

Conifer Chitinases

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ABSTRACT

Over the last two decades scientists have focused much attention on the physiological, molecular and functional biology of plant chitinases and there is considerable evidence suggests that chitinases play important roles in plant defense systems. Chitinases have also been shown to play a role in plant growth and development. Several review articles exist for chitinases of angiosperms but there is no such review for conifer chitinases, despite the economic and ecological significance of coniferous species in the world's forests. Conifer chitinases consist of at least several classes of enzymes that are represented by small gene families. Class II (acidic) and class IV (basic) chitinases, expressed differentially over time and space, have been shown to be the major defense players in many conifer pathosystems. Class I and III chitinases are also reported in some conifers. This review discusses the current body of knowledge regarding conifer chitinases, including the molecular structure of chitinase genes and their regulation and function in conifer plants. Future potential uses for conifer chitinases as biopesticides and agents of biofuel production are also discussed.

Keywords: biocontrol, biofuel, chitin binding domain, growth and development, host defense, PR proteins Abbreviations: AFP, antifreeze protein; AGP, arabinogalactan protein; DF, Douglas-fir; ECP, endochitinase-like protein; EST, expressed sequence tag; LCO, lipo-chitooligosaccharides; PCD, programmed cell death; PEM, pro-embryogenic masses

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INTRODUCTION

Conifer trees are the dominant species in both boreal and temperate forests around the globe, wherein they play vital roles in ecosystem functions (Bonello *et al.* 2006). Regeneration of conifer forests, either naturally or by planting high quality seedlings, is essential for maintaining the world's large forested areas as active carbon dioxide (CO_2) sinks after harvesting (Holopainen *et al.* 2009) and natural disturbances. The future composition of the world's forests and their sustainability will be greatly affected by both global warming and increased pressure by pests and pathogens, many of which are expected to expand in range and ampli-

tude (Niemelä *et al.* 2001; Sturrock *et al.* 2006). To successfully manage the present and future pathogens affecting the health of conifer forests we must understand host-pathogen interactions at a molecular level, including knowledge of the regulation and function of major pathogenesis-related genes and proteins in conifer pathosystems. Plant chitinases (EC 3.2.1.14) are of particular impor-

Plant chitinases (EC 3.2.1.14) are of particular importance to fungal pathosystems because all true fungi contain chitin as a primary structural component of their cell walls (Wessels 1994). Chitin is a linear homopolymer of *N*-acetyl-D-glucosamine and it is hydrolyzed by chitinases into smaller oligomers or monomers (Bishop *et al.* 2002; Xiao *et al.* 2007; Xu *et al.* 2007; Nakamura *et al.* 2008). Many stu-

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dies suggest that conifer chitinases play their most significant roles in conifer defense against pathogens. In addition to that, some conifer chitinases are also induced by abiotic stresses.

During the past decade, chitinases in general have received increased attention because of their wide range of potential uses. Chito-oligomers produced by enzymatic hydrolysis have valuable applications in medicine, agriculture, and industry through their antibacterial, antifungal, hypocholesterolemic, and antihypertensive properties. They also have use as a food quality enhancer (Patil et al. 2000; Bhattacharya et al. 2007). Recent papers provide some details on the prospects chitinases have in biocontrol (Koga 2005; Quecine et al. 2008) and biofuel production (Vaaje-Kolstad et al. 2005; Himmel et al. 2007; Eijsink et al. 2008). Although there are many research papers available on plant chitinases, including several review articles that highlight chitinases of short-lived angiosperm crops (Flach et al. 1992; Collinge et al. 1993; Punja and Zhang 1993; Beintema 1994; Graham and Sticklen 1994; Meins et al. 1994; Araki and Torikata 1995; Iseli et al. 1996; Hamel et al. 1997; Selitrennikoff 2001; Bishop et al. 2002; Kasprzewska 2003; Lucca et al. 2005), there is no broad-scale report on conifer chitinases. To the best of our knowledge, this is the first review article on the current state of knowledge on conifer chitinases, including their regulation and function.

