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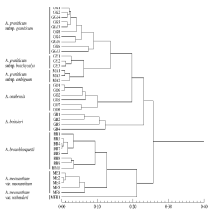
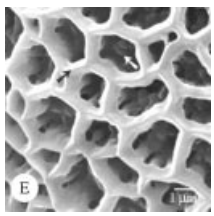
John Bryant takes a closer look at some of this month's Original Articles



### Allozymes aid *Antirrhinum* assignment

One of the functions of taxonomy is to help us understand the evolutionary relationships between organisms. Furthermore, the range of tools available to taxonomists is becoming ever more versatile, especially as different types of molecular analysis can be utilized to investigate relatedness. All this is evident in the paper by **Mateu-Andrés and Segarra-Moragues from Valencia and Zaragozo, Spain (pp. 647–655)**. They have worked on groups of species within the genus *Antirrhinum* in which the use of morphological characters to assign certain species to sub-generic groups has proved difficult. The authors used a proteomic approach (looking at differences in protein populations) and in particular focused on eight enzymes that are readily assayable *in gelo* after electrophoresis. The electrophoretic banding patterns exhibited by these enzymes revealed 14 loci (i.e. some of the enzymes were encoded by more than one genetic locus) providing a total of 51 alleles across the range of species and sub-species studied. Based on a detailed analysis of the distribution of the alleles, the authors calculated genetic distances between the species and sub-species and this in turn led to the construction of a dendrogram. The dendrogram clearly demarcates the two groups of species, previously named subsections *Streptosepalum* and *Antirrhinum*. The authors were then able to re-assign particular species between the two groups and to lower the rank of one 'species' to that of sub-species. The data have thus thrown light on the evolution and divergence of these groups in the genus *Antirrhinum*. In respect of speciation, it is noted that all the species studied are inter-fertile but pollinators can distinguish between them. Hybrids are thus rare and, for some pairs of species, this is reinforced by geographical separation. Thus we have a snapshot in the process of speciation: as the authors comment, reproductive isolation leads to gradual divergence until reproductive barriers appear.



### Ethylene signals route to ferric foraging

The interface between plant and soil via the root system is very dynamic. In response both to nutrient deficiency and nutrient abundance many plants are able to modify root morphology and/or to alter the allocation of overall resources between root and shoot. A specific and unusual example of this is seen *Casuarina glauca*, which forms cluster roots under conditions of soil iron deficiency. One of the interesting questions that arise in these situations is how the morphogenic events are controlled within the plant. The primary signal is nutrient deficiency but this signal must be transduced to cause the production and/or activation of meristems. It is this question that has been addressed by **Zaid *et al.* (Rabat, Morocco and Créteil, France, pp. 673–677)**. They grew casuarina plants in Fe-sufficient and Fe-deficient conditions and then tested the effects of ethylene inhibitors and ethylene precursors on cluster root formation. Iron deficiency led to the formation of four times as many cluster roots compared with plants supplied with iron. Addition of the ethylene precursor ACC (1-aminocyclopropane-1-carboxylic acid) had no effect on cluster root formation in Fe-deficient conditions, but when added to the nutrient solution in Fe-sufficient conditions it led to formation of cluster roots as if the plants were Fe-deficient. This is strong indication that ethylene is involved in cluster root formation. This idea is supported by the results of experiments with inhibitors of ethylene synthesis or of ethylene action: all of these prevented the four-fold increase in cluster root formation normally seen in Fe-deficient conditions. Based on their data, the authors suggest that a very early response to iron deficiency is a marked stimulation of ethylene biosynthesis. This leads, presumably *via* a 'standard' signal transduction pathway, to the regulation of gene expression and morphogenesis in this developmentally plastic root system.

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### Sunbirds' and squirrels' sweet treats help to set seed

Reproductive biology features strongly in this issue of the journal and we focus here on one of the papers that deals with this topic. *Butea monosperma* is a leguminous tree, well-known in India because of its beautiful orange-red flowers and several useful products. The flowers are visited by birds but there is a question as to whether these are effective pollinators. To answer this and several related questions, **Tandon *et al*, Delhi and Bangalore (pp. 715–723)** have carried out an extensive study of the reproductive biology of *B. monosperma*. Here we concentrate mainly on pollination. Three species of bird were recorded as feeding on nectar, but only one, the purple sunbird (*Nectarinia asiatica*) was a legitimate collector. The other two species gained access to the nectar by making a hole in the calyx. The authors also noted legitimate collection of nectar by a mammal, the three-striped squirrel (*Funambulus tristiatus*), whereas the only insect observed to forage nectar *via* the holes in the calyx made by birds was the giant Asian bee. Pollen was presented only to the legitimate foragers of nectar that press down on the keel of the flower. Pollen could be observed on the heads of sunbirds and on the snouts and heads of squirrels as they retreated from the flowers and this pollen transferred easily to the stigma of the next visited flower. Thus, there are two effective pollination agents, a bird and a mammal, a very unusual situation that has been revealed by careful observation in the field. But how effective are they? In manual pollinations, the authors obtained 5 % fruit set in inbred and 22 % in outbred fertilizations. In the wild, fruit set is about 5 %, suggesting that pollinations are mainly inbred. This is borne out by the behaviour of the pollinators, which visit many flowers on the same tree.

### Bats get two innings in the rain forest

Those of us whose research is largely lab-based and focused on a small range of model species, forget all too easily that there is a huge range of botanical biodiversity 'out there'. Much of this is inadequately described or even unknown and there is still enormous scope for careful observation and recording in the field. The paper by **Sazima *et al*., from Campinas, São Paulo, Brazil (pp. 725–730)** illustrates this beautifully. They describe aspects of the reproductive biology of *Dyssochroma viridiflorum*, an epiphytic member of the Solanaceae that grows in the Atlantic rain forest. This species is pollinated by nectar-seeking-bats, which are attracted by a 'mushroom-like' scent. The flowers open early in the night and are available for visiting for about 48 h. During the day, the flowers may also be visited by hummingbirds but these do not act as pollinators. Instead, they 'steal' the nectar by making a hole in the base of the corolla (the corolla tube in *D. viridiflorum* being too long for the particular hummingbird species). Furthermore, the dependence on bats does not finish with pollination. The fruits of *D. viridiflorum* are also attractive to bats, but to frugiverous species as opposed to the nectarivous pollinators. The seeds embedded in the fruit pass through the bats' alimentary system and are dispersed in the faeces. Three different bat species, one pollinator and two seed dispersers are thus involved in the reproductive biology of *D. viridiflorum*. However, the story does not end there. This species produces flowers all the year round and thus flowers and fruit are usually present together, so that an individual plant may be visited by nectar-seeking and fruit-eating bats at the same time. This must be a remarkable sight, a phenomenon that ensures that we lab-based botanists cast our gaze from time to time at a wider botanical world.

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