Unraveling the Origin of Cotton

The origin and evolution of *Gossypium hirsutum*, the most widely planted cotton species, is an unsolved puzzle because of its hybrid origin from Old and New World species. To better understand the evolution of cotton, Palmer et al. shotgun sequenced 454 2000-year-old archaeological samples of cotton from Africa and South America. On the basis of their results and comparisons with genetic data from extant species, they assigned the African lineage to the species *G. herbaceum* and the South American lineages to the species *G. barbadense*. From these data, the authors show that *G. barbadense* shows overall genome stability with few changes in the placement and number of transposable elements over the past 2000 years. In contrast, *G. herbaceum* showed significant differences in transposable element composition over time. On the basis of these results, the authors postulate that the ancient *G. herbaceum* lineage is more like the ancestral form of one of the original species parents of *G. hirsutum* than that of the extant lineages. Furthermore, they suggest that cotton genome evolution is characterized by bursts of transposable element activity followed by genome stability. — LMZ

The Great Gene Giveaway

The vast majority of genes in eukaryotes are inherited vertically; that is, they are transferred through sexual or asexual reproduction from parent(s) to offspring (i.e., from one generation to the next). Prokaryotes are not quite so obliging. Among bacteria and archea, there is a substantial amount of lateral (or horizontal) gene transfer; that is, genes being exchanged between unrelated organisms independent of reproduction.

Christin et al. use comparative studies of DNA sequences (phylogenetics) to provide evidence of repeated lateral gene transfers occurring in plants. Different species of the grass lineage Alloteropsis use either the C3 or the more recently evolved C4 photosynthetic pathway to fix carbon from the air. Analysis of two enzymes critical for the C4 pathway reveals that individual C4 Alloteropsis species seem to have picked up these nuclear genes from four other genera of grass: Setaria palmifolia, found in South Africa; Themeda quadrivalvis, in Australia; and a Cenchrinae species; with the species divergence of Alloteropsis. Lateral transfer may have occurred because of the close physical proximity of the different plant species, all of which are wind-pollinated, resulting in the transfer of pollen between them. Acquisition of the C4 genes may then have provided a selective advantage, because C4 is more efficient than C3 photosynthesis. — GR


What’s Fed to the Fish

Human activities send a dizzying number of organic small molecules into various bodies of water, and the first step in assessing the dangers they may pose is to determine how much of each compound gets sequestered (and possibly transformed) in fish and other aquatic organisms. Direct uptake measurements are time-consuming and challenging, so validated models would be of great use, but thus far studies that compare different models across a broad spectrum of experimental data have been scarce. Stadnicka et al. strive to make progress in this vein by measuring correlations of model predictions with literature data on the uptake of 39 organic compounds in two different fish species: rainbow trout and fathead minnow. In particular, they compare the accuracy of one-compartment models treating fish as a single continuous system with that of a physiologically based toxicokinetic model incorporating more fine-grained distinctions between accumulation in fatty tissue and in organs such as liver and kidneys. On the whole, the models fared similarly, matching measured concentrations to within an order of magnitude for 68% of the compounds, though predictions were poor for minnow accumulation of certain polar compounds, such as phenol and its derivatives. — JSY