CLASSIFICATION AND STRUCTURAL DIVERSITY OF CONIFER CHITINASES

In most plants, including conifers, chitinases occur as diverse groups that differ in their primary structure, isoelectric point and cellular localization (Collinge et al. 1993; Beintema 1994; Graham and Sticklen 1994; Meins et al. 1994; Kasprzewska 2003; Hietala et al. 2004; Fossdal et al. 2006, 2007; Islam et al. 2010). In general, chitinases have been classified into two glycosyl hydrolase (E.C.3.2.1.14) families: family 18 and family 19 (Henrissat and Bairoch 1993). Family 18 chitinases consist of general types: a 'plant type' with endogenous activity that generates products of varying length, and a 'bacterial type' with exogenous activity releasing chitobiose or chitotriose from the non-reducing end of chitin (van Aalten et al. 2001; Andersen et al. 2005; Ubhayasekera et al. 2009). Family 18 chitinases hydrolyze the glycosidic bond with retention of the anomeric configuration, whereas family 19 chitinases have a different protein structure with an α -helical fold and hydrolyze with inversion. Family 18 chitinases occur in bacteria, fungi and some plants while family 19 glycosyl hydrolases occur mostly in plants. It is reported that chitinases within one family share similar three-dimensional structure and the same mechanism of hydrolytic action (Iseli et al. 1996).

The classification of plant chitinases has focused on the presence of auxiliary domains - namely, a chitin-binding domain, a hinge domain and a carboxy-terminal extensionflanking the main catalytic domain (Hamel et al. 1997). Plant chitinases are divided into seven classes (I-VII) based on their primary structures (Collinge et al. 1993; Meins et al. 1994; Neuhaus et al. 1996; Brunner et al. 1998; Gomez et al. 2002; Kasprzewska 2003). These seven classes fit into three of the 17 identified pathogenesis-related (PR) protein families (Neuhaus et al. 1996; Kasprzewska 2003). The family PR-3 includes chitinases of class I, II, IV, VI and VII; family PR-8 includes class III chitinases; and family PR-11 includes chitinases of class V (Neuhaus et al. 1996; Kasprzewska 2003). Additionally, some proteins of the family PR-4 with low endochitinase activity were found (Melchers et al. 1994; Neuhaus et al. 1996).

Based on previous reports (Collinge *et al.* 1993; Neuhaus *et al.* 1996; Hamel *et al.* 1997; Wiweger *et al.* 2003; Ubhayasekera *et al.* 2009), the schematic structural difference between classes of plant chitinases is presented in **Fig. 1**. Class I, II, IV and VII chitinases belong to the family 19 glycosyl hydrolase and share a high amino acid sequence identity within their catalytic domain. Further-



Fig. 1 Schematic representation of the structural differences between classes of plant chitinases. Signal peptides (blue), chitin binding modules (gray), hinge domains (green), and catalytic domains of chitinase family 19 (red) and two distinct groups of chitinase family 18 (pink and purple). Differences in the loop structures of catalytic domains of chitinase classes are indicated by the letters **a** (residues 164–170), **b** (217–222), **c** (235–257), **d** (308–311) and **e** (325–332) (adopted from Collinge *et al.* 1993; Hamel *et al.* 1997; Neuhaus *et al.* 1996; Wiweger *et al.* 2003; Ubhaya-sekera *et al.* 2009).



Fig. 2 Crystal structure of a basic class IV chitinase of *Picea abies*. (A) The chitin binding module (CtBM) of a class IV chitinase of *Picea abies* (color-coded from green to blue; disulfide-forming residues in gold). (B) General structure of the catalytic module (CM) of the same chitinase; residues that may be catalytically important are shown in pink (modified from Ubhayasekera *et al.* 2009). Letters show disulfide-forming cysteine residues (C), and catalytically active glutamic acid (E) and arginine (R) residues.

more, class I and IV chitinases have a cysteine-rich chitinbinding domain followed by a variable hinge region. The chitin-binding domain is absent in class II chitinases (Neuhaus et al. 1996; Ubhayasekera et al. 2009). Although classes IV and VII resemble classes I and II respectively, the former are significantly smaller due to some deletions. It is proposed that a basic class II chitinase is a putative ancestor of basic class I and acidic class II chitinase (Ohme-Takagi et al. 1998). Class IV chitinase genes, which are phylogenetically related to class I and II chitinase genes, are thought to have evolved from a class I chitinase gene by four deletions in the coding sequence (Araki and Torikata 1995). The protein genealogy of chitinases also suggests that class I and class II chitinase genes evolved from the same ancestral gene (Shinshi et al. 1990; Araki and Torikata 1995). In contrast, chitinases of class III, V and VI belong to the family 18 glycosyl hydrolase, are distributed in a wide range of organisms, including bacteria, fungi, plants, insects, mammals and viruses, and posses a common $(\alpha/\beta)_8$ barrel domain (Watanabe et al. 1999; Hollis et al. 2000).

