Global Trends in Plant Genomics Research to Improve Crop Productivity at PAG XXIV Conference

Shadi Rahimi¹, Kwon-Kyoo Kang^{2*}, Yong-Gu Cho^{1*}

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Horticulture, Hankyong National University, Anseong 17579, Korea

ABSTRACT Increasing demand for food commodities and energy supply highlight the necessity to further improve crop productivity. At the Plant and Animal Genome Conference (PAG XXIV), recent developments and future plans for genomics research of plants and animals were presented. PAG XXIV provided a forum to explore crop genomes with the aim of providing new opportunities for crop breeding and the foundation for functional genomic studies to improve agriculture production and help feed the growing population. Genetic diversity and population structure studies of crops have allowed us to explore alleles related to different characteristics important for plant breeding. Several useful databases were introduced in PAG XXIV. They were developed to integrate a growing set of commonly used data types and analysis tools with new capabilities for visualization, exploration, and predictive analysis. This review highlights the global trends in plant genomics presented at PAG XXIV by focusing on crop productivity.

Keywords PAG XXIV, Plant, Genomics, Biomass, Grain yield, Abiotic stress

INTRODUCTION

Global human population is expected to exceed 9.6 billion by 2055. To meet the increasing demand for food commodities, crop productivity in sustainable agricultural systems must be improved considerably to face changing climates and increasing biotic and abiotic stresses. Achieving this will require holistic and systematic approaches by combining a wide range of disciplines including agronomy, physiology, genomics, genetics, breeding, physics, and modeling. The key to successful breeding programs for crop improvement is to understand the extent of genetic variations among crops. Advances in sequencing and data analysis techniques have greatly improved our ability to dissect and mine genomes for specific genes underlying significant traits and allelic variations.

Environmental stresses are the most serious factors limiting the productivity of agricultural crops. Recent

studies have linked increased frequency of severe abiotic stress events to global warming, emphasizing the urgent need to develop crops with enhanced tolerance to abiotic stresses. Abiotic stress tolerance is particularly important for crop productions because they must be grown under low-input conditions to maximize net carbon ratio or on marginal land to minimize competition with food crops (Sade *et al.* 2016).

The Plant and Animal Genome Conference (PAG XXIV) provided a forum on recent developments and future plans for plant and animal genome projects. Consisting of technical presentations, poster sessions, exhibits and workshops, the conference provided an excellent opportunity to exchange ideas and applications on this internationally important genome project. PAG XXIV opened avenues for understanding aspects of plant biology such as plant responses to environmental stresses, plant-pathogen interactions, and trait improvement. This review summarized the new trends in plant genomics with focus on crop

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***Corresponding authors** Kwon-Kyoo Kang, kykang@hknu.ac.kr, Tel: +82-31-670-5104, Fax: +82-31-670-5109

Yong-Gu Cho, ygcho@cbnu.ac.kr, Tel: +82-43-261-2514, Fax: +82-43-273-2242

*These authors contributed equally to this paper as co-corresponding authors.

Table 1. The databases were introduced in PAG XXIV.

