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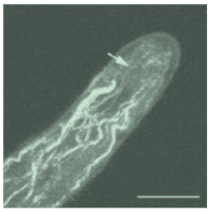
John Bryant takes a closer look at some of this month's Original Articles



Tipped for growth

Root hairs are an excellent subject for the study of tip growth. The existence of mutants and the use of real-time microscopic techniques on living cells have recently added significantly to our knowledge, including features of behaviour of the cytoskeleton. However, there are still many details to be elucidated. This has led **Xue He *et al.* (Beijing, China, pp. 49–55)** to look at the relationships between the distributions of actin and of calcium in relation to growth of wheat (*Triticum aestivum*) root hairs. Instead of using living material, they fixed whole seedlings (which provided root hairs at different stages of development) and used specific antibody staining techniques to examine actin distribution. In root hairs that were still growing at the time of fixation, F-actin was organized in bundles along the axis of growth. However, the bundles were absent from the apical 5–10 μm, the actual growing zone, but there were some very fine F-actin filaments. By contrast, G-actin was at its highest concentration in this zone, organized as a tip-focused gradient. There was no tip-located G-actin in hairs that had finished growing. Instead, the F-actin bundles extended right to the tip, suggesting that the apical location of F-actin bundles was related to the cessation of growth and that G-actin was involved in active growth. To investigate the relationship between actin dynamics and Ca^{2+}, roots were treated with BAPTA-AM, a disrupter of cellular Ca^{2+} distribution known to inhibit root hair growth. In these experiments it inhibited the tip-focused Ca^{2+} gradient characteristic of growing hairs and also inhibited the tip-focused gradient of G-actin. At the same time it caused an accumulation of a dense mesh of F-actin in the tip, more characteristic of hairs that have ceased growing. All this suggests an intimate relationship between Ca^{2+} distribution, actin dynamics and root hair growth.

Tale of the sting

I can still remember very vividly an incident from my childhood when I fell off a fence that I was climbing, straight into a bed of stinging nettles (which I now know as *Urtica doica*). Of course, I knew nothing of the chemistry of the process but I certainly knew that it was very painful! The stinging power of nettles has been known for a very long time, but strangely there is still no consensus on what makes the sting so painful. **Han Yi Fu *et al.* (Taipei and Taoyuan, Taiwan, pp. 57–65)** have analysed the exudate from the stinging hairs of *U. thunbergiana.* The main components were histamine, oxalic acid and tartaric acid, with a trace of formic acid. Several compounds that had previously been thought to be involved in generating the persistent pain, including serotonin and acetylcholine, were not detected in these assays. The next phase of the work was to record pain-related behaviour in rats injected with these compounds. Of the compounds present in the nettle-sting exudate, both oxalic acid and tartaric acid caused pain with a similar persistence to that caused by the exudate itself. Histamine and formic acid (and acetylcholine) were ineffective. Interestingly, serotonin, not detected in the extracts, was very effective in pain induction. The authors conclude that in *U. thunbergiana*, the pain inducers are oxalic and tartaric acids, two compounds widely distributed in the plant kingdom. It would be interesting to know whether in nettle stings they act synergistically and also whether histamine, although not on its own having any effect, may increase the pain-inducing properties of the acids. The inflammatory response to wasp stings, which are much more complex chemically than nettle stings, is at least partly caused by histamine, serotonin and acetylcholine; furthermore, other compounds in the venom induce the production of more histamine from the victim's mast cells.

