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Deciphering and prediction of transcriptome dynamics under fluctuating field conditions

Monday 24 June 2013 11.00am – 12pm

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Slatyer seminar room R.N. Robertson Building (Bldg. 46), Linnaeus Way, ANU



Recent advances in plant molecular biology have revealed large effects of the circadian clock, organism age, and environmental stimuli on transcriptomes under simple, controlled laboratory conditions. However, the factors that control transcriptomes under natural conditions are largely unknown. We have developed statistical models using extensive field transcriptome data and the corresponding meteorological data (1). We named this approach as "field transcriptomics". Here we show that the transcriptome dynamics of rice leaves in a paddy field were mainly governed by ambient temperature and endogenous diurnal rhythms, as well as by plant age and solar radiation. We also found diurnal gates for environmental stimuli, detected associations between the thresholds for plant response to solar radiation and signal-to-noise ratios for day-length change, and predicted

transcriptomes under given environmental conditions. Our models comprehensively describe transcriptome dynamics under complex field conditions and will help researchers to translate the vast molecular knowledge amassed in laboratories into solutions to problems in agricultural and natural environments.

For further field transcriptomic study, we established a highly-parallelized cost-effective RNA-Seq system. Now, several new field-transcriptome projects have started with the RNA-Seq system. We would like to introduce them and discuss about potentials of field transcriptome.

Presented by
ANU College of
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& Environment

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