

Focus on Weed Control

There were many reasons for the editors to suggest that it was timely for *Plant Physiology* to develop a Focus issue around the topic of weed control. While this journal has published many formative papers in the past relating to weed science and herbicide mode of action, this activity has declined in recent years. Based on the importance of weed control in ensuring global food security, it seemed incongruous that one of the most important plant science publications should not be actively promoting the associated high-quality underpinning research on plant physiology, biochemistry, and molecular genetics. The challenges of weed control are immense, and the potential for input from the wider plant science community is largely unrecognized. Many figures are available from public and private sources with respect to the scale of the endeavor. Of the 8,000 plants described as agronomically significant weeds, some 200 to 250 species figure prominently, with up to 50 to 300 million associated seeds infesting the typical acre of farmland in the United States. Figures for the losses in food production associated with weed control are mirrored by the scale of investment made by farmers in associated crop protection measures. Based on current expenditures, 13% and 30% of global agrochemical sales are committed to the purchase of nonselective and selective chemical weed control agents, respectively. Based on projected growth in the sector, by 2018, the crop protection industry will be conservatively worth \$71.3 billion US. As such, at a time when the plant science community is being encouraged to engage in wealth creation, weed science offers many potential prizes to the innovative researcher.

As reviewed by Kraehmer et al. (2014a) in this issue, herbicides remain our front-line defense against weeds and represent the greatest global agrochemical input into crop production. Despite their importance, due to a plethora of factors, there has been no new class of herbicide mode of action commercialized in over 25 years. Some of these factors fall outside the realm of science and have been driven by the increasingly rigorous stance taken by government regulatory bodies with respect to minimizing the effect of agrochemicals on the environment and human health (Kraehmer et al., 2014a). Taken together with the advances in analytical chemistry that have radically reduced minimal levels of detection from parts per million to parts per billion, many new promising compounds have failed in development based on their environmental impact assessments. However, with respect to scientific innovation, it is also clear that the view in the 1980s that the next herbicide silver bullet was only a decade away based on an almost infinite set of yet to be discovered potential modes of action was unfounded.

This brings us to a second reason for sponsoring the Focus Issue on Weed Control: the relatively low level of research undertaken in the academic sector on studying herbicide mode of action. This is reflected by the fact that only one of the Focus issue articles examines the mode of action of a promising herbicide lead (Brabham et al., 2014). In an elegant set of studies harnessing state-of-the-art biochemical and bioimaging approaches and using characterized *Arabidopsis* (*Arabidopsis thaliana*) mutants, the authors demonstrate that the herbicide indaziflam disrupts cellulose biosynthesis through a previously unknown mechanism of action. In a second approach, the importance of understanding herbicide mode of action is demonstrated through engineering a target site, 4-hydroxyphenylpyruvate dioxygenase, to enhance herbicide tolerance in soybean (*Glycine max*) using an optimized expression cassette (Siehl et al., 2014). This article nicely illustrates the level of sophistication in which we can now manipulate important crop protection input traits in agriculture through genetic modification. As described in the review articles on the current status and recent achievements in herbicide development (Kraehmer et al., 2014a, 2014b), the major focus and effort on herbicide research remain in the industrial sector, with many interesting chemical leads and new approaches to deliver compounds in the field currently under development. In particular, the safeners are singled out as a means of enhancing selective weed control through increasing the tolerance of cereal crops, most notably to graminicides. The forward look includes a very different approach to weed control, with the paradigm shifting from a heavy reliance on chemical control to integrated weed management systems that call on a wider range of technologies and cultural practices (Kraehmer et al., 2014b), a theme that nicely links to the topics highlighted in the following sections.

