

Creating rare from common species – seed sourcing and restoration of iconic yellow box (*Eucalyptus melliodora*)

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Yellow box (*Eucalyptus melliodora*) is a valuable and iconic tree once broadly distributed from western Victoria, New South Wales and southeastern Queensland. The soils coinciding with this distribution are favourable to cropping, horticulture and grazing which has resulted in severe loss and fragmentation of this species and the ecological community in which it resides. This ecological community is now protected under both Commonwealth (EPBC) and State (NSW) legislation. Yellow box is valued for its shade, shelter and timber qualities as well as being important for wildlife habitat and honey production. As such it is important restoration species throughout its distribution. However, given the high levels of fragmentation that this species has undergone it is likely that low genetic diversity and elevated inbreeding may limit the utility of some populations to act as restoration quality seed sources. Seed collected under current seed sourcing protocols from across the southern tablelands of NSW were assessed for levels of genetic diversity to help improve yellow box restoration within this region. Excess seedlings from this analysis were later planted into two provenance trails and similarly assessed to determine how much diversity was captured during this process. Finally, mating patterns and pollen dispersal were assessed in five reproductively mature restored sites to determine whether these would be suitable seed sources for future restoration projects.

Plant breeding systems in alpine ecosystems in the southern South American Andes – searching for signs of vulnerability under climate change

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Alpine plants may cope with climate change by upward migration along steep altitudinal gradients. The ability of plants to keep up with the pace of climate change will be influenced by dispersal capacity and breeding system. Among species with different breeding system, those with strong autonomous selfing capacity should be best adapted for migration along altitudinal gradients on account of their capacity to produce seed without the intervention of biotic pollinators. At the other extreme, successful migration of self-incompatible and sexually dimorphic species with specialized pollination might be impeded if pollinators and plants migrate upward at different rates, as would be expected from their respective life history attributes. The autonomous selfing hypothesis posits that generally cold temperatures and variable weather conditions at high elevations will select for autonomous selfing in high elevation ecosystems, which might suggest that alpine plants are well adapted to cope with climate change. Here using data from a published community study for the Patagonian alpine (50°S) in southern Chile and a parallel ongoing study in

the central Chilean Andes (33°S) (together >200 species) we investigate the incidence of breeding systems along the self-incompatibility (SI)-self-compatibility (SC) gradient. Considering the dominant perennial herb life-form, where good breeding systems records are most abundant, both alpine sites show a wide range of breeding systems, there being large contingents of self-incompatible and partially self-compatible species habitually serviced by biotic pollinators, in addition to strongly autogamous species. Contrary to expectation, the frequencies of SC and SI species in the warm and sunny central Chilean alpine and the cold and windy Patagonian alpine are similar, despite wide community-level differences in flower visitation rates. Large breeding system data sets are scarce worldwide. The available information suggests that in spite of the cold and variable weather conditions at higher elevations, SI in perennial herbs is as well represented in the high South American Andes as in some lowland communities, and that many alpine species in this region of the world could indeed be vulnerable under climate change. Research financed by Fondecyt Grant 1085013 and IEB grants, Chile.

Plant architectural and genetic diversities in *Coffea* native from Madagascar: towards an architectural-functional plant growth model applied to *Coffea* biodiversity perservation

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The *Coffea* genus includes 103 species with 53 endemic to Madagascar (namely Mascarocoffea). The three main centres of species diversity for coffee trees are Madagascar (naturally low-caffeine species), Cameroon and Tanzania. However, Madagascar has the higher *Coffea* diversity in terms of total number of species due to the great variety of forest types including littoral, evergreen, gallery, mixed deciduous, dry, xerophytic and high-altitude. During these last 20 years, deforestation in Madagascar has become dramatic and has drastically reduced the distribution area of *Coffea* species. The collection maintained at the Kianjavato Research Station is unique since no living material is authorized to be conserved out of Madagascar. Conservation strategies based on scientific data are needed and become urgent in terms of biodiversity preservation and sustainable development. Recent studies in *Coffea* trees showed that their phenotypic plasticity could be explain the restricted distribution of *Coffea* species. Our recent preliminary results showed a high architectural diversity (i.e. architectural model, growth process, branching degree, branch location) between *Coffea* species and an interspecific variability of functional traits (Leaf Area Mass, wood density). The functional-structural model GreenLab is a dynamic model taking into account architectural plasticity of the plants and biomass allocation to organ level. Potentials of GreenLab model to represent environment x genotype interactions, in particular through its stable endogenous parameter as such the organ sink functions have been demonstrated in some species and they will be tested for *Coffea* species.