To date, class I, II and IV chitinases have been reported from conifers (Davis *et al.* 2002; Karlsson *et al.* 2003; Hietala *et al.* 2004; Nagy *et al.* 2004; Karlsson 2005; Liu *et al.* 2005; Fossdal *et al.* 2006; Adomas *et al.* 2007; Fossdal *et al.* 2007; Adomas *et al.* 2008; Islam *et al.* 2010). However, the rapid progress in expressed sequence tags (ESTs) sequencing and molecular research is revealing additional classes of chitinases in conifer plants. For example, class III chitinase- (glycosyl hydrolase family 18) like ESTs were identified from several conifer species (Kusumi *et al.* 2002) and a class V chitinase (CrChii-A) was identified from *Cycas revoluta* Thunb. (Taira *et al.* 2009). Very recently the X-ray structure of the chitin-binding module and the catalytic module of a class IV chitinase has been reported from *Picea* abies (L.) H. Karst. (Fig. 2; Ubhayasekera et al. 2009). This protein shows high homology with other conifer class IV chitinases (Liu et al. 2005; Islam et al. 2010). In addition, several PR-4 genes were identified from Douglas-fir (DF; *Pseudotsuga menziesii* (Mirb.) Franco) seedlings infected with *Phellinus sulphurascens* Pilát. These PR-4 genes were found to be upregulated significantly after *P. sulphurascens* infection. The nucleotide sequences of these genes showed very low identity with DF chitinase genes suggesting that DF PR-4 proteins may have a differential defense mechanism in infected DF plants (unpublished data). Further research is required to resolve this enigma.

PHYLOGENY OF CONIFER CHITINASES

The alignment of amino acid sequences for selected classes of chitinases from gymnosperms and angiosperms displays the sequence variability occurring within and between different chitinase classes (Fig. 3). In conifers, sequence similarity within class I is over 90%, whereas class II shows 37 to 98% and class IV shows 66 to 98% homology. Between conifer classes sequence identity is comparatively lower, ranging from 31 to 59%. When conifer peptide sequences were compared with relatively distant angiosperm species, the sequence identity was even lower, ranging from 3 to 68%. Based on the alignment data, a phylogenetic tree was constructed using MEGA version 4.0 (Tamura et al. 2007). Class V and VI were not included in this study because they are not very common in planta and to our best knowledge there is no record available for these classes in conifer species. The phylogenetic analysis revealed the presence of several distinct clades for gymnosperm and angiosperm classes. Conifer chitinases form two major groups. One group consists of class II and class IV chitinases; this group shares high homology with angiosperm class IV chitinases but forms a sub-group in the tree. The second group consists of class I and II conifer chitinases along with angiosperm class I, II and VII chitinases. Angiosperm class III chitinases were found to be very distinct in the tree (Fig. 4).

Although conifer chitinases of class I, II and IV show significant sequence similarities, like angiosperm chitinases they differ in several ways: 1) the chitin-binding domain of class IV has cysteines at seven of eight positions in common with class I chitinases, but the remainder of their sequences vary greatly, while class II lacks this domain; 2) there are four deletions in class IV chitinases, one within the chitin-binding domain and three within the catalytic domain, shortening the final protein product compared to class I chitinases; and 3) a C-terminal extension found in most class I chitinases is missing in both class II and IV chitinases (Graham and Sticklen 1994). It is reported that both class II and IV chitinases are secreted to the apoplast (Graham and Sticklen 1994; Singh et al. 2007) and these two classes show high homology in their catalytic domain; however, they do not show any significant homology with class III and V chitinases (Beintema 1994; Kasprzewska 2003).

SUBCELLULAR LOCALIZATION OF CONIFER CHITINASES

To better understand the functions of chitinases in plants, investigators have used different techniques to study their localization. In angiosperms, for example, subcellular localization of a tomato (*Lycopersicon esculentum* Mill.) chitinase (molecular mass of 26 kD) was studied using tomato root tissues infected with *Fusarium oxysporum* Schltdl. The enzyme was found to accumulate in areas where host cell walls were in close contact with fungal cells. In contrast, the enzyme could not be detected in vacuoles and intracellular spaces (Benhamou *et al.* 1990). It was also reported that beet necrotic yellow vein virus, the causal agent of rhizomania, induced accumulation of a chitinase protein in cell walls and extracellular spaces in sugar beet (Burketová *et al.* 2003), while a basic class IV chitinase was found to be

localized in the extracellular space of cucumber (Boller and Metraux 1988). Asiegbu *et al.* (1995) reported the occurrence and accumulation of chitinase in seedling roots of *P. abies* following challenge by the root-rot pathogen *Heterobasidion annosum* (Fr.) Bref. Using transmission electron microscope (TEM) and immunogold labelling techniques, they demonstrated that the enzyme was localized in protein aggregates in host tissues and in the cell walls of intercellular hyphae. The labelling intensity increased with infected roots than in non-infected seedling roots. A similar labelling pattern was observed when this experiment was repeated using root samples inoculated with the saprophyte *Phlebiopsis gigantea* (Fr.) Jülich.