Name	Source	Website	Description	Reference
Plant Reactome database	Model and crop plant species	http://plantreactome.gramene.org/	Gene products, small molecules and macromolecular interactions into reactions and pathways in context of their subcellular location	Jaiswal <i>et al.</i> 2016b
KBase	Microbes, fungal, and plant genomes	http://kbase.us	Metabolic models of specific microbes, fungal, and plant genomes and their interactions, to understand plant microbial and mycorrhizal interactions	Kumari <i>et al.</i> 2016
Plant Wikipathways portal	Plants	http://www.wikipathways.org/index.php/Portal:Plants	Rice stress-response gene-network	Naithani <i>et al.</i> 2016a
DNA polymorphism annotation database (DNApod)	Plants and crops	http://tga.nig.ac.jp/dnapod/	Integration of SRA-driven genotypic data and public phenotypic data	Mochizuki <i>et al.</i> 2016
DNA Data Bank of Japan		http://www.ddbj.nig.ac.jp	Public data center of nucleotide sequences established at the National Institute of Genetics	Kodama <i>et al.</i> 2016
Araport	Arabidopsis	https://www.araport.org	Access to a new generation web-based data platform	Chan <i>et al.</i> 2016
Ensembl Genomes	Farm animals and crop plants, from pests, pathogens and pollinators and symbionts	http://ensemblgenomes.org	Genome-scale data, covering bacteria, protists, fungi, plants and invertebrate metazoa, supplementing the coverage of vertebrate species	Kersey 2016
Plant Genome DataBase Japan	Plants	http://pgdbj.jp/en/	Access information extracted from many plant genome-related databases	Ichihara <i>et al.</i> 2016
HRGRN	Arabidopsis	http://plantgm.noble.org/hrgm/	Model and decipher Arabidopsis signaling transduction, metabolism and gene regulation networks using graph theory	Dai and Zhao 2016
PeanutBase	Peanut	http://peanutbase.org	Genome browsers, genetic map viewers, sequence search tools, and a database of traits and QTLs	Cannon <i>et al.</i> 2016
Cool Season Food Legume Genome Database	Pea, Lentil, Faba Bean and Chickpea	http://www.coolseasonfoodlegume.org	Genetic maps, molecular markers, and QTL data	Humann <i>et al.</i> 2016
LegumeIP	Legume	http://plantgm.noble.org/LegumeIP/	A web-based comparative genomics and gene expression atlas platform that integrates large-scale genomics, transcriptomics data and bioinformatics tools	Li <i>et al.</i> 2016
LIS ²⁾	Common bean, chickpea, pigeonpea, Medicago truncatula, Lotus japonicus, mungbean, soybean, and two Arachis species	http://legumeinfo.org	A resource for trait genetics and comparative genomics for nine species of legumes including	Dash <i>et al.</i> 2016
FragariaCyc	Strawberry	http://pathways.cgrb.oregonstate.edu/pgdb/fragariacyc.shtml	A metabolic pathway network for diploid strawberry <i>Fragaria vesca</i>	Naithani <i>et al.</i> 2016b
Intronless Genes Database	Sorghum bicolor, Zea mays, Setaria italica, Panicum virgatum and Brachypodium distachyon	http://pigd.ahau.edu.cn/	A database for intronless genes in the Poaceae	Fan 2016
Phytozome	Plants	http://www.phytozome.net	Gene family construction and analysis	Phillips <i>et al.</i> 2016
Plant Omics Data Center	<i>Nicotiana tabacum</i> , <i>Zea mays</i> , <i>Arabidopsis thaliana</i> , <i>Solanum lycopersicum</i> , <i>Solanum tuberosum</i> , <i>Oryza sativa</i> , <i>Sorghum bicolor</i> , <i>Vitis vinifera</i> , <i>Medicago truncatula</i> , and <i>Glycine max</i>	http://bioinf.mind.meiji.ac.jp/podc/	An integrated web repository for interspecies gene expression networks with NLP-based curation	Terashima <i>et al.</i> 2016
Planteome initiative	Plants	http://www.planteome.org	A resource for common reference ontologies and applications for plant biology	Jaiswal <i>et al.</i> 2016a
Online Resource for Community Annotation of Eukaryotes	Eukaryotes	http://bioinformatics.psb.ugent.be/orca/	Online resource for community annotation of Eukaryotes	Sterck <i>et al.</i> 2016
GSP	Polyploids	http://probes.pw.usda.gov/GSP	A web-based platform for designing genome-specific primers in polyploids	Gu <i>et al.</i> 2016

²⁾LIS: legume information system; GSP: genome-specific primers; SRA: sequence read archive; QTL: quantitative trait loci; NLP: natural language programming.

productivity and biomass increase that were introduced in PAG XXIV. In addition, several useful databases were revealed in PAG XXIV. They were developed to integrate a growing set of commonly used data types and analysis tools with new capabilities for visualization, exploration, and predictive analysis (Table 1) (Cannon *et al.* 2016; Chan *et al.* 2016; Dai and Zhao 2016; Dash *et al.* 2016; Fan 2016; Gu *et al.* 2016; Humann *et al.* 2016; Ichihara *et al.* 2016; Jaiswal *et al.* 2016a, 2016b; Kersey 2016; Kodama *et al.* 2016; Kumari *et al.* 2016; Li *et al.* 2016; Mochizuki *et al.* 2016; Naithani *et al.* 2016a, 2016b; Phillips *et al.* 2016; Sterck *et al.* 2016; Terashima *et al.* 2016).

FLOWERING TIME VS. BIOMASS

Flowering time is one key factor that affects the biomass yield as delaying flowering time can prolong the period of vegetative growth, which in turn can increase the biomass. However, delayed flowering also increases susceptibility to winter mortality, thus decreasing productivity in following years. Therefore, understanding flowering time regulation in crops will be helpful to improve biomass yield. Genetic variations associated with flowering time and plant biomass have provided important bases for identifying quantitative trait loci (QTLs) in switchgrass (*Panicum virgatum* L.) that is important for cellulosic biofuel production (Taylor *et al.* 2016). To decipher natural allelic variations responsible for biomass yield and quality traits, a Nested Association Mapping population of switchgrass has been developed (Ali *et al.* 2016). Exome-capture genotyping over one million single nucleotide polymorphisms (SNPs) in switchgrass individuals has been used to identify their associations with heading date measured over three years (Grabowski *et al.* 2016). SNP variation studies have revealed a non-conservative amino acid substitution located in a protein-arginine deiminase domain in Phytochrome B (a photoperiod responsive gene) in correlation with flowering time phenotypes (Bahri *et al.* 2016).

