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Genetic approaches to develop salt tolerant germplasm

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Abstract

Forty percent of the world's food is produced under irrigation, and this is directly threatened by over-exploitation and changes in the global environment. One way to address this threat is to develop systems for increasing our ability to use lower quality water, in particular saline water. Low cost partial desalination of brackish water, use of saline water for cooling and increases in the salinity tolerance of crops can all contribute to the development of this new agricultural system.

In this talk, the focus will be on the use of forward genetic approaches for discovery of genes related to salinity tolerance in barley and tomatoes. Rather than studying salinity tolerance as a trait in itself, we dissect salinity tolerance into a series of components that are hypothesised to contribute to overall salinity tolerance (following the paradigm of Munns & Tester, 2008).

For example, one significant component of tolerance of most crop plants to moderate soil salinity is due to the ability to maintain low concentrations of Na^+ in the leaves, and much analysis of this aspect has been done (e.g. Roy *et al.*, 2013, 2014). A major site for the control of shoot Na^+ accumulation is at the plasma membrane of the mature stele of the root. Alleles of *HKT*, a major gene underlying this transport process have been characterized and, in work led by Dr Rana Munns (CSIRO), have now been introgressed into commercial durum wheat and led to significantly increased yields in saline field conditions (Munns *et al.*, 2012).

The genotyping of mapping 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 4500m² growth facility that provides non-destructive phenotyping of large populations of plants (<http://www.plantphenomics.org.au/>). New genetic loci for previously under-studied components of salinity tolerance discovered using this new approach will be presented.

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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, especially in the face of global environmental change. However, this needs to be tested in the field, such as done by Munns et al (2012) and Schilling et al. (2014). To this end, work will be described where mapping populations are grown in the field, and also grown in the Accelerator, and loci for traits are being compared with loci for tolerance in the field.

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