

Plant	Stress	Proteomics techniques	IP <sup>a</sup>	Major findings	References
Rice	Dehydration	2-DE LC-TOF MS	94	Dehydration-responsive proteins mainly involved in a variety of functions, including carbohydrate metabolism, cell defense and rescue, cell wall modification, cell signaling and molecular chaperones	Pandey et al., 2010
Rice	Hydrogen peroxide	2-DE MALDI TOF/TOF MS	54	These proteins identified are involved in a variety of processes, including redox homeostasis, cell wall modification, signal transduction, cell defense and carbohydrate metabolism, indicating a complex regulative network in the apoplast of seedling roots under H <sub>2</sub> O <sub>2</sub> stress	Zhou et al., 2011
Maize	Water deficit	2-DE Q-TOF MS	152	Water stress-responsive proteins were identified and categorized, into five groups; apoplastic ROS level increases in the apical region of the elongation zone of water stressed maize roots and hence provides novel information about the complex mechanisms regulating root growth under water stress	Zhu et al., 2007
Maize	Pathogen	2-DE MALDI-TOF MS	12	Secretion of a new class of putative enzyme inhibitor, the apparent recruitment of classical cytosolic proteins into the cell wall, and the change in phosphorylation status of extracellular matrix proteins	Chivasa et al., 2005
Chickpea	Dehydration	2-DE LC-TOF MS	134	More than hundred extracellular matrix proteins with a variety of cellular functions which are cell wall modification, signal transduction, metabolism, and cell defense and rescue, play crucial roles in dehydration stress sensing and tolerance mechanism	Bhushan et al., 2007
Soybean	Flooding	2-DE MALDI-TOF MS and nanoLC MS/MS	16	Two lipoxygenases, germin-like protein precursors, glycoprotein precursors, super oxide dismutase were decreased, and then lignification was suppressed under flooding stress	Komatsu et al., 2010
Wheat	Flooding	2-DE nanoLC MS/MS Gel-free nanoLC MS/MS	18 15	Four proteins were upregulated and 14 proteins were down-regulated by flooding stress. Both gel-based proteomic system and LC-MS/MS-based proteomic system under flooding stress, most were disease/defense proteins	Kong et al., 2009

<sup>a</sup>IP, Number of identified proteins.