The power and potential of genomics in weed biology and management

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Abstract

There have been previous calls for, and efforts focused on, realizing the power and potential of weed genomics for better understanding of weeds. Sustained advances in genome sequencing and assembly technologies now make it possible for individual research groups to generate reference genomes for multiple weed species at reasonable costs. Here, we present the outcomes from several meetings, discussions, and workshops focused on establishing an International Weed Genomics Consortium (IWGC) for a coordinated international effort in weed genomics. We review the 'state of the art' in genomics and weed genomics, including technologies, applications, and on-going weed genome projects. We also report the outcomes from a workshop and a global survey of the weed science community to identify priority species, key biological questions, and weed management applications that can be addressed through greater availability of, and access to, genomic resources. Major focus areas include the evolution of herbicide resistance and weedy traits, the development of molecular diagnostics, and the identification of novel targets and approaches for weed management. There is increasing interest in, and need for, weed genomics, and the establishment of the IWGC will provide the necessary global platform for communication and coordination of weed genomics research.
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1 INTRODUCTION

In their 2017 State of the World's Plants report, Royal Botanic Gardens Kew estimated that whole-genome sequences are now available for 225 plant species.[1] Of sequenced vascular plants, 58% were crop species, 18% were crop wild relatives, and 22% were model species and their wild relatives. Clearly, the commercial and societal value of plants for providing food, materials, fiber, energy, and medicinal products has been a major motivating factor in plant genomics efforts. However, it is notable that weeds that compete with crops, and result in an average 30% annual yield loss across several crops,[2] are currently under-represented. Indeed, only four weed genomes have been published to date (not including crops with closely related weed species, see Section 2). Weed genomics also lags behind studies of the genomes of arthropods that are plant pests (> 30 sequenced as of December 2017)[3,4] and plant pathogens (275 sequenced as of May 2017).[5]

The power and potential of weed genomics to provide biological insight into the discovery of new herbicide targets and new weed management approaches have long been recognized. A symposium addressing the potential impacts of biotechnology and genomics for weed science was held at the Weed Science Society of America (WSSA) meeting in Toronto in 2000.[6] Here, various speakers discussed the potential of genomics for discovering new

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herbicide targets,[7] providing insights into weed diversity[8] and for identifying the genetic basis of weedy traits, invasiveness, seed dormancy, allelopathy, biological control, and reproductive characters.[9]

Later, at the WSSA meeting in 2007, an Emerging Technologies Symposium[10] considered how advances in genomics, transcriptomics, proteomics and bioinformatics might be applied to studies of weed biology. This was followed by another WSSA symposium in 2015 on the integration of 'omics' approaches in weed science.[11] Many other researchers have considered the potential of weed molecular biology[12] and weed genomics[13–15] to contribute to advances in basic and applied weed science and have called for the pooling of resources towards a community effort to generate genomic data and resources for major weed species.[16] Detractors of weed genomics argue that existing plant model genomes should be sufficient, but this view is incorrect because there is a great diversity of weedy traits and variation in the evolutionary strategies of weeds that is not represented in wild and domesticated model plants such as *Arabidopsis* and rice.[17] We need reference genomes representing the full diversity of weedy traits and evolutionary strategies. Sustained advances in sequencing technologies exponentially increase the rate at which genome sequence data in non-model organisms can be generated at rapidly diminishing costs. Considering these advances, it is timely to review the aspirations and potential for an international, community-based effort by weed scientists to sequence the genomes of important, global weed species.

Here, we review the global status of weed genomics research, the impacts that new sequencing technologies have on the availability of genomic data from weeds and present the outcomes of several recent international workshops, discussions and surveys that have attempted to visualize a global effort in weed genomics, through the auspices of an International Weed Genomics Consortium (IWGC). Although these efforts remain preliminary, we feel it is timely to present our first efforts to determine global priorities for weed genomics, including major species to be sequenced, biological questions and models to be addressed, and the novel weed management tools, resources, targets, and approaches that may arise from such an effort.

2   THE STATE OF THE ART IN GENOMICS AND WEED GENOMICS

Discovery in genomics is primarily being driven by advances in sequencing technologies. When second (next) generation sequencing was first developed, the cost per base pair plummeted and opened up genomics and transcriptomics[18,19] to non-model organisms. Third-generation sequencing technologies that provide the ability to sequence long DNA molecules (> 5 kb) are highly advantageous for weed genome sequencing efforts.[20,21] The production of longer individual sequences imparts more complete and accurate recapitulation of complex regions of the genome. Reads from third-generation sequencing technologies are long enough to span most repetitive regions (simple sequence repeats [SSRs], tandem DNA arrays, long stretches of homopolymers, low-complexity sequence, repetitive DNA elements, telomeres, etc.) and can therefore resolve these areas and accurately scaffold large contiguous DNA sections (contigs). Previously, short-read-only assemblies (so-called 'shotgun' assemblies) could not resolve complex regions and assemblies remained highly fragmented, regardless of the amount of short-read data used in their generation.[22,23] Highly repetitive, gene-poor regions such as centromeres and telomeres remain difficult to assemble, even with long-read data, and still require other strategies such as Hi-C sequencing, mate-pair sequencing, linkage mapping, and optical mapping to construct sequences for entire chromosomes. Computational assembly algorithms have also advanced to handle hybrid data sets (second and third generation), and can also manage higher numbers of heterozygous sites and the ability to split haplotypes, which is crucial for outcrossing species.[24,25]

