



Review

Systems biology approach in plant abiotic stresses

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ABSTRACT

Plant abiotic stresses are the major constraint on plant growth and development, causing enormous crop losses across the world. Plants have unique features to defend themselves against these challenging adverse stress conditions. They modulate their phenotypes upon changes in physiological, biochemical, molecular and genetic information, thus making them tolerant against abiotic stresses. It is of paramount importance to determine the stress-tolerant traits of a diverse range of genotypes of plant species and integrate those traits for crop improvement. Stress-tolerant traits can be identified by conducting genome-wide analysis of stress-tolerant genotypes through the highly advanced structural and functional genomics approach. Specifically, whole-genome sequencing, development of molecular markers, genome-wide association studies and comparative analysis of interaction networks between tolerant and susceptible crop varieties grown under stress conditions can greatly facilitate discovery of novel agronomic traits that protect plants against abiotic stresses.

1. Introduction

Nature constantly changes, and plants must maintain their inherent capacity to survive within their ecological niche by natural genetic variation and adaptive mechanisms. Along with natural variations, induced variants have led to the domestication of plants and development of agriculture, altering human civilization and feeding the increasing global populations at present. However, crops cultivated in agricultural fields are constantly exposed to a variety of biotic and abiotic stresses. According to the IPCC (Intergovernmental Panel on Climate Change) report (2014), plants will have to simultaneously adapt to heat, drought and pathogenic stresses in the future. In 1982, Boyer reported that environmental factors might limit crop production up to 70% (Boyer, 1982). The impacts of different abiotic stresses on the growth and development of plants are evident from the developing ecological challenges of climate change (Bellard et al., 2012). The physiological constraints to crop production are aggravated by the increasing human population and competition for environmental resources, creating further problems for crop production. A Food and Agriculture Organization (FAO) report (2007) stated that only 3.5% of global land area is unaffected by environmental factors. Although it is difficult to

accurately estimate this number, it is clear that abiotic stresses will continue to have dominant effects on plant production. The global average temperature is estimated to have risen by 0.13 °C per decade since 1950, and the impact of this change on agriculture is still poorly understood (Lobell et al., 2011; Solomon et al., 2007). The increase in abiotic stresses results in a decrease in the crop yield potential of major food crops including rice, maize, and wheat. The global production of maize and wheat has been estimated to decrease by 3.8% and 5.5%, respectively due to the increase in global temperature. No such negative indications have been reported so far for rice and soybeans. This suggests that a single stress factor should not be expected to be solely responsible for the yield potential of all the crops, meaning that it is important to understand the specific physiological characteristics of each individual crop plant. To understand the specific physiological characteristics of each and every individual plant, it is highly important to decipher its complete genomic potential. In the era of next-generation sequencing technology and the advancement of genomic data analysis techniques facilitate the discovery of potential genes of interest, the introduction of valuable traits and further biotechnological applications. The ongoing increase in the global population, together with the continued reduction in fertile arable land, global warming and

Abbreviations: FAO, Food & Agricultural organization; NGS, Next-generation sequencing; BAC, Bacterial artificial chromosome; QTL, Quantitative trait loci; BLAST, Basic Local Alignment Search Tool; HMM, Hidden Markov model; PSI-BLAST, Position Specific Iterative Basic Local Alignment Search Tool; SSR, Small sequence repeat; SNP, Small nucleotide polymorphism; EST, Expression sequence tag; ISBP, Insertion site-based polymorphism; MAS, Marker-assisted selection; WGAS, Whole genome-association study; GWAS, Genome-wide association study; SAGE, Serial analysis of gene expression; MPSS, massively parallel signature sequencing; TILLING, Targeting local lesions in genomes; ROS, Reactive oxygen species; RNS, Reactive nitrogen species; ABA, Abscisic acid

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the reduction of water resources are the major challenges to overcome to feed the next generation. Understanding plant traits through advancement and implementation of genomic approach will be the most important route to producing desirable traits of agronomic importance. This review discusses advanced genomic technologies and systems biology approaches that can be useful for the production of stress tolerance traits in plants.