Similarly, an endochitinase-like protein (ECP) was found to be localized in the apoplastic fluid of DF needles (Zamani *et al.* 2003). Immunolocalization studies further suggested that this ECP protein is specifically localized in host cell membranes of DF seedlings (Islam *et al.* 2009). Infected host cell membranes frequently formed papillae where ECP were intensely localized. However, there was little or no localization of ECP observed in host cell walls, intercellular spaces, and cytoplasm of infected DF root tissues (**Fig. 5**; Islam *et al.* 2009). It is also reported that DF seedlings and mature trees contain multiple ECP isoforms (Zamani *et al.* 2003; Islam *et al.* 2009).

The localization of a class II chitinase in pine trees was successfully studied using suspension cell cultures of *Pinus elliottii* Engelm. (slash pine) and *Pinus taeda* L. (loblolly pine). Immunoreactive proteins were identified in the medium of both slash and loblolly pine cultures. In addition to that, one or more immunoreactive proteins approximately 32 kDa in size were detected in loblolly pine whole-cell extracts, suggesting the presence of other chitinase homologs that are localized in the vacuole (Davis *et al.* 2002). Based on the presence of a putative C-terminal vacuolar-sorting determinant (LIKTVV), this protein was designated as a class I chitinase as recommended by Neuhaus and Rogers (1998).

Collinge et al. (1993) and Neuhaus et al. (1996) have demonstrated that a short C-terminal extension of about six amino acids present in a tobacco basic class I chitinase is necessary for vacuolar localization. So far, vacuolar chitinases have been reported from several conifer species such as P. abies (Salzer et al. 1997a, 1997b; Hietala et al. 2004), Pinus halepensis Mill. and P. taeda (Davis et al. 2002; Sathyan 2004) and Cryptomeria japonica (L. f.) D. Don (Kusumi et al. 2002; Kado et al. 2003). Except for class I chitinases, no other conifer chitinases were recorded as vacuolar proteins. However, a class IV chitinase was recently cloned from yam that contains an additional sequence composed of eight amino acids at the C-terminal, when compared with class IV chitinases from other plants (Mitsunaga et al. 2004). In order to clarify the role of this C-terminal extension in cellular localization, Mitsunaga et al. (2004) conducted further studies using plants and suspensioncultured cells of Nicotiana tabacum L. These cultures, which were transformed with either the cloned yam class IV chitinase gene carrying the C-terminal extension or its truncated gene using the Agrobacterium-mediated method, suggest that the C-terminal extension of class IV chitinase plays an essential role as a targeting signal for plant vacuoles (Mitsunaga et al. 2004).

REGULATION OF CONIFER CHITINASES

Conifer plants exhibit both local and systemic expression of chitinases, regulated constitutively or induced by chemicals and pathogen infections. These systemic or inducible defense systems have evolved to deter or kill insects and inhibit or exclude pathogens physically and/or chemically (Bonello *et al.* 2006). Recent fossil evidence suggests that the defense mechanisms in conifers have been operating for at least the past 45 million years in the Pinaceae (Labandeira *et al.* 2001; Bonello *et al.* 2006).

