A functional-structural model of rice (*Oryza sativa* L.) linking morphogenesis with quantitative trait loci

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Rice (*Oryza sativa* L.) is the most important staple food in East and Southeast Asia. Possessing the shortest genome of the Gramineae crops, it is furthermore a model plant of crop plant genetics, with a fully sequenced genome and many studies on quantitative inheritance of agronomical and morphological traits on offer for modelling (e.g., Zhang et al. 2006).

Previous architectural modelling approaches dealing with rice have been largely descriptive and based on morphometric datasets (Watanabe et al. 2005). Buck-Sorlin and Bachmann (2000) introduced a simple method to link virtual genes (Mendelian and quantitative) with morphogenetical rules, the latter implemented as L-system production rules, at the example of barley. Buck-Sorlin et al. (2005) showed how a virtual genotype could be connected to a biosynthesis network and rules simulating architectural development, using relational growth grammars which are an extension of the L-system formalism.

We have created a conceptual model of rice architectural development to reproduce different morphological phenotypes from a genotype consisting of a set of virtual QTLs for spikelet and tiller number as well as other agronomical traits considered as yield components (Wu et al. 1999, Kato 2004, Zhang et al. 2006). The relational growth grammar of the model will be implemented in XL within the modelling platform GroIMP. (Kniemeyer 2004). Using this example, we show how mechanisms of quantitative inheritance could be generalised for use in ecophysiological FSPMs, by implementing a generic description of QTL x environment interactions (Yang & Zhu, 2005) into a virtual rice model. The implications for "virtual breeding" will be discussed, where the latter means the design of rice ideotypes using FSP modelling.

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