Once complete, reference genomes become valuable tools for studying structural variation, DNA rearrangements, association genetics, and polyploid genome evolution.[26] Reference genomes, including non-coding regions, are essential for bridging genomics to weed management by enabling studies to understand evolution, domestication, phylogeny, reproduction, invasiveness, and herbicide resistance in weedy species. In short, technological advancements have drastically enabled genome reconstruction efforts to deliver more complete, contiguous, and accurate genome assemblies for more complex species, which is necessary to deliver on the promise of weed genomics to improve weed management.

Recently, sequencing of complex crop genomes has been completed for multiple species, e.g. sugar beet, quinoa, grain amaranth, millet, and sorghum.[27–31] These results greatly aid efforts to sequence weed genomes because some of these crops, e.g., grain amaranth, foxtail millet, quinoa, and perennial ryegrass, have weedy relatives (Fig. 1). One of the most ambitious recent genomes to be published is the hexaploid wheat genome (15.3 Gb).[32] The wheat sequencing effort makes it clear that almost no genome is out of reach for a dedicated research group.

Despite the increasing ease with which long-read sequence data can be generated and assembled, the genomes of few economically important weed species have been fully sequenced. By contrast, numerous *de novo* transcriptomes have been completed for investigation of herbicide resistance,[33] and weed biology and evolution.[34,35] Weed genome assemblies have been published for *Conyza canadensis* (horseweed),[36] *Echinochloa crus-galli* (barnyardgrass),[37] *Thlaspi arvense* (field pennycress),[38] and *Raphanus raphanistrum* (wild radish).[39] A genome assembly has been published for the perennial grass forage species *Lolium perenne*[40], which is closely related to the weed species *L. rigidum* (annual ryegrass) and *L. perenne* ssp. *multiflorum* (Italian ryegrass). However, these genomes remain fragmented and are not presented as chromosome-scale pseudomolecules, making some types of analysis impossible. Importantly, these projects do not represent the broad diversity of weed species and

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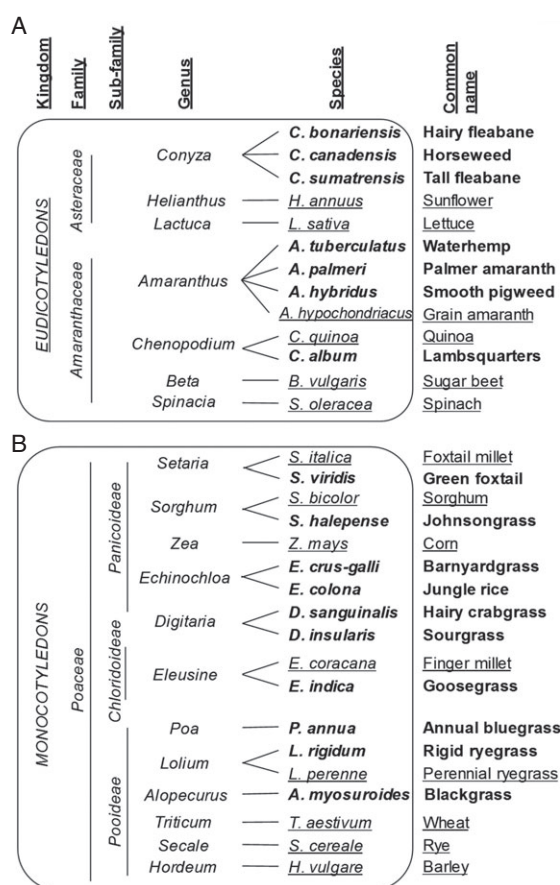
Figure 1. Simplified phylogenetic relationship between selected weed species (bold) and cultivated crops (underlined). Selected weeds that are: (A) eudicots along with important crops, pseudo-cereals, and vegetables; and (B) grass weeds along with cultivated cereal crops.

remain relatively isolated efforts. Currently, several projects are underway to sequence the genomes of additional weed species, including *Amaranthus palmeri* (Palmer amaranth), *A. tuberculatus* (waterhemp), *Echinochloa colona* (junglerice), and *Kochia scoparia* (kochia). These assemblies have not yet been completed or made publicly available. There likely are additional weed genome sequencing efforts underway of which we are not aware. Furthermore, it is very likely that multiple groups are independently sequencing the genomes of the same species, which is an inefficient use of resources and could be better coordinated via the IWGC platform.

