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Pathogenesis Related Protein – A brief abridgment of types and functions.

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Abstract: Ever since the emergence of human civilization, plants hold an accountable value for the source of medicines, health products, pharmaceuticals, food supplements, cosmetics, etc. Many derivatives are used as an overriding compound for their antioxidant activity, anti-tumor activity, cytotoxic-activity, gene toxicity, anti-diabetics, hepato-protective, anti-diabetic, anti-lice activity, etc. as they are reported to contain a wide range of flavonoids, alkaloids, carbohydrates, fixed oils, tannins and phenolic compounds, which are commonly used in folkloric medicine for the treatment of various diseases. On such an account plants are also known to produce a class of proteins called the Pathogenesis Related (PR) proteins against pathogen attack. These proteins play a determining role in plant defense against pathogens. Expression of PR genes can take place due to abiotic factors that cause stress such as oxidation stress, osmotic stress, wounding, and UV light. Their involvement in humans as allergens makes it salient for their exploration. The present review attempts to encompass the comprehensive literature analysis on the Pathogenesis related proteins with respect to their importance owing to its pharmacological activities such as anti-microbial activity, antioxidant activity, and tumor resistant activities and their applications.

Keywords: Pathogenesis related proteins, PR proteins, types of PR proteins, functions of PR proteins, allergenomics.

1. INTRODUCTION

Plants are exposed to an outsized number of pathogens, although they do not possess an immune system, they have evolved with potent defense mechanisms, that includes the synthesis of certain low-molecular- weight compounds, proteins, and some peptides that exhibit anti-fungal activity (Caruso *et al.,* 1996). These proteins are involved in either induced or consecutive resistance to pathogenic attacks. It's a testimony to the potency of the defenses that plants, animals, and humans act well against pathogens. Tobacco plant infected with the mosaic virus was the first case that aided to uncover PR proteins in plants (Van Loon and Van Kammen, 1970). When a plant experiences a pathogen encounter, both the adjacent healthy cells and within the plant cells that are infected produces PR protein (Oliveira *et al.,* 2016).

Numerous PR proteins were identified in alfalfa, cereal grass, sorghum, barley, tomato, grapevine, bean, chickpea, rice, wheat, barley, sunflower, carrot, maize, pepper, pepper, celery, rubber, soybean, and many other plants. The distribution and localization of the PR are recounted on to the tactic and essence of the pathogen infection. The PRs are divided into several groups based on their sequence homology (Sudisha *et al.,* 2011). The isoelectric points of PR proteins are acidic or basic, even though with similar functions. Acidic PR proteins are usually found in intercellular gaps, while basic PR proteins are mostly found in vacuoles (Oliveira *et al.,* 2016). 1,3-glucanases, ribosome-inactivating protein, chitinases, oxalate oxidase, peroxidases, defensins, oxalate-oxidase-like proteins, thionins, nonspecific lipid transfer proteins, and thaumatin-like proteins are among the 17 families based on their characteristics and activities (Oliveira *et al.,* 2016; Mahesh *et al.,* 2017).

The two crucial hydrolytic enzymes that are abundant in most plant species after encountering infections with differing types of pathogens among these PR proteins are the β-1,3-glucanases and chitinase. They play a pressing role within the defense reactions against fungal pathogens by mortifying their cell walls which contain chitin and β-1,3-glucan as major structural components (Ebrahim *et al.,* 2011; Oliveira *et al.,* 2016). A number of those proteins area unit antimicrobial, assaultive molecules among the cytomembrane of a microorganism or plant life. Whereas the role of others could operate as signals that unfold "news" of the infection to the cells accessible. Infections conjointly stimulate the cross-linking of molecules among the cell wall and thus the deposition of polymer, responses that supported a district barricade that slows the unfold of the infectious agent to different elements of the plant (Campbell, N.A. and Reece, J.B., 2005). Salicylic acid plays employment within the resistance to pathogens by causation the assembly of pathogenesis-related proteins (Van Huijsduijnen RAMH *et al.,* 1986).

