Unravelling complex adaptive traits using crop modelling: physiology and genetics of tillering in sorghum

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Abstract

Recent advances in functional genomics generated a huge amount of genetic information of high value for crop improvement. However, DNA sequences alone have little value in unravelling the genetic and physiological bases of complex traits controlled by a large number of genes. This emphasises the importance of approaches combining genetics with physiology, to dissect complex traits into basic biological processes less prone to environmental variations and related to a smaller number of genes. In this context, modelling is essential to identify and quantify such processes and their interactions with environment resulting in complex trait expression. This work aimed to show the added value of formalizing physiological knowledge in models to analyse the genetic control of sorghum tillering, a complex agronomic trait of interest. Detailed physiological analyses were previously realised to implement and test modelling concepts in which tillering is controlled by plant internal competition for carbon assimilates, depending on genotypic characteristics (demand for large vs. many organs) and environment (resource availability). These concepts were used to analyse experimental data acquired on eight BC2F2 populations of sorghum, derived from a cross between *Sorghum arundinaceum* and an elite tester. This analysis largely confirmed the modelling concepts previously developed and allowed to test the link between three putative QTLs and model based coefficients. The implications of this approach for reducing QTL*E effects in QTL detection and potential for future model assisted genetic analyses are discussed. This study illustrates how modelling can assist genetic studies on complex traits and assist breeding programs.

Media summary

Integrating knowledge gained in crop physiology through crop modelling can support the genetic analysis of complex traits, thereby enhancing breeding efficiency.

Key words

Plant internal competition, carbohydrate supply/demand ratio, QTL detection

Introduction

Knowledge of plant genomes is advancing very rapidly, but its utility in plant breeding requires understanding the phenotypic consequences of DNA sequences. Such understanding can be gained by 'dissecting' complex traits into underpinning biological processes that are under simpler genetic control than the complex trait itself and hence more context independent (Hammer *et al.*, 2005). Traditional crop models, which describe consequences of physiological processes, lack the functionality to adequately capture phenotypic consequences of differences at the genome (QTL) level, but such predictive capability can be achieved by incorporating biological knowledge into such models. This can improve the genetic analysis and breeding of complex traits (Yin *et al.*, 2004; Hammer *et al.*, 2006).

Tillering is a complex agronomic trait and a key component of grain yield in sorghum. Key morphogenetic traits, interacting with environments, have been used to explain tillering of five sorghum genotypes across five suboptimal environments (Kim *et al*., unpublished). Results were used to implement a modelling framework simulating tillering dynamics as a result of plant internal competition for assimilates (C), i.e. ratio between C supply and demand (S/D), which is a function of genotype and environment. The present study aims to demonstrate the added value of modelling to dissect complex traits for application in genetic analyses.

Methods

Tillering model framework: S/D is used as a determinant state variable explaining tillering rate across environments and genotypes; key morphogenetic traits involved and computed in this study to formalize S/D and in particular plant C demand in competition with tillering, were: main stem successive leaf width and length increment rate (LWIR, LLIR respectively) among leaves developing during the tillering period.

Phenotyping : Eight contrasting BC2F2 populations of an initial cross between S*orghum arundinaceum* (*s.a*., high tillering wild-type) and an elite tester (low tillering recurrent parent) were grown in a field experiment at Gatton (Australia) during summer 2007. Each population contained over 150 plants, and was sown in a single row at a density of 5 plants per linear metre. Tiller rank appearance, maximum and fertile tiller number (TNmax, FTN), main stem leaf number, length and width of main stem leaf 4 to 9 (developing during tillering period), anthesis date, and plant height were measured on each plant for modelling application.

Genotyping : BC1F4 parent lines of each population were genotyped with DArT technology, which allowed the identification of genomic regions still segregating (indicating introgressions of *S. a.* in the elite tester background). Segregating regions among the BC1F4 lines were screened with a sorghum consensus map including SSR. Polymorphic SSR around the segregating regions were chosen to genotype selected BC2F2 individual plants. QTL analysis was first performed with single-marker regression, to test independence in segregation between one SSR and field observations. A similar approach was used to detect putative QTLs linked with model based genetic coefficients among the segregating regions.

