



Research to Deliver Wheat for the Future

Molecular Dissection of Spike Yield Components in Wheat

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Abstract

Urgent action is needed to sustainably increase global wheat production. However, limited knowledge of the genes controlling wheat yield is hampering efforts to advance towards this goal using science-based solutions. The aim of this proposal is to define, characterize, and manipulate genes that regulate the early stages of spike and carpel/grain development and that govern spike yield components (grains per spike and grain weight). We will apply innovative sequencing-based approaches to exploit novel sources of induced genetic variation in these two traits to increase the genetic yield potential of wheat. We will test if this potential is realized in elite wheat varieties. Understanding the genes controlling different yield components will allow us to combine and exploit variation across all three homoeologous genomes, and to overcome the perennial problem of functional redundancy observed in polyploid wheat. The combination of novel allelic variants in genes affecting grain number and weight represents an opportunity to generate significant increases in wheat yield potential not previously exploited in wheat improvement programmes.

We propose an ambitious programme that will address the following specific objectives to increase wheat grain yield potential:

1. Define the changes in the wheat transcriptome associated with early spike and grain development
2. Identify key genes determining spike yield components through forward genetics
3. Implement reverse genetic tools to discover and characterise genes improving spike yield components
4. Engineer and deploy allelic combinations for increased wheat yield potential and characterise their pleiotropic effects and epistatic interactions

The main direct outcomes expected from this research are:

- Identification and characterisation (molecular, physiological and agronomic) of novel gene variants controlling wheat spike yield components
- Creation of double and triple mutants targeting all homoeologs for the selected genes to overcome functional redundancy
- Generation of adapted germplasm with new allelic combinations affecting complementary spike yield components