Looking forward, several new weed genome sequencing projects will be initiated and the pace at which sequence data become available to weed researchers will accelerate dramatically. Indeed, it may soon be possible for researchers to move beyond sequencing a single individual to embark on pangenomics projects[41] that aim to elucidate gene and genome diversity across a species range, and provide opportunities for studies of the adaptation and eco-evolutionary dynamics of weed populations in specific environments.

3   BUILDING A GLOBAL WEED GENOMICS COMMUNITY

We believe the weed science community is now ready to successfully engage in a community-based approach to weed

genomics through the IWGC. First, advances in sequencing technology have reduced the cost of *de novo* genome assembly such that multiple weed genomes may be successfully completed. Second, a critical mass of interested and motivated scientists from academia and industry have joined together to both drive the genomics effort and utilize the resulting genomics resources. Here, we report on recent efforts to launch the IWGC.

Initially, a 'Grass and weed genomics workshop' held in Prague at the seventh International Weed Science Congress in 2016 (IWSC; http://iwss.info) brought together over 30 weed scientists from academia and industry. This workshop aimed to determine global priorities for weed biology and management, and highlighted the importance of developing weed genomics databases and skills to address those priorities in key weed species. A fundamental output of the workshop was the establishment of an international working group focused on developing weed genomics resources.

Following the IWSC 2016, this working group, which included members from North America, South America, Europe, Africa, Asia and Australia, met at the first official IWGC workshop at Rothamsted Research (UK) in March 2017. The aim of this meeting was to better define the overall effort including the organization, structure, objectives and financing of the consortium. The IWGC concept was then presented to the weed science community during a keynote session at the Global Herbicide Resistance Challenge (GHRC) in Denver in May 2017. A workshop that addressed the question 'how do we bridge the gap between weed genomics and weed management?' was also held at the conference with the intention of identifying key applications of weed genomics and activities of the IWGC (see below). These meetings were followed by an online survey of the weed science community to assess the level of interest in the IWGC concept (see below).

The main objectives of the IWGC are to obtain reference genomes for the most globally important weedy species, to provide open-access to the data, and to offer user-friendly genome analytical tools and training. The expectation is that the IWGC and its associated website will become a central resource not only for a broad array of scientists with diverse areas of expertise and interests around the globe, but will also represent a key platform for stimulating: data sharing; partnerships between academia and industry; collaborations between international research groups; education of the next generation of weed scientists; the transfer of knowledge and experience to developing countries; and an open forum for discussion.

4   FOCAL SPECIES FOR A GLOBAL WEED GENOMICS INITIATIVE

Initial feedback on the IWGC proposal highlighted the importance of careful selection of 'priority' weed species for genome sequencing. A survey circulated among the weed science community following the GHRC addressed this point through two questions. The survey consisted of 245 participants that represented a range of geographic regions and research interests (Figs S1 and S2). Analysis of the distribution of the survey's participants highlighted over-representation of the Americas and Europe, whereas Africa and Asia were clearly under-represented (Fig. S1). Participants were asked to choose three priority species from among a preselected list of 10 species that could be targets for future sequencing efforts, based on the output of previous workshops and discussions, and for which genome assembly projects were not completed or known to be in progress as of March 2017. For example, *Amaranthus palmeri* and *Conyza canadensis* were
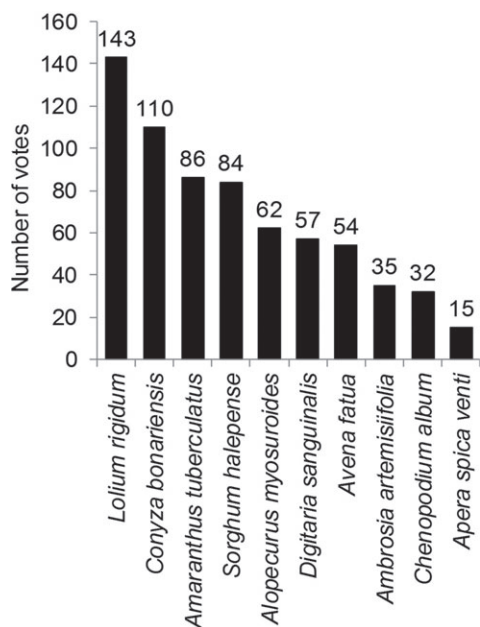
Figure 2. Weeds selected as high-priority species among the preselected species. A list of 10 species was proposed, preselected based on the output of previous workshops and discussions, and for which genome assembly projects were not completed or known to be in progress as of March 2017. For example, *Amaranthus palmeri* and *Conyza canadensis* were not included in the preselected list because their genomes were sequenced or in progress at the time of the survey. Participants were asked to select up to three species. Total number of participants: 245.

not included in the preselected list because their genomes were sequenced or in progress at the time of the survey. As this list of species may not have reflected the needs of the entire community, a second question offered the possibility of nominating two additional unlisted weed species.