Several proteins found in wine area unit grape pathogen-related proteins (Waters EJ *et al.,* 1996). Those embody thaumatin-like proteins and chitinases. Several pathogenesis-related super molecule families conjointly coincide with teams of human allergens, whereas the hypersensitivity reaction could do not have something to do to try to with the defense operate of the proteins (Sinha, Mau *et al.,* 2014). Grouping these proteins by their sequence options permits for locating potential substance proteins from sequenced plant genomes, a field of a study dubbed "allergenomics".

As PR proteins are synthesized when plant structure is stressed, various ways of stress signaling are employed to "bait" the plant into expressing PR genes, which are used for identification. Useful stressors include an actual infection or just defense signals like salicylate and methyl jasmonate. The proteins may be identified by isolation, peptide digestion, and matching against the genomic sequences (protein sequencing). The sequences obtained can then be checked against known PR protein families for categorization (Elvira, M. I. *et al.,* 2018 and Sabater-Jara, AB *et al.,* 2011).

2. Pathogenesis-Related Proteins

PR proteins are churned out in plants resulting in an event of a pathogen attack (Loon 1985). They are induced as an element of systemic acquired resistance. Infections activate genes that produce PR proteins. PR proteins are antimicrobial, attacking molecules within the tissue layer of a bacterium or fungus. Infections also stimulate the cross-linking of molecules within the cytomembrane and the deposition of lignin, responses that founded a part barricade that slows the spread of the pathogen to other parts of the plant (Campbell, and Reece, 2005). Salicylic acid plays a task within the resistance to pathogens by inducing the assembly of pathogenesis-related proteins (Van *et al.,* 1986).

Many pathogen-related proteins found in grape wine include thaumatin-like proteins and chitinases (Waters *et al.,* 1996). Plants when exposed to pathogens like fungi and viruses produce low-molecular-weight antimicrobial compounds called phytoalexins, antimicrobial peptides, and tiny protein (example thionins, defensins (Bloch *et al.,* 1998 and Broekaert, W. F. *et al.,* 1995) hevein-like proteins, knottin-like peptides (Segura *et al.,* 1993) up-regulate sort of antimicrobial proteins. These plant proteins are called Pathogenesis-Related (PR) proteins and are classically divided into many groups PR-1, PR-2, PR-3, PR-4, PR-5, and so on, supported by serological and amino-alkanoic acid sequence analyses. to date, 17 families of PR proteins are named (Sinha, Mau *et al.,* 2014). Most of those have known functions or activities - as an example, PR-2 is additionally a β-1,3-glucanase; PR-3, -4, -8, and -11 are differing types of chitinase; PR-5 is additionally a thaumatin-like protein; PR-6 is additionally a proteinase inhibitor; PR-7 is additionally an endoproteinase; PR-9 is additionally a peroxidase; PR-10 might be a ribonuclease, and PR-12 may well be a defensin, PR-13 might be a thionin, and PR-14 may well be a lipid-transfer protein(reviewed by van Loon and van Strien, 1999).

Some Pathogenesis Related proteins are said to possess antifungal and antibacterial properties (Bowles, 1990). The PR proteins are classified in line with their functions, serological relationship, amino-alkanoic acid sequence, relative molecular mass, and certain other properties. they're either extremely acidic or extremely basic, which makes them highly soluble and reactive. a minimum of 17 classes of PR proteins are recognized (Van Loon *et al.,* 2006) during which are better known are antioomycete, antifungal, glucanases, chitinases, proteinase inhibitors, thaumatin-like proteins, defensins, thionins, osmotin-like proteins, glycine-rich proteins, cysteine-rich proteins, lipoxygenases, peroxidases and more. Ethylene, the polypeptide systemin, xylanase, jasmonic acid, and 2-hydroxybenzoic acid, are the signaling compounds accountable for PR proteins. the sorts of PR proteins and their roles are tabulated below(Table 2.1)

Table 2.1 – PR Proteins and their functions.

