

Korean plant proteomics: pioneers in plant stress physiology

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Abstract Plant proteomics is the large-scale studies of proteins, particularly on their structures and functions, governed by the physiological metabolism of plant cells. With the development of techniques and strategies in proteomics, proteomics approach is moving forward in systems biology handling sophisticated components of major signaling and biochemical pathways in plants responding to their environment. In Korea, pioneers in plant proteomics are trying to catch up with global trends in plant proteomics; these researchers are not only improving existing techniques in protein extraction but also developing new techniques in proteomics context. In the hot field of abiotic and biotic stress proteomics, 29 and 9 out of 74 papers have been published during the review period from 2005 to 2010, respectively. This present review article provides an overview on the output of Korean plant proteomers while paying special attention to both abiotic and biotic stress proteomics.

Keywords South Korea, Plant, Proteomics, Abiotic, Biotic, Stress Physiology

Plant proteomics in Korea – an overview

What is the focus of plant proteomics?

Proteomics is fast becoming a powerful tool for physi-

ological and genetic studies in plants, in the post-genomics era (Rossignol 2001; Agrawal and Rakwal 2008). With the availability of huge genomics information and the advancements of analytical technology, proteomics plays a crucial role in the study of many different aspects of plant functions. Proteins mainly contribute to major signaling and biochemical pathways so that studies on plant proteomes provide knowledge about plant growth, development, and interactions with their environment (Pandey and Mann 2000; Sixue and Harmon 2006; Agrawal and Rakwal 2008). Thus, the proteomics provides new perspectives to understand the complex functions of model plants and crop species at different levels (Cánovas et al. 2004; Agrawal and Rakwal 2008).

Where is the Korean plant proteomics?

Over the last decade, proteomics has generated a relatively large number of reports on human, yeast, and plant; the volume of work in plant biology accounts for about 10 percent of the total fields (Heazlewood and Millar 2006). In Korea, the plant community has published 74 papers containing ‘plant proteomics’ or ‘plant proteome’ plus ‘Korea’ against the Science Citation Index Expanded (SCIE) and Korea Citation Index (KCI) from the year 2005 to 2010 (Fig. 1). Except for 2005, about 15 articles related to plant proteomics were published each year, and these results are marked about 5 percent out of global plant proteomic studies surveyed by Jorriin-Novo et al. (2009).

The published papers corresponded by Korean authors can be divided into subcategories according to plant systems, proteome types, and biological processes (Table 1). In the classification of plant types, cereals including rice and wheat hold dominant positions as 31 and 7 out of 76 species, respectively. Arabidopsis takes the second place ranked as 21, and research on soybean and lettuce follow them with 3 papers each. Interestingly, there are some initial

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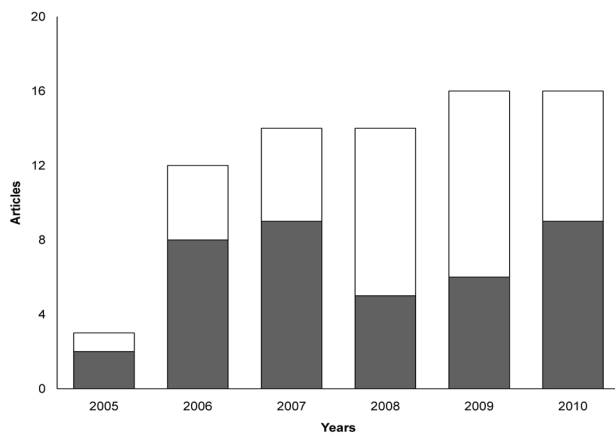


Fig. 1 The numbers of plant proteomics articles corresponded by Korean authors from 2005 to 2010. Published papers were counted by selecting Korean corresponding authors after searching with the keywords, ‘plant proteomics’ or ‘plant proteome’ plus ‘Korea,’ against the Science Citation Index Expanded (SCIE) and Korea Citation Index (KCI) from 2005 to 2010. The black boxes indicate the number of articles focusing on stress physiology, and the opened boxes mean the number of other research areas

studies to identify protein expression patterns of ornamental flowering plants such as *Anoectochilus formosanus* and *Eschscholtzia californica*. With regards to the proteome maps, the Korean proteomers provided about 113 maps at the specific levels of plant development or transgenic plants (cloning and overexpression of genes and mutation lines without target genes). Based on biological processes, the subcategories could be roughly divided into 5 subheadings, including abiotic stress, biotic stress, development/growth, symbiosis, and so on. Each subheading consists of 29, 9, 17, 1, and 3 out of the total 74 papers, respectively. About 40 papers concentrate on stress physiology corresponded to the abiotic and biotic stress areas. This tendency of focusing on stress suggests that it is worthwhile to review diverse researches of Korean proteomers dealing with plant response and networking to its environment.

