Project 2_1 Precision Breeding in Protected Cropping: Addressing Plant Recalcitrance

PC Hub Theme (see list here)
Theme 2: Plant Breeding – Rapid Candidate Gene Identification, Validation and Engineering
Principal supervisors
Prof. Monika Doblin Prof. Mathew Lewsey

Most crops currently grown in protected cropping systems have been bred for traditional/outdoor agricultural systems. As a result, they are not optimised for the environmental conditions and rapid generation cycling typical of protected cropping environments.

The main goal of Theme 2 is to **implement rapid, generalisable, species-agnostic PC approaches** for:

1. Identifying candidate genes controlling traits in crops of commercial value
2. Developing PC-optimised crop cultivars

An efficient genetic transformation system provides a foundational platform for both functional genomics research and molecular breeding in crops. It enables not only the functional validation of a candidate gene post-discovery but also the improvement of desirable agronomic traits such as high yield and quality, and increasingly the development of novel traits artificially engineered into the plant.

With the rapid advancement of gene editing tools such as CRISPR and synthetic biology approaches, the demand for highly efficient transgenic methodologies is anticipated to grow.

However, despite the tremendous potential of modern biotechnology for enhancing crops, the generation of transgenic plants remains technically challenging. A major

bottleneck is the 'recalcitrance' of many plant species to *in vitro* regeneration (Figures 1 & 2), coupled with substantial genotype-dependent transformation efficiency (Figure 3).

This project aims to unravel some of the constraints associated with the transformation of horticulture/medicinal plant species and provide solution(s) to overcome them to enable precision breeding applications for enhanced performance of PC crops.

The PhD candidate will:

- Conduct experiments to discover the underlying molecular players and pathways that result in plant recalcitrance.
- Combined with microscopy modalities, use various methodologies to determine the molecular state of tissue/s showing differences in regeneration and/or transformation competency in a spatiotemporal manner. Analyses include determining gene expression competency (chromatin state, e.g. ATAC-Seq), changes in gene expression (single cell RNA sequencing), metabolite and protein content (GC and LC-MS, tissue imaging (MALDI)-MS).
- Use multiple analyses to identify candidate genes that may play a role in determining recalcitrance.
- Apply biotechnological solutions such as targeted gene expression changes (e.g. over/ectopic expression and/or knock-out/down using CRISPR) to reduce or overcome recalcitrance to deliver a precision breeding outcome of relevance to the PC Hub.

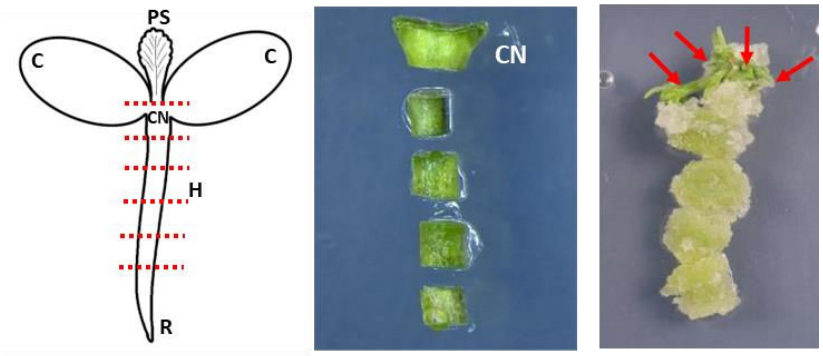

Figure 1: Example of the impact of explant type on regeneration competence. De novo regeneration is indicated by the red arrows.

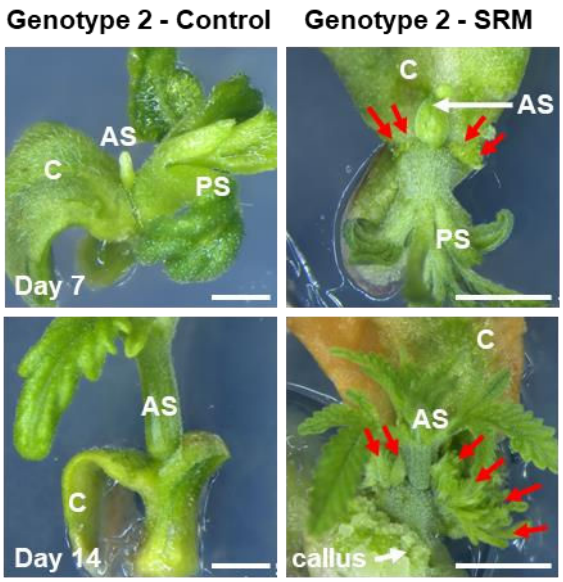

Figure 2: Example of how differences *in vitro* growth media (plant growth regulators) impacts the ability of plant tissue to regenerate. De novo regeneration is indicated by the red arrows.

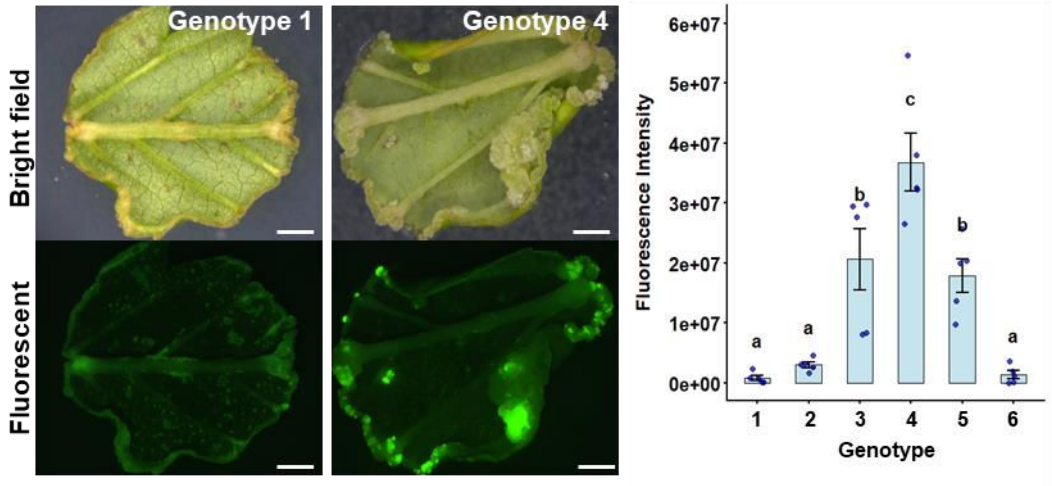

Figure 3: Example of the difference in genetic transformability between various genotypes of a single plant species. Transformed cells are indicated by expression of the fluorescent reporter VENUS. Different letters in the bar graph indicate significant differences in transformability between genotypes.

How to apply

The PC Hub offers a limited number of competitive scholarships.
To apply, please email the following documents to pchub@latrobe.edu.au by **15 February 2026:**

- Application form completed.
- Up-to-date CV
- University transcripts

Only shortlisted applicants will be contacted.