

The age of *Arabidopsis*

Arabidopsis thaliana, a flowering plant of the family Brassicaceae and order Brassicales, is the primary genetic model in plant biology. Although researchers use *A. thaliana*'s evolution and genetic history to understand key events in developmental biology, the timing of divergences within the Brassicaceae and Brassicales has remained under dispute. Mark Beilstein et al. (pp. 18724–18728) reexamined the fossil evidence for evolutionary reference points within the order Brassicales, and uncovered several previously overlooked fossils that permitted the reestimation of divergence dates based on updated molecular dating methods and phylogenetic relationships. The researchers found that *A. thaliana* diverged from its closest relatives approximately 13 Mya and that *Arabidopsis* and *Brassica* (broccoli, cabbage, canola) split 43 Mya, two to three times earlier than researchers previously believed. The findings suggest that researchers' understanding of gene, genomic, and developmental evolution will require revision, the authors report. Notably, the timing of some of the inferred splits suggests that the Cretaceous–Paleogene mass extinction may have driven radiations within the plant family Brassicaceae, and that Brassicaceae codiversified with period butterflies that specialize on the plants, according to the authors. — J.M.



Thlaspi arvense growing near Crested Butte, Colorado.

Indian insects in amber reveal global phylogenetic affinities

India's highly endemic biota is thought to have evolved during 100 million years of near isolation, after the Indian subcontinent broke from Gondwana and drifted equatorward to collide with Asia. Jes Rust et al. (pp. 18360–18365) examined approximately 150 kg of amber from 50 million-year-old Cambay Shale deposits in western India, and identified a distinctive chemical signature of resin produced predominantly by Dipterocarpaceae, a



Fungus gnat, *Palaeognoriste*, in Cambay amber.

globally widespread family of tropical trees. Using solvents to dissolve the amber, the authors were able to extract entire preserved specimens that could be examined with high-resolution electron microscopy. The authors found more than 700 arthropods belonging to 14 orders and more than 55 families, as well as abundant plant and fungal remains. The insects in particular revealed unexpected biogeographical connections: numerous species shared phylogenetic affinities with insects from Asia, Australia, and New Guinea, and with older species found in Mexico, tropical America, and the Baltic region. The findings offer direct fossil evidence that the Cambay Shale Formation contains an early record of a diverse tropical forest with

arthropod fauna, and that precontact India may not have been as biologically isolated as believed, according to the authors. — T.J.

Tracing language evolution in the human brain

The physiological basis of asymmetrical language processing in the human brain remains under debate, with competing theories pointing to auditory asymmetry and hand preference as its functional origin. To determine which brain regions demonstrate intrinsic asymmetry at speech-specific neural frequencies, Benjamin Morillon et al. (pp. 18688–18693) used simultaneous EEG and fMRI to monitor brain activity in 16 human study participants while the participants rested or watched a video. Brain areas associated with syllabic hearing, basic sensory processing, and mouth and hand movements demonstrated activity patterns characteristic of left-brain dominated speech, both during the video and at rest. The results suggest, according to the authors, that these areas are hard-wired for asymmetry, and may form the basis for asymmetrical speech and language functions in modern humans. The researchers further noted that brain activity in areas that direct mouth and hand movements and auditory cortex shared intrinsic similarities at frequencies that correspond to syllabic but not phonemic speech rhythms. The finding suggests that the brain is