The aim in this review is to provide graduate students and advanced researchers with information about the “who and who” of Korean plant proteomics, detailing the various

Table 1 Studies, objectives, and contributions of the plant proteomics papers published by Korean authors from 2005 to 2010

Plant (76) ^a	Proteomes (115)	Biological Processes (74)
Model systems	Genotypes/ Mutants/ Transgenic (35)	Abiotic stresses (29)
<i>Arabidopsis thaliana</i> (20)		Agrochemicals (2)
<i>Physcomitrella patens</i> (1)		Arsenic (2)
		Cadmium (2)
Cereals	Organ/tissue/cells	Cold (6)
Rice (31)	Cells, calli (4)	Copper (1)
Wheat (7)	Leaves (24)	Drought (4)
	Roots (8)	Heat (2)
Legumes	Sap (6)	Hormone (2)
Soybean (3)	Seeds (14)	Light (2)
	Seedling (17)	Salt (3)
Other Crops	etc (6)	Sterol deficient (1)
Buckwheat (1)		Toxic VOC (1)
Lettuce (3)	Subcellular fractions	Waterlogging (3)
Onion (1)	Cell wall (2)	
Pepper (2)	Nuclear (1)	Biotic Stresses (9)
Perilla (1)	Chloroplast (1)	
	Mitochondria (1)	
Pumpkin (1)		Development (17)
Tall Fescue (1)		Leaves (6)
Tomato (2)		Pollen (1)
		Programmed cell death (2)
Others (2)		Seeds (8)
<i>Anoectochilus formosanus</i>		
<i>Eschscholtzia californica</i>		Symbiosis (1)
		etc. (18)

^aNumber of published papers.

* This table was drawn according to the criteria for classification as used by Jorin et al., 2007.

plant proteomics territories areas of expertise in the plant stress physiology area. The following sections introduce eye-opening achievements by Korean scientists in the abiotic and biotic stress proteomics fields.

Plant stress proteomics in Korea

Since plants lack locomotion, they are directly influenced by various stresses in their environment. These stresses ranging from chemicals, drought, salt, pathogen, and to insects, negatively affect plant growth and agriculture production in major cereal crops such as rice (Agrawal et al. 2006; Agrawal et al. 2009; Agrawal and Rakwal 2011). In order to achieve profitable outcomes in plants, including producing new cultivars with high quality compounds, and plants for phytoremediation, it is necessary to first investigate and understand their physiological characteristics. Despite numerous challenges, such as their complexity, and in order to explore the plant world in full proteomics can help leap over these hurdles as proteins are the de facto controller of a cellular and organismal milieu. We

discuss below the abiotic and biotic stress responsive proteomes.

Abiotic plant proteomics

From Korea, at least 29 papers reporting the proteins alterations in plants exposed to abiotic stress such as chemicals, cold, high temperature, drought, waterlogging, and salt, have been published, and are listed in Table 2. Most of these studies have been carried out using leaves and roots of rice and Arabidopsis.

Agrochemicals

The effects of two agrochemicals - glyphosate and glufosinate - on the leaf proteome of rice cultivars have been investigated. In the study on the leaf proteome of rice post-treatment with glyphosate (herbicide used to inhibit aromatic amino acid metabolism), 25 differentially expressed proteins including antioxidant enzymes and photosynthetic/metabolic-related proteins were identified (Ahsan et al. 2008b). Moreover, the effects of glufosinate, inhibiting glutamine synthetase to catalyze ammonia assimilation, on rice leaf

Table 2 A summary of published papers on abiotic stress proteomics during the reviewed period

