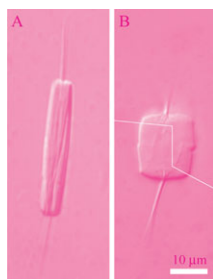




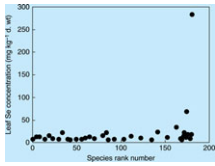
A whiter shade of pale – one partner's reaction to living together

When we talk to our students about legume–*Rhizobium* symbiosis, we usually emphasize the mutual benefits to the partners – the plant and the bacterium – in this relationship. However, living together may not be quite so straightforward, as illustrated by the work of [Okazaki *et al.* at Sendai, Japan \(pp. 55–59\)](#). They point out that the symbiont *Bradyrhizobium elkanii* produces a metabolic inhibitor, rhizobitoxine, which is also produced by a plant pathogen *Burkholderia andropogonis*. Rhizobitoxine inhibits specifically two enzymes, cystathione- β -lyase, which catalyses a late step in methionine biosynthesis, and ACC synthase, mediating the penultimate reaction in ethylene biosynthesis. Further, the biochemist in me notes that methionine is needed to generate the substrate for ACC synthase, and thus the two reactions are linked. In terms of evolution of nodulation, the synthesis of rhizobitoxine ‘makes sense’: ethylene inhibits nodulation and so inhibition of ethylene biosynthesis encourages nodulation. However, nodulation is not the only effect seen in soybean (*Glycine max*) inoculated with *B. elkanii*; the plants also exhibit an obvious chlorosis. The authors have set out to discover whether this is linked to the production of rhizobitoxine. Firstly, mutants of *B. elkanii* that do not produce rhizobitoxine do not cause chlorosis (and are less efficient nodulators than wild-type). Secondly, plants inoculated with wild-type *B. elkanii* show reduced levels of methionine and increased levels of methionine precursors, especially aspartate and homoserine, consistent with inhibition of cystathione- β -lyase (no data on ACC synthase were reported). Thirdly, supply of methionine, but not of ACC, via the plants’ nutrient solution relieved the chlorosis. All of these results are consistent with the view that chlorosis results from methionine deficiency, which is caused in turn by rhizobitoxine-induced inhibition of cystathione- β -lyase. Since the chlorosis is often severe enough to more than counteract the benefits to the plant of nodulation, the hunt is clearly on for rhizobitoxine-resistant varieties of soybean.



Tails – you win: getting a handle on forisome function

Over a period of several decades, many observations of phloem sieve tubes appeared to show protein bodies (P-protein), blocking the sieve-plate pores; how then did translocation occur? It was suggested that this blockage was a fixation artefact but that still did not tell us anything about P-protein function. Then came the discovery that plants in the sub-family Faboideae contain P-protein bodies that, in response to Ca^{2+} , but independently of ATP, expand to plug or partially plug the sieve pores. These were named forisomes, or gate bodies (from the Latin *foris*, the wing of a gate). Now a joint German–American group ([Peters *et al.*, pp. 101–109](#)) has used forisomes from the climbing faboid, *Canavalia gladiata* (sword bean) to study reactions to Ca^{2+} *in vitro*. Forisomes from this species have two main advantages. First they are very large (up to 55 μm long) and secondly they possess tails that allow them to be handled without touching the main contractile part. The authors were thus able to study individual isolated forisomes under the microscope. In the absence of Ca^{2+} (the ‘resting’ state), forisomes had a square cross-section and thus resembled a long box. When forisomes were irrigated with Ca^{2+} the rectangular cross-section was retained but the length decreased by about 30 % and the cross-sectional dimensions increased by up to 4-fold. Overall, this process took between 10 and 15 seconds and, strangely, final length took longer to achieve than final thickness. Especially important for the plugging function, the mean changes in dimension were calculated to increase forisome volume 9-fold. Evidence that the trigger for these changes was indeed Ca^{2+} was obtained by flooding the forisomes with a chelating agent: they reverted to the resting state and, again strangely, this reversion occurred ten times faster than the response to Ca^{2+} . *Canavalia* forisomes thus have great potential for study of calcium-regulated protein contraction.



Life on the high Se...S

In many western countries a visit to a so-called health-food shop will often reveal fashionable food supplements aimed at satisfying equally fashionable anxieties about dietary deficiencies. Amongst these supplements are those offering selenium (Se) as a key ingredient, reflecting a view that modern diets do not contain enough. This is not to say that we do not need Se. We do need it, but only as a trace element (approx. $50 \mu\text{g d}^{-1}$); too much Se is actually toxic. Understanding the mechanism and kinetics of Se uptake by plants is thus important on two counts – the dietary need for small amounts of Se and the toxic effects of any excess. Further, there is the possibility that plants that take up Se may be used in bioremediation of contaminated soil. All this forms the background to the work of [White *et al.* \(Dundee, Warwick and Nottingham, UK, pp. 111–118\)](#). Se is very similar chemically to sulphur (S); selenate and sulphate are generally taken up by the same plasma-membrane high-affinity sulphate transporters (HASTs). However, an earlier survey by the research group revealed that some plants select in favour of sulphate while a few are able to select in favour of selenate. The authors have now surveyed 39 angiosperm species across the range of Se-accumulation phenotypes, grown them hydroponically and studied their ability to take up Se and S. Most of the species did not discriminate between S and Se but two species, *Astragalus recemosus* (Fabaceae) and *Stanleya pinnata* (Brassicaceae) were very obviously Se accumulators, with concentrations of Se in leaves and leaf Se/S quotients very markedly higher than the other species. This ability to discriminate in favour of Se probably lies in the molecular structure of one or more root-located HASTs, which now become important research targets.



Bioinformatics for chocolate lovers: getting a tag on cocoa

One of the recurring themes in surveys of global agricultural research is the comparative lack of effort expended on tropical crops. This is even true of crops of major economic importance, as is illustrated for *Theobroma cacao* (cocoa) by the work of [Gesteira *et al.*, a Franco–Brazilian research group \(pp. 129–140\)](#). The authors indicate that more than 20 million people, many of them in very poor countries, depend directly on cocoa for their livelihood: the importance of the crop extends far beyond the needs of chocolate lovers. Despite this, knowledge of interactions between *T. cacao* and its various pests and pathogens is very limited; thus the authors' work on witches broom disease of cocoa, caused by the fungus *Moniliophthora perniciosa*, is very welcome. They have selected *T. cacao* cultivars that are resistant or susceptible to *M. perniciosa*. Apical meristems of 4-week-old plantlets in both groups were inoculated with spores of *M. perniciosa*; control plants were mock-inoculated. Apical meristems were harvested and rapidly frozen 24, 48 and 72 h after inoculation, and thereafter every 5 d until day 90. Disease development was monitored over the same period. RNA extracted from the harvested meristems was used to construct cDNA libraries. From these libraries clones were randomly selected and partially sequenced to give expressed sequence tags (ESTs), the first EST analysis of the *T. cacao*–*M. perniciosa* interaction. From a total of 6884 ESTs, 2926 individual sequences were identified, of which 54 % could be allocated to genes of known function. Comparison of the ESTs revealed differences that included the greater representation in the ESTs from resistant plants of 'genes involved in the resistance process' and in the ESTs of susceptible plants of genes involved in the oxidative burst and in programmed cell death. Thus, as the authors themselves state, this work will lead to the development of strategies to control witches broom disease in this very important crop.

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