

HUMAN EVOLUTION

Chewing the fat

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One quandary in human evolutionary research is how to explain the dramatic reduction in chewing tooth size and mandibular musculature seen in early species of the genus *Homo* compared with that of earlier australopithecines. Katherine Zink and Daniel Lieberman of the Department of Human Evolutionary Biology, Harvard, now propose that the change began when stone tools were used for slicing or pounding meat and root vegetables to improve their edibility.

Making food easier to eat lowers the required muscular effort and increases efficiency of mastication. It was previously suggested that fire was the first processing agent to make meat and tough, fibrous plants more easily consumable. However, other food preparation techniques would have been available before the advent of cookery.

Volunteers were asked to eat stringy goat meat and woody root vegetables including carrots, beetroots and jewel yams, to

replicate foodstuffs available two million years ago on the African savannah. The researchers then compared the amount of chewing needed to eat unprocessed, pounded/sliced and cooked mouthfuls. 40,000 daily chews are needed to consume an unprocessed 'vegetarian' diet but pounding tough plant foods could reduce this by 5%, and by 17% when combined with meat processed in similar ways. Such a reduction in the extent and force of chewing may have facilitated the evolution of hominin teeth and jaws. *LNE*

IMMUNITY

Decoys everywhere

BMC Biol. **14**, 8 (2016)

Plants must detect pathogens to combat infection. Membrane receptors recognize generic foreign molecules, which leads to a basal immune response. Endogenous sensors containing a conserved nucleotide-binding leucine-rich repeat (NLR) structure perceive specific pathogen-secreted effector proteins to initiate another type of strong immune response. NLRs can sense an effector either by direct interaction or by monitoring its effect on a 'guarded' host protein.

Recently, a few examples of an integrated mechanism have been characterized: decoy domains, duplicated from plant proteins and fused to the NLR to act as bait to pathogenic effectors. This new class of immune receptors is named NLR-ID (integrated domain). By binding to the decoys instead of their actual target, the effectors alert the plant of an invading pathogen. Ksenia Krasileva and colleagues in Norwich,

UK, performed a systematic bioinformatics search for NLR-IDs in 40 plant genomes and discovered that they exist in almost all plant lineages, hinting at a probable conserved defence mechanism in flowering plants. The decoy domain is variable, with a high proportion of kinases and transcription factors such as WRKY domains.

The functional validation of this long list of NLR-IDs will need some time, but their widespread existence can already be integrated into strategies to engineer more efficient disease resistance in crops. *GT*

PHOTOSYNTHESIS

Compartment control

Plant Cell **28**, 454-465 (2016)

The evolution of C_4 photosynthesis from the C_3 pathway involves increased expression of multiple enzymes and their compartmentalization into mesophyll or bundle sheath cells. Current knowledge regarding the mechanism, however, remains limited to a few regulatory elements that each affect a single gene in a specific lineage. Ben Williams, at the University of Cambridge, UK and colleagues have now discovered an untranslated region (UTR) motif that directs multiple C_4 enzymes to accumulate preferentially in the mesophyll cells of *Gynandropsis gynandra*, the closest C_4 relative of *Arabidopsis*.

To understand the mechanisms regulating multiple enzymes in the C_4 pathway, the researchers used a GUS reporter system to examine the *cis*-elements on *CARBONIC ANHYDRASE4 (CA4)* of *G. gynandra* for their ability to affect *CA4* abundance in C_4 leaves. Both the promoter and introns of this gene elevated the abundance of the GUS reporter, presumably through loss of *cis*-elements that repress *CA4* expression in C_3 species.

The UTRs of *CA4* and two other C_4 enzymes caused strong preferential protein accumulation in mesophyll cells. Deletion analysis combined with computational motif detection identified a nine-nucleotide motif shared by all the UTRs (MEM2) that directs the preferential enzyme accumulation with another element immediately upstream of the start codon.

However, MEM2 does not cause differential expression of transcripts between mesophyll and bundle sheath cells, suggesting that the preferential enzyme accumulation was triggered by MEM2 post transcription. *JL*

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ARCHAEOBOTANY

Millet on the move

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Advances in ancient DNA (aDNA) research are facilitating understanding of prehistoric crop exchange and movement. Chunxiang Li, of Jilin University in China, and colleagues now add to that knowledge by analysing aDNA from broomcorn millet (*Panicum miliaceum*).

Broomcorn millet was domesticated in China about 10,000 years ago before spreading throughout Eurasia, but the precise ancestry, centres of domestication and spread of various millet landraces remain uncertain. The researchers successfully extracted aDNA from 4,000-3,500-year-old millet grains that were preserved in the dry conditions of the Xiaohe cemetery, Xinjiang Province (northwest China).

Comparing the aDNA sequence with 190 accessions of modern broomcorn millet revealed that as many as six single nucleotide polymorphism (SNP) sites on the Xiaohe specimens are shared with multiple Russian and Indian landraces, but only one Chinese landrace.

Li and colleagues suggest that the Xiaohe type could be an extinct variety, ancestral to more recent European millet species. In any case, Xinjian emerges as an important Neolithic and Bronze Age staging post in the spread of millet from northern China to Central Asia, southern Siberia and eastern Europe. *LNE*