

In 1997, the maize gene *tb1* was reported as the first domestication QTL to be cloned (4). *tb1* controls the complex differences in plant architecture between maize and its progenitor, teosinte. In 2000, a major QTL (*fw2.2*) contributing to the massive increase in fruit size that was a central feature of tomato domestication was cloned (5). In 2005, the maize domestication QTL *tga1*, which provides naked grains to maize (as opposed to the covered grains of teosinte), was cloned (6). And thus far in 2006, in addition to the two rice shattering genes, cloning of the wheat *Q* gene was reported (7). *Q* controls the compaction and fragility of the ear of wheat and also the ease with which the grain can be separated from the chaff.

A notable feature of this list of six domestication genes is that five of the six encode transcription factors that regulate other (target) genes by directly binding to their DNA. Transcription factors represent only about 5% of genes in plant genomes (8, 9) but 83% of the domestication genes listed above. Interestingly, the five domestication transcription factors belong to five separate families: TCP (*tb1*), SBP (*tga1*), AP2 (*Q*), MYB3 (*sh4*), and HOX (*qSH1*). This suggests that the exaggerated proportion of transcription factors among domestication genes is the product of some general feature of transcription fac-

tors and not of one particular class of transcription factors. The predominant role of transcription factors in domestication mirrors their equally large role in controlling plant development (10), which supports the view that they have properties that predispose them to become the major genes contributing to morphological evolution in plants (11).

Another remarkable feature of this list is that the domesticated alleles of all six genes are functional. If domestication involved the crippling of precisely tuned wild species, one might have expected domestication genes to have null or loss-of-function alleles. Rather, domestication has involved a mix of changes in protein function and gene expression. As a consequence of domestication, *sh4* shows changes in protein function and expression level (2), *qSH1* shows a change in the spatial pattern of its expression (3), *tb1* shows increased expression (4), *tga1* shows a change in protein stability or protein function (6), *fw2.2* shows a heterochronic shift in its expression (5), and *Q* shows changes in protein function and gene expression (7). Given that the cultivated allele of not one of these six domestication genes is a null, a more appropriate model than “crippling” seems to be adaptation to a novel ecological niche—the cultivated field. Tinkering and not disassembling is the order of

the day in domestication as in natural evolution, and Darwin’s use of domestication as a proxy for evolution under natural selection was, not surprisingly, right on the mark.

A consequential question now is whether modern plant breeders might borrow from the playbook of their Neolithic predecessors. Might one tinker with the expression patterns or protein functions of known domestication genes to create superior alleles? Can every transcription factor in the genome be manipulated in a systematic manner to generate a pool of new trait variation? Knowledge of past successes should help to intelligently guide future crop improvement.

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PLANETARY SCIENCE

Exploring Other Worlds to Learn More About Our Own

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The exploration of our solar system was originally driven primarily by curiosity and the search for answers to the eternal question: Are we alone? As the first spacecraft began to visit our neighboring planets in the solar system, hopes of finding life quickly faded and instead the focus began to shift toward gaining a more scientific understanding of their nature and history. After a generation of exploratory robotic spacecraft missions from the 1960s through the 1980s, it became clear that most planets—except Mercury—and some moons had permanent and substantial atmospheres. These atmospheres can be subdivided into three large families: those composed primarily of nitrogen (Earth, Titan, Triton, Pluto), carbon dioxide (Venus, Mars), and hydrogen/helium (Jupiter, Saturn, Uranus, Neptune). On page 1366 of this issue, Forbes et

al. (1) provide fresh insights into the effects of variations in solar radiation intensity on the upper atmospheres of Mars and Earth, which have now been simultaneously observed.

Numerous space missions, along with Earth-based observations and theoretical models, have given us an unprecedented understanding of planetary atmospheres. Yet some of their fundamental prop-

Energy flow on Mars. Solar ultraviolet radiation heats the dayside to 300 K; winds transport some of this energy toward the nightside, where temperatures are typically lower by 100 K. On the dayside, vertical conduction and adiabatic cooling offset solar heating, whereas the nightside temperatures are raised by adiabatic heating. A portion of the solar energy is radiated back into space through infrared cooling by CO₂.

Simultaneous observations of the drag of satellites through the upper atmospheres of Mars and Earth reveal how carbon dioxide is differentially cooling their upper atmospheres.

erties are still poorly understood, including the atmospheric energy balance (see the figure). What are the sources of energy incident upon an atmosphere, how is this energy redistributed