The two major external stimuli used by temperate cereals to coordinate flowering are temperature and light through vernalization and photoperiod pathways (Shaw *et*

al. 2016). These pathways converge on Flowering Locus T1 (FT1). FT belongs to small multigene phosphatidyl ethanolamine-binding protein (PEBP) family (Shaw *et al.* 2016). There are six FT-like members in wheat. While data suggests that *FT1* is a key gene in the induction of flowering, its deletion has resulted in delayed flowering for less than one month, suggesting that other *FT-like* genes may have overlapping functions (Shaw *et al.* 2016). *FT2* homologs have been characterized in temperate grass *Brachypodium distachyon*, barley, and wheat (Shaw *et al.* 2016). It has been found that *FT2* is not essential for flowering. However, it does contribute to the promotion of flowering in both *Brachypodium* and wheat (Shaw *et al.* 2016). It was also found that *FT2* gene expression profiles are different from those of *FT1*, suggesting that these two genes may have independent roles in the regulation of flowering in temperate cereals (Shaw *et al.* 2016).

Wheat cultivars exposed to optimal photoperiod and vernalization treatments still exhibit differences in heading time (Alvarez *et al.* 2016). This variation, known as earliness per se (*Eps*), is important for fine-tuning flowering time and the adaptation to different environments (Alvarez *et al.* 2016). It has been previously found that the *Eps-A^m1* locus in *Triticum monococcum* can significantly delay flowering while increasing the number of spikelets per spike (Alvarez *et al.* 2016). However, wheat ortholog of circadian clock regulator *EARLY FLOWERING 3 (ELF3)* is different from the previous *Eps-A^m1* allele in four amino acids associated with altered transcription profiles of *PIF-like*, *PPD1*, and *FT1*, the downstream targets of *ELF3* (Alvarez *et al.* 2016).

FLOWERING LOCUS M (FLM) has been recently described as an important regulator of ambient temperature-regulated flowering (Lutz 2016). It has been proposed that modulation of *FLM* abundance is an important mechanism for the adaptation of plants and flowering to changing ambient temperatures (Lutz 2016). Therefore, elucidating the genetic control of flowering time should help breeding efforts and the development of resources to enhance the adaptabilities and yield potentials of crops.

GRAIN YIELD

Grain yield and quality traits are key contributors to the amount of usable energy available as food and feeds. High grain yield is one of the most important traits that require improvement in rice breeding programs. The genetic basis of spikelets per panicle (SPP) and grain weight (TGW) could be used to determine grain yield of rice. Both *qSPP6* and *qTGW6* alleles are involved in the improvement of rice yields (Ahn *et al.* 2016). In addition, inflorescence architecture has been proposed as a key agronomical factor determining grain yield (Zhu and Sun 2016).

Wheat is one of the most important crops worldwide. In recent years, there has been significant interest in improving this crop to meet current and future global demands. Therefore, increasing sink strength of the spike is crucial for wheat breeding. Guo *et al.* (2016) have suggested that *VRN*, *Ppd*, *FT*, *Rht*, and *Q* genes are involved in the regulation of assimilate distribution among competing plant parts, supporting that manipulating assimilate partitioning is an important strategy to improve grain yield of wheat.

Bread wheat (*T. aestivum*) is an allohexaploid (AABBDD) with a large (17 Gb) genome. Mapping efforts have been underway for many years. Wheat breeders have considered grain protein concentration as the principal trait of interest to wheat producers. A genome-wide association study has found several putative loci associated with grain protein concentration on chromosomes 2A, 4A, and 2D (Dao *et al.* 2016). Whereas, several putative loci associated with test weight on chromosomes 1B, 2B, 3B, and 4B (Dao *et al.* 2016).

The starchy endosperm of wheat kernel is a major source of carbohydrates worldwide (Schönhofen *et al.* 2016). Starches with higher proportions of amylose will have higher content of resistant starch, a fermentable dietary fiber that can provide health benefits. A strategy to increase the levels of resistant starch is to pyramid mutations in *STARCH BRANCHING ENZYME II (SBEII)* isoforms *SBEIIa* and *SBEIIb* in the three homoeologs present in A, B, and D genomes of common wheat (Schönhofen *et al.* 2016). Quintuple mutant line (mutated *SBEIIa/b* in A and B genomes, and *SBEIIa* in D genome) has significant

differences in starch viscosity parameters (Schönhofen *et al.* 2016). The release of common wheat germplasm combining five *SBEII* mutations is expected to expedite the development of varieties with increased amylose and resistant starch contents (Schönhofen *et al.* 2016). Thus, studies on compositional grain traits can help crop breeders to increase grain yield and improve grain quality.

