Oral sessions | Farming System | O23: Crop Modeling: Recent Progress and Applications

[O23] Crop Modeling: Recent Progress and Applications

Chair: Hiroshi Nakagawa (National Agriculture and Food Research Organization, Japan)
Chair: Xinyou Yin (Wageningen University and Research, Netherlands)
2021年9月9日(木) 17:00 〜 19:00 Room 2 (Oral) (Farming System)

18:25 〜 18:40

[O23-06]Determination and Genetic Analysis of Genotype-Specific Parameters of Crop Growth Model Using Large-Scale Data of Rice Cultivation Tests in Japan

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There is a gap between our molecular level understandings of crop responses to environments and the actual crop growth and yield in the field. Further development of the crop growth model toward integrating the genomic or other omics data will help us bridge the gap and simulate the robust genotype under the changing environments. The objectives of our study were to clarify the variation in the "genotype-specific" parameters of crop growth simulation model and to analyze the linkage between those empirically determined parameters and genomic information by GWAS. We utilized a large-scale database of rice cultivation tests which consists of rice growth data for total 38 years at 101 sites in Japan, while the number of data and the included environmental combinations of year x site were different among genotypes. We firstly determined genotype-specific parameters for phenological development of 1860 genotypes. Then, we simulated the above-ground biomass and yield of those genotypes grown at various environments by rice growth model GEMRICE and estimated the genetic and environmental effects (excluding the effects of phenology and weather conditions, respectively) by applying a linear mixed model against the gap between observed and simulated growth and yield of rice. Integrating the environmental effects into GEMRICE, finally genotype-specific parameters for biomass growth and yield formation were determined. We report the GWAS results of those parameters for 110 genotypes and discuss the methodology for integrating the genomic data into the crop growth simulation model.