A sharp decline in the availability of arable land and sufficient supply of irrigation water along with a continuous steep increase in food demands have exerted a pressure on farmers to produce more with fewer resources. A viable solution to release this pressure is to speed up the plant breeding process by employing biotechnology in breeding programs. The majority of biotechnological applications rely on information generated from various "-omic" technologies. The latest outstanding improvements in proteomic platforms and many other related advances in plant biotechnology offer various new ways to encourage the usage of these technologies by plant scientists for crop improvement programs. A combinatorial approach of accelerated gene discovery through genomics, proteomics, and other associated "-omic" branches of biotechnology, as an applied approach, is proving to be an effective way to speed up the crop improvement programs worldwide. In the near future, swift improvements in "-omic" databases are becoming critical and demand immediate attention for the effective utilization of these techniques to produce next-generation crops for the progressive farmers. Here, we have reviewed the recent advances in proteomics, as tools of biotechnology, which are offering great promise and leading the path toward crop improvement for sustainable agriculture.

Keywords: biotechnology, crop improvement, proteomics, sustainable agriculture

INTRODUCTION

A sharp decline in the availability of arable land and sufficient supply of irrigation water along with a continuous steep increase in food demands have exerted a pressure on farmers to produce more with fewer resources. A viable solution to release this pressure is to speed up the plant breeding process by employing biotechnology in breeding programs. The majority of biotechnological applications rely on information generated from various "-omic" technologies. The latest outstanding improvements in proteomic platforms and many other related advances in plant biotechnology offer various new ways to encourage the usage of these technologies by plant scientists for crop improvement programs. A combinatorial approach of accelerated gene discovery through genomics, proteomics, and other associated "-omic" branches of biotechnology, as an applied approach, is proving to be an effective way to speed up the crop improvement programs worldwide. In the near future, swift improvements in "-omic" databases are becoming critical and demand immediate attention for the effective utilization of these techniques to produce next-generation crops for the progressive farmers. Here, we have reviewed the recent advances in proteomics, as tools of biotechnology, which are offering great promise and leading the path toward crop improvement for sustainable agriculture.

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The knowledge of key proteins that play crucial roles in the proper growth and development of a plant are critical to propel the biotechnological improvement of crop plants. These proteins maintain cellular homeostasis under a given environment by controlling physiological and biochemical pathways. A search of the published research literature revealed that genomics and proteomics are the two major wheels that keep the discovery of novel genes rolling, which can eventually be placed into the pipeline for crop improvement programs. Two-dimensional electrophoresis (2-DE) and mass spectroscopy (MS), two of the most widely used proteomics methods, are used to catalog and identify proteins in different proteome states or environments. Advances in 2-DE have been extremely helpful in bringing proteomics close to biotechnological programs; however, due to some drawbacks and disadvantages associated with gel-based proteomics, e.g., labor intensiveness, insensitivity to low-copy number proteins, low reproducibility and the inability to characterize complete proteomes, many gel-free proteomic techniques have also become a valuable tool for scientists (Baggerman et al., 2005; Lambert et al., 2005; Scherp et al., 2011; Jayaraman et al., 2012).

**PROTEOMIC TECHNIQUES OFFER NEW TOOLS FOR PLANT BIOTECHNOLOGY**

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**COMPARATIVELY, IT IS NOW A FULLY MATURE SCIENCE AND IS PROUD TO BE ON THE LIST OF MOST QUICKLY ADOPTED CROP TECHNOLOGIES IN THE WORLD.**

Biotechnology provides the capabilities to breeders to achieve certain goals that would otherwise be impossible through conventional plant breeding approaches. Globally, today genetically modified crops are grown in fields at a commercial scale. Thus, the biotech crop area has increased from 1.7 million ha in 1996 to 160 million ha in 2011 (Khush, 2012). This trend was well-expected by Dixon (2005) when he stated that “Genomics (originally DNA- and transcript-based, but recently extended to integrate the proteome and metabolome) would play a major role in driving plant biotechnology.” This review corroborates his long vision and focuses on the use of proteomics for genetic improvements in food and biofuel crops including food quality, safety, and nutritional values, tolerance to abiotic and biotic stresses, manufacturing plant-based vaccines and proteomics-based fungicides. Apart from these, proteomics is being used for several other crop improvement programs such as, pre- and post-harvest losses, and crop quality characteristics but that is not a part of this review because of space constraints.
Table 1 | A short overview of recent gel-based and gel-free proteomics methods as biotechnological tools that could provide knowledge for crop improvement programs.