PHOTOSYNTHESIS VS. BIOMASS

Different aspects of plant biomass provide important feedstocks for energy production, providing a promising solution to sustainable energy challenge in the 21st century. Sugarcane has a C4-type of metabolism for carbon fixation, allowing it to produce enormous amounts of biomass in tropical and subtropical regions. Genetic improvement of photosynthetic efficiency can be theoretically achieved by targeting higher photosynthetic rates/unit of leaf area and by developing the most photosynthetically effective canopy (Kannan *et al.* 2016). Recent modeling work has indicated that the C4 photosynthetic machinery could be currently limited by inadequate pyruvate orthophosphate dikinase (PPDK) levels (Kannan *et al.* 2016). Field performance of transgenic sugarcane with reduced chlorophyll content, altered chloroplast size and elevated levels of PPDK has been examined using RNAi suppression of candidate genes to enhance light transmission into the canopy and PPDK level (Kannan *et al.* 2016).

Both leaf and seed starch biosynthesis are important for cereal crop yields. Carbohydrates are stored transiently as starch in leaves and as starch in seeds in long term (Oiestad *et al.* 2016). Adenosine diphosphate (ADP)-glucose pyrophosphorylase (AGP) is the rate-limiting step in starch biosynthesis (Oiestad *et al.* 2016). Enhanced rice growth and whole plant metabolism have been found to be conferred by increased leaf and seed AGP activity through overexpressing leaf and seed AGP (Oiestad *et al.* 2016). Artificial microRNA (amiR) strategy to silence NADP-malic enzyme family in *Arabidopsis thaliana* has been used to manipulate carbon flow to impact plant biomass (Paoli *et al.* 2016). Taken together, managing carbon flow within plant metabolism could improve

different aspects of biomass feedstocks, thus advancing current plant capabilities for fiber and fuel production.

LIGNIFICATION AND BIOMASS

Ideal feedstock needs to produce biomass in high amounts while maintaining the quality. This is directly linked to cell wall composition (Yanagui *et al.* 2016). Energy cane is a high-biomass dedicated crop selected during the Saccharum breeding program to fit particular industrial needs of 2G bioethanol production (Yanagui *et al.* 2016). Transcriptional profile of elongating energy cane internode has revealed insights about vascular bundle lignification. The expression profiles of lignification genes have a gradient pattern, with higher expression in sections having complete lignified vascular bundles compared to sections without lignifications (Yanagui *et al.* 2016).

Grasses cover approximately 20% of terrestrial land provides 50% of human calories. When dried, secondary cell walls (SCW) are the bulk of grass biomass. Therefore, genome-scale network analysis has been used to identify rice SCW associated regulators that can control SCW biosynthesis in grasses to improve fuel, feed, and fiber production (Zhao *et al.* 2016).

PLANT-ASSOCIATED MICROBES

One approach in developing sustainable agriculture techniques is to utilize plant-associated microbes for plant growth promotion, biological nitrogen fixation, or biocontrol. Bacteria have been isolated from the rhizosphere and endophytic compartments of *A. thaliana* and the effect of these isolates on *Setaria viridis* plant health has been evaluated under various nutrient starvation stresses, especially phosphate starvation stress (Mucyn 2016). Symbiosis with microbial endophytes can enhance nitrogen fixation, confer drought tolerance, reduce reactive oxygen species, increase plant growth, and improve photosynthetic parameters during drought stress in hybrid poplars (Doty *et al.* 2016).

Populations of bacterial endophytes have been identified

within *Miscanthus* that can be grown on low grade land with minimal requirements (Cope-Selby *et al.* 2016). The most diverse population of endophytes has been found in the seedling (Cope-Selby *et al.* 2016). Therefore, vertical transmission through seed has been suggested as an important process for sustaining bacterial endophytes in *Miscanthus* with potential of sustainable crop production (Cope-Selby *et al.* 2016).

BIOTIC AND ABIOTIC STRESSES

Exposure of crops to environmental stresses threatens agricultural sustainability (Hendrickson *et al.* 2016). Accordingly, new tools are needed to improve their tolerance to environmental stress to ensure long-term sustainability in crop production (Hendrickson *et al.* 2016). Alternative splicing (AS) of precursor messenger RNAs is a widespread phenomenon in plants. Approximately 42% to 61% of intron-containing genes exhibit AS (Filichkin *et al.* 2016). Differential intron retention has been identified as a key component in AS-driven adaptation to osmotic (dehydration or high salinity) and thermal stresses (heat or cold) in the transcriptome of western poplar (*Populus trichocarpa*) (Filichkin *et al.* 2016).