In summary, responses to these two questions revealed a consensus towards sequencing weed models within the genera of *Conyza*, *Sorghum*, *Poa*, *Lolium*, *Amaranthus*, *Echinochloa*, and to a lesser extent *Alopecurus*, *Eleusine* and *Digitaria* (Figs 2 and 3). Analysis of preferences based on the 10 listed species (Fig. 2) revealed two species that were globally important: *Lolium rigidum* (rigid ryegrass) and *Conyza bonariensis* (hairy fleabane). A cluster of four species, namely, *Amaranthus tuberculatus* (waterhemp), *Sorghum halepense* (Johnsongrass), *Alopecurus myosuroides* (blackgrass) and *Digitaria sanguinalis* (hairy crabgrass) were viewed as being next in importance. Respondents also identified several additional genera, consisting of multiple target weed species (Fig. 3). Several species appeared in the second list (Fig. 3A) for which genomes are in progress or complete, such as *Amaranthus palmeri* and *Conyza canadensis*, indicating their importance to the North American weed science community and a need for improved communication about the status of genome sequencing projects in weeds.

Fortunately, several of the species identified as being of high priority have closely related crop relatives whose genomes and genome annotations (Fig. 1) will be highly useful for annotating new weed genome assemblies. Additionally, genomes of several of the identified priority species or related species within the same genus are in progress and/or published, including the published *C. canadensis*[36] and *E. crus-galli*[37] genomes and the sequencing of a bacterial artificial chromosome genomic library from *A. palmeri*,[42] with a whole-genome assembly in progress.
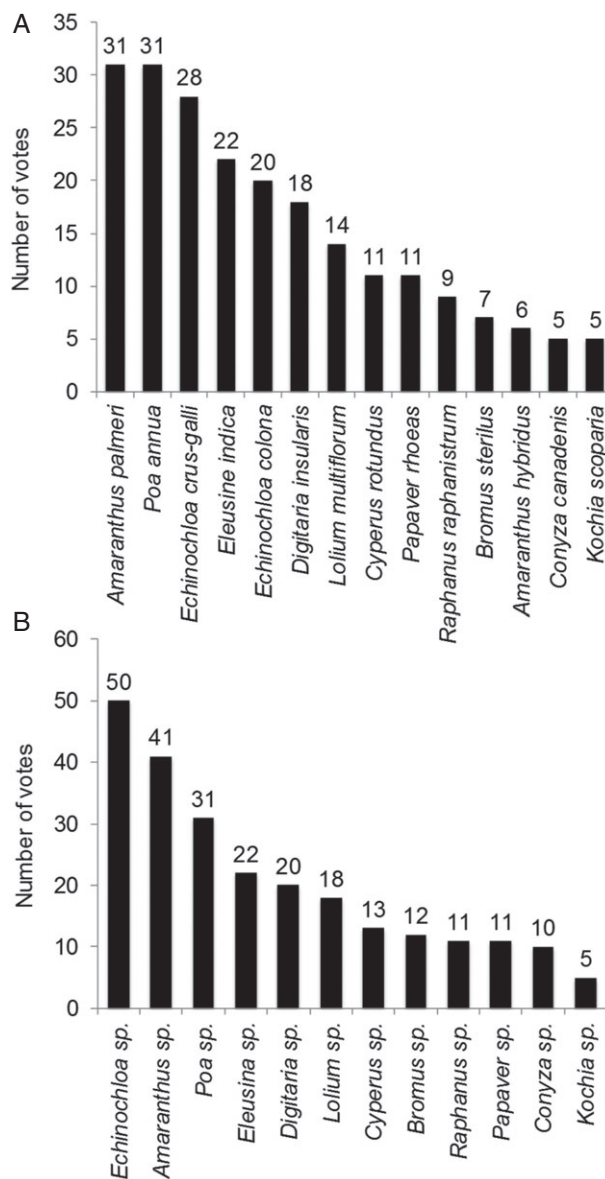

Figure 3. Additional weed species selected as high-priority species. Participants were asked to choose up to two additional species that were not preselected. (A) Highest ranked species and (B) highest ranked species by genus. Several species appear in this list for which genomes are in progress or complete, such as *Amaranthus palmeri* and *Conyza canadensis*, indicating their importance to the weed science community and a need for improved communication about the status of genome sequencing projects in weeds. Species and genera receiving fewer than five votes are not shown. Total number of participants: 245.

