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Post Translational Modification of Proteins in Plants under Biotic Stress

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Proteins play most important role in the regulatory mechanism of plants cells in various metabolic processes which coordinate their life cycle. Post translational modifications (PTM) are covalent process that involves addition of group to one or several amino acid residues or removal of group which changes its properties and function. Modified proteins play different roles in plant growth, metabolism, development and signaling pathways. PTM of plant proteins are extensively involved in physiological process of growth and development modifying the enzymes in metabolic pathways. PTM are important for plant defense responses and involved in all aspect of growth and development. Methylation, hydroxylation, acetylation, Phosphorylation, ubiquitination, sumoylation, glycosylation, and nitrosylation are the common PTMs that are important for defense against pathogens. These modifications are important for plants for their adaptability to long term stress memory.

Different post translational modifications of proteins in plants

Methylation refers to the addition of methyl group to lysine of arginine residue of a protein. Methyltransferases are the enzymes that catalyzes methylation. This occurs widely in histones were histone methylation activates genes. Hydroxylation is another type of modification which adds hydroxyl group to the proteins and catalyzed by hydroxylases. Acetylation and deacetylation are another forms of PTMs which have ctritical role in gene regulation. Phosphorylation involves the addition of phosphate group on serine, threonine and tyrosine residues by kinases. They have vital role in cellular processes, cell cycle and signal transduction pathways. Glycosylation refers to the addition of oligosaccharide to either a nitrogen atom or oxygen atom termed as N-linked glycosylation or O-linked glycosylation. Ubiquitinaton is the process based on polypeptides which involves the addition of protein termed ubiquitin to the lysine residue of a substrate. Proteolysis refers to the breakdown of proteins into smaller polypeptides or aminoacids catalyzed by proteases. Deamidation can change protein structure by removal or conversion of asparagine or glutamine residues to another functional group.

Post translational of proteins in plants under biotic stress

MAPK cascade: A major conserved signalling cascade activated by biotic and abiotic stress in plants is the MAPKcascade (Pedley and Martin, 2005; Zhang et al., 2006). The cascades consist of three functionally linked proteinkinases. A stress signal causes phosphorylation and activation of the most upstream MAPK kinase kinase (MAPKKK). Then the MAPKKK phosphor-ylates and activates a MAPK kinase (MAPKK), then it phosphorylates the MAPK (MPK). Further The MAPK phosphorylates downstream target(s) and transfer the signal downstream. The Arabidopsis genome encodes 60 putative MAPKKKs, ten MAPKKs and 20MAPKs, and other several protein phosphatases that control the cascade by dephosphorylating the MAPK cascade components (Ichimura et al., 2002; Martín et al., 2005)

CDPK-mediated signalling: CDPKs consists of calmodulin-like domain with Ca 2+ binding sites and which represent a class of kinases. The kinase domain of CDPKs is not phosphorylated in absence of Ca 2+ which directly regulates Ca 2+ (Ludwiget al., 2004). Tobacco NtCDPK2 was the first CDPK reported to be involved in plant defence signaling. It is required for hypersensitive response (HR) develop-ment which is activated by phosphorylation.

Ubiquitination in defence signalling: Ubiquitination regulates the immune responses in plants by tagging proteins for degradation or altering their function/location via the ubiquitin-proteasome system (UPS). E1, E2 and E3 are the ligases which determine specificity, signaling components and protein turnover to either activate or degradation of proteins thereby enabling plants to adapt and survive infections. The E1 enzyme activates ubiquitin (Ub) using ATP and the activated Ub is transferred to an E2 enzyme and then E3 ligase brings in the target protein. The E3 ligase attaches Ub to a lysine residue on the target protein. Which inturn degrades the target protein by 26S proteasome or regulates the protein activity by interactions. Several proteins with E3 ubiquitin ligase activity play significant role in defence signalling which proves ubiquitination is important for resistance of plants to pathogens. For example in Arabdiopsis the closest orthologue of ACRE276 which is PUB17 needed for the expression of RPM1- and RPS4 resistance genes against Pseudomonas syringae pv. tomato elicitors AvrB or AvrRPS4 (Yang et al., 2006).

Sumoylation: The process involves the Small Ubiquitin-like Modifier (SUMO) target the target proteins which alters their function and help the plant to safeguard against various pathogens. The process enhance resistance in plants by affecting salicylic acid (SA) signaling. The sumoylation process in plants increased upon heat shock and pest attack (Kurepa et al., 2003; Saracco et al., 2007).

Conclusion

PTMs always help to adapt and survive the limited genome of an organism under various stress conditions. They regulate protein localization and activity to balance responses in the cell. They normalize proteins interaction with in the plant cell and balance the responses in cell due to biotic stress without prerequisite of protein synthesis. With the aid of recent biotechnological tools many of the unidentified signaling cascades related to defense mechanism in plants which are regulated by PTMs can be identified for developing host plant resistance.

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