Plant	Genotype	Growth stage /tissue	Treatments	Proteomics approach	Main features	Reference
Agrochemicals						
Rice	Ilpumbyeo	Leaf	1, 2, and 3 mM Glufosinate for 72 h	2-DGE ^a /MALDI ^b	13 proteins participating in reactive oxygen scavenging mechanisms and amino acid synthesis were analyzed	Lee YW et al. 2008
Rice	Dongjin	Leaf	2.5 mM Glyphosate for 12 h	2-DGE/MALDI	25 differentially expressed proteins including antioxidant enzyme and photosynthetic/metabolic-related proteins were identified	Ahsan N et al. 2008b
Heavy Metal Toxicity						
Rice	Dongjin	Leaf	50 or 100 mM Arsenic (As) for 4 d	2-DGE/MALDI & ESI ^c	14 spots representing energy and metabolism-related proteins were investigated	Ahsan N et al. 2010
Rice	Dongjin	Root	50 or 100 mM As for 4 d	2-DGE/MALDI	23 As-regulated proteins were identified. GSH is important in protecting cells under As treatment	Ahsan N et al. 2008a
Rice	Dongjin	Root/Leaf	100 μ M Cadmium (Cd) for 24 h	2-DGE/MALDI	A total of 36 proteins were identified. Total glutathione levels were significantly decreased.	Lee K et al. 2010
Rice	Hwayeong	Seedling	0.2 to 1.0 mM Cd for 4 d	2-DGE/MALDI	21 proteins playing a role in detoxification, biosynthesis and germination were up regulated at the treatment of Cd	Ahsan N et al. 2007d
Rice	Hwayeong	Seedling	0.2 to 1.5 mM Copper (Cu) for 4 d	2-DGE/MALDI	25 proteins were MS analyzed generated the expression of antioxidant enzymes and the inhibition of seed germinations	Ahsan N et al. 2007b

Table 2 Continued

Plant	Genotype	Growth stage /tissue	Treatments	Proteomics approach	Main features	Reference
Cold						
Arabidopsis	<i>msrb3</i>	Seedling	4°C for 3 d	2-DGE/MALDI	A total of 8 chloroplast proteins and 3 cytosol proteins were identified. MsrB3 becomes tolerant in cold by scavenging MetO and ROS	Kwon SJ et al. 2007
Arabidopsis	GRP2	Mitochondria	11°C for 3 d	2-DGE/MALDI	Several mitochondrial proteins were regulated by GRP2 under cold stress	Kim JY et al. 2007
Rice	Dongjin	Root	10°C for 24 h or 72 h	2-DGE/MALDI & ESI	27 up-regulated cold stress responsive proteins participating in energy metabolisms, vesicular trafficking, and detoxification were identified	Lee DG et al. 2009
Rice	Dongjin	Leaf	5°C for 12, 24, 36 h 10°C for 24, 72 h	2-DGE/MALDI & ESI	By using polyethylene glycol to eliminate the high-abundant proteins, 12 up-regulated low-abundant proteins related to cold stress were separated.	Lee DG et al. 2007b
Tall Fescue	EN-transgenic	Leaf	4°C for 24, 48, 72 h	2-DGE/MALDI	In Tall Fescue by the overexpression of NDP Kinase, NDP kinase 2, HSP70, and GSTs were identified	Lee SH et al. 2009
Heat						
Arabidopsis	<i>35S:DRE-B2C</i>	Leaf	37°C for 24 h	2-DGE/MALDI	There is no change of proteome between wild and transgenic plant at 22°C. At 37°C, the change of proteins and transcripts levels in the transgenic were detected	Lee K et al. 2009
Rice	Dongjin	Leaf	42°C for 12, 24 h	2-DGE/MALDI	Among 73 proteins on the 2-D maps, 48 proteins were recognized as HSPs, energy and metabolism, redox homeostasis, and regulation proteins	Lee DG et al. 2007a

were reported (Lee et al. 2008). A total of 13 proteins responding to ammonia accumulation were identified. In these papers, RuBisCO large subunit (LSU) was significantly decreased by the treatment of both herbicides. Increase of some antioxidant enzymes after treatment of rice cultivars with these herbicides suggested that glyphosate and glufosinate treatment possibly generate oxidative stress in plants. These results also imply usefulness of proteomics in elucidating the unknown biochemical processes of agrochemicals as shown by glufosinate and glyphosate treatments.

