Translating Nitrogen Use Efficiency from models to crops

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Proposal Title	Translating Nitrogen Use Efficiency from models to crops
The Idea	Optimizing biological nitrogen (N) use is pivotal to maximizing crop yields and ameliorating the adverse environmental impacts of excess agricultural N application. Most cereal crops only take up about 50% of the applied N (Robertson, 1997). The other 50% of applied nitrogen is lost either to soil microbes, leeched from the soil during rains or chemically lost to the environment. New opportunities exist to provide gains in efficiency via the translation of basic research into application in crop species. With the advent of the wheat genome the opportunity now exist to indentify novel targets for breeding of N efficient crops in the most import UK crop species. However to translate our understandings of genes involved comparison of more distant plant species to the original model species is increasing difficult as little experimental evidence exists to help identify orthologous genes other than sequence alone. In wheat the problem is further complicated as polyploidy triples the potential targets one could study for nitrogen use efficiency. The proposal seeks to help better indentify orthologous genes as well as indentify how much variation exists in NUE targets in wheat. We are proposing to collect RNA Seq data on the eight parents of a widely distributed and publically available mapping population (MAGIC elite) to add experimental evidence to help build connections between current knowledge in model species and wheat. We will grow these eight lines under both sufficient N and low N conditions to add further evidence of the effect N has on expression and better predict orthologs.
Who We Are	Dr. Mariana Fazenda University of Cambridge ml745@cam.ac.uk Mariana is currently working as part of a large Netwon fund grant between Cambridge University, NIAB and two Indian Institutes Punjab Agricultural University and ICRIST called CINTRIN. Mariana helps to coordinate the project and drives communication between breeders, molecular biologists and agronomist to improve NUE in wheat and other crop speices. Dr. Matthew Milner NIAB matthew.milner@niab.com Matthew is a post doctoral researcher also working as part of the fore mentioned CINTRIN grant and is a molecular biologist working on characterizing nitrogen use efficiency genes in wheat. Prof. Mario Caccamo NIAB mario.caccamo@niab.com Mario is the head of Crop Bioinformatics at NIAB is was integral as part of the sequencing effort of the wheat genome and is currently working with the IWGSC to help develop consistent nomenclature for genes in wheat and other crop species. Dr. Dan Swan Earlham Institute daniel.swan@earlham.ac.uk Dan leads the Platforms and Piplines group at Earlham and is part of the team which runs most of the NGS technology at Earlham from start to finish.

Implementation	Project Aims 1. Grow the eight MAGIC elite parents in hydroponics for 14 days on either 0.25 mM NH_4NO_3 or 1.5 mM NH_4NO3. 2. Run samples on Illumina HiSeq for expression of nitrogen related genes. 3. Compare transcripts to known model systems for similarities and differences. 4. Look for differences in the parents of the MAGIC elite population and correlate this to publish data set for protein content, yield and other growth characteristics. Methods 1. Grow the eight MAGIC elite parents in hydroponics for 14 days on either 0.25 mM NH_4NO_3 or 1.5 mM NH_4NO3. And extract RNA from pooled plants for RNA Seq 2. Run RNA Seq on illumina HiSeq 2500 for the eight parents and align reads to best current genome for wheat 3. Compare with other known data sets to start to develop networks and orthologs with known NUE genes in rice and Arabidopsis. 4. Look for differences in ortholog expression and differences in the parental lines and start to understand how the genetics and polyploidy effects response to N limitation.
Benefits and outcomes	I. Reveal if expression and sequence similarity can help bioinformatic prediction of orthologs in newly sequenced plant species. Ii. Indentify differences in the genetics of NUE in wheat. Iii. Release expression data to a public database such as wheat-expression.com (Uauy lab at JIC). For public dissemination. Iv. Add to marker data for current MAGIC population (http://www.niab.com/pages/id/402/NIAB_MAGIC_population_resources)
Sponsor for the research and cost centre	Dr. Dan Swan, Earlham Institute, Head of Platforms and Pipelines, daniel.swan@earlham.ac.uk
Budget	2 lanes 100 Single End HiSeq 2500 Rapid Run 12 TruSeq RNA library preps This should still deliver you ~30M reads per sample Total inc. VAT: £3996.94 RNA extraction kit and media/cost of growing plants/ bioinformatic time covered by NIAB