During plant growth and development, plants are exposed to a variety of abiotic stresses including drought, flood, salinity, freezing, cold temperature, hot temperature, high and low intensity lights, heavy metal toxicity, ozone, carbon dioxide, sulfur dioxide pollution, soil pH, UV irradiation and several others. Among these stress factors, drought, heat, salinity and metal toxicity are major causes of crop loss. Plants may resist the effects of these stresses to some extent, but it will be challenging for a plant to overcome the combined stress condition. Understanding and identifying the crucial regulatory factors involved in multiple stress responses in plants is a complex process. It is critical to determine traits that can confer tolerance to such environmental stresses, and genomic studies can answer these questions. The combination of structural and functional genomics along with a systems biology approach will be very helpful to understand and identify potential traits of interest. Therefore, this review discusses the role of structural and functional genomics and system biology approaches toward the discovery of stress-tolerant traits.

2. Genomics approach

2.1. Structural genomics

Structural genomics addresses the characterization of the structure of the genome. The main focus of structural genomics is to identify and understand the physical structure of the genome and to locate and identify the genomic features of the chromosomes. Understanding the structure, location and genomic features of the genome of an individual organism is useful for efforts to manipulate any gene or DNA of interest to generate a valuable agronomic trait. Structural genomics uses techniques with a high analytical resolution to characterize a genome at its full length and breadth and to develop tools for structural analysis including prediction and annotation.

2.1.1. Genome sequencing

Sequencing of genes and genomes started with the pioneering work of Sanger, and the completion of the genome sequencing of *Arabidopsis thaliana* was one of the most important breakthroughs in genomic research in plant biology (Sanger et al., 1977; Sanger and Coulson, 1975; The Arabidopsis Genome Initiative, 2000). Over the last decade, enormous progress has been made in DNA sequencing technology, enabling the generation of an enormous amount of sequencing data within a short span of time in a cost-effective manner compared with the Sanger-based capillary method. High-throughput next-generation sequencing technologies have gained enormous interest for genome sequencing, with prominent next-generation sequencing (NGS) platforms including the Illumina/Solexa AB SOLiD Genome analyzer (<https://www.illumina.com/>) and Roche 454 GS FLX Titanium (www.454.com). The advancement of NGS technology has opened the door to the study of plant genomics to produce improved crop varieties for breeding purposes. Following the sequencing of the *A. thaliana* genome in 2000, the genome sequence data of more than 380 plant species are now available in the public domain (<https://www.ncbi.nlm.nih.gov/genome/browse/>) for exploitation. The genomic details of a few selected plant species are mentioned in Table 1. Using the NGS platform, it is now possible to resequence the plant genome and the whole transcriptome in greater depth. In addition, sequencing hundreds or even thousands of related genomes within and between germplasm pools is possible as a way to understand genetic diversity. To overcome certain drawbacks of these second generation sequencing technologies,

Table 1
Genomic details of few model plant species.

