IWYP International Wheat Yield Partnership

Research to Deliver Wheat for the Future

AVP1, PSTOL1 and NAS – Three High-Value Genes for Higher Wheat Yield

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Abstract

Aim: Enhancing wheat yield by exploiting and building synergy of three high value genes (AVP1, PSTOL1 and NAS) and enabling molecular breeding.

Project Objectives:

1. Develop two-gene and three-gene pyramiding combinations of *AVP1*, *PSTOL1* and *NAS* using available transgenic wheat lines and quantify additive effects on yield in multi-location field and greenhouse trials (as a proof of concept).

2. Identify wheat orthologs and allelic variants of *TaAVP1*, *TaPSTOL1* and *TaNAS* and design molecular markers to the best alleles for marker-assisted breeding.
3. Provide basic understanding of the physiological and molecular mechanisms behind improved yield and select wheat lines with the best allelic combination and field performance.
4. Assess the necessity for using genome editing technologies to optimize gene function and enhance positive effect on wheat yield by modifying expression of the wheat alleles.

The genes *Vacuolar Proton Pyrophosphatase 1* (*AVP1*), *Phosphorus Starvation Tolerance 1* (*PSTOL1*) and *Nicotianamine Synthase* (*NAS*) have been shown to improve plant biomass production and grain yield. Over-expression of these genes results in improved biomass production and grain yield in a range of plant species, including cereals (rice, barley, wheat), in optimal growing conditions. The enhanced yield of the plants is believed to be due to improved sugar transport from source to sinks (*AVP1*), enhanced root growth and nutrient uptake (*AVP1*, *PSTOL1*) and increase in shoot biomass and tiller number (*AVP1*, *PSTOL1*, *NAS2*). Identifying and pyramiding the wheat orthologs of these high-value genes provides a real opportunity to produce wheat with significantly improved field performance and higher grain yield.

Transgenic wheat plants with constitutive transgene expression of the above genes have been generated and are available for this project. Preliminary data for *AVP1*, *PSTOL1* and *NAS*, derived from soil-based phenotyping experiments, already indicate that the genes are functional in wheat, improving nutrient uptake, biomass production and grain yield. Based on bioinformatics analyses of wheat genomes and evidence from other monocots, we have identified the evolutionarily conserved putative wheat orthologs of the three genes and allelic variation is likely to exist in wheat as has been observed in other species, e.g. the *AVP1* homolog *HVP10* in barley or the *PSTOL1* homologs in sorghum (see below).

Within this project we will provide the opportunity to use available transgenic wheat lines as a proof of concept for the optimal combination of the three genes to improve wheat yield; while in parallel, screening of diverse germplasm will identify the best natural alleles of the wheat genes for introgression into elite wheat cultivars and breeding lines.

Within this project, we will also characterize the mechanisms underlying the observed positive gene effects on plant growth and yield, and will use the data derived from the transgenic lines to guide development of molecular markers to the best alleles of the wheat homologs of *AVP1*, *PSTOL1* and *NAS2,* to facilitate the production of non-GM wheat line with enhanced grain yield.