| Major crops | Technique used | Trait studied | Plant part | Reference |
|-------------|----------------|---------------|------------|-----------|
| Wheat       | 2-DE           | Desiccation   | Embryo     | Irar et al. (2010) |
|             | iTRAQ and 2D-DIGE | Drought       | Leaves     | Ford et al. (2011) |
|             | 2D-DIGE        | Salinity      | Leaves     | Gas et al. (2011) |
|             | 2-DE           | Senescence and oxidative stress | Stem | Bazargani et al. (2011) |
|             | 2-DE           | Flooding stress | Root | Kang et al. (2010) |
|             | 2-DE           | Metabolism post anthesis | Endosperm amyloplast | Dupont (2008) |
|             | 2-DE           | Fusarium head blight | Kernels | Foroud et al. (2008) |
|             | 2-DE           | Heat          | Kernels    | Laina et al. (2010) |
| Maize       | 2-DE           | Unintended effects of GM | GM vs. non-GM leaves | Barros et al. (2010) |
|             | nanoLC-LTQ-Orbitrap | C_4 leaf development | Leaves | Majeran et al. (2010) |
|             | 2-DE           | Desiccation   | Embryo     | Huang et al. (2012) |
|             | Shotgun proteomics | Photosynthesis | Chloroplast thylakoid membrane | Liu et al. (2011) |
|             | Shotgun proteomics | Desiccation   | Embryo     | Amara et al. (2012) |
|             | 2-DE           | Drought       | Xylem sap in root and stem | Alvarez et al. (2008) |
|             | iTRAQ          | Ear rot infection | Ears | Mohammadi et al. (2011) |
|             | LC-MS          | Greening of cotyledons | Leaves | Shen et al. (2008) |
| Soybean     | 2-DE           | Tolerance to Phytophthora | Hypocotyls | Zhang et al. (2010) |
|             | 2-DE and blue native PAGE | Flooding stress | Roots and hypocotyl | Komatsu et al. (2011) |
|             | 2-DE           | Oxidative stress | Leaves     | Galant et al. (2012) |
|             | 2-DE           | Heat stress    | Leaves     | Wang et al. (2012) |
|             | 2-DE           | Flooding stress | Roots, Hypocotyl, and leaves | Khatson et al. (2012) |
|             | 2-DE           | Osmotic stress | Roots      | Toorchi et al. (2009) |
|             | iTRAQ          | Enhancing water and nutrient uptake after inoculation with Bradyrhizobium | Root | Nguyen et al. (2012) |
| Rice        | 2-DE           | Response to selenium | Leaves     | Gong et al. (2012) |
|             | 2-DE           | Embryogenesis  | Embryo     | Zi et al. (2012) |
|             | Shotgun proteomics | Grains development | Grains | Lee and Koh (2011) |
|             | 2-DE           | Heat stress    | Spikelet   | Jagadish et al. (2010) |
|             | 2-DE           | Drought stress | Rice peduncles | Multhuajen et al. (2011) |
|             | iTRAQ          | Cold stress    | Leaves     | Neilson et al. (2011) |
|             | 2-DE           | Bacterial blight defense signaling | Leaves | Mahmood et al. (2009) |

could be lost (Boyer, 1982). To increase crop productivity, genes and proteins that are responsible for stress tolerance and disease resistance have to be identified continuously. In this direction, a snapshot of the cellular proteome map at a given time and under given conditions facilitates the identification of changes in protein expression (Hashiguchi et al., 2010). Advancements in MS-based proteomics platforms have been considered to be “New Genomics” because MS has become an indispensable tool for the investigation of the PTMs to proteins, and protein interactions. These data provide an unprecedented insight into how cells make decisions and are thus a cornerstone of systems biology (Cox and Mann, 2007). None-the-less, the knowledge about the interacting protein partners, essential for the success of the function of a particular protein, might be a good target for gene pyramiding in species that lack the interacting protein(s). In the recent past, several successful projects have been completed to create proteome maps of various crops using 2-DE and/or other proteomic approaches. For example, in wheat a reference map has been created for leaves (Donnelly et al., 2003), roots (Song et al., 2007), endosperm (Vensel et al., 2005), and amyloplasts (Balmer et al., 2006).
As with any living organism, crop plants also have to cope with various biotic and abiotic stress conditions. Contrary to greenhouse nurseries, plants in the field experience a combination of various stresses throughout the growing season (Tester and Bacic, 2005; Mittler, 2006).