5 WEED GENOMICS PROVIDES NOVEL INSIGHTS INTO WEED BIOLOGY

As mentioned above, a workshop was also held at the GHRC to examine and discuss the desired weed biology and management focus for the IWGC. Prior to the workshop, participants were asked to submit up to five biological questions and/or weed management applications in which they thought weed genomics could or should make a significant contribution. In total, 91 responses were submitted (Table S1). These responses were analyzed to identify major emerging themes and areas where potential new insights and advances could be made given access to weed genomics

Figure 4. A word map depicting the frequency that keywords were mentioned when delegates at the weed genomics workshop (Denver, 2017) were asked to identify priority areas for research that informs weed management through increased access to weed genomic resources.

resources (Table S2). From this analysis, several focal areas for weed biology research and weed management application were identified (Fig. 4). These areas are discussed below. Broadly, three areas in which weed genomics can make significant advances were identified: (1) understanding of the fundamental molecular, physiological, genetic, ecological, and evolutionary processes that underlie weed adaptation (basic plant biology); (2) insights into new targets and new approaches for weed management (translational plant science); and (3) management strategies that make weed adaptation (applied evolutionary biology) more difficult, or slower, to evolve.

5.1 Herbicide resistance

To date, our understanding of the molecular basis of herbicide resistance has been largely informed by single-gene sequencing and identification of single-point mutations causing target-site resistance (TSR). More recently, second-generation sequencing technologies have also enabled transcriptomic approaches (e.g., RNA-Seq) to identify candidate genes underlying more complex non-target-site resistance (NTSR) mechanisms, such as herbicide metabolism and translocation. Genomics offers the promise to go beyond transcriptomics to provide further novel insights into the genomic basis of complex resistance traits such as NTSR. For instance, as specific NTSR genes such as cytochrome P450s[43] are identified, researchers will use functional genomics to determine why differential regulation of TSR and NTSR genes occurs (and thus provide insights into regulatory mechanisms), determine what types of mutations produce this adaptive molecular variation (such as copy number variation or changes in gene promoters), and the relationship between a weed's genome and its resistance phenotype. This knowledge will inform the design of specific weed management programs for different types of resistance mechanisms.

Gene expression can be controlled by a variety of mechanisms; however, mutations in *cis* and *trans* regulatory elements and in the transcription factors that bind them can only be understood with genomic tools. Additionally, gene copy number variation (CNV) and the resulting changes in gene expression have been shown repeatedly to underlie herbicide resistance in multiple weed species.[44,45] Genomic and computational resources are essential to answer questions related to CNVs. In addition, epigenetic mechanisms are likely to play an as yet unknown role in herbicide resistance[46] and weed adaptation to changing environmental and

management conditions, yet without genomic resources, all work on epigenetics is currently restricted to model species with reference genomes, such as *Arabidopsis*. Further, research into CNVs and epigenetics will undoubtedly generate new insights into whether herbicide resistance mechanisms are linked to abiotic stress responses, such as tolerance to flooding, drought, heat, cold, or xenobiotics, and thus provide information on how different weed species will respond to changing climate and weed control practices. Such knowledge is key to developing effective and sustainable weed management strategies for the future.

Some important research needs in weed biology and herbicide resistance evolution identified in the GHRC 2017 workshop include: (1) identifying the mechanistic basis and frequency of novel molecular variation in NTSR genes; (2) determining whether NTSR mechanisms are linked to stress responses, such as responses to flooding, drought, heat, or cold tolerance; (3) discovering whether NTSR genes are genetically linked and/or co-regulated with such stress response pathways; (4) asking if pre-adaptation for NTSR occurs in weed populations that are adapted to stressful environments; and (5) determining why enhanced metabolic resistance appears to be relatively common in grass weeds, but relatively less common in broadleaf weeds.

5.2 Weed evolution

Over 60 years ago, Harper (1956)[47] surmised that 'arable weeds constitute an ecological group … that have been selected by the very practices that were originally designed to suppress them'. The relative importance of 'general-purpose' genotypes,[48] phenotypic plasticity and rapid, ongoing adaptation for explaining the prominence of some plant species as agricultural weeds has been the subject of ongoing debate,[48–50] leading to a recognition that weed species may be ideal models for studying adaptation in plants.[51] Given that the evolution of herbicide resistance provides evidence of the importance of, and potential for, rapid weed adaptation, it is also likely that ongoing selection for other weedy traits is a pervasive force that impacts all weed management efforts.

Many weedy traits (including NTSR) have complex genetic architecture, and understanding the evolution of those traits in the face of novel management and environmental challenges requires knowledge of the additive genetic variation that underlies traits and the resulting trait heritability. Approaches based on quantitative genetics and population genomics, including genome-wide association studies and whole-genome diversity scans, can deliver increased power to unravel the genetic basis of complex traits in weeds, their phylogenetic histories, and the demographic and population genetic processes that mediate responses to environment- and management-based selection pressures. These approaches will be enabled by greater access to genomic resources for weed species.

