

NEWS:

Proteomics and metabolomics for plant improvement

Although QTLs/candidate genes/alleles have been used in breeding programmes, it has been observed that structural/expression variation identified at the genetic level are not always translated into the “predicted” phenotype. Additionally, mechanisms involved in stress tolerance can be complicated, e.g., the involvement of metabolites, multigenes and post-translational modifications (PTM) which cannot be investigated by genomics or transcriptomics approaches. In this context, with high resolution LC-MS/MS, proteomics and metabolomics (1) are efficient approaches to enhance our understanding of functional molecules on specific aspects of multigene families and PTMs (2), instead of analyzing the genetic code (DNA) or transcript (RNA) abundance which may not correlate with their corresponding proteins. Even the large genomes limitations (3) are no longer a problem and the LC-MS/MS dynamic range is sufficient after simple prefractionations.

- (1) Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. Ramalingam A. and all. 2015 <http://www.ncbi.nlm.nih.gov/pubmed/26734026>
- (2) Proteome-Wide Identification of Lysine Succinylation in the Proteins of Tomato (*Solanum lycopersicum*). Jin W and all. 2016 <http://www.ncbi.nlm.nih.gov/pubmed/26828863>
- (3) Opportunities for wheat proteomics to discover the biomarkers for respiration-dependent biomass production, stress tolerance and cytoplasmic male sterility. Jacoby RP and all. 2016 <http://www.ncbi.nlm.nih.gov/pubmed/26915586>

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