Components of salinity tolerance in wheat

A thesis submitted in fulfilment of the requirements for the degree of Doctor of Philosophy at the University of Adelaide

By

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List of abbreviations

ABA : Abscisic acid
ACS : Australian Commodity Statistics
ANOVA : Analysis of variance
APW : Australian Premium White
CCD : Coupled Charge Device
CIM : Composite Interval Mapping
CIMMYT : International Maize and Wheat Improvement Centre
DArT : Diversity Array Technology™
DH : Doubled Haploid
dS/m : deci-Siemens/meter
Ec_e : Electrical conductivity of saturation extract
ESP : Exchangeable sodium percentage
F_2 : Second filial generation
FAO : Food and Agriculture Organization of the United Nations
GLM : General Linear Model
H^2 : Broad sense heritability
IBLS : Image Based Leaf Sum
IDRC : International Development Research Centre
kPa : Kilopascal
LOD : Log of odds ration
LRS : Likelihood Ratio Statistics
M : Molar
MCIM : Mixed linear Composite Interval Mapping
mM : millimolar
NILs : Near Isogenic Lines
NLWRA : National Land and Water Resources Audit
P : Probability
PCR : Polymerase Chain Reaction
PEG : Polyethylene glycol
PVC : Polyvinyl chloride
QTL : Quantitative Trait Loci
R^2 : Regression co-efficient
RILs : Recombinant Inbred Lines
ROS : Reactive Oxygen Species
rpm : Revolutions per minutei
SARDI : South Australian Research and Development Institute
SD : Standard deviation
SIM : Simple Interval Mapping
SSR : Simple Sequence Repeats

List of publications and conference presentation from this dissertation

Journal publications

Rajendran, K, Tester, M and Roy.S. Quantifying three major components of salinity tolerance mechanisms in cereals. Plant Cell and Environment.32: 237-249, 2009.

Golzarian.MR, Frick.RA, Rajendran.K, Berger.B, Roy.S, Tester.M and Lun,D.S. Accurate inference of shoot biomass from high-throughput images of cereal plants. Plant Methods.7:2, 2011.

Publication in progress

Rajendran, K, Tester, M and Roy.S. Identification of new source of genetic variability and QTL for osmotic component of salt stress in bread wheat (*T. aestivum*) through non-destructive image analysis.

Rajendran, K, Hudson, I, Tester, M and Roy.S. Use of EM algorithm to evaluate genotype × seasonal interaction on growth and health of genotypes with diverse combinations of three major salinity tolerance components – a case study with bread wheat (*T. aestivum*).

Oral presentations

Rajendran, K, Tester, M and Roy.S. Imaging growth and senescence through time to separate components of salinity tolerance. The Genomics of Salinity. ACPFG Symposium -2009, Adelaide Australia.

Abstract

Soil salinity causes osmotic and ion specific stresses and significantly affects growth, yield and productivity of wheat. The visual symptoms of salinity stressed wheat include stunted shoot growth, dark green leaves with thicker laminar surfaces, wilting and premature leaf senescence. There are three major components of salinity tolerance that contribute to plant adaptation to saline soils: osmotic tolerance, Na^+ exclusion and tissue tolerance. However, to date, research into improving the salinity tolerance of wheat cultivars has focused primarily on Na^+ exclusion and little work has been carried out on osmotic or tissue tolerance. This was partly due to the subjective nature of scoring for plant health using the human eye.

In this project, commercially available imaging equipment has been used to monitor and record the growth and health of salt stressed plants in a quantitative, non-biased and non-destructive way in order to dissect out the components of salinity tolerance. Using imaging technology, a high throughput salt screening protocol was developed to screen osmotic tolerance, Na^+ exclusion and tissue tolerance of 12 different accessions of einkorn wheat (*T. monococcum*), including parents of the existing mapping populations. Three indices were used to measure the tolerance level of each of the three major components of salinity tolerance. It was identified that different lines used different combinations of the three major salinity tolerance components as a means of increasing their overall salinity tolerance. A positive correlation was observed between a plant's overall salinity tolerance and its proficiency in Na^+ exclusion, osmotic tolerance and tissue tolerance. It was also revealed that MDR 043 as the best osmotic and tissue tolerant parent and MDR 002 as a salt sensitive parent for further mapping work. Accordingly, the F_2 population of MDR 002 × MDR 043 was screened to understand the genetic basis of osmotic tolerance and tissue tolerance in *T. monococcum*. Wide variation in osmotic tolerance and tissue tolerance was observed amongst the progenies. The broad sense heritability for osmotic tolerance was identified as 0.82.

Similar, salinity tolerance screening assays were used to quantify and identify QTL for major components of salinity tolerance in Berkut × Krichauff DH mapping population of bread wheat (*T. aestivum*). Phenotyping and QTL mapping for Na^+ exclusion and osmotic tolerance has been successfully done in this mapping population. There existed a potential genetic variability for osmotic tolerance and Na^+ exclusion in this mapping population. The broad sense heritability of osmotic tolerance was 0.70; whereas, it was 0.67 for Na^+ exclusion. The composite interval mapping (CIM) identified a total of four QTL for osmotic tolerance on 1D, 2D and 5B chromosomes. For Na^+ exclusion, CIM identified a total of eight QTL with additive effects for Na^+ exclusion on chromosomes 1B, 2A, 2D, 5A, 5B, 6B and 7A. However, there were QTL inconsistencies observed for both osmotic tolerance and Na^+ exclusion across the three different experimental time of the year. It necessitates re-estimating the QTL effect and validating the QTL positions either in the same or different mapping population.

Declaration

I, Karthika Rajendran certify that this work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

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*Rajendran, K, Tester, M and Roy.S. Quantifying three major components of salinity tolerance mechanisms in cereals. Plant Cell and Environment.32: 237-249, 2009.

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