FAMILY	PROTEIN	FUNCTIONS
PR- 1	PR-1 a, PR-1 b, and PR-1 c	Antifungal (CAP)
PR- 2	β-1,3-Glucanases	Cleaves β-1,3-glucans
PR- 3	Chitinase types I, II, IV, V, VI, and VII	Endochitinase
PR- 4	Barwin domain - chitinase I/II	Antifungal and chitinases- Pro-heveins
PR- 5	Thaumatin-like	Antifungal
PR- 6	Potato protease I	Proteinase inhibitor
PR- 7	Cucumber chitinases	Chitinase III
PR- 8	Tomato endoproteinase *P69*	Endoproteinase
PR- 9	Tobacco lignin-forming peroxidase	Haem peroxidase III
PR- 10	Parsley "PR-1"	Ribonuclease-like

PR- 11	Tobacco chitinase V	Tobacco chitinase V
PR- 12	Radish *Rs-AFP3*	Plant Defensisns
PR- 13	Arabidopsis *THI2.1*	Thionin
PR- 14	Lipid transfer proteins	Shuttling of phospholipids and fatty acids
PR- 15	Barley *OxOa*	germin; Oxalate oxidase
PR- 16	Barley *OxOLP*	germin-like
PR- 17	Tobacco *NtPRp27*	late blight resistance

2.1 Pathogenesis-Related (PR) Protein-1

Pathogenesis-Related-1 proteins are accumulated to high levels after pathogen infection and are antifungal both in planta (transgenic plants over-expressing tobacco PR-1) and in-vitro species (Tahiri-Alaoui *et al.,* 1993). PR-1 proteins are found in wheat, tobacco, *A. thaliana*, maize, barley, rice, and far of plants (Rauscher *et al.,* 1999). PR-1 proteins have antifungal activity at the micro-molecular level against an expansion of plant pathogenic fungi including rust fungus, Potato late blight fungus, and *Blumeria graminis* (Niderman *et al.,* 1995). PR1 proteins have molecular masses of ~15 to 17 kDa, which has homology to the cysteine-rich proteins superfamily. Although the express mechanism of antifungal activity incomprehensible for plant PR-1 proteins, PR-1-like protein, helothermine for Mexican banded lizard linked with the membrane-channel proteins of target cells, inhibiting the discharge of Ca^{2+} (Morrisette *et al.,* 1995). Whether antifungal plant PR-1 proteins act by this mechanism was not known but it is suspected.

2.2 Pathogenesis-Related Protein-2

The β-Glucanases, pathogenesis-related protein-2 has endo-glucanase activity in vitro and has been grouped into three classes on the concept of amino-alkanoic acid sequence analysis (Payne *et al.,* 1990). Class I glucanases are basic proteins of ~33 kDa is found in plant vacuoles. there are classes II and III of β-glucanases that include acidic, extracellular proteins of about 36 kDa. The foremost structural difference between class I proteins and thus the selection of two classes is that class I proteins are synthesized as pre-proproteins that are processed before being enzymatically active. PR-2 proteins are found in quiet oversized plants including tobacco, *A. thaliana*, peas, grains, and fruits (Kim *et al.,* 1997). The proteins are active in vitro at micro-molecular levels (~ 50 mg/ml) against an outsized number of fungi, including human and plant pathogen (example *Rhizoctonia solani, C. albicans,* and *Aspergillus fumigates*). The antifungal activity of PR-2 proteins is convincingly exemplified by diffusion of whole-cell assay and in vitro enzyme assay (Stintzi *et al.,* 1993) as in plant using transgenic plants over-expressing a PR-2 protein (Jach *et al.,* 1995). The antifungal activity of plant (1,3) β- glucanases is assumed to occur by PR-2 proteins hydrolyzing the structural(1,3) β-glucan present within the fungal cytomembrane, particularly at the hyphal apex of filamentous molds where glucan is most exposed, leading to a cytomembrane that's weak. This weakened cytomembrane finally ends up in cell lysis and necrobiosis.

2.3 Pathogenesis-Related Proteins-3

The styles of enzymatic assays have shown PR-3 proteins to possess in vitro chitinase activity. Most PR-3 proteins have molecular masses between 26 and 43 kDa (Watanable *et al.,* 1999). Chitinases (both plant PR-3 chitinases and chitinases from other sources) are divided into five groups. Class I chitinases include a 40-amino-acid N-terminal cysteine-rich domain (sometimes referred to as the nutrient agglutinin domain), a chitin-binding hevein-like domain, a highly conserved middle section, and therefore the hinge region; most class I proteins have molecular weights of 32 kDa. Class II proteins are similar in amino-alkanoic acid sequence to class I proteins, but they lack N-terminal cysteine-rich domain and have molecular masses of 27 to twenty-eight kDa. The category IV proteins resemble class I chitinases but are significantly smaller due to four major deletions. Class III proteins don't share compound sequence homology to the chosen class and have a molecular mass of ~28 to 30 kDa. The category V chitinases, on the other hand, have molecular weights of 41 to 43 kDa and have sequence similarities with bacterial exochitinases. Apart from the present, antifungal chitinases (chitosan is de-acetylated chitin) from *Streptomyces* strain *N174* have been isolated and their X-ray structure characterised (Bull *et al.,* 1992).