Heavy metal toxicity

At least five studies on rice proteome affected by heavy metal such as arsenic (As), cadmium (Cd), and copper (Cu) have been reported. Two-week-old seedlings of rice exposed to 50 or 100 mM As were separated on two-dimensional gel electrophoresis (2-DGE), and 14 proteins

were identified by using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) (Ahsan et al. 2010). This analysis revealed that the increase of several proteins related with energy production and metabolism such as RuBisCO LSU and chloroplast 29 kDa ribonucleoproteins. In order to elucidate the interference of seed germination by Cd stress, 4-day-old rice seedlings were exposed to Cd solutions ranging between 0.2 and 1.0 mM. Twenty-one proteins associated with detoxification, biosynthesis, and germination on rice seed were found to be up-regulated by Cd treatment (Ahsan et al. 2007d). In a series of studies, these identified proteins provided new insight to better understand the physiological and biochemical networking in responses to stress conditions derived from AS, Cd, and Cu in plants (Table 2).

Table 2 Continued

Plant	Genotype	Growth stage /tissue	Treatments	Proteomics approach	Main features	Reference
Drought						
Arabidopsis	<i>nagB#1</i>	Seedling	1 mM GlcN for 6 h	2-DGE/MALDI	Although RuBisCO LSU was down-regulated in wild-type Arabidopsis on the GlcN medium, RuBisCO was not reduced in the transgenic plant	Chu SH et al. 2010
Rice	NA	Grain	RT and 15°C for 10 d after drying at RT, 40, 60°C	2-DGE/MALDI	The activities of 32 proteins decreased storing at 60°C. Heat shock protein 70 and GST can be used as a marker for tracing drying temperature	Shin PG et al. 2008
Soybean	Taegwang	Root	After 5 d of 79, 62, 46, 29, 23% FC, & re-watering for 4 d	2-DGE/MALDI	5 proteins were increased, 21 were decreased, and 2 protein spots were newly expressed in drought stress	Alam I et al. 2010b
<i>Anoectochilus formosanus</i>	Hayata	Leaf	withholding water supply for 30 d	2-DGE	A total of 17 proteins were detected on the differential expressed maps. 15 out of 17 proteins were down-regulated and 2 proteins were up-regulated after drought.	Pandey DM et al. 2006
Waterlogging						
Tomato	Koma	Leaf	waterlogging for 24, 48, 72 h	2-DGE/MALDI & ESI	33 proteins were identified as photosynthetic, disease resistance, stress, and defense proteins	Ahsan N et al. 2007a
Tomato	Koma	Root	waterlogging for 24, 72 h	2-DGE/MALDI	16 down-regulated and 13 up-regulated proteins were identified in waterlogged tomato roots.	Ahsan N et al. 2007c
Soybean	Asoagari	Root	waterlogging for 3, 7 d	2-DGE/MALDI & ESI	Increased proteins were recognized as anaerobic proteins imply the plant try to meet its need for energy by using fermentation pathway due to lack of oxygen	Alam I et al. 2010a

Light and temperature

Proteomics studies on light and temperature stress in plant are few, compared with those on water and nutrient status (Rossignol et al. 2006); researches in these areas are progressing smoothly in Korea (Table 2).

With respect to plant response to light intensity, Hong et al. (2006) carried out an interesting study on the effect of elevated ultraviolet-B (UV-B) radiation on yield in Perilla (*Perilla frutescens* L.). Ten out of 30 proteins affected by UV-B were identified as photosynthetic and stress-related proteins. The authors suggested that the decreased yield in Perilla was due to the inhibition of photosynthesis by damaged DNA and photosynthetic apparatus from exposure to UV-B.

The Korean proteomers have been focusing on the long-term exposure to low temperature for 3 days in Arabidopsis, rice, and transgenic Tall Fescue plants (Table 2). Lee DG

et al. (2007b, 2009) reported the response in leaf and root of rice Dongjin cultivar to chilling stress conditions. A total of 12 and 27 up-regulated proteins were identified by MALDI-TOF-MS and electrospray ionization-tandem mass spectrometry (ESI-MS/MS) analysis. Acetyl transferase, phosphogluconate dehydrogenase, NADP-specific isocitrate dehydrogenase, fructokinase, PrMC3, putative alpha-soluble *N*-ethylmaleimide-sensitive factor (NSF) attachment protein, and glyoxalase 1 were identified as proteins involved in energy metabolism, vesicular trafficking, and detoxification under cold-stress. Interestingly, another study on the long-term exposure to cold environment was performed on transgenic Tall Fescue overexpressing NDP Kinase (Lee SH et al. 2009). By 2-DGE analysis of wild-type and transgenic Tall Fescue plants, eight up-regulated proteins including heat shock protein 70 (HSP 70) and glutathione S-transferase (GST) were identified by MALDI-TOF-MS.