There are two major ecotypes of switchgrass: 1) the one originates from the lowland of the southern east coastal region of the United States, and 2) the one originates from the upland the northern regions of the United States. Late-flowering lowland varieties have the potential to be more productive than adapted upland varieties in the north. However, they are more susceptible to winter damage. Therefore, it would be desirable to combine the late-flowering lowland trait with the adaptation traits of upland varieties (Tornqvist *et al.* 2016). Lowland ecotypes are typically favorable due to their high biomass yield and tolerance to heat and drought. In some areas, the upland ecotypes are favored due to their adaptability to cold conditions. Genome wide methylated DNA immunoprecipitation-sequencing has revealed higher methylation level in AP13 of lowland than that in VS16 of upland (Crampton *et al.* 2016). Transcriptome analysis has identified genes involved in stress responses to drought, heat, flooding,

salinity, or pathogen. RNA binding proteins, Mei2-like, pumilio, and RNA recognition motif (RRM) domain containing proteins have been implicated in post-transcriptional gene regulation (Fiedler *et al.* 2016).

Plants have an internal clock that mediates almost all daily activities and coordinates internal molecular responses with the environment. Interestingly, day-dependent responses to abiotic stress have been shown in *Oryza sativa* (Desai 2016).

Aquaporin (AQP) genes are responsible for water transportation in plants. Their functions are to transport water and nutrient molecules through living membranes. They might be essential for survival under salt and drought stresses. Differential expression profiles of 22 members of the *BrPIP* subfamily against biotic and abiotic stresses have provided a basis to elucidate stress-related biological functions of specific *PIP* genes in abiotic and biotic stress tolerance in *Brassica rapa* (Kayum *et al.* 2016).

Histone deacetylases (HDACs) are important regulators of chromatin structure and function (Hayford *et al.* 2016). HDACs have been found to play key roles in plant developmental processes (Hayford *et al.* 2016). They also respond to environmental cues (Hayford *et al.* 2016). For example, *Arabidopsis HDA6* can regulate transcription of ribosomal RNA and play a role in cold acclimation (Hayford *et al.* 2016). Up-regulation of *HDA6* in common bean is age dependent (seedling > flowering > maturity). Spatial distribution analysis has revealed more *HDA6* transcripts in flowers and pods. Accordingly, a crucial role of *HDA6* in the growth and development of common beans has been proposed (Hayford *et al.* 2016). In addition, *HDA6* also appears to be involved in cold response (Hayford *et al.* 2016).

TIFY family novel plant-specific group of genes have been widely reported for their important functions related to biological processes such as plant development and responses to stress and hormone in different crop species. A total of 36 *TIFY* genes have been characterized and classified under four subfamilies (JAZ, TIFY, ZML, and PPD) in *B. rapa* (Saha *et al.* 2016). Among them, nine *JAZs* have been shown to be differentially up-regulated against cold stress and jasmonic acid treatment (Saha *et al.* 2016). *BrTIFY3a*, *3b*, *6a*, *9a*, *9b*, and *9c* have been shown to have

corresponsive expression against salt, drought, *Fusarium*, ABA, and SA treatment, respectively (Saha *et al.* 2016).

One of the most severe pathogens that threaten wheat production worldwide is stripe rust caused by *Puccinia striiformis* f. sp. *Tritici* (Nazarov 2016). Genetic resistance to rust has been proven to be the most economically efficient method to control this pathogen (Nazarov 2016). High temperature adult plant resistance (HTAP) has been previously reported as a promising trait that can grant resistance to a broad range of stripe rust pathogens with high level of resistance, especially in warm climatic conditions (Nazarov 2016). A novel HTAP locus has been reported in wheat after performing further synteny analysis utilizing wheat SNP database followed by target amplifications and restriction essays, leading to the mapping of polymorphic marker of HTAP locus on the short arm of chromosome 2B (Nazarov 2016). In addition, the suppressor of *rps4-RLD 1 (SRFR1)* has been identified as a negative regulator of effector triggered immunity against bacterial pathogen *Pseudomonas syringae* pv (Nguyen *et al.* 2016). Recessive *srfr1* mutation in tomato has been found to be able to confer *enhanced disease susceptibility1 (EDS1)* dependent resistance to DC3000 (avrRps4) in *Arabidopsis* leaves (Nguyen *et al.* 2016). In addition, *srfr1-1* plants have increased resistance to herbivory by beet army worm *Spodoptera exigua* and parasitism by cyst nematode *Heterodera schachtii* (Nguyen *et al.* 2016).