A recent estimate suggested that the increased temperatures of the past two decades have caused a loss of approximately $5 billion by impacting the yields of major food crops such as wheat, rice, maize, and soybeans (Peng et al., 2004). Temperatures reaching 35°C in the field cause rice and maize to show sterility. Such high heat conditions in the field also lead to flowering and fruiting failure in other crops. Molecular plant physiologists know very well that heat stress increases membrane damage and impairs metabolic functions (Taux and Zeiger, 2010). A plant breeder needs to activate the proper protection systems in a crop plant to enable the survival of the plant’s cells under such heat stress conditions. Heat stress tolerance is a complex mechanism and is controlled by multiple genes and proteins involving a number of physiological and biochemical changes in the cell, e.g., adjustments in the membrane structure and function, tissue water content, protein composition, lipids, and primary and secondary metabolites (Huang and Xu, 2018). Global proteomic profiling projects are useful techniques for increasing the knowledge base of plant breeders. For example, a study comparing various wheat cultivars with different heat tolerance capabilities revealed low molecular weight (16–17 kDa) heat shock protein (HSPs) and other metabolic proteins crucial for the heat tolerance phenotype (Majee et al., 2004). Proteins from the HSP family and the transcription factors upstream of these HSPs have been found to have crucial roles in providing thermotolerance to the crop. Disarming the function of HSP100 by introducing an antisense construct in tomato plants resulted in their poor survival under heat stress conditions (Yang et al., 2006). However, in another study, transgenic lines overexpressing a different HSP protein (HSP90) showed superior thermotolerance in soybean plants (Zhai et al., 2006). Furthermore, protein–protein interaction studies have proved that HSP90 interacts with calmodulin-binding protein (CBP) (Vindi et al., 2009). Thus, the studies by Zhang et al. (2009) showed that the knockdown of calmodulin resulted in reduced thermotolerance. Proteins other than HSPs, e.g., CBP in the above study, have been identified in other proteomic studies as differentially expressed proteins during heat stress conditions. Sule et al. (2004) proposed S-adenosylmethionine synthetase as a molecular marker for screening heat-tolerant germplasms. Even with this information, knowledge on the systemic response of plants during heat stress remains limited because plant perception and response to a single stress is different than to a combination of multiple stresses.

There is another major constraint to world agriculture in the form of limited water availability for crop irrigation. Recent climate variability from year to year predicts a worsening situation in the future. World climatologists predict that global warming will result in more frequent and severe droughts in the coming years.

Drought stress causes a decrease in carbon usage by the photosynthetic machinery that result in net yield losses on the farm. Physiological experiments have shown that drought conditions inhibit plant photosynthesis within a short time of a limited water supply resulting in a drop in the CO₂ assimilation rates (Ribas-Carbo et al., 2005). To minimize water loss, plants need to close their stomata under water deficient conditions. The guard cells help the plant in the process of controlling the opening and closing of the stomata. The closure/opening of the stomata is controlled by the plant hormone, abscisic acid (ABA). In a plant cell, ABA flux concentrations are controlled in response to the availability of water to the plant. ABA has been found to play an indispensable role in the plant response to drought conditions by inducing many transcription factors. In this direction, the guard cell proteome profiling by Zhao et al. (2008) revealed 336 proteins responsive to water stress conditions, with a further 52 proteins considered to be signaling proteins. Abiotic stresses in general cause a water deficit condition in cells that results in a myriad of complex cellular and physiological responses at the plant cellular and organismal levels. In general, the net photosynthesis rate is reduced either because of stomatal closure or via metabolic impairment (Reddy et al., 2004). The changes in mitochondrial respiration and the photosynthetic electron transport chain lead to the generation of highly toxic reactive oxygen species (ROS), such as superoxides and peroxides, and cause chemical damage to the DNA and proteins. This damage has serious effects on cellular metabolism (Mittler, 2002).