Table 2 Continued

Plant	Genotype	Growth stage /tissue	Treatments	Proteomics approach	Main features	Reference
Salt/Multiple						
Arabidopsis	<i>atRZ-1a</i>	Seedling	100 mM NaCl 100 mM mannitol	2-DGE/MALDI	<i>atRZ-1a</i> serves as a negative regulator of germination and growth in the Arabidopsis	Kim YO et al. 2007
Arabidopsis	<i>CaPUB1</i>	Seedling	Multiple	2-DGE/MALDI	26S proteasome regulatory subunit RPN6 was clearly down-regulated in the <i>35S::CaPUB1</i>	Cho SK et al. 2006
<i>Physcomitrella patens</i>	NA	protonema/ gametophore	Multiple	2-DGE/MALDI	90 out of 1500 soluble protein in protonema and gametophore of <i>Physcomitrella patens</i> were identified. Most of them were categorized into energy or primary metabolism.	Cho SH et al. 2006
Light						
Arabidopsis	Wild	Seedling	660, 730, 450 nm	2-DGE/MALDI	A total of 49 proteins responded from light treatment were detected. Most of them were metabolic enzymes regulating metabolic changes induced by various wave lengths	Kim DS et al. 2006
Perilla	Manchu	Leaf	UV-B 2 h for 30 d	2-DGE/MALDI	10 out of 30 proteins affected by the UV-B were identified as photosynthetic, stress related proteins	Hong SC et al. 2006
Etc.						
Arabidopsis	<i>cyp51A2</i>	Seedling	None	2-DGE/MALDI	Photosynthesis related proteins were reduced on the mutant line on the sterol deficiency	Kim HB et al. 2010
Arabidopsis	Wild	Seedling	formaldehyde/ toluene for 24 h	2-DGE/MALDI	14 and 22 proteins were displayed on the 2-D maps under formaldehyde and toluene treatment	Park MA et al. 2009
Wheat	4 cultivars	Grain	-20 to -10°C for 4 months	2-DGE/MALDI	Among more than 140 proteins were detected, 124 proteins were regarded as abiotic stress responsive proteins	Kamal A et al. 2010a

^{a)} Two dimensional gel electrophoresis

^{b)} MALDI-TOF/MS.

^{c)} ESI-MS/MS.

On the one hand, leaf proteome of rice exposed to 42°C for 12 and 24 h was investigated (Lee DG et al. 2007a). Seventy-three out of 1000 proteins were separated by 2-DGE, and after heat treatment 48 proteins were recognized as HSPs, energy and metabolism, redox homeostasis, and regulation proteins. In transgenic Arabidopsis, a study on changes of proteins and transcripts levels in the transgenic plants overexpressing DREB2C was performed using proteomics and RT-PCR (Lee K et al. 2009). A total of 11 proteins were recognized as peptidyl-prolyl isomerase ROC4, GST 8, pyridoxal biosynthesis, protein PDX1, and elongation factor Tu.

These investigations of leaf protein expression and iden-

tification of some novel proteins could be helpful in better understanding the molecular basis not only of heat but also of cold stress responses in plants.

Drought and waterlogging

Proteomics articles on plants under drought (4 papers) and waterlogging (3 papers) conditions have been published. In contrast to other areas of stress proteomic, various species were selected as experimental plants including Arabidopsis, rice, soybean, tomato, and *Anoectochilus formosanus*.

Alam et al. (2010b) have carried out the proteomics analysis of soybean roots under drought stress. Five up-regulated proteins and 12 down-regulated proteins, and

Table 3 A summary of published papers on biotic stress proteomics during the reviewed period

