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Deciphering wheat grain protein content

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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 nitrogen input on plants and preserving our environment, the genetic improvement of the GPC appears as a good way to maintain the product’s quality and to ensure a good productivity 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 Bils 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 popula on during the grain filling period, from anthesis to maturity.

![Spectrometer calibers on fresh leaf and dry leaf](image)

The spectra obtained of a fresh flag leaf at anthesis and a dry flag leaf at maturity.

**Sta ssical Analysis**

For each plant, we obtained 30-40 spectra that were converted into value of nitrogen content thanks to a robust calibra on of the device (R²=0.93, Ecarnot and Roumet, submitted). 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 es mate 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 correla ons between two traits were es mated 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 correla ons between traits were es mated with the pearson coefficient between pairs of traits. The values of individual heritability were calculated as the additive variance divides by the sum of the additive and the residual variance for each trait.

![Jitter, boxplot and distribution of values](image)

<table>
<thead>
<tr>
<th>Trait</th>
<th>GPC</th>
<th>Maturity</th>
<th>GPW</th>
<th>GPW</th>
<th>Nmat</th>
<th>Area</th>
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<th>Area</th>
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</tbody>
</table>

**Conclusion**

We used a new device for phenotyping present ng the advantage to be non destruct ve for the plants and allowed us to follow the remobiliza on of nitrogen in the flag leaf of a durum wheat popula on.

The trait chosen is an underlying mechanism of the GPC elabora on. Heritability of its components being of the same order of magnitude than the GPC, the remobiliza on of 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 absorp on for example.

The remobiliza on on t0 and t1 are nega ve correlated with GPC but posi ve with GPW. It is relevant with the nega ve correla on on exis ng between GPC and the yield since a late remobiliza on increase the yield but by a dilu on effect, reduce the GPC but not the protein weight in the spike.

![Graphs of nitrogen content and yield](image)