During evolution, plants have developed several strategies to address ROS, e.g., avoidance by anatomical adaptation, photosynthesis suppression and photosystem and antenna protein complex modulations. Several metabolites, such as ascorbate and glutathione, and enzymes, such as peroxidases and superoxide dismutases, help to scavenge the ROS (Mittler, 2006). Another plant strategy to address drought conditions is to maintain the turgor pressure of plant cells by the overproduction of osmolytes, such as proline, glycine betaine, and trehalose. These metabolites provide secondary protective effects to proteins against misfolding (Hare et al., 1998). Moreover, dehydration responsive proteins, such as dehydrins and HSPs, are over produced to protect the intracellular metabolic machinery (Wang et al., 2003). In short, with such a wealth of knowledge, drought-tolerant plants can be generated by the modification of these mechanisms, e.g., ABA signaling can be adjusted for the better survival of a crop plant under such stress conditions. The level of sphingosine-1-phosphate, a messenger molecule, is controlled by ABA through the sphingosine kinase protein. In another study using a sphingosine-1-phosphate lyase mutant, the accumulation of sphingosine-1-phosphate decreased the fresh weight loss of plants under drought stress conditions.
controlling water loss from the stomata (Nishikawa et al., 2008). Hajheidari et al. (2005) report the predominance of proteins that are related to ROS management and protein stability after investigating the proteomic profiling of field-grown plants under drought stress conditions.

Proteomic approaches are useful in the study of the molecular mechanism involved in the interaction between a plant and its pathogens (Zhou et al., 2006). This group inoculated the wheat spikelet with the fungal spores of Fusarium graminearum and subjected the total proteins from the infected spikelet to 2-DE for proteome profiling under normal and infected conditions. They discovered that 41 proteins were differentially regulated due to Fusarium infection. The gene ontology (GO) annotation revealed that the up-regulated proteins were from the antioxidant and JA signaling pathways, pathogenesis-related response, amino acid synthesis and nitrogen metabolism, whereas the down-regulated proteins were from the photosynthesis pathway. A DNA-damage inducible protein was found to be up-regulated and glycosylated (a type of PDM) in a Fusarium-infected spikelet. Furthermore, utilizing the TargetP software, several identified plant proteins were predicted to localize to the chloroplast. This knowledge further strengthened the previous finding that the chloroplast is the organelle most affected by Fusarium infections. Several fungal proteins were also identified and found to possess antioxidant and carbon-acquiring functions from the plant through the glycolysis reaction during a compatible interaction between Fusarium and the plant. Studying the proteome response of the resistant wheat cultivar Wangshuibaizi, Wang et al. (2005) found that expression of the carbon metabolism and photosynthesis genes decreased significantly after 6, 12, and 24 h of spike inoculation with the fungus Fusarium. In a separate study, the global proteomic analysis of germinating maize embryos after infection with Fusarium verticillioides highlighted the contribution of protein synthesis, protein folding, and stabilization, and oxidative stress tolerance proteins (Campo et al., 2004). Chivasa et al. (2005) studied a maize cell suspension culture with pathogen elicitors and showed that the responses to the pathogen attacks were localized to the extracellular matrix. The elicitor treatment of the cell cultures induced a rapid change in the phosphorylation status of extracellular peroxidases, the disappearance of the putative extracellular b,N-acetylglucosaminidase, and the accumulation of glyceraldehyde-3-phosphate dehydrogenase and a fragment of a putative HSP were observed at the start of the defense response time. Konishi et al. (2001) identified protein expression changes in rice leaves infected with the blast fungus Magnaporthe grisea. They found a correlation between quantitative expression changes in blast responsive proteins and the amount of applied nitrogen fertilizer. The large and small Rubisco subunits were among the proteins that were increased by the nitrogen applications, whereas the small Rubisco subunit was reduced after a nitrogen application. After the Magnaporthe infection, PR1 was among the proteins that were induced by the nitrogen application. Based on the results of this study, these proteins were proposed to potentially be involved in the incompatible interactions between the plants and the fungus and thus might be good candidates for approaching through plant biotechnology.

