

# ContentSelect

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

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## Waterproof genes?

Mention of rice cultivation will lead many to picture paddy fields with the rice plants rooted under water. Indeed, many rice varieties are grown in this way but there are also flood-intolerant varieties, while even paddy rice is vulnerable to total submergence. The main factor in flooding is O<sub>2</sub> deprivation, and it is of great interest to understand the mechanisms involved in toleration of hypoxia. One approach to this is to investigate the array of genes activated during O<sub>2</sub> deprivation, as reported extensively by **Agarwal and Grover (University of Delhi, India, pp. 831–844)**. At the heart of the methodology was the construction of 'subtraction' cDNA libraries, which enabled a comparison between flood-tolerant (variety FR13A) plants exposed to control conditions or to O<sub>2</sub> deprivation and, secondly, comparison between the responses of FR13A with those of a flood-intolerant variety, PB1. These libraries were then used in expression profiling, using reverse Northern analysis, which identified specifically the cDNA clones, 293 in all, that represented genes up-regulated in FR13A during O<sub>2</sub> deprivation. Partial sequencing of these clones then provided the same number of ESTs (expressed sequence tags). It is a major advantage for this work that the rice genome has been sequenced and this has enabled the authors to make at least a partial identification of the up-regulated genes. The detail lies outside the scope of this commentary; here we focus on the overall classification of these genes. The largest group, representing 68 % of the transcripts, are as yet 'anonymous' within the rice genome. The remaining 32 % may be grouped into six categories, which, starting from the largest category, are N and C metabolism (including the electron transport chain), transport, RNA binding and recognition, transcription factors, signalling pathways and anti-oxidant metabolism. This is a great start to understanding the molecular biology of flood tolerance in rice and bodes well for future breeding or gene transfer programmes.

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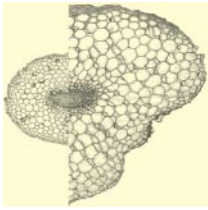


## Alien on the loose causes strife for natives

Earlier today, while walking beside a local river, I was pleased to see *Lythrum salicaria*, purple loosestrife, along the water's edge. However, for readers in North America, it would be a much less welcome sight. In many parts of the USA and Canada, *L. salicaria* has become aggressive, often dominating the vegetation in wetland habitats, as described by **Houghton-Thomson et al. (Michigan State University, USA, pp. 877–885)**. *Lythrum salicaria* was probably introduced accidentally into North America in the early 1800s but it was not until the 1930s that it began to become a problem. Since then, the pattern of invasion has elements that one might meet in a science fiction plot: in each new area that it reaches, it remains, as the authors say, 'unobtrusive' for at least 20 years, after which it becomes dominant in suitable habitats in less than 3 years. The authors wondered whether this pattern of invasion was at least in part due to hybridization between *L. salicaria* and the native North American species, *L. alatum* (winged loosestrife). To test this idea they carried out a careful analysis, based both on diagnostic morphological traits and on an AFLP screen, of populations of *L. alatum* and of European and North American populations of *L. salicaria*. The results are clear: genetically and morphologically, the two species are clearly separate; however, the North American *L. salicaria* form a distinct subgroup within the *L. salicaria* populations. Further, some of the characters that mark out the North American populations are actually from *L. alatum*. In other words, hybridization between the two species has occurred at some time in the past but the level of introgression of *L. alatum* genes into the *L. salicaria* genome is actually very low; too low, the authors suggest, to explain the invasiveness of *L. salicaria*. For the present, then, the secret of the alien's success remains hidden.

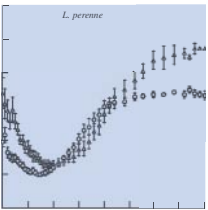
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### A root in a hard place

It was apparent in one of the symposia sponsored by the *Annals of Botany* at the recent International Botanical Congress in Vienna that laboratory studies of root development may tell only part of the story. This is because, in contrast to laboratory conditions, agricultural and natural habitats are often far from ideal for root growth. One common shortcoming is soil compaction, studied here by **Hanbury and Atwell (South Perth and Sydney, Australia, pp. 913–924)**. These authors imposed an air pressure of 15 kPa on the coarse sand in which roots of *Lupinus angustifolius* seedlings were growing, thereby mimicking the effects of impedance in a hard soil. Within 1 h, the extension rate of roots declined, and by 20 h the rate was less than 25 % of that in control roots. There was no effect on the root meristem; the effect on root extension being due to a dramatic reduction in cell elongation. Two other morphological effects were also very clear. Firstly, the zone of cell elongation was pushed towards the meristem. Secondly, the impeded roots were nearly twice as thick as control roots. This did not involve the generation of new cell files but was based entirely on increased lateral expansion of the cells. The authors then determined O<sub>2</sub> requirements for elongation. Control roots achieved their maximum elongation rate at approx. 10 % soil atmosphere O<sub>2</sub> whereas the corresponding figure for impeded roots was approx. 22 %. Overall, impeded roots consumed 80 % more O<sub>2</sub> per unit of elongation growth than control roots. In both situations O<sub>2</sub> requirement was much greater in the apical 5 mm, the zone containing the root meristem, but because, in impeded roots, cell elongation was initiated so close to the meristem, cell elongation in this zone was very vulnerable to lower O<sub>2</sub> tension. Thus, morphological responses to impedance made the roots more vulnerable to hypoxia, a situation likely to be exacerbated in hard soils where gaseous diffusion may be hindered.



### Key role for polyploidy in promoting leaf length in *Lolium* species

It is obvious that both cell division and cell enlargement are essential processes in plant growth. However, that simple statement raises some very interesting questions concerning the control and integration of the two processes in the production of organs of particular shapes and sizes. Thus, the recent discovery of genes that regulate the cell cycle in relation to leaf size is very exciting. Equally interesting is the evidence that in many, but certainly not all species, the phase of cell enlargement is preceded or accompanied by endo-reduplication of DNA (replication of DNA in the absence of mitosis). Taken with observations that across the plant kingdom cell size is positively correlated with genome size, this suggests a role for genome size in regulating cell enlargement. The data presented here by **Sugiyama (Hirosaki, Japan, pp. 931–938)** certainly point in this direction. The author compared diploid and tetraploid populations in two *Lolium* species with respect to leaf size, leaf cell division and leaf cell enlargement. In both species, but especially in *L. perenne*, the tetraploids had longer leaves than the diploids. This was not due in any way to differences in cell division: cell cycle times and cell production rates showed no significant differences between diploids and tetraploids. Instead, as shown by detailed analysis of cell lengths from the leaf bases up through the zones of division and elongation, the greater leaf lengths were clearly correlated with greater cell lengths at maturity. Statistical analysis showed that although the tetraploids exhibited both a greater rate of cell elongation and a longer phase of cell elongation than the diploids, it was the increased rate of elongation that made by far the major contribution to increased cell length. The challenge now is to discover the mechanism(s) by which genome size affects so specifically this particular facet of cell growth.

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