

Exploration of Life-Course Factors Influencing Phenotypic Outcomes in Crops

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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 agronomically important traits and on understanding crop–environment interactions.

During the last decade, advances in multiple areas of large-scale biology and information technologies have presented new opportunities to deeply investigate plant responses to environmental change and gain insights into plant–environment interactions that could help contribute toward crop improvement. High-throughput sequencing-based applications have dramatically improved our accessibility to genome-scale information, facilitating the development of genomic resources and tools for gene discovery and breeding in various crop species (Wang et al. 2018, Nguyen et al. 2019, Tanaka et al. 2020). Combinatorial use of multiple high-throughput methods for -omics analyses has been widely used to monitor physiological alterations in plants in response to environmental stimuli (Yoshida et al. 2015, Zander et al. 2020). Statistical and computational modeling has further provided strategies that aid our understanding of the relationships between factors involved in plant physiological responses to environmental conditions (Satake et al. 2015, Fodor et al. 2017). Moreover, advances in sensors and analytics in computer vision have assisted in building frameworks for high-throughput plant phenotyping to continuously and non-invasively monitor growth and environmental responses in plants (Fujita et al. 2018, Mochida et al. 2019).

Field-grown plants are continuously exposed to temporal environmental fluctuations throughout their life cycle. Such crops continuously sense changes in various environmental

factors simultaneously to regulate their physiological conditions and keep healthy, as well as to determine the timing of developmental transitions (Mochida et al. 2015). Agronomic traits in crops often appear during their later growth stages, as a result of cumulative effects on crop–environment interactions endured throughout their life cycle (Fig. 1). Therefore, understanding the relationship between crop varieties and their temporal physiological responses to environments throughout their life-course could provide insights into 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 pleiotropic 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

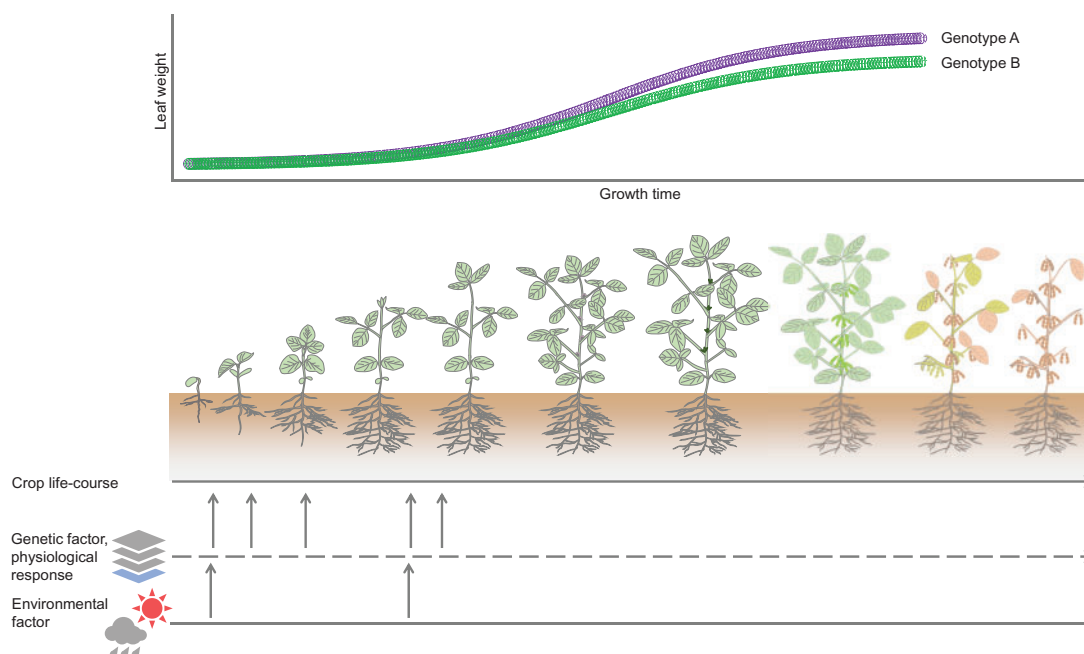


Fig 1 Plant—environment interactions during the crop life-course. A life-course approach allows the elucidation of the relationships between earlier experiences and later outcomes, such as yield. Growth curves of two soybean genotypes are represented, showing relative leaf weights over time, which were 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.

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

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.

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Disclosures

The authors have no conflicts of interest to declare.

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