

Treatments	Crop species and tissue	Common points	Difference	References
Nitric oxide	<i>Gossypium hirsutum</i> , leaf	<ol style="list-style-type: none"> 1. Distribution of pS and phosphorylated Ser accounts for most of distribution and phosphorylated sites. 2. 34 common phosphorylated proteins were detected, such as CTR1, STN7, Phosphoenolpyruvate carboxylase 2, phototropin-2, Chloride channel protein CLC-c, Dynamin-2B, Monosaccharide-sensing protein 2, TBC1 domain family member 15, Serine/threonine-protein kinase HT1, Nitrate reductase, dehydrin, Heat shock protein 81, Nuclear Transcription factor Y subunit B-3, Aquaporin PIP2-7, Peptidyl-prolyl cis-trans isomerase, Sodium/hydrogen exchanger, Eukaryotic translation initiation factor 4G, DEAD-box ATP-dependent RNA helicase 3, Transcription factor RF2b, Sugar Ion/protein transporter ERD6-like 6, 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1, TPR repeat-containing protein, Chaperone protein dnaJ, Meiosis protein mei2, Polyphosphoinositide phosphatase, LRR receptor-like serine/threonine-protein kinase, Inositol hexakisphosphate, Chlorophyll A-B binding protein, Stem-specific protein TSJT1, Ankyrin repeat-containing protein, Zinc finger family protein, Bromodomain containing protein, KH domain containing protein and diphosphoinositol-pentakisphosphate kinase. 3. There are no significant fold change in CTR1, STN7, Phosphoenolpyruvate carboxylase 2, phototropin-2, Chloride channel protein CLC-c, Dynamin-2B, Monosaccharide-sensing protein 2, TBC1 domain family member 15, Serine/threonine-protein kinase HT1, Nitrate reductase, DEAD-box ATP-dependent RNA helicase 3, dehydrin, Nuclear Transcription factor Y subunit B-3, Aquaporin PIP2-7, Eukaryotic translation initiation factor 4G, Transcription factor RF2b, Sugar Ion/protein transporter ERD6-like 6, 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1, TPR repeat-containing protein, Meiosis protein mei2, Polyphosphoinositide phosphatase, Inositol hexakisphosphate, 60S acidic ribosomal protein and diphosphoinositol-pentakisphosphate kinase. 	<ol style="list-style-type: none"> 1. 34 up-regulated DEPPs and 50 down-regulated DEPPs were detected in the reference, but in this study only 12 up-regulated DEPPs and 12 down-regulated DEPPs were found. 2. LRR receptor-like serine/threonine-protein kinase, Stem-specific protein TSJT1, 60S acidic ribosomal protein and Chlorophyll A-B binding protein were up-regulated, and Peptidyl-prolyl cis-trans isomerase, Zinc finger family protein and Chaperone protein dnaJ were down-regulated in the reference. 	Quantitative phosphoproteomics analysis of nitric oxide-responsive phosphoproteins in cotton leaf

		<ol style="list-style-type: none"> Heat shock protein 81, Sodium/hydrogen exchanger were up-regulated in both of two studies. Ankyrin repeat-containing protein, Bromodomain containing protein, KH domain containing protein were down-regulated in both of two studies. 		
Drought	<i>Triticum aestivum</i> L., leaf	<ol style="list-style-type: none"> Three interesting function categories, such as signal transduction, RNA transcription/processing and stress defense stood out in both of studies. 9 common phosphorylated proteins were detected, such as LRR receptor-like serine/threonine-protein kinase, Monosaccharide-sensing protein 2, TBC1 domain family member 15, Serine/threonine-protein kinase HT1, Peptidyl-prolyl cis-trans isomerase, FACT complex subunit SSRP1-B, Serine/threonine-protein kinase CTR1, Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2, Zinc finger family protein. LRR receptor-like serine/threonine-protein kinase, Serine/threonine-protein kinase HT1, Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 were down-regulated. Monosaccharide-sensing protein 2 were up-regulated. 	<ol style="list-style-type: none"> TBC1 domain family member 15, Zinc finger family protein were up-regulated in this reference. Peptidyl-prolyl cis-trans isomerase, FACT complex subunit SSRP1-B were down-regulated in this reference. But it was up-regulated in this study. There is no significant change of Serine/threonine-protein kinase CTR1 in this reference. 	Phosphoproteome analysis reveals new drought response and defense mechanisms of seedling leaves in bread wheat (<i>Triticum aestivum</i> L.)
Drought	<i>Triticum aestivum</i> L., grains	<ol style="list-style-type: none"> 7 phosphoproteins including DEAD-box ATP-dependent RNA helicase, heat shock protein 90, Nuclear transcription factor Y subunit B, Eukaryotic translation initiation factor 4G, DnaJ homolog subfamily C member, CTR1, Putative LRR receptor-like serine/threonine-protein kinase were detected in both of studies. DEAD-box ATP-dependent RNA helicase, heat shock protein 90 and CTR1 were up-regulated. DnaJ homolog subfamily C member was down-regulated. 	<ol style="list-style-type: none"> Cellular protein modification, carbohydrate metabolism, and the nucleobase-containing compound process accounted for about 50% of all phosphoproteins in this reference. Nuclear transcription factor Y subunit B-4 did not change significantly in this reference. Eukaryotic translation initiation factor isoform 4G, Putative LRR receptor-like serine/threonine-protein kinase were up-regulated in this reference. 	Comparative phosphoproteome analysis of the developing grains in bread wheat (<i>Triticum aestivum</i> L.) under well-watered and water deficit conditions