

Selecting Radiation Use Efficiency to Boost Yield Potential

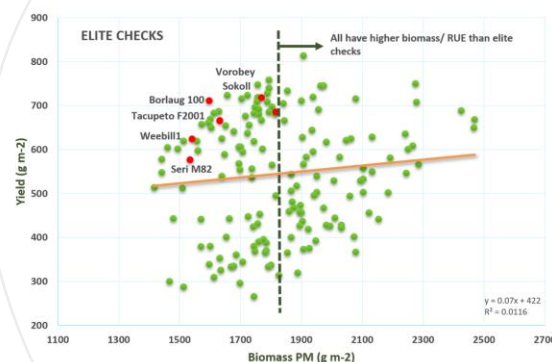
The dynamics of photosynthesis generally determines crop productivity in farmers' fields. It drives the fixation of carbon into sugars and their conversion into the myriad of metabolites necessary for growth. However, ancestral feedback mechanisms favoring survival over productivity greatly reduce carbon fixation below the theoretical maximum and hence the potential production of biomass and grain yield. A major challenge in breeding, and a high priority for IWYP, has been to select for both more efficient carbon fixation (photosynthesis) and an optimized regulation of the numerous downstream processes, including photorespiration, that feedback to limit supplies of photosynthesis products for optimal agricultural output. The primary trait addressing this challenge is Radiation Use Efficiency (RUE), defined as the biomass achieved relative to the light intercepted by the crop canopy. High RUE is essential at specific times in crop growth to achieve the highest grain yields.

Genetic variation in RUE has been screened in large numbers of elite and exotic hexaploid wheat lines grown in plots at the IWYP Hub at CIMMYT. Amongst a panel of 150 primary synthetic lines containing D genome segments from different *A. tauschii* genotypes, outstanding sources of higher biomass resulting from high RUE have been identified (**Figure 1**). Such lines have proved valuable as parents in crosses designed to produce progeny with higher yields. For example, a higher yielding line was selected from a cross whose parents included a high biomass landrace and a synthetic genotype. The line expressed 25% higher biomass and 30% higher RUE than either parent during the vegetative and grain filling stages. As expected, these traits correlated with higher grain yield. Lines with high RUE are now routinely crossed with lines that express high harvest index and related traits, leveraging higher expression of both RUE and harvest index to boost yield. Replicated field trials of an IWYP diversity panel (HiBAP) have been used to genetically dissect RUE using growth and hyperspectral reflectance analyses together with genome-wide molecular markers. Several key loci and potential gene candidates were correlated with RUE ([Joyson et al., 2021](#)) and these should help select for high RUE in breeding programs using relevant germplasm. Other IWYP research projects have also delivered lines with exceptional photosynthetic efficiency including ones containing chromosomal segments from wild species ([IWYP Science Brief No.1](#)) and lines that show a speedier return to maximum photosynthetic efficiency following release from shading ([IWYP Science Brief No.22](#)).

Physiological pre-breeding has delivered the proofs of concept that alleles affecting RUE at specific growth stages can boost yield, and that high sink strength genes can further boost RUE through increasing demand for photosynthesis during grain growth. These types of conclusions validate the IWYP-Hub's physiological pre-breeding approach of crossing parents with optimized 'source' and 'sink' traits to improve source:sink balance in the resulting progeny ([Reynolds et al. 2017; 2021](#)).

Given the importance of RUE for achieving high yields, it is recommended that wheat breeders use high RUE lines as parents to cross with locally adapted lines having high harvest index and fruiting efficiency. Genetic markers and phenotypes should be used to select progeny expressing high RUE at the best developmental stages for local conditions. To help screen breeders' germplasm, the IWYP Hub at CIMMYT continues to improve trait-specific diagnostic genetic markers as well as remote and proximal sensing techniques for phenotyping photosynthesis related traits.

Figure 1. Primary synthetic hexaploids: many lines express extraordinary RUE under high yield potential conditions



Measuring photosynthetic characteristics in HiBAP I using a ASD hyperspectral unit

