

Nodulation in the crotalarioid *Lotononis s.l.* clade (Research in Context)

doi:10.1093/aob/mct095

Comparatively few studies have examined nodulation or rhizobial association in the basal legume tribe Crotalariaeae. Within the *Lotononis s. l.* clade, **Ardley et al.** (pp. 1–15) characterize the rhizobia associated with *Listia*, *Leobordea* and *Lotononis s.s.*, and examine infection and nodule initiation in species of *Listia*. They find that the lupinoid nodules of *Listia angolensis* and *L. bainesii* have uniformly infected central tissue and develop in the outer root cortex, and infection occurs without root hair curling or the formation of infection threads. Five genera of rhizobia nodulate *Lotononis s.l.* hosts, but specificity has developed within *Listia*, which is nodulated only by species of *Methylobacterium* and *Microvirga*. The seasonally waterlogged habitat of *Listia* species may favour the development of symbiotic specificity.



C₃–CAM plasticity in epiphytic orchids

doi:10.1093/aob/mct090

A positive correlation between tissue thickness and crassulacean acid metabolism (CAM) expression has been suggested. **Rodrigues et al.** (pp. 17–29) study tissue morphology and photosynthetic mode in response to drought in leaves, pseudobulbs and roots of a thick-leaved (*Cattleya walkeriana*) and a thin-leaved (*Oncidium 'Aloha'*) epiphytic orchid. They find that although *Oncidium* is considered as a C₃ genus, it expresses facultative CAM in its non-leaf organs under drought, whilst *C. walkeriana*, which is considered a constitutive CAM species, displays a clear drought-induced up-regulation of CAM in its thick leaves but not in its non-leaf organs. Thus water availability modulates CAM expression in an organ-compartmented manner in both orchids, with distinct regions of the same plant displaying different photosynthetic pathways and variable degrees of CAM expression in response to drought.



Adaptation of cotton bracts to high CO₂

doi:10.1093/aob/mct091

The rapid respiration rate of cotton (*Gossypium hirsutum*) fruits produces a microenvironment with intercellular CO₂ concentrations of 500–1300 $\mu\text{mol mol}^{-1}$, and **Hu et al.** (pp. 31–40) hypothesize that the adaptations that have evolved in response to this can provide insights relevant to future increases in atmospheric CO₂. They compare morphological and physiological traits of bracts and leaves of cotton, and find that bracts show significantly lower stomatal conductance, which results in a significantly higher water use efficiency. Both gas exchange and protein content show a significantly greater RuBP regeneration/RuBP carboxylation capacity ratio ($J_{\text{max}}/V_{\text{cmax}}$) in bracts than in leaves, which agrees with theoretical predictions regarding

adaptation to elevated CO₂. They conclude that cotton bracts provide readily available material for studying adaptations to elevated CO₂.



Cytokinins can trigger hypersensitive-like responses

doi:10.1093/aob/mct092

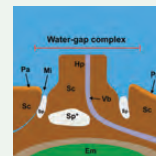
The mechanisms involved in plant defence against pathogens are of considerable scientific and agricultural interest. **Novák et al.** (pp. 41–55) use activation of the gene *ipt* to produce high levels of cytokinins in tobacco, *Nicotiana tabacum*, and find that this is sufficient to trigger fast cell death without intervening chlorosis, which is characteristic of the hypersensitive response. The results are consistent with the suggestion that the molecular processes underpinning this hypersensitive-like response are orchestrated by increases in cellular hydrogen peroxide levels. The hypersensitive-like response includes inhibition of photosynthesis, increases in stress hormone levels, oxidative damage to membranes and stomatal closure. Thus, cytokinins may act as signals and/or mediate plant defences against pathogen attack.



Cytokinins are implicated in keeping green kiwifruit green

doi:10.1093/aob/mct093

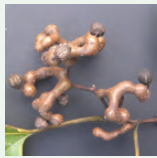
Kiwifruit species that have either green flesh (*Actinidia deliciosa* 'Haywood') or gold flesh (*A. chinensis* 'Hort 16A') at harvest provide an interesting comparative system to investigate the mechanism of degreening in ripening fruit. **Pilkington et al.** (pp. 57–68) find that fruit of both species have elevated levels of cytokinins during ripening, yet only the green kiwifruit has elevated expression of genes coding for cytokinin synthase. Additionally, high levels of *O*-glucosylated cytokinins are detected only in green kiwifruit, as is also the case for the expression of the gene for zeatin *O*-glucosyltransferase, an enzyme responsible for glucosylating cytokinins. The results strongly suggest that the green fruit are perceiving cytokinin whereas the gold fruit are not.



