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Deciphering wheat grain protein content

**Gene c analysis of temporal dynamic nitrogen content resorption in flag leaves**

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### Introduction

Grain protein content (GPC) is a targeted trait in breeding for durum wheat since it has a strong impact in industrial transformation. However, its improvement is compromised by the complexity of its genetic architecture (many QTL have been highlighted) and by a negative correlation with the yield. Nevertheless, in view of the necessity to feed more and more people, reducing the fertilizer input on inputs and preserving our environment, the gene c improvement of the GPC appears as a good way to maintain the product’s quality and to ensure a good production to farmers.

In response to this economical and environmental context, we propose to decipher this trait and to focus on an underlying mechanism to the elaboration of the GPC, the nitrogen remobilization on in the flag leaf.

### Material and Method

#### Phenotyping

We phenotyped 282 flils coming from a half diallel (4 parental lines, lloyd, neodur, ixos and primadur) in a greenhouse. We used a portable near infrared spectrometer (Labspec®) covering a wide range of wavelengths (350 to 2500 nm) to measure the flag leaves of our population during the grain filling period, from anthesis to maturity.

The curves were modelled using a non-linear method based on a Gauss Newton algorithm. Variables coming from the curves and other variables measured at anthesis or at maturity.

### Results

A mixed model was defined to evaluate the variance components and to predict the gene c values (BLUP) using the ASReml-R package (Butler et al., 2007). The block was considered as fixed and the genotype as random with the pedigree associated. The gene c correlation between two traits was evaluated with bivariate models as the ratio between the genetic covariance for a pair of traits and the product of their own additive variance. The phenotypic correlation between traits was evaluated with the linear coefficient between pairs of traits. The values of individual heritability were calculated as the additive variance divided by the sum of the additive variance and the residual variance for each trait.

### Conclusion

- We used a new device for phenotyping presenting the advantage to be non-destructive for the plants and allowed us to follow the remobilization on nitrogen in the flag leaf of a durum wheat population.
- The trait chosen is an underlying mechanism of the GPC elaboration on. Heritabilities of its components being of the same order of magnitude than the GPC, the remobilization on nitrogen could be improved as well as the GPC but with the advantage to be combined with other underlying traits for GPC as the efficiency of nitrogen absorption on for example.
- The model of remobilization on t0 and t1 are negatively correlated with GPC but positively with GPC and the yield since a late remobilization increases the yield but by a dilution on effect, reducing the GPC but not the protein weight in the spike.