As the costs decline and accessibility increases for genomic data in non-model organisms, many researchers envision that we are rapidly moving towards the age of pangenomics,[41] where genome sequencing efforts focus on multiple individuals and populations to capture the full range of genetic diversity within a species. This may be particularly important for species where understanding adaptation is a major focus (such as weeds), as there is an increasing realization of the importance of gene duplication, genomic rearrangements, and neo-functionalization in rapid plant adaptation to environmental stress.[44,52–54] Although these pangenomics approaches may be a longer-term aspiration for the IWGC, they can only be possible by initial access to reference genomes for key weed species.

5.3 Weedy traits and stress tolerance

Through natural and human-mediated selection, weeds have been and continue to be selected for optimal fitness in agricultural environments. Because weeds are not constrained by conscious breeding efforts that may deliberately select for only a few specific traits, especially related to yield and pest resistance, natural selection acts on a host of weedy traits that make weeds well-adapted to compete with crops. Important weedy traits include prolific seed production causing high rates of population increase, extended seed dormancy, high dispersion rates, adaptive germination traits, abiotic stress tolerance, and competitiveness. Additional weedy traits of high interest for weed management and crop improvement are allelopathy and seed shattering. These life history and resistance traits have been shaped by evolution in response to human and environmental pressures. Identifying and understanding the genetic bases of these traits will be facilitated by access to the genomes of weed species.

Many weed species have high tolerance to abiotic stresses such as drought and flooding, cold, and heat.[55] Identifying the gene(s) responsible for these abiotic stress tolerance traits would open new avenues for crop improvement[56] to breed crops that may, for example, be more resilient to drought and heat stress associated with changing climate. In theory, genes responsible for weedy traits may be incorporated into crop varieties (via introgression if the crop and weed are sexually compatible, or via transgenic approaches where they are not) or the corresponding crop gene may be modified to mimic the function of the weed gene (via genome editing). Although functional genomics in weeds remains at a preliminary stage, genomic resources for weed species developed now will pay large dividends in the years to come.

5.4 Weed taxonomy and identification

Where closely related weed species coexist, and where definitive identification via morphological traits is not possible, genomic resources may play a role in assigning species identity. This may be particularly important in instances where control options and efficacies differ between closely related weed species and where hybrid complexes between co-occurring species have been reported. For example, two related aquatic plant species of the *Myriophyllum* genus, and their hybrid, were distinguished using three Kompetitive Allele-specific PCR (KASP) markers.[57] Molecular diagnostics may also enable confirmation of species identity where novel invasions of weed species beyond their normal range are suspected. One example used species diagnostic KASP markers to confirm the recent invasion into Brazil of populations of *A. palmeri*, distinguishing this species from the complex of other weedy *Amaranthus* species previously documented in Brazil.[58] Increasing access to genomic resources and sequence data for closely related weed species will continue to enable and inform these efforts.

5.5 Weed dispersal and gene flow

Elucidating the spatial dynamics of weed dispersal (via seed, fruits, and propagules) and gene flow (via seed and pollen) is important for understanding the evolution and spread of weeds and weedy traits. This knowledge can, in turn, inform the design of effective weed management strategies that limit seed production and/or movement locally and/or over larger, continental areas. Where dispersal is limited, weed management interventions can be planned and implemented at a local (field to farm) scale, whereas for highly mobile species, studies over large areas and integrated approaches may be warranted. The degree to which the evolution and spread of herbicide resistance over large distances is determined by multiple independent evolutionary events versus rarer, isolated events with subsequent spread remains incompletely understood, and likely varies for different resistance traits and species.[59] Studies to quantify the dispersal of herbicide resistance alleles have used a variety of methods. Manipulative field experiments[60,61] and field observations of gene flow between herbicide-resistant and -susceptible crop varieties have been conducted.[62] Population genetics analyses have used the sequence and/or frequency of herbicide target genes,[63] amplified fragment length polymorphism (AFLP) markers[64] and microsatellites/simple sequence repeats.[65,66]

With access to less expensive sequencing technologies, it becomes possible to generate orders of magnitude more data (tens of thousands of markers) for genotyping-by-sequencing and population genomics studies.[67] These approaches will significantly increase the power to determine genetic structure, and associated gene flow and dispersal processes in weed populations. Associated with this, the greater genome coverage achieved provides extra power to determine the areas of the genome that are under selection at landscape scales in weed populations, not just for resistance to herbicides, but for weedy traits in general.

A related issue that has elicited much discussion within the weed science community has been the potential for 'transgene escape' via introgression of transgenic crops and their weedy relatives. Several mitigation strategies have been proposed, which link crop protection traits with other traits that will lower the fitness of weedy populations should introgression occur.[68] Increased access to weed genomes will facilitate efforts to identify candidate 'fitness-reducing' traits that can be coupled with crop protection traits in tandem constructs.