	Name of the species	Genome Size Mb/ Gb	GC%	Genes	Proteins
Monocots					
1	<i>Aegilops tauschii</i>	4.32 Gb	46.37	54769	55,713
2	<i>Brachypodium distachyon</i>	24.64 Gb	–	84423	84,423
3	<i>Brachypodium stacei</i>	234	–	29898	36,257
4	<i>Dichanthelium oligosanthes</i>	589.166	47.50	26468	26,468
5	<i>Eleusine coracana</i>	1.19 Gb	44.80	85243	126,312
6	<i>Eragrostis tef</i>	607.318	45.50	27756	38,333
7	<i>Hordeum vulgare</i>	5.3 Gb	–	39734	248,180
8	<i>Lolium perenne</i>	481.479	46.30	28455	–
9	<i>Leersia perrieri</i>	266.688	42.60	29078	40,521
10	<i>Musa acuminata</i>	472.231	40.73	34100	47,707
11	<i>Musa itinerans</i>	455.349	35.40	32456	32,456
12	<i>Oropetium thomaeum</i>	243.175	45.30	28446	–
13	<i>Oryza barthii</i>	308.272	42.08	26803	29,549
14	<i>Oryza brachyantha</i>	259.908	41.10	24793	26,803
15	<i>Oryza glaberrima</i>	303.295	42.80	33164	–
16	<i>Oryza glumipatula</i>	372.86	43.73	25896	–
17	<i>Oryza longistaminata</i>	362.064	43.08	31686	–
18	<i>Oryza meridionalis</i>	354.611	43.20	29308	45,737
19	<i>Oryza nivara</i>	337.95	42.94	36313	50,032
20	<i>Oryza punctata</i>	393.817	42.81	31762	46,255
21	<i>Oryza rufipogon</i>	384.518	43.90	37071	50,219
22	<i>Oryza sativa</i> subsp. <i>indica</i>	426.337	43.73	40745	88,438
23	<i>Oryza sativa</i> subsp. <i>japonica</i>	374.423	43.58	35679	97,751
24	<i>Panicum hallii</i>	554	–	37232	49,852
25	<i>Panicum virgatum</i>	734.4	–	91838	–
26	<i>Phoenix dactylifera</i>	556.481	40.11	28270	38,570
27	<i>Secale cereal</i>	7.9 Gb	46.70	27784	–
28	<i>Setaria italica</i>	405.86	46.17	31092	32,964
29	<i>Setaria viridis</i>	394.9	–	35214	48,594
30	<i>Sorghum bicolor</i>	732.2	–	34129	47,121
31	<i>Spirodela polyrhiza</i>	158	42.72	19623	19,623
32	<i>Triticum aestivum</i>	17 Gb	–	217907	273,739
33	<i>Triticum dicoccoides</i>	1.04 Gb	46.08	61821	–
34	<i>Triticum urartu</i>	3.74 Gb	46.00	29190	24,169
35	<i>Zea mays</i>	2.13 Gb	46.91	47800	58,291
36	<i>Zoysia marina</i>	203.914	38.90	20855	20,648
37	<i>Zoysia japonica</i>	334.384	42.60	59271	–
Dicots					
38	<i>Actinidia chinensis</i>	616.1	35.20	39040	–
39	<i>Aethionema arabicum</i>	192.488	36.20	23167	–
40	<i>Amaranthus hypochondriacus</i>	502.148	42.20	24829	–
41	<i>Amborella trichopoda</i>	706.495	38.10	19354	31,494
42	<i>Ananas comosus</i>	382.056	38.54	27024	35,775
43	<i>Aquilegia coerulea</i>	306.5	–	30023	43,440
44	<i>Arabidopsis halleri</i>	221.14	37.10	25008	26,911
45	<i>Arabidopsis lyrata</i>	207	37.60	34280	39,161
46	<i>Arabidopsis thaliana</i>	135	36.05	27655	48,456
47	<i>Arabis alpina</i>	308.033	37.93	30216	23,286
48	<i>Arachis duranensis</i>	1.25 Gb	37.67	–	88,643
49	<i>Arachis ipaensis</i>	1.56	37.77	–	94,419
50	<i>Artocarpus camansi</i>	631.308	33.20	49089	–
51	<i>Asparagus officinalis</i>	1308	39.36	32073	36,763
52	<i>Azadirachta indica</i>	261.458	43.20	20000	22,760
53	<i>Beta vulgaris</i>	566.55	37.30	27429	32,874
54	<i>Brassica juncea</i>	954.861	37.34	80050	–
55	<i>Brassica napus</i>	848.2	37.80	101040	101,040
56	<i>Brassica nigra</i>	591	36.32	49826	–
57	<i>Brassica oleracea</i>	488.954	37.33	53670	56,687
58	<i>Brassica rapa</i>	284.129	35.83	48731	52,553
59	<i>Cajanus cajan</i>	529.971	33.71	31549	31,549
60	<i>Camelina sativa</i>	641.356	37.49	97832	107,481
61	<i>Cannabis sativa</i>	820	38.80	30000	–
62	<i>Capsella grandiflora</i>	112.3	–	24805	26,561
63	<i>Capsella rubella</i>	133.064	35.90	26776	28,713
64	<i>Capsicum annum</i>	2.93 Gb	35.41	45131	57,266
65	<i>Carica papaya</i>	369.782	39.00	28629	–
66	<i>Chenopodium pallidicaule</i>	337.011	35.70	–	–

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