

Notat

SEGES, Landbrug & Fødevarer F.m.b.A.
PlantInnovation

Status på genetisk kortlægning af proteinindhold	Ansvarlig	NHKR
	Oprettet	13-12-2021
	Side	1 af 1
Projekt: OPTICROP - WP3		

Identification of the genetic elements underlying a negative grain protein deviation, i.e. high grain protein content and high yield

Last year we performed an RNA-Seq experiment involving varieties with high grain protein content and high yield (i.e. negative grain protein deviation) and varieties with lower grain protein content and high yield (i.e. positive grain protein deviation). We focused on flag leaf samples harvested in a time series between the point of anthesis and up to four weeks after anthesis. Based on this experiment, we established a set of candidate genes potentially involved in the regulation of wheat grain protein content. We identified close to 500 candidate genes specific to the variety with the highest negative grain protein deviation. There is considerable overlap with genomic regions reported in the known literature. However, our results highlight some new genomic regions potentially involved in the regulation of grain protein content. Candidates include genes involved in senescence, nitrogen uptake and transport, nitrogen metabolism, a series of transcription factors, phytohormones, stress response genes. A total of 30 candidate genes are of special interest due to showing differential expression specific for the variety with best grain protein deviation and, at the same time, harboring SNPs identified only in this specific variety. Genomic regions of high interest are located on chromosomes 7A, 2B, 1B, 2A, 2D, 3B, 4A, 4B, 5B, 6A, 6B, 7D.

We performed another RNA-Seq experiment this year, from flag leaf samples but also from developing grains, and the results are currently being processed. Besides the varieties tested last year, we included two extra varieties of interest, one with high and the other with lower grain protein content.

All the varieties included in the RNA-Seq experiments were phenotypically assessed in the field trial at Flakkebjerg this year.

The QTL mapping based on last year's results highlighted two genomic regions, on chromosomes 4A and 6A, with the region on chromosome 6A suggested by a preliminary analysis of this year's data as well.