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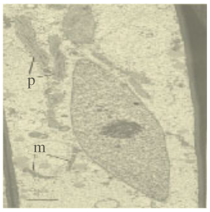
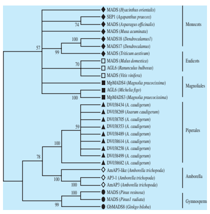


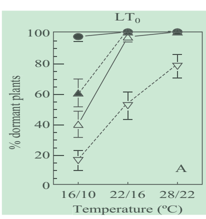
Skeleton holds key to cell reconstruction

The ability of many mosses to recover from severe dehydration is astonishing and there has been extensive research on the effects of desiccation and re-wetting on cellular membranes and on key biochemical processes. However, as pointed out by **Pressel *et al.* (Queen Mary, London and Caserta, Italy, pp. 67–76)**, little work has been done on transport systems. Focusing specifically on *Polytrichum formosum*, they have turned their attention to leptoids, food-conducting cells, generally considered to be the functional equivalent of phloem sieve elements in vascular plants. Shoots of plants collected from the field were allowed to dry over a period of 18 days, reaching a water content of only 7.5 %. In this state, they were able to survive for several weeks. Rehydration was achieved by immersing the shoots in distilled water. Throughout the dehydration–rehydration procedure, samples were taken and fixed for light and electron microscopy. In the hydrated state, leptoid cells have an 'elaborate cytoplasmic architecture' with a very obvious polarity along the long axis of the cell; this polarity is largely lost during desiccation. Microtubules disappear, as do the stacks of ER, the latter being replaced with 'membranous tubules' aligned across the cell; the elongated shapes of nucleus, plastids and mitochondria convert to more rounded forms; small vacuoles accumulate in the cytoplasm; plasmodesmata become plugged. On rehydration, the start of the reversal of these changes is visible within 30 min and is well under way by 2 h. Recovery proceeds in an orderly way with some events being completed early and others taking 12–24 h. One of the early events is the re-establishment of the microtubular cytoskeleton. Indeed, it is likely that this event plays a key role in the re-ordering of cellular structure during recovery: in shoots rehydrated in the presence of oryzalin, a disrupter of microtubules, leptoids failed to regain their normal structure.



Method in the MADS-boxes: ESTimation of evolutionary relatedness

Alterations in anatomy, morphology, cell biology and biochemistry are significant events in the remarkable transition from a vegetative to a floral apex. Underlying these are changes in the expression of a hierarchy of homeotic genes that are activated in an ordered sequence culminating in the formation of functional flowers. The most well known of these are the 'ABCD' genes that set up the floral organ identities after the establishment of the floral apex. These homeotic genes are classified as MADS-box genes in respect of a sequence motif that they possess and that is involved in their function as transcription factors. **Yinhe Zhao *et al.* (Kunming and Beijing, China; Köln, Germany; Houston, Texas, pp. 157–163)** are interested in the origin and evolution of this system. They have looked at the expression of flowering-related genes in *Asarum caudigerum*, a herb with simple flowers and regarded as primitive. They constructed a floral cDNA library and then sequenced 1920 randomly selected cDNA clones. The sequences were aligned with each other and with known sequences in the databases, resulting in the identification of 567 separate cDNAs. About 40 % of these represented either novel genes or genes encoding unknown proteins. The remainder could be assigned with confidence to different functional groups. Here we concentrate on the MADS-box homeotic genes, of which 38 were identified. Twenty-nine of these were of the *APETALA3* family, corresponding to the B-genes in the ABCD model and very similar in sequence to the corresponding genes in *A. europaeum*. Very interestingly, the other nine formed a cluster in the phylogenetic sequence comparison with MADS-box genes from *Amborella*, regarded as the most basal living angiosperm, and from gymnosperms. The authors suggest that this indicates an origin of *A. europaeum* intermediate between the gymnosperms and angiosperms, and that study of flower development in this species will provide new insights into the evolution of angiosperm flowers.



Lazy days of summer: a correction

In the April issue (97: 4), the Select article concerning the work of **Ofir and Kigel (pp. 659–666)** mistakenly stated that in the flowering ecotypes, higher temperatures induced earlier flowering, whereas in fact higher temperatures induced later flowering, consistent with the inhibiting effects of high temperature on flowering and the accelerating effects on dormancy, as described in the article.

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