CIHEAM
Options Méditerranéennes

Genetic analysis of nitrogen accumulation and protein composition in wheat kernel

Charmet G., Martre P.

in

Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.).
Cereal science and technology for feeding ten billion people: genomics era and beyond

Zaragoza : CIHEAM / IRTA
Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81

2008
pages 387-389

Article available on line / Article disponible en ligne à l'adresse :

http://om.ciheam.org/article.php?IDPDF=800886

To cite this article / Pour citer cet article

Charmet G., Martre P. **Genetic analysis of nitrogen accumulation and protein composition in wheat kernel.** In : Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.). *Cereal science and technology for feeding ten billion people: genomics era and beyond.* Zaragoza : CIHEAM / IRTA, 2008. p. 387-389 (Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81)

CIHEAM

http://www.ciheam.org/
http://om.ciheam.org/

Genetic analysis of nitrogen accumulation and protein composition in wheat kernel

G. Charmet* and P. Martre**
*INRA-University B Pascal, UMR ASP, France
**INRA UR Agronomie, 234 av du Brézet, F63100 Clermont-Ferrand, France

---

SUMMARY – The maximum rate and duration for grain dry matter (DM) and nitrogen (N) accumulation were evaluated for 194 recombinant inbred lines (RILs) from a cross between two French wheat cultivars. Grain protein composition was analysed by capillary electrophoresis (CE) and size-exclusion high performance liquid chromatography (SE-HPLC). Correlation analyses revealed that DM and N accumulation rates were closely related, and that protein composition was primarily influenced by the total quantity of N per grain. A genetic map of 254 molecular markers allowed us to identify 7 quantitative trait loci (QTL). Five QTLs were significantly associated with the kinetics of DM and N accumulation, and two of them also influenced protein composition. Two QTLs affected only the protein composition. We also used the *SiriusQuality*1 wheat simulation model to analyze genotype × environment interactions for grain protein composition. QTLs for the genotypic key parameters of total grain nitrogen partitioning were detected.

Introduction

Grain protein concentration reflects the accumulation kinetics of both nitrogen (N) and dry matter (DM), the latter consisting of 60-70% starch. The genetic correlation between grain yield and protein concentration has consistently been reported as highly negative (see Oury *et al.*, 2003 for a review). It can thus be postulated that common genetic factors are involved in the control of both sets of kinetics. However, no formal study of the genetics of protein and DM accumulation in wheat kernel has been reported to date. The accumulation of the different protein fractions is highly asynchronous. One consequence is that either genetic or environmental factors that affect the duration of grain filling are likely to modify the balance between the different protein fractions. The most effective factors are high temperature (either moderately high, 25-32℃, or heat stress >35℃) and drought during the grain filling period (Sofield *et al.*, 1977). Genotypic differences in the response of DM and N accumulation to environmental variations have also been documented. The rate of DM accumulation is most important as a selection criterion, since the duration of accumulation is influenced to a much greater extent by the environment than by the genotype (Stone and Nicolas, 1995; Whan *et al.*, 1996; Robert *et al.*, 2001). We found that the French cultivars 'Renan' and 'Récital' had contrasting values with respect to maximum rates and durations of DM and N accumulation. Here we report a genetic analysis of grain filling parameters and final protein composition using a recombinant progeny from a cross between 'Renan' and 'Récital'.

Results and discussion

Seven chromosome regions were identified as having significant effects on either grain filling parameters or protein composition (Fig. 1). QTL for grain filling parameters were found in five regions on chromosomes 2B, 3A, 6A, 7A and 7D. The region on chromosome 3A displayed only QTL for grain filling parameters, while the other four also explained variations in the composition of grain protein. The strongest QTL, on chromosomes 2B and 7A, explained about 21 and 19% in the variation of the rates of DM and N accumulation, respectively, and were detected in both harvest years. Positive additive effects for the rates of DM and N accumulation, grain dry weight and quantities of total protein, LMW-GS and gliadins were associated with the presence of the 'Récital' allele at the 2B QTL, although this parent had the smallest grain dry weight and protein content. A similar picture was found on chromosome 7A, but as expected the allele from 'Renan' increased the rate of N accumulation grain dry weight and the quantities of total protein, as well as those of LMW-GS. The QTL for grain filling parameters and protein composition found on chromosomes 6A and 7D were less robust for most traits, i.e. detected in less than 75% of boo strap samples, with the exception of the quantity of LMW-GS.