As a further priority, we wanted to capture emerging thinking with respect to developing new strategies for weed control, with two Update articles of significance here. The review on natural products as new leads for herbicides (Dayan and Duke, 2014) is very timely, based on our rapidly emerging knowledge of plant and microbial secondary metabolism. The natural world is well versed in waging chemical warfare on plants in the form of allelochemicals and phytotoxins, and here the authors propose that some of these agents are interesting new leads for herbicides. Using a completely different strategy, it is proposed that multicopy transposons carrying unfit genes could be used to help control weeds by reducing their competitiveness against crops (Gressel and Levy, 2014). Four potential scenarios are described relating to different weeds, with the introduced transposons only activated under conditions induced by selective environmental conditions or by spraying with specific agrochemicals. The theme of understanding the competitiveness of weeds is also at

the heart of the article detailing the impact of using non-genetically-modified Clearfield imazethapyr-resistant rice (*Oryza sativa*) as a weed control strategy on the evolution of weedy rice (Burgos et al., 2014).

Understanding the impact on weed populations of imposing strong new selective pressures through the repeated use of a restricted range of chemistries, often linked to genetic modification-mediated herbicide-resistant crops, takes us to a further emergent theme of the issue, namely the steady emergence of herbicide resistance in weeds and our understanding of its molecular basis. Roundup-ready technology has been a massive global success but has driven the emergence of glyphosate resistance in problem weeds. Two such resistance mechanisms are detailed in this Focus issue. One well-described method for evolving glyphosate resistance in weed population lies in the enhanced expression of the enzyme targeted by the herbicide, 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS). In the case of the pernicious U.S. weed *Kochia scoparia*, a newly identified mechanism underpinning this via the tandem duplication of 10 copies of the EPSPS gene at a single locus is described after visualizing its amplification using fluorescence in situ hybridization (Jugulam et al., 2014). In contrast, a completely different mechanism of glyphosate resistance is described in horseweed (*Conyza canadensis*), where ³¹P-NMR has been used to demonstrate the active sequestration of the herbicide in the vacuole mediated by active transporters (Ge et al., 2014). Herbicide resistance is not confined to glyphosate and is widely observed in all types of crop production systems. Of particular international concern is the growth of nontarget site-based herbicide resistance (NTSR), which challenges the effectiveness of weed control measures irrespective of the mode of action applied. In a comprehensive review, Yu and Powles (2014) detail the scale of the problem, focusing on NTSR in grass weeds affecting cereal productivity. Attention is directed at the role of cytochromes P450 (CYPs) in promoting NTSR in annual ryegrass (*Lolium rigidum*), and therefore it is timely that in two elegant studies, new insight into the identity and roles of CYPs involved in herbicide detoxification are presented in this issue. First, the gene encoding CYP72A31 is shown to confer tolerance to two different herbicides (bispiribac sodium and bensulfuron-methyl) that both act on acetolactate synthase in rice and Arabidopsis (Saika et al., 2014). In a second report, the CYP76C enzyme family in Arabidopsis is shown to oxidatively metabolize phenylurea herbicides and, interestingly, provides a bridge beyond herbicide research by also elucidating the natural function of CYP76Cs in planta, which is linked to monoterpene secondary metabolism (Höfer et al., 2014).

Finally, a further theme emerging from this Focus issue relates to the way in which new technologies relating to next-generation sequencing are allowing the research community to gain unparalleled knowledge of the molecular biology of hitherto understudied weed species. Using a range of sequencing platforms, a draft genome has been assembled for horseweed and used to

study associated differences in glyphosate-resistant and -susceptible biotypes of the weed (Peng et al., 2014). Using similar technology, but with a transcriptomics focus, genes involved in the process of dodder (*Cuscuta pentagona*) parasitizing crops through forming invasive feeding structures in crop hosts have been identified, offering new strategies for controlling this highly destructive weed (Ranjan et al., 2014). The pervasive impact of these technologies is further illustrated by their application for genotyping by sequencing in the earlier mentioned study of weedy rice populations (Burgos et al., 2014).

Whether you are new to the field or already familiar with weed science, we hope this Focus issue will both highlight the excellence of some of the continuing research on this topic as well as encourage the broader plant science community to think of addressing the many challenges inherent in modern weed control. In addition to the authors of the papers presented, we particularly thank the reviewers of the articles who have responded so enthusiastically in delivering this Focus issue of *Plant Physiology*.

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