Proteins from the rice plasma membrane were studied by Chen et al. (2007), who analyzed the early defense responses involved in Xa21-mediated disease resistance. Xa21 is a receptor kinase in rice, and is predicted to detect the pathogen (Xanthomonas) signal on the cell surface. In this investigation, 20 proteins were found differentially expressed by Xanthomonas infection after 12 and 24 h of inoculation. Eight of these proteins were plasma membrane-associated proteins and had potential functions in rice defense, whereas two proteins were not associated with the plasma membrane. By comparing two partially resistant lines with a susceptible control tomato line over time (72 and 144 h post-inoculation), plant proteins were found to be regulated in response to Clavibacter michiganensis sp. Michigananesis infection. Using a 2-DE approach, 26 differentially regulated plant proteins were discovered, with 12 being stress response proteins and related to defense protein families (PR3 and PR9; Coaker et al., 2004). The resistant tomato line showed the up-regulation of PR3, SOD, thioredoxin, and S-adenosylhomocysteine hydrolase genes. In Medicago truncatula, a global proteomic analysis was used to characterize the plant response to the pathogenic bacterium Pseudomonas aeruginosa (Mathesius et al., 2003). The study established that 154 proteins were accumulated upon exposure to P. aeruginosa, with 21 of those proteins reported to be related to the defense and stress response mechanisms. Afroz et al. (2009) reported the differential expression of proteins in bacterial wilt-sensitive and wilt-resistant tomato cultivars using 2-DE and Edman sequencing. Molecular chaperones and proteins related to defense storage were highly expressed in the resistant cultivars compared with the susceptible cultivars.

All of the studies described above, and many that are not included here because of space limitations, are decent examples that prove that proteomics is highly capable of discovering novel genes/proteins that could be potential candidates for further studies via biotechnological approaches. We hope that, with time, the data sets for crop proteomics will strengthen further and that we will be able to see examples in which such proteomic-based knowledge is used directly for the improvement of the stress tolerance of a crop plant (Agarwal et al., 2012).

MANUFACTURING PLANT-BASED VACCINES IS A POSSIBILITY IN NEAR FUTURE

An antigen of interest, when overexpressed in plant tissues by a biotechnological approach, is considered to be a plant-based vaccine (Chergeygue et al., 2001). In situations dealing with a poorly characterized pathogen, a genomic or proteomic approach is specifically useful to identify the candidate antigens that possess favorable characteristics (Scarselli et al., 2005; Streathfield, 2005). A major advantage of plant-based vaccines is “no safety concerns” (Tacket et al., 1998a, 2000; Kapusta et al., 1999). The production of vaccine antigens in plants can be achieved through either stable expression or transient expression systems. The stable genetic transformation produces a genetically engineered plant producing the antigen, and this plant can be propagated either asexually through stem cuttings or sexually through seeds (Tacket et al., 1998b, 2000). On the other hand, transient expression uses recombinant plant virus that carries the vaccine gene and directs the plant to produce the antigen via systemic infection (Koprowski 2000).

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and Yuasbov, 2001). Tomato is good alternative for edible vaccines and was used to express orally immunogenic respiratory syncytial virus (RSV) fusion (F) protein in the fruit (Sandhu et al., 2000). Banana is also another good alternative for edible plant vaccines since it is widely grown and transformation has been reported (May et al., 1995). Potato is considered a good model for edible vaccines and the first edible vaccine was tested in potatoes (Tacket et al., 1998b). However, from an economic point of view, it would be better if major crops such as soybean, alfalfa, or corn can also be made efficient plant systems for recombinant antigen protein production (Sanford et al., 1993). Enterotoxigenic bacteria such as Escherichia coli and Cholera cause diarrhea due to the secretion of toxins that specifically bind to GM1 gangliosides present on epithelial cell surfaces of small intestine (Sixma et al., 1991). Cholera toxin (CT) and E. coli bile tolerant (LT) are homologous multi-subunit proteins in which the non-toxic B subunit mediates GM1 and thus can be candidates for vaccines that can neutralize toxin activity. Both LT-B (Mason et al., 1998) and CT-B (Arakawa et al., 1998) expressed in transgenic potatoes produced toxin-protective intestinal antibody responses after ingestion, and this shows that plants produced correctly folded proteins and assembled native GM1-binding parametric complexes. LT-B potatoes have been used in a clinical study to test the edible plant vaccine (Tacket et al., 1998b). This study successfully shows that transgenic plant material expressing the antigen, are capable of simulating the antibody response in humans. Similarly, several clinical trials have also been performed for other projects, e.g., rabies (Modecki et al., 1998), and E. coli O157:H7 (Judge et al., 2004). A step ahead, Witz et al. (2012) described a fully automated “factory” that uses tobacco plants to produce large quantities of vaccines and other therapeutic biologics within weeks using a biotechnology approach, representing a perfect example and motivation for future endeavors in this direction.

