Exploration of Life-Course Factors Influencing Phenotypic Outcomes in Crops

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(Received 3 May 2020; Accepted 22 June 2020)

Keywords: Crop • Life-course approach • Plant–environment interaction.

The rapidly increasing global population will require more food in the future, but global food security is facing challenges from climate change, and limited arable land and water resources (Bailey-Serres et al. 2019, Gupta et al. 2020). To cope with the concerns of global food security, climate-resilient crop varieties are expected to play a key role in innovating the farming system and facilitating climate-smart agriculture. Therefore, there has been much interest in research on the gene discovery of agriculturally important traits and on understanding crop–environment interactions, which would facilitate the breeding of climate-resilient crop varieties.

In this Special Focus Issue (SFI) of Plant and Cell Physiology, we introduce approaches to understanding plant–environment interactions in various crop species, highlighting how the diversity in physiological responses to environmental changes can influence growth and agronomically important traits.

The mini review by Mochida et al. (2020) introduces recent advances in two disciplines, i.e. a multi-omics analysis combining a life-course approach with plant phenomics, which can synergistically facilitate advances in our understanding of plant–environment interactions. In their paper, the authors showcase recent examples in both disciplines, highlighting the latest emerging technologies that can facilitate the modeling of genotype-to-phenotype in crops (Mochida et al. 2020).

With the advent of high-throughput genotyping and phenotyping technologies in crops, genome-wide association study (GWAS) has become a useful strategy to identify genes associated with phenotypes in various crop populations (Connorton and Balk 2019, Alqudah et al. 2020). In this issue, the review article by Li (2020) provides a comprehensive insight into recent advances in GWAS, including the identification of genes that may be used to improve salt tolerance in plants. Moreover, by applying multivariate GWAS (mGWAS) approaches to analyze phenotypic datasets of inflorescence and leaf architecture in a genotyped diversity panel of maize (Zea mays), Rice et al. (2020) demonstrate the ability of mGWAS to identify pleotropic quantitative trait loci, which are associated with multiple inflorescence-related traits observed in different maize organs. They also conducted a simulation to show that it is possible for...
mGWAS to yield higher true positive detection rates than univariate GWAS approaches when at least one of the correlated traits have low-to-medium heritability. Integrative analysis of multiple -omics spectra has been used to monitor physiological responses to environmental changes in various crops, both under controlled and field conditions. In this issue, Hirayama et al. (2020) provide the first report of a diversity of endogenous phytohormone levels in barley (*Hordeum vulgare*) under field conditions. In this study, they simultaneously assessed the endogenous levels of five phytohormones, such as auxin, cytokinins, abscisic acid, jasmonate and salicylic acid, in leaves sampled weekly and throughout the life-course of plants from eight diverse barley accessions grown under field conditions, illustrating the diversity of the physiological dynamics of field-grown barley accessions (Hirayama et al. 2020). In addition, Abdelrahman et al. (2020b) provide an example of a comparative multi-omics approach combined with genetic variation analysis in Asparagus. To gain insights into the diversity of Phomopsis disease resistance, they applied metabolome and transcriptome analyses for susceptible *Asparagus officinalis* and resistant wild *Asparagus kiusianus* and assessed the association between their patterns of multi-omics signatures and genetic variation (Abdelrahman et al. 2020b). Temperature is a primary environmental factor that affects plant growth and development, but the elevated temperature will negatively impact crop production, especially that of cool-season cereals, such as wheat (*Triticum aestivum*). In this issue, Abdelrahman et al. (2020a) provide a comprehensive review of recent advances in understanding the cellular response to heat stress conditions in the wheat, particularly highlighting membrane lipid reprogramming (Abdelrahman et al. 2020a). As previously discussed in *Plant and Cell Physiology*’s SFI on ‘Plant Responses to CO₂’, rising atmospheric CO₂ conditions can also impact plant carbon metabolism (Terashima et al. 2014), which will influence crop growth and yield. In this issue, the research article by Palit et al. (2020) reports findings of a physiological and transcriptional response to elevated CO₂ conditions in chickpea (*Cicer arietinum*). In this study, they assessed the alteration in various physiological parameters and transcriptome in response to elevated CO₂ conditions at different growth stages in two popular cultivars of chickpea and demonstrated stage- and genotype-specific patterns of physiological responses to the elevated CO₂ conditions in chickpea (Palit et al. 2020). Collectively, the papers in this SFI have highlighted several approaches aimed at elucidating crop–environment

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**Fig 1** Plant—environment interactions during the crop life-course. A life-course approach allows the elucidation of the relationships between earlier experiences and later outcomes, such as yield. Growth curves of two soybean genotypes are represented, showing relative leaf weights over time, which were estimated using the R Package ‘qrNLMM’ (Quantile Regression for Nonlinear Mixed-Effects Models) and its ‘Soybean’ data (Galarza et al. 2018). Representative growth stages of soybean are illustrated to exemplify the crop life-course. Various genetic and environmental factors interact to shape crop development during its life-course. Physiological responses mediate crop development in response to such factors, which may be observed through time-series analyses using various diagnostic methods, including omics analysis. Timing of environmental exposures and genetic variation between crop varieties may cause different developmental consequences.
interactions, with examples given in various crop species. We hope that this SFI will provide readers with useful information to better understand the significant crop–environment interactions that take place during a plant’s life-course history, especially when designing novel climate-resilient crop varieties and devising climate-smart agriculture strategies.

Funding

Grant-in-Aid for Scientific Research (B) [grant no. 15KT0038 to K.M. and T.H.] and a Grant-in-Aid for Scientific Research (C) [grant no. 19K11861 to K.M.] of the Japan Society for the Promotion of Science (JSPS) and Core Research for Evolutionary Science and Technology (CREST) of the Japan Science and Technology Agency (JST) [grant no. JPMJCR1604 to K.M. and T.H.].

Acknowledgments

We thank Professor Hitoshi Sakakibara, former Editor-in-Chief, and Professor Wataru Sakamoto, Editor-in-Chief of Plant and Cell Physiology, for providing us the opportunity to organize this SFI. We also thank Dr. Liliana M. Costa, Managing Editor, and all the contributors and anonymous reviewers of these articles for their great efforts with this SFI even under the COVID-19 pandemic.

Disclosures

The authors have no conflicts of interest to declare.

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