2.4 Pathogenesis Related Protein 4

Pathogenesis-Related Protein-4 (PR-4) is also a chitin-binding protein, has molecular masses 13 to 14.5 kDa, and is classed into two groups (Van Damme *et al.,* 1999). Class I proteins are members of the chitin-binding lectin superfamily and feature amino-alkanoic acid sequences that are comparable to hevein, a chitin-binding polypeptide (Friedrich *et al.,* 1991). The category II proteins lack the chitin-binding domain. PR-4 proteins are isolated from potato, tomato, barley, tobacco and many other plants (Hejgaard *et al.,* 1992) noted that the PR-4 proteins from the various sources share common sequences. Both classes of proteins have potent antifungal activity against a limitless form of human and plant pathogens (example, *Trichoderma harzianum, Fusarium culmorum, F. graminearum,* and *B. cinerea).* The antifungal activity of sophistication 1 protein is probably the result of protein binding to nascent fungal membrane b-chitin. By a mechanism not understood, this ends in disrupted cell

polarity, with concomitant inhibition of growth (Boemann *et al.*, 1999). The mechanism of action of two proteins that lack kite in binding hevein domain but are antifungal nonetheless is understood.

2.5 Pathogenesis Related Protein 5

These are TLPs (Thaumatin-Like Proteins), which show a significant sequence similarity to thaumatins, a sweet-tasting protein derived from the West African plant *Thaumatococcus daniellii*. Antifungal activity, anti-freezing action, and osmotic stress tolerance are all activities of the PR-5 family in plant disease resistance. Around 24 different PR-5 genes have been discovered in *Arabidopsis*. TLPs possess a molecular mass of 20 to 26 kDa, with ~200 residues possessing 16 conserved cysteine residues forming eight disulfide bonds. The antifungal activity of osmotin and zeamatin from maize is due to membrane permeabilization to fungus. The gene PgPR-5 that was isolated from the leaf tracheophyte was characterized. Results revealed that when PgPR-5 was induced by salt stress, chilling stress, heavy metals, UV, and pathogen infection, the results played a vital role within the molecular defense response of ginseng to antibiotic and pathogen attack (Kim *et al.*, 1997).PR5 family consists of TLP, osmotin, osmotin-like proteins (OLP), and zeamatin. As demonstrated by Zamani *et al.*, the Thaumatin-like Protein (TLP) gene, which was isolated from cereal rye (*Secale cereal L.*) and expressed in Canola (*Brassica napus L.*), confers antifungal activity while also increasing resistance to the pathogen *Sclerotinia sclerotiorum*, which causes stem rot disease (2012).

2.6 Pathogenesis Related Protein 6

Protease Inhibitors (PI) are small proteins that act as natural antagonists of proteases. In plants, the Proteinase inhibitors are present mainly in storage tissues (tubers and seeds) and aerial parts inhibiting the function of proteases. PI weights 4 to 85 kDa, are responsible for plant defense and are induced in response to various stress including pathogens and insect attacks, wounding, and various environmental stresses. The first isolated and well-characterized cysteine PI is Oryzacystatin (*OC-1*). Over expression of the *Solanum americanum* serine proteinase inhibitor gene (*SaPIN2a*) in transgenic tobacco has been shown to improve resistance to the lepidopteran insects *Helicoverpa armigera* and *Spodoptera litura*, which cause significant economic losses in cotton, tobacco, sunflower, corn, pepper, and tomato plants (Sumant Pratap Singh and Shambhoo Prasad, 2020). The Pathogenesis-Related protein (PR-6) isolated from the embryogenic callus of ginseng is known as *PgPR6*. The peak-level expression of *PgPR6* was observed within the premise as revealed by quantitative real-time PCR. Signaling molecules, sucrose, mechanical wounding, heavy metals, salt, freezing, and mannitol stress all significantly increased *PgPR6* expression, indicating that *PgPR6* may play an essential part in ginseng's molecular defensive response to a variety of environmental stressors (Myagmarjav *et al.*, 2017).