**ANALYSES OF FOOD QUALITY, SAFETY, AND NUTRITIONAL VALUES ARE MORE MEANINGFUL**

The field of proteomics has been used to analyze the differences between the nutritional values of food crops through the analysis of their proteomes. Ishwahi and Hossoda (2000) reported that heat stress increased the expression of invertases in tomato fruits, thus increasing their sucrose content and producing sweeter tomatoes. As physiological disorders appear in crop if they are not harvested at right stage and may result in huge economic losses (Elso et al., 2007; Pedreschi et al., 2007, 2008, 2009), proteomic-based approaches have become useful to detect biomarkers for optimal harvest maturity (Abdi et al., 2002). Analysis of post-harvest withering process in grapes is very critical to produce high quality wines, and thus gel-based proteomics analysis of this process has been employed for improving grape quality (De Casti et al., 2011). Also understanding the ripening and post-harvest physiology during storage will not only have impact on food quality but also on the optimization of the technological processes involved. Proteomics have investigated the reason that heat treatment for peach fruits will improve the peach fruit quality and shelf-life, and the reason was the differentially expressed proteins that were involved in fruit development and ripening (Zhang et al., 2011a). On the other hand, in cereal industry, proteomics was used for investigating the protein biomarkers for the selection of suitable durum wheat cultivars for pasta making (De Angelis et al., 2008). Flour quality is highly correlated with protein composition and functional quality, thus proteomics can be very useful to identify protein markers for suitable cultivars for flour making (Yahata et al., 2005). The proteomic analysis of wheat kernels for amphiphilic proteins increased the knowledge of the physiologic and technological functions of wheat kernels (Amiour et al., 2002). Salt et al. (2005) used 2-DE approach to identify the soluble proteins that play an important role in stabilizing the gas bubbles in dough and influencing the crumbling structure of proteins. Proteomics has also helped in the construction of proteome map investigating the level of protein modification during barley malting and detecting the proteins associated with beer quality (Iimure et al., 2010). Proteomics also had a role in food authenticity, through using sensitive protein biomarkers (Pischetsrieder and Baeuerlein, 2009). Proteomics was used to identify cheaper substituents for cheaper cultivars of coffee varieties through the use of specific biomarkers (Gil-Agusti et al., 2005). Plant or fruit extracts used in formulas can also be authenticated by the use of protein biomarkers to assess the genuineness of the formula or product (D’Amato et al., 2011; Faoli et al., 2011).