Results

Phenotyping: Across populations, there was little variability in phenology, with final main stem leaf number

varying from 16.5 to 18.0 leaves, resulting in a one week difference in anthesis date between the earliest and the latest population. Tiller appearance and fertility frequency of each tiller rank (T1 to T6) are represented in Fig. 1 for each population. The main difference between high (F2_R05422, 29, 34, 30 and 26) or low (F2_R05425, 36 and 21) tillering populations was in the proportion of plants that produced tillers in the axils of Leaf 1 (T1) and Leaf 2 (T2). Tiller number (TNmax and FTN) was clearly related to the identified leaf morphogenetic parameter LWIR for three to four of the populations (Fig. 2). However, the response to LWIR varied among populations, indicating other factors were involved in regulating tillering.

QTL analysis: Among segregating regions based on polymorphic SSR, those related to tillering ability across populations were selected and are presented in Fig.3. The link between those loci, observations and model based coefficients (mainly, LWIR and S/D threshold enabling tillering) is currently being tested.

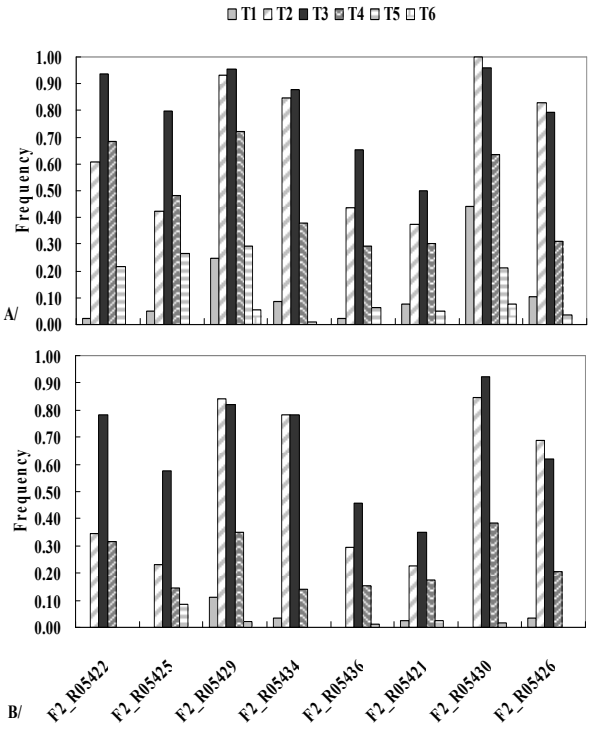

Figure 1: Distribution of appearance (A) and fertility (B) proportion for each tiller rank (T1 to T6) for each population.

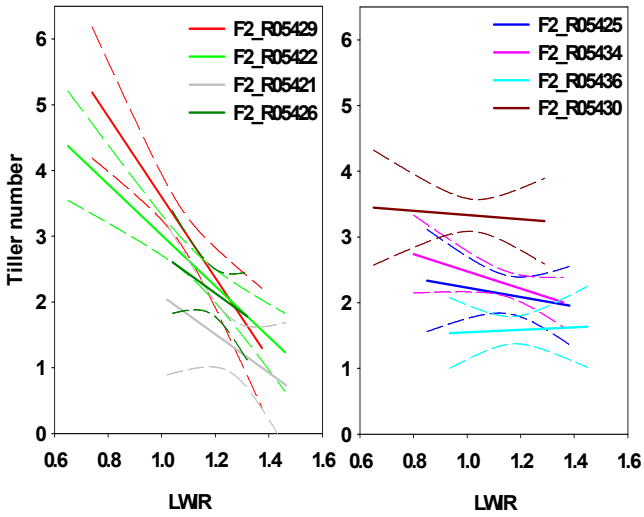

Figure 2: Relationship between leaf width increase between main stem Leaf 4 and 9 (LWIR) and tillering among lines of a given population. Regression (plain lines) and 95% confidence interval (dashed lines) are represented for each population.