B. rapa cysteine protease 3 (CP3) is an endopeptidase member of C1A family (papain-like) and CA clan of cysteine protease (Niño *et al.* 2016). Members of papain-like CP have emerged to be key enzymes involved in cell death in response to biotic and environmental stresses (Niño *et al.* 2016). Regulation of rice resistance through cysteine protease activity is evident in over-expression lines of *BrCP3* with enhanced immunity to three isolates of *Xanthomonas oryzae* pv. *oryzae* (Niño *et al.* 2015, 2016).

Remarkable projects in the area of crop stress tolerance presented at PAG XXIV could represent attractive initial points for functional characterization of plant genes. This will support future efforts to improve crop productivity during biotic and abiotic stresses. Some studies on abiotic stresses that could threaten crop productivity are discussed

in the following sections.

DROUGHT STRESS

Climate models have predicted that a gradual increase in temperature and CO₂ concentration can lead to the escalation of drought incidence and duration in many regions around the world (Tavakol 2016). *Miscanthus*, a genus of C4 perennial grasses, is of great interest for the production of biorenewable energy and chemicals due to its high biomass potential even in temperate regions (Malinowska *et al.* 2016). Yield of *Miscanthus* strongly depends on water availability. Many places across Europe where irrigation and temperature are favorable for *Miscanthus* cultivation with limited water supply. Therefore, the response of diverse genotypes of *Miscanthus* to reduce water availability has been investigated. This will help identify pathways responsible for drought resistance and sensitivity to improve selections of plants with good biomass production under water stress (Malinowska *et al.* 2016). A QTL (*qDHY.3BL*) located on chromosome 3BL has been found to be associated with increased grain and plant biomass under drought and heat stresses in bread wheat (Thomelin *et al.* 2016).

Uridine diphosphate (UDP)-glucose 4-epimerase (UGE) catalyzes the reversible conversion of UDP-glucose to UDP-galactose (Lee *et al.* 2016). A potential role of *BrUGE1* in improving rice growth performance under optimal and water deficit conditions has been proposed. In addition, rice with *BrUGE1* overexpression has been shown to have enhanced tolerance to salt and bacterial infections caused by *X. oryzae* pv *Oryzae* (Lee *et al.* 2016).

Increased water soluble carbohydrate concentration in stem bases contributes with stable wheat grain yield under terminal water deficit (Ovenden 2016). Initial studies have indicated moderate broad sense heritability of this trait. However, molecular marker technologies could facilitate greater genetic gain for this complex trait. Water soluble carbohydrate accumulation is subjected to the dynamics of supply from photosynthesis and demand from maturing grains and other sinks. It is also influenced by phenology, plant size, stem diameter, and canopy senescence under the

influence of declining water availability during grain fill. Thus, genetic contribution of water soluble carbohydrate concentration to yield has been studied in contrasting environmental conditions (Ovenden 2016).

Fructans are naturally occurring plant oligo- and polysaccharides composed of fructose molecules (Veenstra *et al.* 2016). These polymers are known as carbon stores with potential to protect plants against water deficit.

Utilizing materials from a multi-year multi-environment study, factors influencing variation of wheat grain fructan content in 289 winter wheat varieties have been examined (Veenstra *et al.* 2016). Information regarding the effect of genotype and environment on wheat grain fructan can be utilized to implement recurrent genomic selection in winter wheat and guide future decisions regarding breeding methodologies for total fructan content in wheat.

Post-anthesis drought is a common limiting factor for many temperate wheat growing regions including the USA (Babar *et al.* 2016). The most pronounced significant changes are in amino acids, sugars, and antioxidant compounds. Specifically, L-tyrosine, L-isoleucine, L-serine, L-aspartate, L-glutamate, 3-hydroxy-3-methylglutarate, L-threonine, D-arabinose, and sedoheptulose are strongly expressed. They are potentially associated with drought tolerance in wheat (Babar *et al.* 2016). By comparing molecular, physiological, and compositional responses of plants to drought, we hope to identify pathways responsible for drought resistance and sensitivity so that we can improve selections for plants with good biomass production under water stress.

CADMIUM

Wheat (*T. aestivum* L.) genotypes have different propensities to accumulate cadmium (Cd) that is toxic. Producing low Cd grain is important for safe and healthy food supply. The maximum level of Cd concentration that is allowed to trade on international markets for wheat grain is 0.2 mg/kg (Oladzadabbasabadi *et al.* 2016). Therefore, accumulation of Cd in durum wheat (*T. turgidum* L. var. durum Desf) may threaten its export. Genetic mapping of SNP associated with low Cd uptake has been studied in

durum wheat (Oladzadabbasabadi *et al.* 2016).