Water-gap complexes in species with physical dormancy

doi:10.1093/aob/mct094

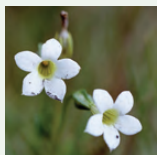
A water-gap complex is a morpho-anatomically specialized area in the seed/fruit coat of water-impermeable species: with breaking of physical dormancy (PY), a pre-determined, small opening forms in the water-gap complex allowing the seed/fruit to imbibe water. **Gama-Arachchige et al.** (pp. 69–84) study the seed/fruit coat anatomy and morphology in 15 species with PY in seven families and report ten new water-gap complexes. Complexes consist of: (1) an opening that forms after PY is broken; (2) a specialized structure that occludes the gap; and (3) associated specialized tissues. Based on these results and other related studies, they introduce a classification system for water-gap complexes in 16 angiosperm families with PY species.



Peduncles elicit mammal endozoochory

doi:10.1093/ob/mct096

Plants have evolved a variety of seed dispersal mechanisms, one of which is to produce seeds embedded in fleshy pulp to facilitate endozoochory. The raisin tree, *Hovenia dulcis*, produces enlarged, fleshy peduncles with outer, dry drupes and **Zhou *et al.* (pp. 85–93)** investigate how this dry-fruited plant disperses its seed. In contrast to previous studies reporting that fleshy appendages entice bird epizoochory, their field observations, combined with experimental manipulations, confirm that *H. dulcis* peduncle sets are adapted primarily to achieve mammal endozoochory, with viable seeds being found in the faeces of species such as bears and martens. The germination rate of egested seeds is higher than that of unconsumed seeds, demonstrating a mutualistic association similar in function to production by the plant of fleshy pulp or foliage.



Variation and evolution of herkogamy in *Exochaenium*

doi:10.1093/aob/mct097

The spatial separation of stigmas and anthers (herkogamy) functions to reduce self-pollination and avoid interference between pollen dispersal and receipt. Little is known about the evolutionary relationships among the main forms of herkogamy. **Kissling and Barrett (pp. 95–102)** examine those relationships in *Exochaenium*, a genus of African herbs, using phylogeny reconstruction. They find that distyly originated once from an ancestor with approach herkogamy, supporting a theoretical model proposed by Lloyd and Webb in 1992. The results demonstrate the lability of sex-organ deployment and implicate pollinators, or their absence, as playing an important role in driving transitions among herkogamic and non-herkogamic conditions.

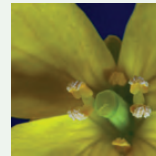


Hydrotropism and root-system development in arabidopsis

doi:10.1093/aob/mct098

The gene *MIZU-KUSSEI 1* (*MIZ1*) has been shown to regulate root hydrotropism in *Arabidopsis thaliana*, but its role in plant growth and survival under natural conditions is not yet fully known. **Iwata *et al.* (pp. 103–114)** establish moisture gradients in soil and examine root system architecture, biomass production and survival of the *A. thaliana* mutant *miz1* in comparison with transgenic plants over-expressing *MIZ1* (*MIZ1OE*) and with wild-type plants. They find that wild-type plants develop their root systems in regions with higher water potential and this asymmetrical pattern is more pronounced in the transgenic *MIZ1OE* plants, but the response is lacking in the *miz1* mutants. Shoot biomass and the number of plants that survive under drought conditions are much greater in *MIZ1OE* plants,

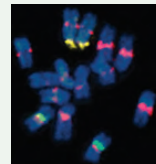
demonstrating that *MIZ1* over-expression has potential for improving productivity in arid areas.



Live time-lapse imaging of pollination in *Brassica rapa*

doi:10.1093/aob/mct102

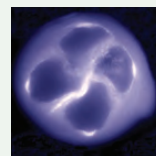
Although pollination has been studied extensively, accurate knowledge of the morphological aspects of the process is still far from complete. **Hiroi *et al.* (pp. 115–122)** use time-lapse imaging to examine the morphological responses of pollen in *Brassica rapa* and classify six representative patterns of behaviour, which occur in both self- and cross-pollinations. The results suggest that regulated hydration of pollen is key for successful pollination, and is achieved by a complex balance of hydration, dehydration and nutrient supply to pollen grains from stigmatic papilla cells. The difference between self- and cross-pollination is manifest in the ratios observed between the six different patterns of behaviour.



Molecular cytogenetics of repetitive DNA in jute species

doi:10.1093/aob/mct103

The genomes and chromosomes of the important fibre crops white jute and Tossa jute (*Corchorus* species) are poorly characterized. Information is essential for breeding and improvement, with characters including environmental adaptability, fibre quality and susceptibility to diseases differing between the species. **Begum *et al.* (pp. 123–134)** use a comparative analysis of a prominent satellite DNA family, identified in this study, to reveal its diversification and emerging subfamily structure in both jute genomes, while the heterogenous distribution along chromosomes is conserved. In combination with ribosomal genes and retrotransposon sequences, they use the chromosome-specific distribution of the satellite DNA for *in situ* hybridization to generate a reference karyotype for both jute species. These sequences and data will be useful for genetic mapping and analysis of hybrid lines.