Conclusion

This study aimed at applying dynamic modelling concepts to dissect a complex trait to more basic biological processes to assist and enhance genetic analysis. Eight BC2F2 populations were phenotyped to compute model based genetic coefficients quantifying the control of sorghum tillering by plant C S/D. The degree of association across populations studied suggests value in this approach. Such model based genetic coefficients could then be used to carry out other QTL analyses on sorghum tillering. In addition, they can be used to improve the way sorghum tillering and morphogenesis are considered in existing model platforms, such as Ecomeristem (Luquet *et al.*, 2006) and APSIM (Wang *et al.*, 2002). Once connected to genetic information and integrated in crop models, such genetic coefficients will allow simulation of QTL effects on tillering behaviour in target environments and help in reducing QTL*E effects in QTL analysis.

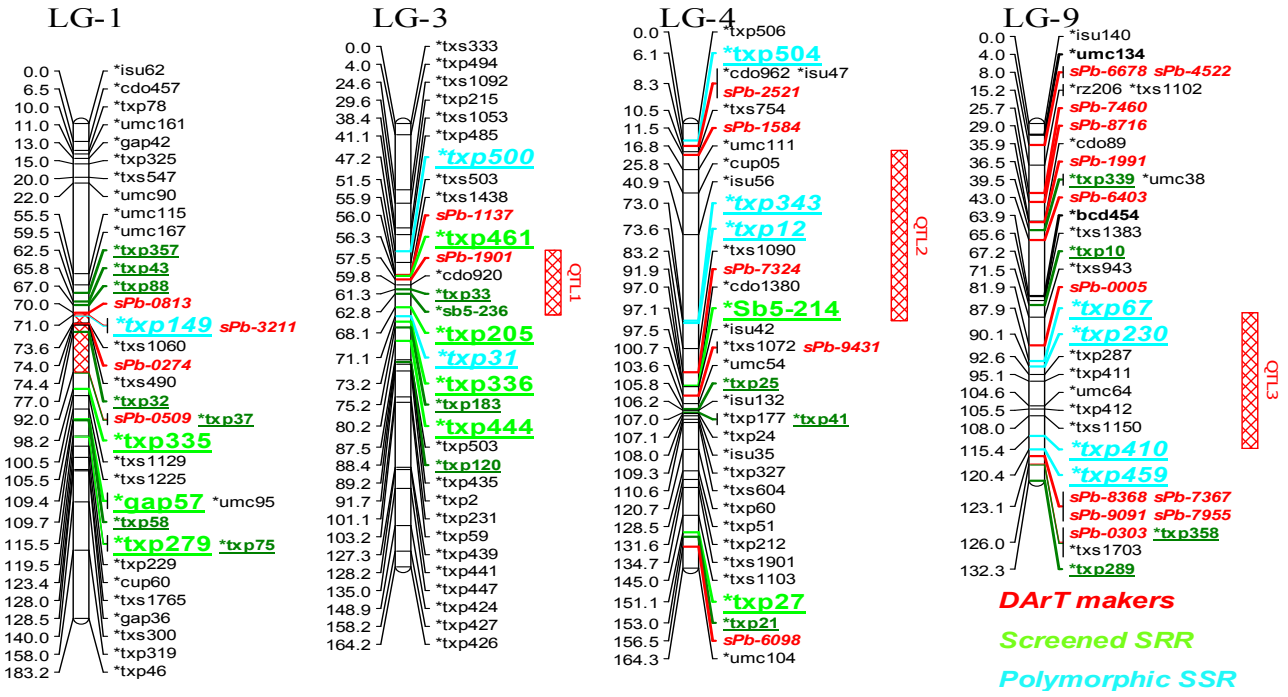

Figure 3: Localisation of putative QTLs linked with tillering component traits or model based genetic coefficients on chromosomes 1, 3, 4 and 9 in BC2F2 populations genotyped with SSR.

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