In field-grown plants, grain Cd concentration is proportional to above-ground plant Cd concentration at flowering (Guttieri *et al.* 2016). In low-volume hydroponic system, high-Cd wheat genotypes have been found to accumulate more Cd in shoots but less Cd in roots than low-Cd wheat genotype (Guttieri *et al.* 2016). It has been shown that Cd-upregulated transcripts include transcripts associated with metal ion binding, whereas Cd-down-regulated transcripts are almost transcripts associated with nicotianamine biosynthetic processes (Guttieri *et al.* 2016). The transcript that responded differently to Cd was homologous to YS1, an iron-phytosiderophore transporter. It was downregulated in the Cd-accumulating genotype, together with the transcripts encoding a group of defense-related Mn-binding proteins that was upregulated in high-Cd genotype (Guttieri *et al.* 2016). In addition, a *plant cadmium resistance 1 (PCRI)* in rice has been found to be able to influence both zinc (Zn) accumulation and weight of rice grain (Song *et al.* 2016). Interestingly, the grains of *OsPCRI*-knockdown lines of rice contain substantially more Zn and less Cd concentration than control rice (Song *et al.* 2016).

ELEVATED OZONE CONCENTRATION

Exposure to elevated ozone concentrations [O₃] can accelerate the rate of leaf senescence, thus decreasing the functional lifespan of leaves and reducing plant productivity. The natural molecular and biochemical components of senescence are accelerated at elevated [O₃], including upregulation of senescence associated genes, down-regulation of photosynthetic genes, degradation of chlorophyll, and loss of Rubisco protein activity (Ainsworth *et al.* 2016). Variation in [O₃]-induced senescence has been reported to be correlated to yield losses in maize and wheat as well as rice (Ainsworth *et al.* 2016). The genotypic diversity in yield and grain quality responses to elevated ozone of diverse inbred and hybrid maize have been studied. It has been reported that yield loss is primarily driven by decreased kernel number on inbreds versus decreased individual kernel mass in hybrids (Rios-Acosta

et al. 2016). Yield loss is also associated with increased kernel protein content under elevated [O₃] (Rios-Acosta *et al.* 2016).

HERBICIDES

Glyphosate, a leading broad spectrum herbicide, is toxic to rice (Cui *et al.* 2016). Therefore, developing glyphosate-resistant rice can broaden available herbicides for rice production and provide more effective weed management strategies. A *japonica* rice transformed by *Isoptericola variabilis-EPSPS**, a novel herbicide-resistant gene isolated from bacterium *I. variabilis*, has been found to be glyphosate-resistant. It can survive when the application dose of glyphosate is 10 times higher than the recommended dose for agricultural application (Cui *et al.* 2016).

Foxtail millet (*S. italica*) is a nutritious plant. It is tolerant to drought and barren conditions. It is an important crop in northern China where there is severe water shortage (Cheng *et al.* 2016). However, foxtail millet is very sensitive to herbicide. Its 1,000-grain weight is only about 3.0 g, making precise seeding difficult (Cheng *et al.* 2016). Traditional thinning seedling and weed control by hand have limited the scale of millet planting. Millet materials with resistance to Sethoxydim, Imazethapyr, and Nicosulfuron are controlled by a single dominant gene. They have been obtained by crossing Chinese cultivated millet varieties with green foxtail (*S. viridis*) herbicide-resistant mutants coming from Canada since 1993. By crossing herbicide-susceptible male-sterile line with herbicide-resistant restoring line, self-crossed sterile line could be killed when herbicide is applied (Cheng *et al.* 2016). The application of herbicide resistant varieties and hybrids has overcome the obstacle of seedling thinning and weed control by hand in the field, leading to large-scale millet production in China for the first time (Cheng *et al.* 2016).

FUSARIUM

Fusarium head blight (FHB) caused by *Fusarium*

graminearum Schwabe (Teleomorph: *Gibberellazeae*) is one of the most devastating diseases that severely affects crop production (Kumar and Kushalappa 2016). Resistance to FHB is highly complex and quantitative in nature (Kumar and Kushalappa 2016). Resistance to FHB can be classified as type-I (resistance to initial infection of spikelets) or type-II (resistance to spread within the spike or rachis resistance). Barley has high level of type-II resistance. It is reported that WIN1 transcription factor can channelize free fatty acids to enforce cuticle in barley spikelets to resist FHB (Kumar and Kushalappa 2016). Dhokane (2016) has dissected the second major QTL (QTL-*Fhb2*) that can impart rachis resistance (Type-II). Basic Helix Loop Helix (*bHLH*) transcription factor, 4-Coumarate-CoA Ligase (*4CL*), Glutathione S-transferase (*GST*), and ABC transporter have been found as putative candidate genes for QTL locus imparting resistance to FHB in wheat. In addition, the wild grass species *Thinopyrum elongatum* has been identified as a source of strong FHB resistance (Ouellet *et al.* 2016). Resistance to FHB has been mapped to the long arm of chromosome 7E in *T. elongatum*. This is of great interest because it can protect wheat against FHB to a high level. In addition, the source is located on a single chromosome arm, possibly at a single locus, in contrast to other sources of resistance that are complex and multi-genic. Thus, Ouellet *et al.* (2016) have developed approaches to characterize and clone the 7EL source of FHB resistance.

