

Studies of Plant Environmental Responses by Field Transcriptomics

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Detailed molecular mechanisms of plant environmental responses have been revealed by laboratory experiments. However, it is not enough to understand plant environmental responses under field conditions. To bridge between laboratory and field, we developed statistical models using extensive transcriptome data of rice leaves in the field and the corresponding meteorological data¹⁾ (Fig. 1). We showed that the transcriptome dynamics of rice leaves in a paddy field were mainly governed by ambient temperature and circadian clock. The statistical model successfully predicted field transcriptome dynamics in Nipponbare, a standard cultivar. However, the effect of genomic background on

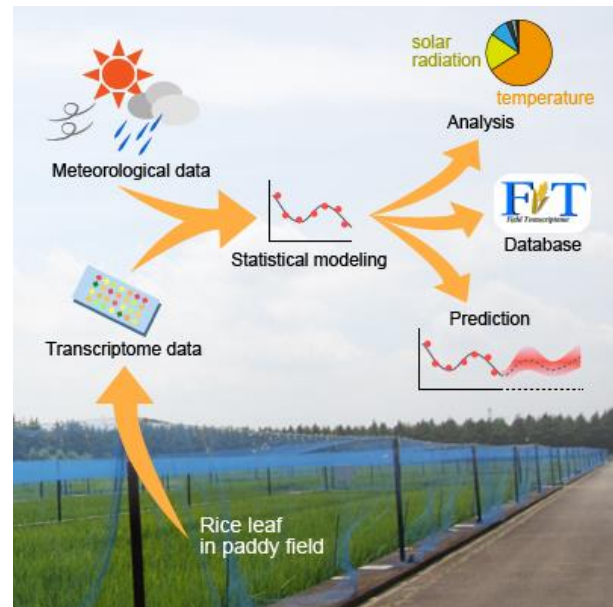


Fig. 1 Scheme of field transcriptomics

transcriptome dynamics is not known. To establish a method of predicting the transcriptome dynamics in various genomic backgrounds, we developed several novel technologies such as automated parallel preparation of RNA-Seq library, a fast and easy-to-use R library for statistical modeling²⁾. Using these technologies, we obtained RNA-Seq data of 1,300 field samples of chromosomal substitution lines between Koshihikari and Takanari, and analyzed the transcriptome data with the corresponding meteorological and genotype data. Two statistical models describing transcriptome dynamics in Koshihikari and Takanari, respectively, were developed. We detected 2,911 genes with different expression dynamics between two cultivars by comparing with predicted transcriptome dynamics of Koshihikari and that of Takanari. Genomic regions controlling the expressional differences were successfully identified in approximately half of the genes with different expression dynamics. Our models enable the prediction of field transcriptome dynamics not only in two parental cultivars but also in their progeny lines.

Reference

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2. Iwayama K, Aisaka Y, Kutsuna N, *Nagano AJ (2017) FIT: Statistical modeling tool for transcriptome dynamics under fluctuating field conditions., **Bioinformatics**, btx049