

Mapping QTL involved in rice early morphogenesis as described by the process based parameters of *EcoMeristem* model

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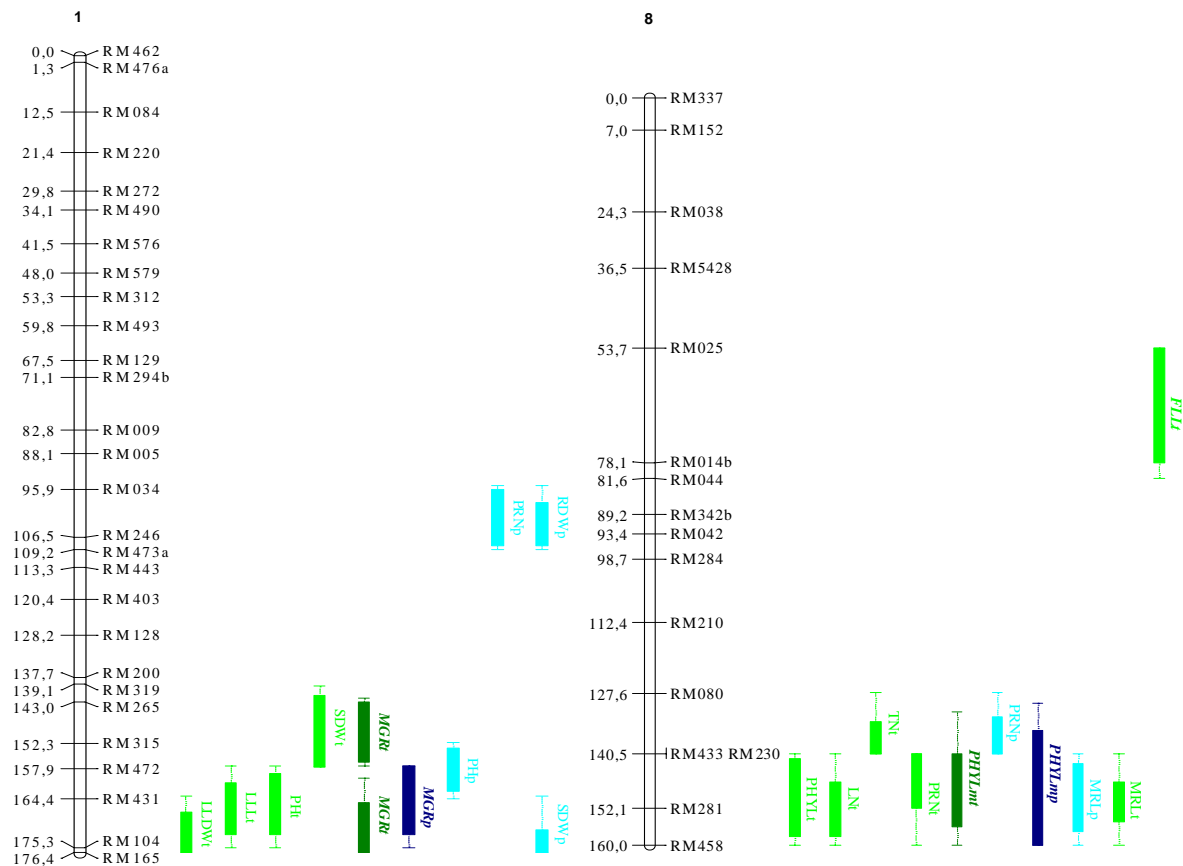
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Introduction: Plant models describing organ or whole plant growth and development as a set of response processes to environment are of great potential for the genetic dissection of complex traits. Indeed, related model parameters can be considered as ‘process based’ traits and are expected to (1) have less complex genetic determinisms than related complex traits accessible experimentally and (2) be less prone to uncontrolled environment effects since model equations separate genotypic parameter (G) from environmental variable (E) effects (Dingkuhn et al., 2005). Proof of this concept was provided for response processes at organ level, e.g. by Reymond et al. (2004) for maize leaf expansion rate response to drought. Recently, the model *Ecomeristem* was developed to address early morphogenesis processes involved in whole plant phenotypic plastic expression in response to E. *Ecomeristem* main originality is to formalize in a simple way and based on a few parameters, the daily control of plant morphogenesis by meristems in response to E. E is mainly characterized at plant level by a state variable I_c , plant internal competition index for carbon, daily computed as the ratio between plant C supply (assimilation) and demand (sum of organ daily demand for growth). Main process based genotypic parameters controlling morphogenesis in the model are MGR (Meristem Growth Rate, pre-dimensioning newly created organs), I_{ct} , a threshold parameter regulating tillering depending on I_c state variable, SLAP (controlling leaf structural thickness depending on its rank) and phyllochron (PHYLm, controlling leaf appearance rate). The objective of the present study is to compare QTLs detected by *Ecomeristem* model parameters and by measured related phenotypic complex traits, for then analysing the stability of parameter-QTLs across different growth conditions.

