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Editorial: Regulation of proteolysis and proteome composition in plant response to environmental stress

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Editorial on the Research Topic

Regulation of proteolysis and proteome composition in plant response to environmental stress

Introduction

Because of their sedentary lifestyle, plants are susceptible to changing environmental conditions. They must cope with miscellaneous abiotic stresses usually enhanced by heavy industry (Labudda et al., 2022). Moreover, changes in climate conditions and agricultural systems are favourable to pests and pathogens gradation on plants (Nykiel et al., 2022; Skoracka et al., 2022). However, plants are not defenceless; they are equipped with a battery of multiple mechanisms (from molecular through biochemical-physiological to structural) that are activated by them to ensure further growth and development and the production of diasporas (Muszyńska and Labudda, 2019; Formela-Luboińska et al., 2020; Tokarz et al., 2020; Tokarz et al., 2021; Fidler et al., 2022; Miernicka et al., 2022). Among these mechanisms, the control of proteolysis and thereby the quality and composition of proteins and pool of amino acids are of fundamental significance (Muszyńska et al., 2019; Labudda et al., 2020; O'Conner et al., 2021; Pan et al., 2021; Szewińska et al., 2021; Tan et al., 2021; Sun et al., 2022; Tanvir et al., 2022; Xing et al., 2022).

Proteolysis is an elementary biochemical process indispensable for protein metabolism. A wide spectrum of proteolytic enzymes is involved in this process, including exopeptidases (amino and carboxypeptidases) and endopeptidases (serine, aspartic, metallo- and cysteine peptidases) (Godson and van der Hoorn, 2021; van der Hoorn and Klemenčič, 2021). As uncontrolled proteolysis can seriously damage plant cells, the activity of peptidases is accurately regulated by their endogenous inhibitors

(Prabucka et al., 2017; Kunert and Pillay, 2022). Thus, an understanding of the mechanisms assuring the accurate regulation of peptidase activity and the dynamic alterations in the proteome and amino acids of plants struggling with environmental stresses is an urgent task undertaken by numerous teams from all over the world.

This Research Topic aimed to widen the understanding on protein and amino acid metabolism mechanisms in plants using an interdisciplinary approach. The Research Topic contains ten papers from several fields across abiotic stress (acid rain, low and elevated temperatures, salt, osmotic, and abscisic acid (ABA) treatments, and phosphate starvation) and biotic stress (infection with *Verticillium dahliae*). Two review articles are a valuable addition to the experimental articles. The first review by Zhang et al. concerns the application of TurboID-based proximity labelling in studying the protein interaction network in plant response to abiotic stress, while the second by Mangena shows the pleiotropic effects of recombinant protease inhibitors in plants.

What new have we learned from this Research Topic?

As Topic Editors, it was our pleasure and honour to review and manage the submitted manuscripts. In this editorial, we recapitulate the main findings of the published articles.

One of the abiotic stress, acid rain (AR) may cause severe damage to plant functioning. This problem is especially noticeable in woody plants. Hu et al. investigated the response of *Taxus wallichiana* var. *mairei* to AR stress. These authors showed that, in *T. wallichiana* var. *mairei* plants grown under AR stress in the soil with low calcium (Ca) level, the net photosynthetic rate and activity of the superoxide dismutase, ascorbate peroxidase, guaiacol peroxidase, and catalase were decreased in leaves; however, these physiological parameters were enhanced in plants cultivated under high Ca level in the soil. Furthermore, the proteomic profiling revealed forty-four differentially abundant proteins in leaves of AR stress-exposed *T. wallichiana* var. *mairei* plants cultivated under different Ca amounts in the soil. Identified proteins were classified into seven groups related to processes such as signal transduction, protein modification and degradation, metabolism, photosynthesis and energy, cell rescue and defence, transcription and translation and unknown proteins.

Another important abiotic stress is low temperature. Liu et al. presented the results concerning the enzyme aminoacyl tRNA synthetase YLC3, which has been shown to take part in the regulation of amino acid homeostasis and chloroplast thylakoid development in *Oryza sativa* plants under low temperature. This article showed a thermo-sensitive rice

mutant *yellow leaf chlorosis3* (*ylc3*) with decreased chlorophyll content, changed thylakoid structure, and increased amounts of aspartate, asparagine, and glutamine in leaves under low-temperature stress.