Microsporogenesis of monosulcate pollen grains in monocots

doi:10.1093/aob/mct104

The monosulcate type is the most common pollen aperture pattern in monocots and basal angiosperms, and is considered as the ancestral condition for flowering plants. **Toghranegar *et al.* (pp. 135–139)** describe microsporogenesis in 30 species belonging to eight monocot families, and find five different pathways associated with the production of monosulcate pollen grains. These pathways differ in the type of cytokinesis, the tetrad shape, and the presence and patterns of additional callose deposition after the formation of intersporal walls. In all the pathways, aperture location seems to be linked to the last points of callose deposition.



Pollination syndromes in Australian epacrids

doi:10.1093/aob/mct105

Floral diversity in Australian epacrids (Ericaceae: Styphelioideae) suggests that they may be adapted to pollinator type. **Johnson (pp. 141–149)** investigates epacrid–pollinator relationships using a multivariate approach based on published literature and field observations, and a novel statistical method is used to identify key floral traits per syndrome. Although most epacrids have generalized pollination systems, a correlation between bird pollination and red, long-tubed epacrids is found. Statistical classification highlights the relative importance of each floral attribute in relation to pollinator type and proves useful in classifying epacrids to bird, fly and bee pollination systems.



Biogeography of sapindaceous lineages

doi:10.1093/aob/mct106

Paleoclimatic data indicate an abrupt climate change at the Eocene–Oligocene (E–O) boundary, which affected tropical forest distribution, and south-east Asia emerged during the same period following the collision of the Eurasian and Australian plates. Little is known about the effect of these abiotic factors on the spatio-temporal history of angiosperms. **Buerki et al. (pp. 151–160)** analyse a combined plastid and nuclear DNA sequence data set and record an increase of dispersals at the E–O boundary in the sapindaceous clade (Xanthocercaceae, Aceraceae, Hippocastanaceae, Sapindaceae), and show that they were connected with the emergence of south-east Asia. This area allowed multiple contacts between Laurasian and Gondwanian lineages. The study thus demonstrates the importance of geomorphological and climatic factors in shaping species' distributions.



Floral ontogeny and gene protein localization in mapaniid sedges

doi:10.1093/aob/mct111

Poorly known, mapaniid sedges (Cyperaceae, subfamily Mapanioideae) possess unique floral forms, markedly different

from stereotypical monocots, and the evolutionary issues of how or why this has occurred have not been resolved. **Prychid and Bruhl (pp. 161–177)** evaluate current knowledge about mapaniid reproductive structures and present an ontogenetic study of a range of reproductive developmental stages in the genus *Lepironia*. Using floral protein localization they present the first floral protein expression maps for the family, leading to the conclusion that a synanthial hypothesis best explains the evolutionary origin of the reproductive unit.



Invasive *Mimosa* does not share symbionts with native relatives

doi:10.1093/aob/mct112

The legume genus *Mimosa* comprises approx. 500 species, most of which are native to the New World, with Brazil being the main centre of radiation, but ancient transoceanic dispersal resulted in the Indian subcontinent hosting up to six endemic species. **Gehlot et al. (pp. 179–196)** examine the nodulation ability and rhizobial symbionts of two of these, *M. hamata* and *M. himalayana*, both from north-west India, and compare them with those of *M. pudica*, an invasive species. In contrast to all Brazilian *Mimosa* species so far examined, which are nodulated by rhizobia in the Betaproteobacterial genus *Burkholderia*, the symbionts of the two Indian species are identified as belonging to the Alphaproteobacterial genus *Ensifer* (syn. *Sinorhizobium*). The invasive *M. pudica* is predominantly nodulated by Betaproteobacteria in the genera *Cupriavidus* and *Burkholderia*, and it does not share symbionts with either native species.



Hydraulic resistances in developing kiwifruit berry

doi:10.1093/aob/mct101

Xylem flows into most fruits decline as the fruit develop, with important effects on mineral and carbohydrate accumulation. **Mazzeo et al. (pp. 197–205)** use pressure chamber and flow-meter techniques to examine changes in xylem hydraulic resistance (R_T) in kiwifruit, *Actinidia deliciosa*, during fruit development. They find that increased R_T in the receptacle zone coincides with slowing of fresh-weight growth, reduced transpiration and rapid starch accumulation by the fruit. Shading of fruit also increases R_T . They conclude that developmental changes in R_T may be connected to changes in phloem functioning and the maintenance of water potential gradients between the stem and the fruit.