

# **Dissecting genetic variation for nitrogen use efficiency in wheat**

A thesis submitted for the degree of Doctor of Philosophy

by

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May 2015

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## **Thesis Abstract**

Nitrogen (N) is essential for high grain yield (GY) in cereals. A major aim of breeding programs is to increase GY while minimising the level of external inputs, such as N fertilisation. Nitrogen Use Efficiency (NUE) is a complex trait controlled by both genetic and environmental factors resulting in variation depending on seasonal growth conditions. Only 30-50% of N supplied is actually taken up by the plants with the extra N lost through run-off, leaching, denitrification and gas emission. These losses have a negative environmental impact, leading to surface and underground water pollution, algae blooms and intensifying global warming. In addition, nitrogen (N) application is costly further emphasising the importance of NUE improvement to reduce the economic and environmental issues associated with N application. NUE of wheat is important in all production areas but little is known about genetic variation for NUE in low-yielding environments such the Mediterranean-type climate of Southern Australia with low rainfall and high temperatures during critical growth periods. Research described in this thesis evaluated variation in NUE in Australian wheat germplasm and then to identify loci regulating NUE traits in a bi-parental mapping population of RAC875/Kukri. Improvement in NUE will require the integration of physiological and molecular aspects of N status in plants under different growth conditions: the highly variable conditions of field trials and controlled environments such as under hydroponics. The assessment of NUE and N response under both field and controlled conditions could facilitate the identification of traits and QTL and lead to the discovery of candidate genes underlying the traits.

The first step of this research involved NUE traits and N response assessment of Australian cultivars in different environments, with varying N input. Genetic variation for NUE was identified in Australian spring wheat cultivars, and the cultivars were ranked for their N-efficiency and responsiveness. The dissection of genetic variation for NUE was investigated in the RAC875/Kukri population across six field trials between 2011 and 2013 covering 16 environment by treatment combinations. Nitrogen responsiveness was compared

with N efficiency and the genotypes were ranked for the consistency of a positive response and high efficiency of N use versus negative responsiveness and low efficiency. Quantitative Trait Loci (QTL) analysis identified the genome regions associated with GY, grain quality and responsiveness to N. In addition, specific-environment associated N QTL were identified. A QTL on chromosome 2A was detected for most of traits studied and across multiple environments. Further stable QTL were identified on chromosomes 1A, 1B, 2A, 3D, 7A and 7B for GY across environments. The physiological response to N was studied at the early stages of growth for selected lines in a hydroponics system that allowed the measurement of N uptake and utilisation. The aim of the experiments was to investigate the physiological basis for the effects seen in the field trials. However, no consistent response was seen in these studies suggesting that future work should focus on later growth stages.

To conclude, the results showed significant genetic variation and transgressive segregation for NUE despite the complex nature of the effect of N on grain yield and quality traits. These genome regions can be used to support marker assistance selection (MAS) for improved NUE and for cloning genes underlying the loci affecting NUE in wheat. The results show that selection for improved NUE is possible and also provide a base for further molecular and physiological studies on efficient use of applied N.

**Declaration**

I 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. In addition, I certify that no part of this work will, in the future, be used in a submission for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

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Saba Mahjourimajd

December 2014

## **Acknowledgements**

I would like to use this opportunity to express my gratitude to all people who helped and supported me throughout my thesis. First of all, I am deeply thankful to Peter, my principle supervisor, for all his guidance, invaluable comments and brilliant views on many issues related to my Ph. D. project and his friendly encouragements during my work. It definitely was his support that made me study and work enthusiastically at the Australian Centre for Plant Functional Genomics (ACPFPG) and the University of Adelaide and drove me to think of new perspectives in plant breeding. I learned lots of scientific and life lessons from him and I am honoured to have been one of his students. My warm thanks to Mamoru, for his kind and patient support and helpful suggestions. I am sincerely grateful to Haydn, for his guidance and his great analytical ideas for interpreting the results of experimental tests.

Thanks to Julian Taylor who assisted me in statistical analysis of the data and thanks also to Glen McDonald, my independent advisor, Ken Chalmers, my postgraduate coordinator, Monica Ogierman, my previous education manager and Ruth Harris, my English tutor for their patiently and positively support and encouragement.

I am sincerely grateful for having a chance to meet so many wonderful people and professionals including supervisors, students, lab managers and Administrative people at the ACPFG who provided kind cooperation and encouragement to enjoy every moment of my study. Also, special thanks to the University of Adelaide and ACPFG manager which provided me with full-scholarship and all required facilities and conducive conditions to do my Ph. D in Australia.

I would also like to thank all organisations including the Australian Grain Technologies team at Roseworthy, barley group, SARDI group at Waite campus, Geranium people at Lameroo, technicians, casuals and everybody who helped me to provide this dissertation.

Last but not least, my great thanks and appreciation to my family, particularly my Mum as my first teacher, for all their support and inspiration throughout my life and education.

## Abbreviations

N	: Nitrogen
NUE	: Nitrogen Use Efficiency
GY	: Grain Yield
RGY	: Responsive Grain Yield
GPC	: Grain Protein Concentration
PY	: Protein Yield
DH	: Doubled Haploid
QTL	: Quantitative Trait Loci
LOD	: Logarithm of the odds
G×E	: Genotype-by-Environment Interaction
SR	: Seeding Rate
BLUP	: Best Linear Unbiased Predictors
NO <sub>3</sub> <sup>-</sup>	: Nitrate
NH <sub>4</sub> <sup>+</sup>	: Ammonium
HATS	: High Affinity Transport System
LATS	: Low Affinity Transport System
<sup>15</sup> N	: Labelled Nitrogen
HN	: High Nitrogen
LN	: Low Nitrogen