Food allergens are a great threat to people suffering from such allergies. However, DNA-based techniques have successfully been used but these techniques have limitations as in many instances DNA was completely absent while high quantities of allergy triggering proteins were still present, as in the case of egg white (Popping and Godefroy, 2011). Proteomics is a crucial field for sensitively detecting and quantifying food allergens. A combination of 2-DE and IgE reactive proteins using an allergic patient’s sera has been applied as an approach to characterize the allergenicity of food proteins (Akagawa et al., 2007; Pischetsrieder and Baeuerlein, 2009). Through a proteomics experiment, in which extracted sesame seed proteins were separated by 2-DE followed by immuno-labeling with individual patient sera from 20 patients with sesame seed allergy, four allergen including 7S vicilin-type globulin, 2S albumin seed maturation protein, and embryogenic abundant protein were identified in this study (Beyer et al., 2002). Petersen et al. (2006) compared the allergenic potency of maize pollen and the native grass Phleum pratense using 2-DE followed by immuno-blotting, and found that maize pollen showed less allergic response in comparison to the native grass due to lower allergen content and lower allergic groups found in maize pollen. Herrndl et al. (2007) also studied apple allergen using 2-DE with IgE-immuno-blotting and identified four new apple allergens known as Mal d 1, Mal d 2, Mal d 3, and Mal d 4. Proteomics analysis of rice leaf, root, and seed showed the presence of many allergenic proteins in the seeds, which implicate the uses of proteomic analysis of foods for the presence of allergens (Koller et al., 2002). Shotgun proteomics was also used to characterize the allergenicity of certain foods (Chassaing et al., 2007; Heik et al., 2011b). The generated information is key for targeted approaches, such as selective reaction monitoring (SRM), which not only detect the allergen but also quantify it (Heic et al., 2011a; Lutter et al., 2011). Recently, multi-allergen detection based on an SRM approach was used in the detection of seven allergenic foods in bread, five of which are plant origin (Heic et al., 2011a). None-the-less, once a protein of
a specific gene or gene families of allergen is confirmed, its expres-
son can be silenced through biotechnological approaches for a
safer human consumption of that food (Thelen, 2009).
Recently, proteomics has been used to investigate "plant-based
bioactives" to improve the nutritional value of food crops. Bioac-
tives are the peptides that are released either during digestion by the
host enzymes or during food processing and ripening by microbial
enzymes (Brambilla et al., 2009). Bioactives were reported from
different plant sources, such as wheat, rice, maize, soybean, mush-
rooms, pumpkins, and sorghum (Möller et al., 2008). Soybean
bioactive peptides, such as lunasin, Bowman–Birk inhibitor, lectin,
and beta-conglycinin, have attracted the attention of researchers
who study their antioxidant activities (de Lumen, 2005) to treat
oxidative stress in the future (Kussmann et al., 2010). Lupin also
contains alpha and beta-conglutins as storage proteins and appears
to have bioactive effects (Brambilla et al., 2009).

**BIODFUEL CROP SCIENCE IS ON RIGHT TRACK TO GET BENEFITED BY
PROTEOMICS**

Biofuels are obtained primarily from plant biomass, and are
believed to have the capacity in the future for substituting fos-
sil fuels for sustainable bioenergy needs (Yuan et al., 2008). Uses
of biofuels make a balance between the consumption and release
of CO2 in the atmosphere. Biofuels, unlike fossil fuels, are made
from clean renewable resources such as plants, algae, or photosyn-
trophic microbes (Schmool, 2010; Somerville et al., 2010). As the
transition from the use of prevalent fossil fuels to the renewable
energy resources is a complicated procedure comprising scientific
and socio-economic problems (Kullander, 2010), it is very impor-
tant to shift from using the first generation biofuel crops, such as
sugar cane or corn, to the second generation biofuel crops, such as
*Manicaria* and *Cordegrass for the production of bioethanol from
 lignocellulosic materials found in plants to make a swift change
to the most recent and third generation biofuel organisms such as
photosynthetic microbes and microalgae. Currently, maize, sug-
arcane, and rapeseed are among major the crops that are being used
for biofuels. One good example of including a new bio-
fuel crop to the list that is under investigation is African grain sorghum. It has been used as food and feed and is now gaining
much attention as energy crop (Calvino and Messing, 2012). The
an in vitro suspension culture of sorghum and the characterization of its
cell secretome using 2-DE and MS/MS have been studied (Ngara
et al., 2008; Ngara and Ndomba, 2011). Another important crop is
a non-domesticated oil crop, *jatropha curcas L.*, has been getting
much attention for its oil, which can be converted to bio-diesel,
and for its ability to be easily cultivated in arid and semi-arid
regions, including wastelands (Johnson et al., 2011). Proteomics
has been used to explore the oil body and identify the proteins
for oil biogenesis (Liu et al., 2009; Yang et al., 2009). These pro-
teins can be used to employ phylogenetic and molecular breeding
strategies in the improvement of this crop (Johnson et al., 2011).
*Populus trichocarpa* is a tree model system for energy crops (Singh
et al., 2011). Kalluri et al. (2009) used a proteomics, a LC-MS/MS-
based approach, and discovered new potential candidate genes in
xylem tissues that play an important role in cell wall biosynthesis
in addition to cellulase synthase, sucrose synthase, and polygalac-
turanase. In this way, the use of proteomics to identify candidate
proteins (and genes) to improve energy crops for their growing on
marginal lands, cheaper breakdown of cellulose and increased total
biomass will be reflected in the yield and quantity of their biofuel
production capabilities. *Chlamydomonas reinhardtii* is considered
as a model system for photosynthetic growth and lipid and
hydrogen production. As these unicellular green algae has been
studied and sequenced in many laboratories, it now serves as a
model of choice for physiological, ecophysiological, and econom-
ical study for the production of biofuels (Huang, 1986; Merchant
et al., 2007). The remarkable metabolism of *Chlamydomonas* for
energy productions was observed based on its proteomic inves-
tigations (Wienkoop et al., 2010). During the investigation, the
metabolism showed pronounced effects of carbon concentrat-
ing mechanism, which makes the CO2 more available for Calvin
cycle using carbonic anhydrases. Nearly, 12 isoforms of carbonic
anhydrases (CAH4) were found in *Chlamydomonas*, and five iso-
forms were measured with targeted proteomics and revealed the
differences of these isoforms in respect of concentration pat-
tterns (attomole/1000 cells). The mitochondrial isoform of CAH4
showed a very high dynamic range and high activity under the
limiting conditions of CO2 (Wienkoop et al., 2010). This indi-
cates to the significant role of carbonic anhydrases in CO2-sensing
pathways in higher plants as well as microalgae, and this novel
information improves our understanding and can be used to
enhance CO2 fixation mechanisms for better biomass production
and for increasing the efficiency of biofuel productions irrespec-
tive of plants or microalgae (Hu et al., 2009; Moroney et al., 2011;
Xue et al., 2011).