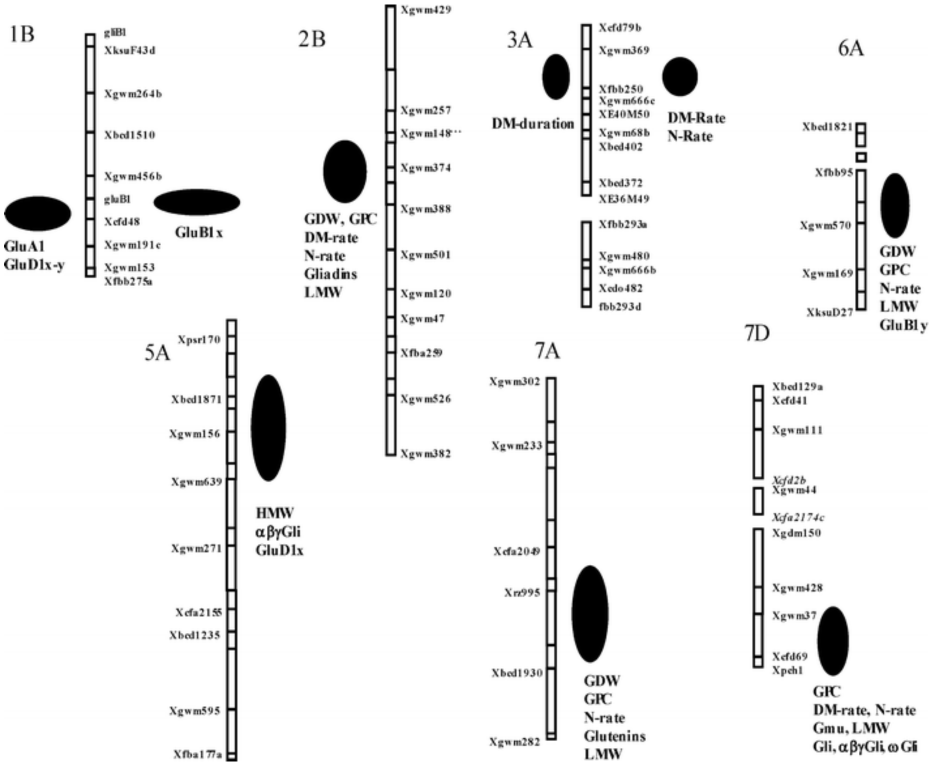

Fig. 1. Locations of QTL for mature grain dry weight (GDW), protein content (GPC), maximum rates and duration of DM and N accumulation, the quantities of glutenins, gliadins and their different subunits.

In addition, a QTL analysis was carried out on the parameters of an eco-physiological modelling of grain protein fractions (Martre *et al.*, 2003). Surprisingly, these QTL do not co-locate with QTL of Table 1 for N accumulation kinetics and grain composition.

Table 1. Detection of QTL for key genotypic parameters of *SiriusQuality*1 (Y = a × Nb)

Protein fraction	Parameter	h^2 (%)	Chromosome	Collocation
Alb-glo	a	10	2D	
	b	7	2D	
Gli	a	24	1A	Glu-A3 Gli-A1
EPP[†]	a	15	1A	Glu-A3 Gli-A1
UPP[††]	a	12	2D	
PPP[†††]	a	12	1A	Glu-A3 Gli-A1

[†] EPP = SDS-Extractable Protein Polymers.
[††] UPP = SDS-Unextractable Protein Polymers.
[†††] PPP = Protein Polymers in the total Protein.

Our preliminary results clearly show that more studies are needed to understand the relationship between N accumulation and grain protein composition, and that modelling gives a new insight into regulation mechanisms in wheat kernel.

Acknowledgements

This study was supported by the French Ministry of Research and Technology within the framework of the National Plant Genomics Programme "Génoplante".

References

Martre, P., Porter, J.R., Jamieson, P.D. and Triboï, E. (2003). Modelling grain nitrogen accumulation and protein composition to understand the sink/source regulations of nitrogen remobilization for wheat. *Plant Physiology*, 133: 1959-1967.

Oury, F.X., Berard, P., Brancourt-Hulmel, M., Depatureaux, C., Doussinault, G., Galic, N., Giraud, A., Heumez, E., Lecomte, C., Pluchard, P., Rolland, B., Rousset, M. and Trottet, M. (2003). Yield and grain protein concentration in bread wheat: A review and a study of multi-annual data from a French breeding programme. *J. Genet. Breed.*, 57: 59-68.

Robert, N., Hennequet, C. and Bérard, P. (2001). Dry matter and N accumulation in wheat kernel: Genetic variation in rate and duration of grain filling. *J. Genet. Breed.*, 55: 297-305.

Sofield, I., Evans, L.T., Cook, C.G. and Wardlaw, I.F. (1977). Factors influencing the rate and duration of grain filling in wheat. *Aust. J. Plant Physiol.*, 4: 785-797.

Stone, P.J. and Nicolas, M.E. (1995). A survey of the effects of high temperature during grain filling on yield and quality of 75 wheat cultivars. *Aust. J. Agric. Res.*, 46: 475-492.

Whan, B.R., Carlton, G.P. and Anderson, W.K. (1996). Potential for increasing rate of grain growth in spring wheat. I. Identification of genetic improvements. *Aust J Agric Res.*, 47: 17-31.