Deciphering wheat grain protein content : Genetıc analysis of temporal dynamic nitrogen content resorption in flag leaves

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Gene?c analysis of temporal dynamic nitrogen content resorp?on in flag leaves

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Introduc?on

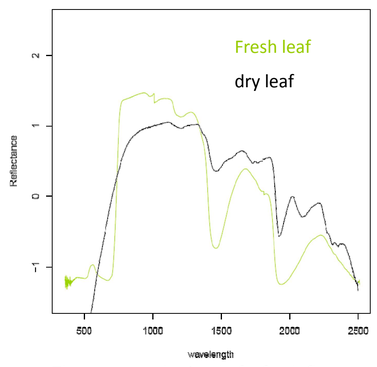
Grain protein content (GPC) is a targeted trait in breeding for durum wheat since it has a strong impact in industrial transforma?on. However, its improvement is compromised by the **complexity of its gene?c architecture** (many QTL have been highlighted) and by a **nega?ve correla?on with the yield**. Nevertheless, in view of the necessity to feed more and more people, **reducing the fer?liza-?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 produc?on 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 elabora?on of the GPC, **the nitrogen remobiliza?on in the flag leaf**.

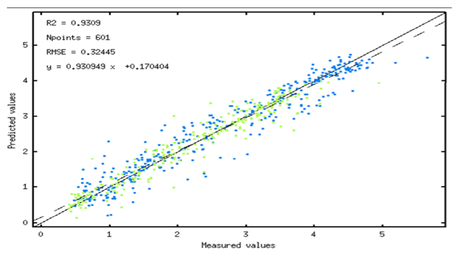
Material and Method

Phenotyping

We phenotyped **282 Rils** coming from a half diallel (4 parental lines, lloyd, neodur, ixos and primadur) in a greenhouse. We used a **portable near infrared spectrome-ter** (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.



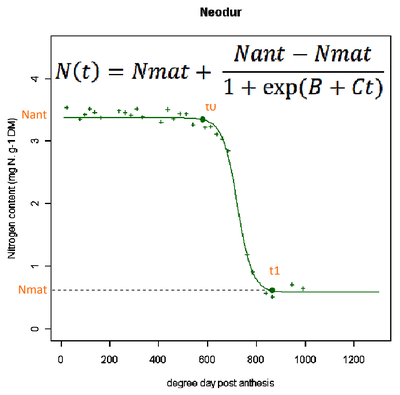
The spectra obtained of a fresh flag leaf at anthesis and a dry flag leaf at maturity



Spectrometer calibra?on

Sta?s?cal Analysis

For each plant, we obtained 30-40 spectra that were converted into value of **nitrogen con-tent** thanks to a robust calibra?on of the device (R^2=0.93, Ecarnot and Roumet, submi?ed). The curves were modelled using a non linear method based on a Gauss Newton algorithm.



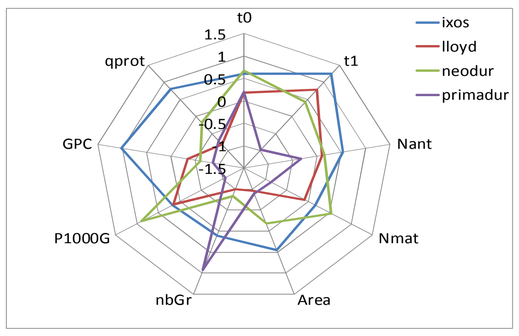
The curve obtained

t0	?me of senescence ini?a?on
t1	?me of senescence ending
Nant	N content in the flag leaf at anthesis
Nmat	N content in the flag leaf at maturity
Area	Flag leaf area at anthesis
nbGr	Number of grain in the spike
TKW	Thousand kernel weigth
GPC	Grain Protein Content in the spike
GPW	Grain protein weigth in the spike

Variables coming from the curves and other variables measured at anthesis or at maturity

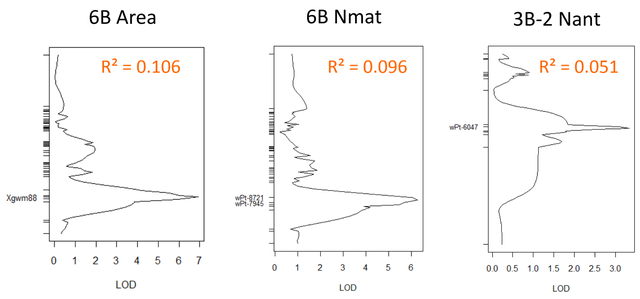
Results

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 ra?o between the gene?c covariance for a pair of traits and the product of their own addi?ve variance. The **phenotypic correla?ons** between traits were es?mated with the pearson coefficient between pairs of traits. The values of **indi-vidual heritability** were calculated as the addi?ve variance divides by the sum of the addi?ve variance and the residual variance for each trait.



- Genitors had contrasted mean values for the studied traits (standardized values), es-pecially ixos and primadur

		correla?on (pearson) between traits (blups)									
		t0	t1	Nant	Nmat	Area	nbGr	TKW	GPC	GPW	h²
Gene?c correla?on (rG)	t0		0.3152	0.3368	0.0049	0.1291	-0.0006	0.4845	-0.2130	0.4709	0.3278
	t1	0.3856		0.2193	0.0502	0.1415	-0.1004	0.3622	1.27 E-0.5	0.3651	0.1730
	Nant	0.4671	0.2319		0.2283	-0.1448	-0.1045	0.4274	-0.0682	0.3190	0.3975
	Nmat	-0.2453	-0.2553	0.2090		0.1763	-0.4530	0.2507	0.4188	0.0058	0.2128
	Area	0.0361	-0.1131	-0.2617	-0.1475		0.0029	0.4105	0.3379	0.6195	0.3150
	nbGr	0.0931	0.0334	-0.0434	-0.4877	0.1869		-0.5372	-0.2272	0.2568	0.4783
	YKW	0.6004	0.4056	0.4485	0.0933	0.3341	-0.4446		-0.0528	0.5579	0.5054
	GPC	-0.4456	-0.4353	-0.2027	0.3533	0.1589	-0.3103	-0.2075		0.1891	0.3731
	GPW	0.5901	0.3519	0.3254	-0.3632	0.5816	0.4208	0.5385	-0.1652		0.4284



- For most of the traits, the gene?c correla?on was stronger than the phenotypic correla?on with some excep?ons.
- The values of heritability were low to moderate, some traits related to senescence presented the same order of magnitude than the one of the GPC or GPW.
- 3 QTL iden?fied based on the BLUP, 2 colocaliza-ted (Nmat and Area)

Conclusion

- We used a new device for phenotyping presen?ng the advantage to be non destruc?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. Heritabili?es of its components being of the same order of magnitude than the GPC, the remobilisa?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 ?me of remobiliza?on t0 and t1 are nega?vely correlated with GPC but posi?vely with qprot. It is relevant with the nega?ve correla?on exis?ng between GPC and the yield since a late re-mobiliza?on increase the yield but by a dilu?on effect, reduce the GPC but not the protein weight in the spike.