

## Increasing photosynthetic efficiency: From phenotype to genotype and back

Photosynthetic and radiation use efficiencies during plant development and in the mature canopies of crops have a large influence on crop yields. Optimizing the rate and efficiency of photosynthesis to increase wheat yields is therefore a primary target for IWYP. However, these traits are complex and thus extremely challenging to select in breeding programs. To accurately phenotype them requires specialized and often expensive equipment, is labor intensive and low throughput. To break this bottleneck, a ground-breaking project led by Anthony Hall, at the Earlham Institute, with colleagues in the UK, Mexico, and Australia, “**Using Next Generation Genetic Approaches to Exploit Phenotypic Variation in Photosynthetic Efficiency to Increase Wheat Yield**”, has combined cutting edge *de novo* genomics technologies and analytical tools with state-of the-art precision phenotyping to discover the genes responsible for controlling these traits and define molecular markers genetically linked to these genes. These linked genetic markers now enable breeders to identify germplasm with higher photosynthetic potential to use as parents in crosses and to accurately select for improved photosynthetic efficiency in progeny. Determination of candidate alleles for enhanced photosynthetic efficiencies has furthered the understanding of the biology underpinning photosynthesis and other traits and will enable development of precision genome engineering tools in the future.

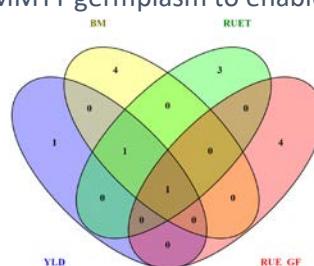
### What Solutions have been Identified?

- A set of molecular markers genetically linked to some photosynthetic and other component traits, including plant biomass, that can be used to screen large numbers of lines to find those with increased photosynthetic efficiency
- Better understanding of the mechanisms underlying improved photosynthetic efficiency and yield that help identify likely new targets for plant improvement
- New re-sequencing and allele mining approaches that enable introgressions from wild wheat into bread wheat to be selected and tracked to select for higher rates of photosynthesis and other desirable traits

### What has been Transferred to Wheat Improvement Pipelines?

- A recommended subset of molecular genetic markers and several lines containing them to enable their validation in elite germplasm in high yielding environments
- Extensive genotypic data on key CIMMYT germplasm to enable discovery of more marker-trait associations and to drive breeding decisions

Trait	Number of MTAs	Chromosomes
BM_E40 ( $\text{g m}^{-2}$ )	2	1B, 3B
BM_InB ( $\text{g m}^{-2}$ )	3	2A, 4B, 7A
BM_PM ( $\text{g m}^{-2}$ )	6	5A, 6A, 7A(2), 7B, 7D
RUE_E40InB ( $\text{g MJ}^{-1}$ )	4	2A, 2D, 3B, 6A
RUE_GF ( $\text{g MJ}^{-1}$ )	5	1A, 1D, 2A, 5A, 6A
RUET ( $\text{g MJ}^{-1}$ )	5	3D, 5A(2), 6A, 7A



**Number of total and common Marker-Trait Associations detected.**  
 RUET (radiation use efficiency from canopy closure to physiological maturity), RUE\_GF (radiation use efficiency from 7 days after anthesis until physiological maturity, RUE\_E40InB (radiation use efficiency from canopy closure to initiation of booting), BM\_E40 (biomass measured 40 days after emergence), BM\_InB (biomass at initiation of booting), BM\_PM (biomass at physiological maturity) and Yield. Molero et al. 2019. doi:10.1111/pbi.13052

