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Understanding and engineering salinity tolerance in crop plants

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Slatyer Seminar room Robertson Building, ANU



Genetics and genomics are powerful tools for gene discovery. In this talk, forward genetic approaches for discovery of genes related to salinity tolerance in wheat and barley will be described.

Increasingly efficient transgenic technologies are generating large numbers of GM crop plants. However, gene expression often needs to be manipulated in more targeted ways by, for example, activating genes in only specific cells or at specific times. Using salinity as an example, it will be shown how gene over-expression in specific cells in the root can increase salinity tolerance, including in rice.

The genotyping of mapping and mutant populations is now highly efficient. However, the ability to quantitatively phenotype these populations is now commonly limiting forward progress in plant science. The increasing power of digital imaging and computational technologies offers the opportunity to relieve this phenotyping bottleneck. The Plant Accelerator™ is a 4500 m² growth facility which provides -omic-scale phenotyping of large populations of plants. New genetic loci for components of salinity tolerance discovered using this exciting new approach will be presented.

The application of these technologies provides opportunities to significantly increase abiotic stress tolerance of crops, and thus contribute to increasing agricultural production in many regions.

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