It is well-known that a plant's response to stress is governed by an intricate network of phytohormones. Among these hormones are auxins. Ma et al. published results on the *Arabidopsis thaliana* endoplasmic reticulum (ER)-localized MAIGO2 (MAG2) complex and its protein homologue MAG2-Like (MAL) as regulators of plant development and vesicle trafficking and auxin homeostasis with functional redundancy. Moreover, it has been proven that MAIGO2 and MAG2-like participated in stress response, and in more detail the salt, osmotic, and ABA treatments have been examined.

Another published article concerned phosphate (Pi) stress. Wang et al. presented changes in phosphorylation and succinylation of *Hordeum vulgare* root proteins in response to phosphate starvation and recovery. The study showed that, the phosphorylated proteins associated with purine, the mitogen-activated protein kinases (MAPKs), pyrimidine, and ATP-binding cassette (ABC) transporters were upregulated in both Pi starved and recovered barley plants. s regards the succinylome, proteins in nitrogen and phenylpropanoid metabolism were significantly upregulated; on the other hand, proteins in lysine and tryptophan metabolism in both Pi-starved and recovered barley plants were significantly downregulated.

Adamiec et al. took a closer look at the role of the *A. thaliana* chloroplast EGY3 pseudoprotease in response to high-light and high-temperature stresses. Based on the molecular, biochemical, and physiological experiments, these authors concluded that, EGY3 mediated plant response to high-light and high-temperature stresses, and its role was related to photosystem I and light-independent reactions of photosynthesis. Moreover, these authors made the conclusion that, EGY3 took part in the regulation of H₂O₂ level through stabilization of the copper/zinc superoxide dismutase 2. Therefore, this matched up, as the authors concluded, to retrograde chloroplast-nucleus signalling.

An important global environmental problem is the soil salinity. Chen et al. using the quantitative proteomics analysis investigated changes in cell wall proteins of *Solanum lycopersicum* root in response to salinity. Two *S. lycopersicum* genotypes were used in this experiment, the salt-tolerant IL8-3 and the salt-sensitive M82 plants. This approach allowed the authors to show the differential responses of two contrasting genotypes. The salinity-tolerant IL8-3 plants presented not only a remarkably decremented Na⁺ level but also a clearly improved redox balance and cell wall lignification in response to salinity in comparison to the salt-sensitive M82 *S. lycopersicum*. The common response of plants from both lines was that the proteins involved in signal transduction and cell wall polysaccharides were upregulated in response to salt stress.

In addition to abiotic stresses, biotic stresses, including fungal infections, contribute to losses in crops of arable plants. Lu et al. performed a comparative proteomic analysis of two *Gossypium barbadense* cultivars differing in *V. dahliae* tolerance (susceptible XH7 and resistant XH21). It was clear from this study that, changes in reduced ascorbate (AsA) and H₂O₂ contents and the gene expression of ascorbate peroxidases (APX) were essential for *V. dahliae* resistance in *G. barbadense*. Compared to susceptible XH7 plants, the resistant XH21 plants presented consonantly higher AsA level and sharply induced the APX gene expression.

An article by Zhang et al. presented proteomic analysis of the ClpX proteolytic complex consisted of a hexameric ATPase ClpX and a tetradecameric peptidase ClpP in the model cyanobacterium *Synechocystis* sp. PCC 6803. One of the used experimental approaches was the comprehensive proteomic identification of proteins which were ClpX-regulated in *Synechocystis*. One hundred seventy-two ClpX-regulated proteins were detected. As the functional analysis showed, these proteins were engaged in glycolysis, nitrogen assimilation, photosynthetic electron transport, ATP-binding cassette (ABC) transporters, and signal transduction.

Taken together, this Research Topic clearly shows that, investigations of various aspects of proteolysis and proteome composition in plant responses to environmental stresses are conducted by numerous teams from all over the world. This topic is timely from the point of view of modern plant biology. Therefore, there is a strong need for further research in this area, not only in the field of responses to environmental stresses, but also in terms of plant growth and development regulation.

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Author contributions

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict.

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