Materials and methods: A mapping population, composed of 178 recombinant inbred lines (RIL) of the IR64 / Azucena cross (Ahmadi et al. 2005), was grown in a phytotron in hydroponic conditions with either optimal or phosphorus deficient (P) nutritive solution, using a alpha lattice design with 2 replications. Twenty-three days after sowing phenotypic traits related to early morphogenesis were measured: plant height (PH), main stem leaf number (LN), tiller number (TN), main stem last ligulated leaf length (LLL), width (LLW) and dry biomass (LLDW), shoot dry weight (SDW), maximum root length (MRL), primary root number (PRN) and root dry biomass (RDW). Data obtained under P conditions are indicated with a *p* subscript. PH, TN, LN, SDW and RDW data were used as targets to apply *Ecomeristem* model in a inverse mode, i.e. to optimize for each line in the population four of its main morphogenetic parameters described above: MGR, I_{ct} , SLAP, PHYLm. Composite Interval mapping procedures of the MapQTL software package (Van Ooijen, 2006) were used for QTL detection.

Results: Model parameters, MGR, I_{ct} and PHYLm, showed normal distribution within the RILs population and transgressive segregations were observed. Significant genetic variation was observed for almost all parameters, under both growth conditions. Significant correlations were observed between model parameters and measured data. Broad sense heritability of model parameters did not exceed the one of measured traits. At least one QTL was identified for each parameter (except SLAP) under both growth conditions, but the percentage of genetic variation explained by each QTL was low, seldom higher than 10%. Under optimal growth conditions, two MGR QTLs, out of 3, were mapped on chromosome 1, near the *Sd1* locus involved in meristem growth via the biosynthesis of GA. This chromosomal area very

often exhibits a QTL for plant height with a bimodal LOD distribution. Interestingly MGR allowed detecting 2 QTLs in this chromosomal segment by contrast with PH. The QTLs for Ict were all mapped in chromosomal areas involved in tillering ability. The 2 QTLs for PHYLM co-localised with QTLs involved in leaf number, tillering ability and vegetative growth duration but didn't co-localise with known QTLs for phyllochron and plastochron. QTLs involved in MGR and PHYLM were mapped in same chromosomal area under the two growth conditions, which was not the case for QTLs involved in Ict.



Conclusion: QTLs mapped for model parameters MGR, Ict and PHYLM were consistent with the ones involved in morphogenesis related complex traits directly measured, i.e. plant height, biomass accumulation, tillering number and leaf number. To the exception of PHYLM, they were also consistent with the literature regarding genetic bases of related traits. Model parameters allowed identifying other genomic areas involved in morphogenesis compared to direct observations. The unexpected instability of Ict QTLs across growth conditions, expression of an inducible phenotypic plasticity, needs further confirmation.

References

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