GENOME METHODOLOGY ADVANCEMENTS

Several novel high-throughput methods in the area of genome technology have been presented at PAG XXIV. Recent advances in genome sequencing and mapping methods, high quality library construction, phenotyping and genotyping technologies, targeted mutagenesis systems, genome amplifications, and genetic improvement approaches were revealed at PAG XXIV. In addition, DNA and RNA extraction kits as well as fast and reliable electrophoresis system that can empower molecular biologist to obtain high yield and high quantities of DNA

with high performance and sensitive separation as well as analysis of DNA fragments were revealed at PAG XXIV. Moreover, FastMiR, an RNA-based sensor for in vitro detection of small RNA designated to revolutionize analyses of small RNAs (21- to 24-nucleotide molecules, including microRNAs (miRNAs) and small interfering RNAs (siRNAs) has been reported (Huang *et al.* 2016). It will shed light on the regulatory roles of small RNAs and miRNAs in plants and animals (Huang *et al.* 2016).

MALE STERILITY AND BREEDING

Male sterility is an important trait. It plays a key role in hybrid breeding in crops. Thermo-sensitive genic male sterility (TGMS) lines that are male-sterile at high temperatures but can be converted to male-fertile at low temperatures have been widely used in two-line hybrid rice breeding. A rice (*O. sativa* L.) *thermo-sensitive genic male sterile gene 5* (*tms5*) locus has been found to confer the TGMS trait through a loss-of-function mutation of *RNase Z^{Sl}* belonging to the metallo- β -lactamase superfamily. The loss-of-function mutation of *RNase Z^{Sl}* can result in failing to mediate the mRNA decay of *UbiL40*, a temperature-responsive ubiquitin-encoding gene family, finally causing over-accumulation of mRNAs in young anthers at high temperatures (Zhou *et al.* 2016). In addition, Voltage-Dependent Anion Channel (VDAC) gene family has been found to be involved in the formation of Honglian-Cytoplasmic Male Sterility in rice (Xu *et al.* 2016).

CROP DOMESTICATION

Cultivated rice *O. sativa* L. originated from tropical regions is now grown worldwide due to concerted efforts of breeding programs. Through the domestication process, many traits from wild rice are lost, including awn phenotype (the elongated spine-like organ at the tip of seeds), functions in seed dispersal, and preventing predation by animals. Therefore, genes responsible for awn development have been identified in rice with possible correlation with the domestication process (Uehara 2016).

Fig. 1. Schematic representation of factors that can positively and negatively affect crop biomass.

The transition from a spread panicle typical of ancestral wild rice (*O. rufipogon* Griff.) to the compact panicle of present cultivars (*O. sativa* L.) is a crucial event in rice domestication. In this case, a SNP6 residing in the regulatory region 11 kb upstream of the spread panicle architecture gene *Panicle Architecture Control 1* (*PAC1*)/*LGI* (laminar joint and ligule development gene) can lead to a compact panicle architecture in cultivars during rice domestication (Zhu and Sun 2016). Therefore, rice inflorescence architecture can be suggested as a major target of rice domestication.

Loss or reduction of hard seededness or impermeability water is a key step that can lead to domestication of many leguminous crops for agricultural production (Sun 2016). Map-based cloning and characterization studies have revealed that a major QTL designated as *Hs1* can control the seed hardedness in *Glycine soja*. *Hs1* encodes a calcineurin-like metallo-phosphoesterase-like transmembrane protein localized in cellular membranes (Sun 2016). The transition from hard seededness in the wild accessions to soft seededness in cultivated soybeans is caused by a

single nucleotide mutation within *Hs1*, resulting in an amino acid change and a recessive mutation allele (*hs1*) (Sun 2016).

CONCLUSION

We propose a model to elucidate factors that may positively or negatively affect the biomass of crops such as rice (Fig. 1). Further investigation on important yield traits contributing to increased biomass production and stress tolerance mechanisms will provide valuable data to improve our understanding on factors that may impact yield production. It will possibly help breeders to manipulate crop biomass accumulation.

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