6 WEED GENOMICS FOR NOVEL AND IMPROVED WEED MANAGEMENT

6.1 Resistance diagnostics

Understanding the underlying genetic basis of herbicide resistance mechanisms and the development of diagnostic methods for those genetic traits is one immediate practical application of weed genomics. Information on the presence and frequency of herbicide resistance is most valuable when available prior to planning and making herbicide applications. Most current diagnostic procedures use either polymerase chain reaction (PCR)-based assays to genotype for known TSR mutations, and/or directly measure herbicide metabolism using analytical procedures.[69] These current diagnostics can be improved (made faster and less expensive) once the molecular variation underlying NTSR is known, i.e., specific mutations in regulatory regions or other functional molecular variants detected using PCR. PCR-based methods for resistance diagnostics would preferably be DNA-based, as DNA is less expensive to extract and easier to manipulate for diagnostics than RNA. Without a full understanding of intron/exon and promoter structure of a gene, as would be possible with weed genomic resources, these DNA-based methods can only rely on inferences from closely related species.

Some resistance mechanisms may be amenable for protein-based detection methods using antibodies (TSR or NTSR protein overexpression). Such methods would work for mechanisms in which the abundance of a given protein (e.g., a cytochrome P450) is much higher in a resistant plant than in a susceptible plant. Antibody-based detection methods can be

adapted to field applications because a leaf can be crushed in buffer and the extraction applied to a strip or column containing the antibody for rapid detection and visualization.

It must be emphasized that DNA- and protein-based diagnostic methods are necessarily specific to known mutations and mechanisms. If a weed population carries an unidentified mechanism that is not tested for in the assay, the diagnosis would produce the false result of herbicide sensitivity. Biological diagnostic assays, which are independent of mechanism, are better at avoiding false results but typically require more time. The RISQ assay[70] is a current leading example of a cost-effective test that can be easily employed for a result within ∼ 2 weeks, but necessary seeds or seedlings are not available at all times of year. A major challenge for resistance diagnostics in the years ahead is to develop simple, inexpensive, and robust molecular diagnostics that encompass all known mechanisms while somehow addressing the potential for as yet unknown mechanisms.

6.2   New targets for weed control
New herbicides are being discovered at a slowing pace and no new modes of action have been marketed in more than 30 years.[71] When new candidate molecules are found, they may not be brought to market for a range of reasons such as insufficient efficacy, narrow range of usefulness, non-selectivity, inappropriate residual activity, and/or mammalian toxicity.[72] Weed genomics can contribute to new herbicide discovery by helping to: (1) identify the mode of action of new compounds with unknown targets using sequence-based approaches; (2) discover the target proteins of existing modes of action for which all molecular targets are not yet known (e.g., synthetic auxins, cellulose biosynthesis inhibitors); and (3) design the chemical structure of candidate inhibitors based on potential new molecular targets discovered in the genome. It should be noted that having genomic sequence is no guarantee of finding new herbicide targets. Gene knockout approaches for chemical discovery have been attempted using *Arabidopsis* by the chemical discovery industry, but no commercial products with new target sites have reached the market from this approach.[71] Gene knockdown may be more promising to identify novel targets because no chemical herbicide completely inhibits a target. Plant death often results from toxic substrates or products that accumulate when a target is inhibited. We anticipate that having the gene sequences of economically important weeds may aid in identifying novel protein targets. Molecules inhibiting the specific enzyme in weeds could be developed and tested. Novel molecular targets may be discovered through computational approaches using the sequences of all expressed genes available from transcriptomes and genomes. Additionally, candidate molecules from other crop protection or medical sectors with known targets could be evaluated against plant targets using complete proteomes available from weed genomes, as has been conducted for antimalarial drugs as candidate herbicides using *Arabidopsis* as a model.[73,74]

Potentially disruptive technologies such as RNAi and gene drive may provide new tools for weed management with facilitation by weed genomics. RNAi targets could function as herbicide synergists, and/or as stand-alone herbicides, depending on the efficiency of transcript silencing that can be achieved.[75] Gene drive technology[76] could be employed to reverse herbicide resistance or to spread deleterious mutations through weed populations that impact reproductive success, competitiveness or other fitness-related traits. The more complete understanding of herbicide resistance mechanisms expected to result from weed genomics could also be utilized to discover and develop chemical

synergists to reverse and/or down-regulate resistance mechanisms. Finally, the discovery of novel herbicide resistance mechanisms that have evolved in weeds can be used to develop new herbicide resistance traits in crops through targeted gene editing.

