

**Flora of China: An international collaborative project to describe the 31,000 vascular plant species of China**

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The *Flora of China* Project is a massive international collaboration between Chinese and non-Chinese botanists to catalogue the estimated 31,000 species of wild vascular plants in China. The project began in 1988 and now has a 21-member Editorial Committee and 11 partner institutions: four in China and seven in the West, coordinated by the Missouri Botanical Garden, St. Louis, and the Institute of Botany, Chinese Academy of Sciences, Beijing. The *Flora* itself is being written in English by over 450 authors and when finished will comprise 24 volumes of text and 24 accompanying volumes of illustrations, plus one introductory volume. Due for completion in 2012, so far 14 volumes of text and 12 volumes of illustrations have been published, accounting for nearly 18,000 species, of which just over 9500 (53%) are endemic to China. The *Flora of China* Project has a website hosted by the Harvard University Herbaria ([flora.huh.harvard.edu/china](http://flora.huh.harvard.edu/china)) and an electronic version of the *Flora* is served by the *eFloras* website ([www.efloras.org](http://www.efloras.org)), where all the paper-published information is freely available online. Also online are web-based interactive identification keys for more than 11,000 species as well as draft treatments for most of the as yet unpublished volumes of the *Flora*.

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**The influence of stream order on riparian biodiversity in the Sabie River: The links between compositional, functional and structural diversity**

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Biodiversity consists of compositional, structural and functional components. However, the study of biodiversity is biased towards compositional diversity, and structural and functional aspects are often neglected. This has been the case in many riparian biodiversity studies. Furthermore, riparian biodiversity research is normally focused upon large perennial rivers, with little attention paid to smaller, lower order streams. Knowledge of how all three components of biodiversity are distributed among rivers of different size will provide a new perspective of riparian biodiversity, and could help focus both research and conservation efforts. Here we present results showing how woody plant compositional and structural diversity change along rivers in the Kruger National Park ranging from first stream order to fifth stream order. Generally woody plant diversity is higher in the fifth orders streams, but is similar in the first, second, third and fourth order streams. We discuss the possible reasons behind these results, and finally consider their broader implications for biodiversity conservation.

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**Co-evolutionary dynamics within the fig–fig wasp mutualism; sycoecine and agaonid fig wasps associated with *Ficus* section *Galoglychia***J.G. Underhill<sup>a,b</sup>, K.A. Tolley<sup>a</sup>, S. Van Noort<sup>c</sup><sup>a</sup>*Leslie Hill Molecular Laboratory, Kirstenbosch Research Centre, South African National Biodiversity Institute, Private Bag X7, Cape Town, South Africa*<sup>b</sup>*Department of Botany, University of Cape Town, Private Bag, Rondebosch 7701, South Africa*<sup>c</sup>*Natural History Division, South African Museum, Iziko Museums of Cape Town, PO Box 61, Cape Town 8000, South Africa*

The fig–fig wasp mutualism has traditionally been distinguished by a one-to-one ratio of host-specificity, whereby each species of fig tree (*Ficus*, Moraceae) is pollinated by a unique species of fig wasp (Agaonidae, Chalcidoidea, Hymenoptera). However, recent studies conclude that extreme host specificity, although frequent, is no longer as ubiquitous as previously considered, thus challenging strict co-evolutionary hypotheses. This study comprises the first molecular phylogeny of the Sycoecinae (Pteromalidae, Chalcidoidea, Hymenoptera) a group of non-pollinating fig wasps that enter the fig to oviposit, imitating the pollinators, in contrast to the majority of externally ovipositing non-pollinators. Internal oviposition requires the sycoecines to face the same selective pressures as the pollinators, potentially promoting the maintenance of host-specificity within this group. Have the sycoecine non-pollinators coevolved with the pollinating fig wasps or do they represent a more recent colonization of the fig niche and subsequent speciation by sequential radiation? Revisions of the molecular phylogenies of *Ficus* section *Galoglychia*, and of the associated African pollinators were also performed. The phylogenetic history and biogeography of the sycoecine and agaonid fig wasps associated with *Ficus* section *Galoglychia* were explored using tests of phylogenetic congruence, molecular dating techniques, and lineage through time plots. Phylogenetic analyses of both nuclear and mitochondrial DNA sequence data using bayesian and parsimony approaches show both wasp lineages to be monophyletic. Preliminary results of this ongoing study hint at a complex history of codivergence between figs and fig wasps, in corroboration with similar, recently published studies.

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**Evaluation of gene expression in wheat upon treatment with a novel plant activator**C.H.J. Van der Merwe<sup>a</sup>, B. Visser<sup>a</sup>, J.C. Pretorius<sup>b</sup>, A.J. Van der Westhuizen<sup>a</sup><sup>a</sup>*Department of Plant Sciences, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa*<sup>b</sup>*Department of Soil-, Crop- and Climate Sciences, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa*

ComCat<sup>®</sup> is a commercially available plant activator used in the agricultural industry to improve root growth and the general condition of plants. Isolated from twelve different wild plants, the product is a complex mixture of compounds. Since the effect of ComCat<sup>®</sup> treatment on plant gene expression has never been tested, this study was initiated to determine the response of treated plants on molecular level. After treating wheat seedlings with a purified fraction of ComCat<sup>®</sup>, referred to as SS, subtractive suppression hybridization (SSH) was used to clone and sequence putative differentially expressed cDNA fragments. The induced expression of some genes was confirmed using RT-PCR. The vast majority of cDNA clones that were identified encoded photosynthetic related proteins. The obtained results indicated that the main benefit of the purified SS fraction of ComCat<sup>®</sup> to treated plants was most probably an increased photosynthetic capacity, making the plants stronger and more robust.

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**How to resolve a comb by sequencing low copy nuclear genes and what we can infer from its trees**T. Van der Niet<sup>a</sup>, F. Bakker<sup>b</sup><sup>a</sup>*School of Biological and Conservation Sciences, University of KwaZulu-Natal Pietermaritzburg, Scottsville 3209, South Africa*<sup>b</sup>*Biosystematics Group, Wageningen University and Research Center, Generaal Foulkesweg 37, 6703 BL Wageningen, The Netherlands*

Species level plant phylogenetics is limited by the availability of suitable markers that are adequately variable and reliable at this taxonomic level. Although low copy nuclear gene sequences offer great potential, they are rarely