**DEVELOPMENT OF PROTEOMICS-BASED FUNGICIDES IS A POSSIBILITY**

This possibility relies on the hypothesis that the majority of drug
targets are proteins and the proteomics can provide the canti-
date protein involved in a specific biological mechanism. Several
changes in the design of chemical fungicides are being undertaken
by the scientific research community by summarizing the available
genomic and proteomic information. Moreover, bioinformatics
can come to help in predicting a protein as a fungicide. Biosyn-
thetic fungicide design that is disease-associated target oriented
has been established as a new focus in fungicide development (Col-
lado et al., 2007; Acero et al., 2011). However, this field is mostly at
its beginning stage but the fungicide design and selection based on
target identification information utilizing proteomics experiments
is going to change the market in the next 10 years (Garrido et al.,
2010; Acero et al., 2011). In depth proteomic and genomic studies
of fungal infection biology are a pre-requisite of such projects. The
use of modified natural compounds provides a potential species-
specific method of controlling plant pathogens by the specific
inhibition of those proteins involved in the infection cycle (Finozo
et al., 2008). The use of these compounds minimizes their environ-
mental impact if they are biodegradable, possess high specificity,
and have the further advantage of poor penetration into the food
chain. In short, such an application of chemo-genomics to protein
targets is named "choemo-proteomics," although a more explicit
definition is target related affinity profiling (TRAP), defined as
the use of biology to inform chemistry (Benna et al., 2003). The
accumulation of proteomic information about fungal plant
pathogens may be an incentive to the development of new and

environmentally friendly fungicides. One of the most promising biotechnologies downstream of proteomics is the use of specific peptide sequences that are able to modify protein activities in the pathogen. One encouraging strategy to combat fungal diseases in the field is the use of a novel chemical proteomics tool called activity-based protein profiling (ABPP). Richard and van der Hoorn, 2010, and that is why understanding the involved biological processes is so crucial. A small-molecule fluorescent probe is used in ABPP; the probe irreversibly reacts with the catalytic sites of catalytic substrates in an activity-dependent manner. By using fluorescent protein gels, the protein activities can be quantified to study these activities in vitro and in vivo (Giu et al., 2010).

CONCLUSION

During the recent past, world agriculture has come under more climatic variability along with less arable land availability per person, which compounds the stress situation on producer groups. In the present scenario, pressure is building upon the plant breeders and plant biologists to come up with “smart crop varieties” that are better suited genotypes with the ability to withstand conditions of future generations along with maintaining/exceeding a wider range of climatic variability to tackle the food insecurity. One encouraging strategy to combat fungal diseases is the use of specific biotechnologies downstream of proteomics. A small-molecule fluorescent probe is used in ABPP; the probe irreversibly reacts with the catalytic sites of catalytic substrates in an activity-dependent manner. By using fluorescent protein gels, the protein activities can be quantified to study these activities in vitro and in vivo (Giu et al., 2010).

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