Plant	Genotype	Growth stage /tissue	Treatments	Proteomics approach	Main features	Reference
Rice	<i>blm</i>	Leaf	None	2-DGE/N ^d &ESI ^c	Oxidative stress marker and pathogen-relative (PR) proteins were identified on various develop stages	Jung YH et al. 2006
Rice	<i>blm</i>	Leaf	<i>Magnaporthe oryzae</i>	2-DGE/N	Some pathogen-relative proteins regarding as pathogenesis-related proteins were analyzed in the <i>blm</i>	Jung YH et al. 2005
Wheat	6 cultivars	Seed	field	2-DGE/MALDI	185 differential expressed proteins were detected and identified as biotic stress response proteins	Kamal A et al. 2010b
Arabidopsis	Col	Secretome	0.5 mM SA for 4 d	2-DGE ^a /MALDI ^b	A total of 18 SA-responsive proteins secreted by the Arabidopsis cell cultures after treating SA were identified	Oh IS et al. 2005
Rice	Jinheung	Secretome	<i>M. oryzae</i> or elicitor	2-DGE/MALDI & ESI	Most of the 21 differential protein spots regulated by fungus and its elicitor were involved in defense	Kim ST et al. 2009
Rice	3 mutants	Leaf	<i>M. oryzae</i>	2-DGE/MALDI	8 up- and down-regulated proteins in susceptible rice mutants were identified	Ryu HS et al. 2009
Rice	Waito-c	Seedling	<i>Fusarium proliferatum</i> KGL0401	2-DGE/MALDI	180 overexpressed proteins were detected on the proteome of rice. Among them, 75 induced proteins were identified	Rim SO et al. 2006
Arabidopsis	Col-0	Seedling	<i>Bacillus subtilis</i> GB03	2-DGE/MALDI & TO ^e	<i>Bacillus subtilis</i> GB03 resulted in the increase of the enzymes expression including ethylene biosynthesis, detoxification, and defense	Kwon YS et al. 2010
Hot Pepper	Bugang	Nuclear	TMV SA	2-DGE/MALDI	Six nuclear proteins responded by TMV or SA were detected.	Lee BJ et al. 2006

^{a)} Two dimensional gel electrophoresis.

^{b)} MALDI-TOF-MS.

^{c)} ESI-MS/MS.

^{d)} N-terminal amino acid sequence.

^{e)} MALDI-TOF/TOF-MS.

newly expressed proteins were identified under drought condition as visualized by 2D maps. The proteins were found to be involved in carbohydrate and nitrogen metabolism, cell wall modification, cell defense, and programmed cell death. Under drought stress, levels of reactive oxygen species (ROS), lipid peroxidation, and proline content increased. These results suggested involvement of these proteins in allowing soybean plants to adapt to the drought conditions. In another study, there was an attempt to apply proteomics to understanding responses of *Anoectochilus*

formosanus, an orchid plant, to drought stress (Pandey et al. 2006). A total of 17 proteins were detected on the differential expressed 2D maps. Fifteen out of 17 proteins were down-regulated while 2 proteins were up-regulated after drought treatment. In addition, 11 proteins were qualitatively up-regulated and 6 proteins were down-regulated.

With respect to waterlogging, tomato and soybean plants have been investigated. The proteomes of tomato leaf and root response to waterlogging conditions for 24, 48, and 72 h were established by using 2-DGE (Ahsan et al. 2007a,

2007c). A total of 33 proteins were identified by MALDI-TOF-MS and ESI-MS/MS in the leaf. Sixteen down-regulated and 13 up-regulated proteins were identified in waterlogged tomato roots. In the study of soybean root proteome against waterlogging stress, 14 proteins were found to be up-regulated, 5 proteins were down-regulated, and 5 proteins were *de novo* expressed (Alam et al. 2010a). These authors suggested that increased proteins recognized as anaerobic proteins might help the plant try to meet its need for energy by activating the fermentation pathway under low-oxygen conditions.

Biotic plant proteomics

Biotic stress is one of the major stresses affecting crop growth and productivity. Several biotic stress proteomic studies have been performed in Korea (Table 3). Most of these studies have also been conducted in rice and Arabidopsis; they were associated with biotic stress response proteins coupled to pathogens or defense-related signals. As a major fungal pathogen, the interaction between *Magnaporthe oryzae* inducing rice blast disease and rice plants was reported by Jung et al. (2005), Kim et al. (2009), and Ryu et al. (2009). In the previous study though secretome analysis in rice suspension-cultured cells treated with *M. oryzae* or its elicitor, 21 differential protein spots regulated by fungus and its elicitor were identified and it was revealed

that most of them are involved in defense response against pathogens (Kim et al. 2009). Furthermore, proteomics analysis using resistant line and susceptible line to *M. oryzae* identified 4 metabolism-associated proteins such as fructokinase, triosephosphate isomerase and 2 defense proteins, GST and aminopeptidase N, indicating that proteomics analysis is a useful approach for identifying novel proteins related in pathogen resistance (Ryu et al. 2009). Meanwhile, this proteomics approach has been also used to investigate physiological interaction between plant and beneficial microorganisms promoting plant growth as well as plant response to pathogen. This method revealed that bacterial volatile-mediated plant growth response was associated with management of plant basal defenses such as endogenous ethylene synthesis pathways and the generation of ROS (Kwon et al. 2010).