2.7 Pathogenesis Related Protein 7

PR-7 family (proteinase or peptidase) play important role in the regulation of various biological processes like growth, development, photosynthesis, and induction of defense response against insects, herbivores, and nematodes. Proteases directly degrade proteins from the pathogen and release peptide-based toxins or activate enzymes from their precursor proteins. *Arabidopsis* genome encodes over 800 proteases. Protease inhibitors inhibit the activity of proteases. Liu *et al.* (2001) demonstrated that in Glycine max *GmMMP2* gene was up-regulated in response to the infection from fungal pathogen *Phytophthora sojae* and bacterial pathogen *Pseudomonas syringae*.

2.8 Pathogenesis Related Protein 8

The class III chitinases belong to PR-8. Chitinases are hydrolytic enzymes catalyzing the hydrolysis of β-1,4- linkage of the N-acetyl glucosamine polymer of chitin. A cDNA encoding class III chitinase (*OschibI*) was isolated from a cDNA library constructed from leaves infected with the blast fungus *Magnap grisea*. The induction patterns of *OschibI* expression suggested that it is visiting be involved in defense response against pathogen infections and will be classified as a member of pathogenesis-related protein 8 in rice (Chan-Ho Park *et al.*, 2003). Molecular characterization of a PR-8 protein gene encoding a category III chitinase in rice is studied. Further, the PR-8 protein also acts as allergens in the case of dermatitis Hevamine (latex), a bifunctional enzyme with lysozyme/chitinase activity having an employment in plugging the latex vessel and halting latex flow. Within the case of oral allergy syndrome, *Ziz-m-1* was produced in Indian jujube because of the PR-8 protein mechanism. Similarly *Cof-a-1* in coffee for eye and airway allergy (Sinha *et al.*, 2014).

2.9 Pathogenesis Related Protein 9

Peroxidases are a ubiquitous class of oxidoreductases weighing about ~32-42 kDa, which catalyze the reduction of peroxide and oxidation of a spread of organic and inorganic compounds. Peroxidase is that the key enzyme involved in plant differentiation, development, auxin catabolism, hormonal signaling, wound healing, lignification, suberization, response to stresses. Recently, demonstrated that tobacco transgenic plants over-expressing the ascorbate peroxidase *SbpAPX* gene from *Salicornia brachiata* shows salt and drought stress tolerance. Sarowar *et al.* (2005) demonstrated that *Capsicum annuum* ascorbate peroxidase-like 1 gene (*CAPOA1*) over expressed tobacco plants exhibited enhanced resistance to the oomycete pathogen, *Phytophthora nicotianae* and shows increased tolerance to oxidative stress.

2.10 Pathogenesis Related Protein 10

PR-10 proteins are classified as ribonuclease-like PR proteins due to the structural similarity to ginseng ribonuclease weighing around 15-18 kDa. PR-10 proteins have RNase and ligand-binding activities, which protect plants during programmed death around infection sites or act directly on the pathogens. The PR-10 proteins play important roles in plant growth, development, and plant defense responses against various biotic and environmental stresses, like drought, high salinity, low and high temperatures, wounding heavy metals, and UV exposure. PR-10 family has been isolated from the bean, soybean, asparagus, sorghum, barley, rice, potato, apple, and trefoil. Fung et al. (2007) demonstrated that in *V. vinifera* these proteins are induced under salt or herbicide stress and exhibit wide spectrum resistance to the mold fungus *Erysiphe necator* (Schw.) Burr. Recently, Xie et al. (2013) demonstrated that over expression of PR10 family gene *ARAhPR10* plays a significant role in legume seed resistance to *Aspergillus flavus*. The rice (*Oryza sativa L.*) gene that's homologous to *sorghum* PR-10 protein genes that were cloned from a cDNA library prepared from 2-week-old jasmonic acid-treated rice seedling leaves. The expression analysis of *JIOsPR10* disclosed that the signaling components of defense/stress pathways, jasmonate, salicylate, and H_2O_2 are significantly up regulated the *JIOsPR10* mRNA upon the cut control, whereas two other stress regulators, ethylene and abscisic acid, didn't induce its expression. Within the identical way protein phosphatase (PP) inhibitors, cantharidin, endothall, and okadaic acid, rapidly and potently up regulated the *JIOsPR10* expression, suggesting the involvement of the phosphorylation/dephosphorylation events (Nam-SooJwa *et al.,* 2001).

