful) conclusions that accurately detail the complex patterns of admixture and selection defining the history

of the domestic species that make modern life possible. □

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