Metabolomics and trait development in crops

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Genetic modification to elicit trait improvements in crops can be pursued through conventional breeding, irradiation, chemical mutagenesis and modern biotechnological approaches. These latter approaches have recently expanded to include both the use of RNAi silencing and the modification of genes encoding regulatory proteins. The emergence of these new biotechnological options coincides with continuing technical and informatics advances in the ‘omics sciences. The purpose of the “Metabolomics and Trait Development” focus of this journal issue is to discuss how metabolomics can integrate with modern biotechnological strategies, as well as with conventional approaches, to drive trait enhancements in major crops.

An introductory review by Harrigan and colleagues considers the potential of metabolomics in assessing natural variation and metabolic diversity in plants. Two original research articles then follow that highlight applications of metabolic profiling in characterizing metabolic variation in tomato during growth and development (Mounet et al.) and exposure to drought (Semel et al.). A third research article describes methodology for assessing sub-cellular compartmentation in the soy metabolome (Benkeblia et al.).

Subsequent articles consider more directly the value of metabolomics in studies of plants modified through modern biotechnology. This is first illustrated by research on the effects of manipulating tomato metabolism through expression of a moss-derived sodium pumping ATPase. The metabolic and phenotypic changes induced by manipulating ion homeostasis are difficult to predict yet a

metabolomics program yielded information that can now guide more detailed mechanism-of-action studies (Jacobs et al.). Hypotheses-driven or “targeted” profiling can also be of immense value in evaluating metabolic changes associated with manipulation of a specific metabolic pathway. Wakasa and colleagues, for example, demonstrate that metabolome changes associated with deregulation of tryptophan synthesis through expression of mutant forms of anthranilate synthase in rice and other crops are quite minimal.

A fundamental concern regarding the use of “non-targeted” metabolic profiling approaches in compositional assessments of crops centers on the fact that the number of acquired data points can greatly exceed the number of experimental samples in a typical study. Indeed, Enot and colleagues emphasize that few studies prescribe “distance metrics” for determining whether there are, in fact, biologically meaningful differences in the metabolomes of different test materials. They describe a hierarchical approach that may provide greater statistical rigor to profiling experiments; this is expanded upon in the follow-up paper by Enot and Draper which posits the value of machine learning in studies using high content data.

RNAi silencing is proving to be an important strategy for effecting loss-of-function mutations. Tang and colleagues present an excellent overview of the technology involved and provide examples of its applications. This article also serves as an introduction to three reviews that describe RNAi silencing approaches, and other transgenic strategies, to the manipulation of a number of important biochemical pathways. These include the pharmaceutically significant benzylisoquinoline pathway in poppy (Larkin and Harrigan), cyanogenic glucoside synthesis in a range of plants (Morant et al.) and flavonoid synthesis in tomato (Bovy et al.). A role for targeted metabolomics in assessing

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the efficacy (and potential for secondary [unintended] effects) of biotechnological approaches to pathway modification is described in all three articles.

In summary, this special issue is intended to highlight possible synergies between metabolomics and emerging and conventional strategies for eliciting trait improvements

in crops. It includes contributions from a diverse range of scientists and over 10 countries are represented. All articles have been peer-reviewed and are of consistently high quality. It is my hope that you will enjoy all these articles and your thoughts can be forwarded to me at the address above.