2.11 Pathogenesis Related Protein 11

Chitinases are hydrolytic enzymes catalyzing the hydrolysis of β-1,4-linkage of the N-acetyl glucosamine polymer of chitin of molecular mass about 25 to 40 kDa. Constitutively present in stems, seeds, flowers, and tubers. Chitinases have lysosomal activity, present in low levels in plants but are strongly and coordinately up regulated by various abiotic and biotic stress conditions. The transgenic plants over expressing chitinases confer increase resistance to pathogen attack. Salzer et al. (2000) demonstrated that class III chitinase genes from barrel-clover *Mtchit3-1* and *Mtchit3-4* are induced in response to infection by pathogenic water mould *P. megasperma, F. solani* within the roots. The constitutive expression of both chitinases and β-1,3- glucanases from lemon seedlings shows the defense response against *Alternaria alternata* which causes early blight disease.

2.12 Pathogenesis Related Protein 12

The protein structures of defensins are small i.e. about 5kDa, basic, *βαββ* architecture of cysteine-rich antifungal peptides ranging up to 45 to 54 amino acids and are charged. They were first isolated from endosperm of wheat and barley. Defensin exhibits a broad spectrum of potent antifungal activity, antibacterial activity, proteinase inhibitory activity, and bug amylase inhibitory activity. The antifungal activities of plant defensins are identified in various plants like pea, tobacco, radish, and Arabidopsis. The mode of action for a defensin relies on the extent to which a plant exhibits potent antifungal activity in vitro at micromolar concentrations against a broad spectrum of filamentous fungi. They'll be morphogenic which reduces hyphal elongation and induce hyper branching or non-morphogenic reducing hyphal elongation with no morphological distortions. In bacteria, permeabilization concurred with the inhibition of RNA, DNA, and protein synthesis and diminished bacterial viability. Antifungal defensins reduce hyphal elongation and induce hyper branching. Defensis like *Rs-AFP2* appears to act primarily at the tissue layer and induces a rapid influx of Ca^{2+} and K^+ efflux in *Neurospora crassa*. One in all the foremost effective characterized antifungal plant defensins was isolated from radish (*RsAFP1* and *RsAFP2*) which confers both in vivo and in vitro antifungal activity.

2.13 Pathogenesis Related Protein 13

Thionins could also be a gaggle of small, low molecular weight (approximately 5kDa) with 45 to 50 amino acids, which include 3 or 4 conserve disulfide linkages, cysteine-rich, basic polypeptides. Thionins are classified into two groups supported by their 3D structure: α/β-thionins and γ-thionins. Thionin has antibacterial, antifungal activities with the flexibleness to inhibit insect α-amylases and proteinases playing a task as plant defense proteins. In transgenic sweet potato expressing barley thionin, αHT showed enhanced resistance to disease caused by *Ceratocystis fimbriata* which severely deteriorates the plant's growth and storage roots (Sumant Pratap Singh and Shambhoo Prasad, 2020). The barley leaf thionin, which is extremely poisonous to pathogens and is important in plant defence against microbial diseases, has also been discovered. Presumably attacking the membrane and making it permeable, this ends within the inhibition of sugar uptake and allows potassium, phosphate ions proteins, and nucleotides to ooze from cells. Y-hydeothionins isolated from *sorghum* was the primary example of a thionin able to inhibit insect amylase.