The present study focuses on 5 species endemic to Madagascar with different phenotypic traits and forest habitats. For each species, architecture and genetic comparative analyses between individuals growing in situ (natural forest) and ex situ (common garden test) will be performed. In addition, we have set up two experimental stands to analyse the site effect. These whole results will be used to introduce genetic factors into the GreenLab model. The global aim of our approach is to analyse the adaptive capacity and phenotypic plasticity at the individual level within *Coffea* populations.

THEME 02: ECONOMIC BOTANY INCLUDING BIOTECHNOLOGY, AGRICULTURE AND PLANT BREEDING

Sym028: Novel approaches to engineering C₄ photosynthesis into C₃ crops – 26 July

C₄ Rice Project

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Future global population increases of some 2 billion people by 2050 will require an extra 250 million tonnes of rice per year in Asia alone. To feed this increased population, agriculture will need to improve food production by some 50% equivalent to a second green revolution that first occurred in the 60's and 70's. The C₄ Rice Project was launched 18 months ago to address this problem and will need substantial financial investment now and in the future if it is to succeed. Excellent initial progress has been made in the project which is predicted take 15–20 years. This talk will provide a description of the consortium, outline the research strategies being employed, give an update on current research progress and outline some of the challenges to be tackled in the coming years.

Engineering the C₄ pathway into rice

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It has been proposed that integrating C₄ photosynthesis into C₃ crops could be used to increase their maximum yields. This is a challenging undertaking because the C₄ pathway is complex and involves alterations to the biochemistry, cell biology and development of leaves. However, C₄ photosynthesis has evolved independently at least 62 times, and this biological precedent implies that changes to a relatively small number of factors may generate the complexity of a C₄ leaf. Recent advances in proteomics, transcript profiling and the release of genome sequences for sorghum and maize, two important

C₄ crops, have filled some of the gaps in our understanding of mechanisms underlying C₄ photosynthesis. Further advances are being made by comparative analysis of closely related C₃ and C₄ plants because this reduces signal noise associated with phylogenetic distance. We will consider both our understanding of global alterations to gene expression in C₄ compared with C₃ leaves, and also provide specific examples of how the regulation of genes has altered as they are recruited into the C₄ pathway. We will discuss evidence that distinct lineages of C₄ plants share regulatory circuitry that generates accumulation of photosynthesis proteins in specific cells. A summary and progress report of current efforts at placing the biochemistry of C₄ photosynthesis into rice will be provided.

Evidence for the essential components of the C₄ mechanism

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Recently there has been a renewed interest in the C₄ photosynthetic mechanism due to the desire to improve yield potential and radiation use efficiency in C₃ crops by introducing elements of the C₄ pathway (C₄ Rice Consortium; <http://beta.irri.org/projects15/c4rice>). To facilitate this process, strategies need to be developed to identify the subset of key genes necessary to transfer a functional C₄-like mechanism to C₃ crops. This presentation describes development of phenotypic screens for 'C₄-ness' which can be used in analysis of transgenic C₃ plants in which partial C₄ pathway components are being installed, analysis of photosynthesis in sorghum with impaired lignification and secondary thickening of leaf tissues, and photosynthetic characterisation of maize husk, and leaf sheath, tissue thought to operate a biochemical and structural blend of C₄ and C₃ photosynthesis. These data are synthesised to delineate the challenges of measuring 'C₄-ness', the role of bundle sheath cell wall properties in the efficiency of the C₄ CO₂ concentrating mechanism and the key steps in attaining a C₄-like C₃ crop plant.

Do rice mutant populations offer variation in traits useful for C₄ engineering ?

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A large proportion of global rice production takes place in conditions where high temperatures induce substantial levels of photorespiration resulting in deterioration of