Challenges for Korean plant proteomics

As shown above, we have reviewed proteomics research cases and trends focusing on plant responses to various stimuli in Korea. Proteomics has been used for the identification and quantification of stress-related proteins, mapping the dynamics of their expression and post-translational modifications. Thus, the knowledge on complexity of the plant response to various environmental stress factors help

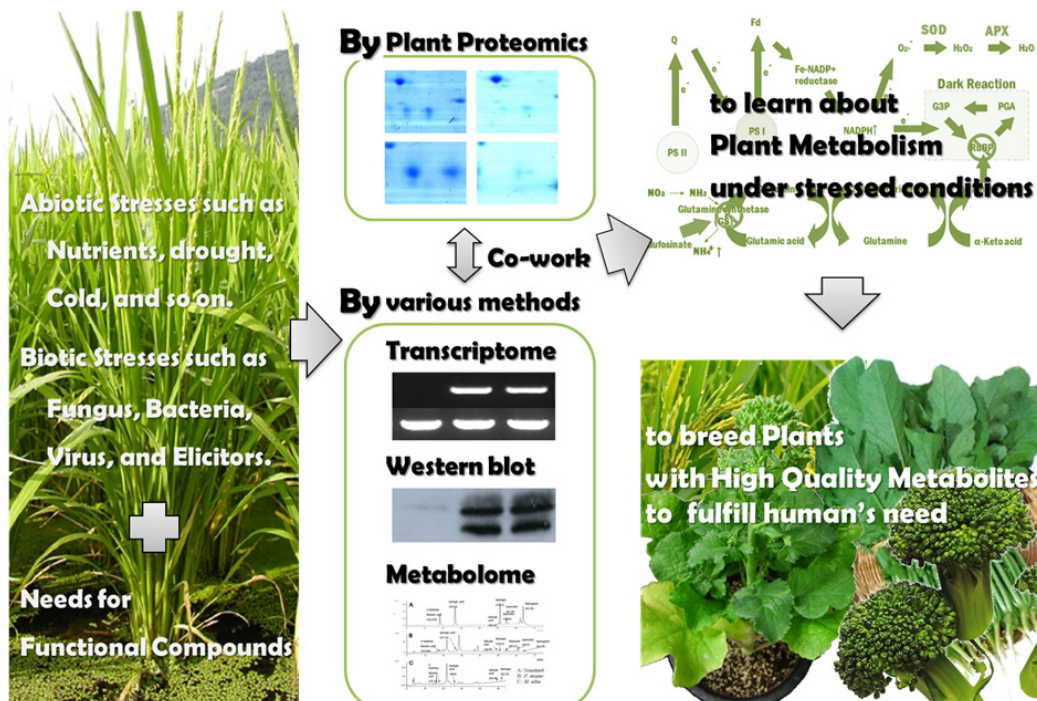


Fig. 2 An overview of the plant proteomics research concerning on the stress physiology to breed new cultivars under stressed conditions.

select biomarkers of plant tolerance to various biotic and abiotic stresses which could be usable by breeders (Vítámvás et al. 2007). In this regard, the information accumulated from these researches might provide optimal tactics for cultivating new crops with high-quality compounds even though the crops are grown under stressful conditions (Fig. 2).

The rise in the number of proteomics articles and of proteomics applications is not as great as compared with other countries including Japan, China, United States, and EU. Consequently, it is time to try proteomics approaches to broaden research areas and include various crops as well as up-to-date methods including MudPIT. There are a few studies to introduce these high-throughput approaches for studying vegetative plants of importance such as lettuce, onion, pepper, etc. Through improvements in both more accurate proteomics methods and diversification of research themes, plant proteomics will open doors for researchers to systematically approach a problem and/or biological question, and help widen the understanding of the network between plant and environment. Finally, these efforts may guarantee that Korean plant proteomers a place in major and important positions in research into plant stress physiology around the world.

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