2.14 Pathogenesis Related Protein 14

Lipid-transfer proteins (LTP) are small (9-10 kDa), a basic, soluble, ubiquitous protein that has the ability to bind lipids and other hydrophobic molecules. LTP has an alpha-helical structure stabilized by four disulfide bonds involving eight cysteine residues, which form a tunnel-like hydrophobic cavity for ligand binding. LTP plays a diverse role in plant development and defense like cutin synthesis, β-oxidation, somatic embryogenesis allergens, pollen adherence, signaling, and plant defense against phytopathogens. LTPs comprise of two families, LTP1 and LTP2. LTP1 is basic with molecular masses of ~10 kDa. Recently Zhu et al. 2012 demonstrated that transgenic *Triticum aestivum* plants overexpressing lipid transfer protein gene

TaLTP5 shows increase resistance to *Cochliobolus sativus* and *Fusarium graminearum* which causes common root rot and Fusarium head blight disease in wheat respectively They are present in higher plants, might enhance the in vitro transfer of phospholipids between membranes, and may bind alcy chains. They participate in membrane biogenesis and regulation of intracellular carboxylic acid pools. The principle of the essay is to observe the transfer of labels within the lipids from the donor to acceptor membranes. They participate in cutin confirmation, embryogenesis, and defense reactions against phytopathogens, symbiosis, and adaptation of plants to varied environmental conditions.

2.15 Pathogenesis Related-Protein 15 And 16

Oxalate oxidase (OXO) in plants is present in low concentrations playing a crucial role in the defense against biotic and abiotic stress. The enzyme catalyzes the aerobic oxidation of oxalic acid and oxygen into CO_2 and hydrogen peroxide H_2O_2. H_2O_2 triggers a signal transduction cascade, which activates plant defense mechanisms leading to the synthesis of pathogenesis-related proteins and phytoalexins. The oxalate oxidase plays various physiological and defense roles like germination, fruit ripening, floral induction, seed development, embryogenesis, nodulation production of H_2O_2, and nitrogen fixation. *Hordeum vulgare* and *Triticum aestivum* were the first plants to have oxalate oxidase isolated and described. OXO exists in two forms in nature: soluble and membrane-bound. Transgenic *Colocasia esculenta* (Taro) converted with the oxalate oxidase gene gf 2.8 from wheat confers enhanced resistance to the Taro disease *Phytophthora colocasiae*, according to Xiaoling et al. (2013).

2.16 Pathogenesis Related Protein 17

Unknown the PR17 proteins play important role in plant defense against pathogens but the exact molecular functions are still not defined. Over expression of the PR17 protein in wheat (*WCI-5*) gives resistance to powdery mildew fungus *B. graminis f. sp. tritici* in wheat. . In tobacco, *NtPRp27* was induced in response to tobacco mosaic virus infection and mechanical wounding. The *HvPR-17a* and *HvPR-17b* proteins weighing 26 and 24 kDa respectively, accumulate in the barley mesophyll apoplast and in leaf epidermis when attack with powdery mildew fungi *Blumeria graminis f. sp. hordei*. (Sumant Pratap Singh and Shambhoo Prasad, 2020).

3. Plant PR Proteins and Allergenicity

By employing such a proteomic method, the term "allergenomics" has been proposed for the quick and thorough study of potential proteinous allergens (allergenome). We can use allergenomics to not only detect and assign putative allergens (proteins that specifically interact with IgE antibodies in a patient's blood) in a short amount of time, but also to analyze the antigens' quantitative and qualitative changes as a function of the allergenic causative's surroundings and environmental conditions (Beyer *et al.*, 2002).

IgE antibodies generated in response to allergen sensitization identify epitopes on the surface of other plant proteins that are similar to those found on the surface of allergens. As a result, re-exposure to homologous plant allergens causes an allergic response in people who have already been sensitized (Wagner and Breiteneder, 2002). Pollen-related food sickness, latex-fruit syndrome, and the birch-mugwort-celery-spice syndrome are only a few of the prevalent allergy disorders linked to PR proteins (Midoro-Horiuti *et al.*, 2000).

A number of PR proteins and homologues of them cause allergic reactions in humans have been identified and described. These proteins are good candidates for eliciting allergic responses due to their size, stability, and resistance to proteases, as well as hydrolytic and membrane-permeabilizing capabilities in certain. Furthermore, due to structural similarities among several of the main proteins, PR proteins are generally linked with a significant degree of cross-reactivity. Many individuals who are sensitive to one type of allergen, such as pollen, develop allergy symptoms when they consume other allergens, such as certain fresh fruits, vegetables, or nuts (Halmepuro *et al.*, 1984 and Asero *et al.*, 2011).

