



Simulating Superior Genotypes for Plant Height based on QTLs: Towards Virtual Breeding of Rice

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Résumé en
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Crop plant researchers and agronomists have in the recent past increasingly turned to crop modeling as a promising tool for the integration and exploration of experimental data from breeding and agronomy. Set up suitably, crop modeling can then also be used to predict performance of future high-yielding cultivars, e. g. of rice, which is one of the major food crops worldwide. Questions such as "Which combination of alleles is likely to have the strongest influence on the development of the individual phenotype?" or "In which way is QTL action modified by a particular environment?" can be tackled with the help of a crop modeling approach. As a further extension of a previously established Functional-Structural Plant model (FSPM) of rice we present here simulated "virtual" reproduction of individuals using QTL information, which can contribute to providing answers to these difficult questions. In this study, we briefly describe the way QTL information has been integrated into the rice model, and sketch the algorithmic implementation of processes leading to the creation of filial genotypes from parental genotypes via simulated sexual reproduction. The phenotype value, which in this case was plant height, was determined with the rules that specify the genetic processes operating on genotypes as intrinsic properties of each individual. The mapping results from the simulated population were compared with the input values for the parental lines. It is shown that the rice model faithfully reflected the genetic properties from the parental lines with low bias, which suggests a reasonable way to integrate QTLs into the plant eco-physiological model with the predictive properties. It could in the future be used as a supporting tool in breeding practice.

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