6.3   Proactive resistance management
The potential for weed genomics to provide additional insight and understanding for resistance management featured heavily in responses and discussions among delegates at the 2017 GHRC conference. In the word cloud depicted in Fig. 4, we distinguish participant responses between the general category of resistance management, and responses specifically recognizing the potential for weed genomic resources to enable more predictive or proactive approaches. In general, proactive resistance management would be facilitated by access to resistance diagnostics and through the identification of novel targets for weed control, which would enable more diverse weed management strategies and moderate selection pressures by reducing reliance on current weed management tools. As these aspects have been discussed above, here we focus on application for proactive resistance management.

Access to comprehensive genome sequences for major global weeds will result in increased efforts to elucidate the herbicide- and stress-responsive pathways that are involved in NTSR. With this insight, it should be possible to gain a better understanding of the relative risks of resistance evolution prior to, or during, the early stages of selection for NTSR. Further, such insights would motivate pre-emptive studies that assess risks of resistance to new herbicides, and even new modes of action. They may also help to answer longstanding and recalcitrant questions about why some weed species are more prone to the rapid evolution of resistance than others. Increased knowledge of the underlying molecular genetic mechanisms of NTSR can inform questions about the molecular basis of cross-resistance patterns, and the repeatability and genetic convergence of evolutionary outcomes.[59] This understanding will inform the rational design of herbicide mixture and rotation strategies to ensure that these do not promote the use of herbicides with cross-resistance NTSR mechanisms. Armed with this basic knowledge, it will be possible to improve the design, testing and implementation of proactive resistance management strategies.

6.4   New traits for crop improvement and crop/weed comparative genomics
Despite the continuous advances made in crop breeding, projection models of crop production suggest a progressive decline in yield for most major crops, which threatens food security globally.[54] There are two main reasons for these predictions. First, breeders have long focused on producing phenotypically, and thus genetically, uniform crop cultivars with specific plant traits, which has led to significant losses in genetic diversity (i.e., genetic erosion).[77] Second, modern varieties have been selected based on their performance in a specific climate and are generally locally adapted as a result. Fluctuations in the environment can result in dramatic crop yield loss, and thus global climate change will significantly impact crop production.

Agricultural weeds and wild relatives of crops are re-emerging as promising sources of genetic diversity for crop improvement.[54] As previously mentioned, many traits increasing weed competitiveness are unknown, and most of the physiological characteristics associated with weed fitness, other than herbicide resistance, have

an unknown genetic basis. Understanding the genetic mechanisms underlying the physiological processes that make weedy species so competitive in agriculture settings will provide new genetic resources for developing new crop cultivars that can out-compete weeds and produce significant crop yields under various climatic scenarios. Among the most interesting traits are developmental traits improving plant biomass production and seed yield, and stress tolerance traits enhancing plant adaptation to environmental challenges.

As an example, the cultivated rice/weedy rice system represents an excellent model for crop/weed comparative genomics because the species belong to the same genus, a high-quality and fully annotated reference genome is available, and many cultivated rice cultivars and wild relatives have been sequenced. Re-sequencing of several rice and weedy rice accessions from China demonstrated that Chinese weedy rice was the result of de-domestication of cultivated rice through exoferality.[78] Using a similar approach, 38 weedy rice accessions from the United States were re-sequenced and compared with > 100 previously sequenced rice genomes, including weedy rice accessions from China.[79] Such work provided insights into evolutionary processes responsible for weedy traits in rice and identified genomic regions that could be used for crop improvement.[80] Importantly, with the more robust genomic tools in rice, we can now detect the difference between exoferal (derived from crop-wild relative hybridization) and endoferal (escaped crop genotypes) weeds.[81,82] Through comparative genomics analyses of exo- and endoferal weedy rice, we can now discover quantitative genetic differences in weedy versus domesticated traits and how population structure may modulate these differences in the field.

7 DELIVERING AN INTERNATIONAL WEED GENOMICS CONSORTIUM

To reach its full potential, weed genomics must connect communities from diverse disciplines of biology such as weed science, plant genetics, molecular physiology, evolution, and ecology. The IWGC is moving forward with members from across these disciplines and plans to initiate the envisaged genome sequencing, website, and training initiatives. Annotated genomes at chromosome-scale assembly will be released in a user-friendly database environment. To provide a platform for community engagement with the IWGC, we have established a discussion forum at Plantae (www.plantae.org), a free online resource for the plant science community. Interested readers are invited to register with Plantae and join the conversation at https://community.plantae.org/discussion/48960691111202710923/international-weed-genomics-consortium. The weed genomics website developed by Scott McElroy, www.weedgenomics.org, may be further developed into the online weed genomics resource for the IWGC, based in part on other successful genome initiatives such as www.rosaceae.org. The weed genomics website will provide genome browsers, searching capability, comparative and diversity genomics tools, and visualization of gene expression and genotyping data sets. The website will also provide a platform for IWGC training in bioinformatics.

SUPPORTING INFORMATION

Supporting information may be found in the online version of this article.

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