Plants grown under various circumstances have been shown to have varying amounts of expression of allergenic PR proteins and their homologues (Midoro-Horiuti *et al.*, 2000). Some of these allergy classes exhibit changes in expression as a result of environmental contaminants (Midoro-Horiuti *et al.*, 2001). A number of allergens categorized as PR proteins are recognized from PR families 1, 2, 3, 4, 5, 8, 10, and 14 (Table 3.1) based on sequence features(van Loon *et al.*, 1999).

Table 3.1 – Types of Allergens produced by different PR Proteins.

FAMILY	DOMAIN	ALLEGENS
PR – 1	IPR034111 IPR001283	Cuc m3 (muskmelon; P83834) – Oral Allergy Syndrome(OAS).
PR – 2	(GH17)	Hev b 2 (latex; P52407) —contact dermatitis. Ole e 9 (olive)—respiratory allergy. Mus a 5 (banana)—oral allergy syndrome(OAS).
PR – 3	IPR016283	Pers a 1 (avocado)—itchy eyes or nose, asthma, swelling, and so forth. Mus a 2 (banana)—food allergy like swelling of lips, anaphylaxis, and so forth.
PR – 4	IPR001153	Pro-heveins: Hev b 6—contact dermatitis.

PR – 5	IPR001938	Jun a 3 (mountain cedar), Cry j 1 (Japanese cedar), and Cup a 3 (Arizona cypress)—rhinitis, conjunctivitis, and asthma. Pru av 2 (cherry), Mal d 2 (apple), Cap a 1 (bell pepper), Act d 2 (kiwi), and Mus a 4 (banana)— OAS.
PR – 8	(GH18)	Hevamine (latex, P23472)—contact dermatitis. Ziz m 1 (Indian jujube, Q2VST0)— OAS. Cof a 1 (coffee, D7REL9)—eye and airway allergy.
PR – 10	IPR024949 IPR000916	Bet v 1 (birch pollen)— allergic rhinoconjunctivitis and asthma. Pru av 1 (cherry), Mal d 1 (apple), Api g 1 (celery), and Dau c 1 (carrot)— OAS. Gly m 4 (soy), Vig r 1 (mung bean), Cor a 1 (hazelnut), and Cas s 1 (chestnut), Act c 8 (golden kiwi fruit), Act d 8 (green kiwi fruit) — OAS.
PR – 14	IPR000528	Par j 1 (weed; P43217)—rhinitis and asthma. Pru p 3 (peach), Mal d 3 (apple), Pru av 3 (cherry), Pru ar 3 (apricot), Cor a 8 (hazelnut), Cas s 8 (chestnut), and Zea m 14 (maize)— OAS.

4. Conclusion

PR proteins are synthesized in response to some sort of stress; their function analogs to the one postulated with heat shock protein might protect the plants from extensive damage. Within the succeeding phase of slow lesion expansion, they reach the best concentration at the lesion margin. During allergies in plants, PR proteins are first detectable in an exceeding ring around a necrosis center. PR proteins play a vital role in disease resistance, seed germination and help the plant to adapt to environmental stress. The escalated knowledge concerning the PR proteins gives a stronger idea aiding the event and munitions of plants.

The first aspects of gene regulation of the PR proteins are understood but the study of the extracting mechanism of gene regulation and receptor cascade will open new ways for the plant biotechnology technology for crop improvement. The PR genes are also considered as "stress-inducible" proteins having various applications in genetic engineering for crop improvement. The antimicrobial properties of PR proteins are used in agribusiness to create genetically modified plants with increased field resistance.

Further, a combination of various PR proteins opens new ways for genetic engineering and provides insights into pathogen defense mechanisms with improved disease resistance for developing new and improved crop varieties. Thus pathogenesis-related proteins potentially help to increase crop production with an increase in plant disease resistance to various pathogens and reduction in the extensive use of the chemical fungicides.

The other major reason to develop various studies in this area is that, many pathogenesis-related protein families also happen to correspond to groupings of human allergens, even though the allergy has nothing to do with the proteins' defensive role. Finding potential allergenic proteins from sequenced plant genomes is made possible by grouping these proteins by their sequence characteristics, an area of study known as "allergenomics."

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