S	ILALVVVGIPAFAE-NCGSQAGG
S	ILALVVVGIPAFAE-NCGSQAGG
MAKVKMLVI5	SMRVISALTALAMM
MASATIGRMK	SMRVI SALTALAMM
MAYTNMKRMM	SMRTTLATTAVATM
VQ	LAACAAAALLAVA
MMRFWLVSL	FCLFCLKYALAQ
MKIWGLRF	FPLMLLAIGGAFAQEQCGRQAGG
MGLWALVA	FCLLSLILVGSAEQCGGQAGG
MPPQKENHRTLNKMKTNLFLF	LIFS <mark>LL</mark> LS <mark>L</mark> SSAEQCGRQAGG
MAYSDALL	FAVTAVASLVTSGG
	ALWIAVVAFLVASGSVVVI
EAIMAKPTPAPK	ATPFLLAAVLSIVVVAASG
MGTTTTDKS	VMARVI.VI.I.I.VGFIVNAON
MGSSSSDKS	VMALVLVLLLVGVSVNAQN
WGRTGGEKW	VMALVLVLLLVGVGVNAQN
B	LMVLLLVLLLVGVTVNAQN
MAGSSGKFDSPRGRV	VVRMSLVLLLVVGVSVNVVNAQN
MQIMATQNSKSNIFWSSS	ASVVLVLLLLVDVGVCQN
F	IFLIALTIVLVVVPRTILAQN
S	ISLVTILLVLQAFSNTTKAQN
L	LTVLLVGALFGAAVAQN
MANSPTPTM	LAFLALGLALLL-SATGQASAQN
F	FIFUTALFIAASLVSAQN
MAFGRRSLFLPVVGV	AAILLLAAGHATAVNTGETV
	TYFT FFTSCSLSKPSDASRGGTA
MIKYS	FLT TALVI.FL.BALKI.EAGDIV
MATESPKHS	SKYGVRSISIPTRSHP
AVCPGCLCCSQYCWCCNTPDHCRVPGC	QSQ <mark>C</mark> GGGSGPSPPS
AVCPGCLCCSQYCWCGNTPDHCRVPGC	QSQ <mark>C</mark> GGGSGPSPPS
AV C PG GLCCS QY GWCG N T PAHCQVPGC	QSQ <mark>C</mark> GGGSGPTP
GTLC	CQVSAQQG
GTLC	CQVSAQQG
SSLC	CYVSAQQG
ASG-	AAAQG
ALOSGGLCCSQYGYCGSTSAYC-STGC	QSQCPSGGSPSTPSTP-TPTPS-
FFAEARWYGPGG	K
RVAEAR-YGPGH	W-NPAAPAP
AEARWYGGGG	GGGYSPSPSP
SALSICR	
SALSI S R	
CG C AT <mark>GLCCS</mark> QY <mark>GYCG</mark> TTSA <mark>YCG</mark> KGCK	TGP <mark>C</mark> YSSGGGSPS
CG C AS <mark>G</mark> V CCS QY G Y CG T T SA YCG KGCK	SGP <mark>C</mark> YSS <mark>GG</mark> GSPS
CGCASCLCCSKFCYCGTTSAYCGTGCQ	SGPCSSSGGGSPS
CGCASCLCCSQYCYCGSSSAYCCAGCK	SGPC-SGGGSPS
CGCASCLCCSKWGYCGTISAYCGNGCQ	SGPC-SGGGSPS
	SGPOYEGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CNCAAGLCCSKHGYCGTTSDYCCEGCO	AGPCTNTAPTGG
VFWGRNKDEGSLREACDTGLYTSVIIS	FLAVFGHG
VFWGRNKDEGTLREACDTGTYTTVIIS	FLRGFGHGAA
IYWGQNGNEGTLTQTCN T GK <mark>Y</mark> SYVNIA	FLNKFGNGQ
IYWGQNGNEGNLSATCATGRYAYVNVA	FLVKFGNGQ
IYWGQNGNEGSLADTCA T NN <mark>Y</mark> AIVNIA	FLVVFGNGQ
STVRVEEEL <mark>S</mark> KLKSLEASSSSSSTPKV	ETICCGLSG
PSGQGVASIITENVFNQMLKHRNEGSC	PGKNFYNYNAFIAAAKAFN-GFG
PSGQGVASIITENVENQMLKHRNEGSC	PGKNEYNYNAFIAAAKAFN-GFG
	FGANEYNINAEIAAAKAFN-GFG Dakcentysaeiaaakafn-gfg
	FANGELLISAELAAANSEP-DEG
	PAKCEVTYSAETAAAMCED_DEC
	PAKGFYTYSAFIAAANSFP-DFG SakgeytysafiaAansfp-dfg

C_japonica_BAE43610_I C_japonica_BAD02536_I T distichum BAD02824 I P_abies_AAT09427_II P sitchensis ABK25320 II P storbus U57410 II O sativa AAL34317 II N_tabacum_BAA33971_II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S_bicolor_XP_002457689_VII O_sativa_EAY73581_VII P sitchensis ABK22545 II P menziesii GU063812 II P abies AAQ17050 IV P glauca AAA85364 IV P menziesii GU063815 IV P_monticola_AAS83984_IV P sitchensis ABK22417 IV C_japonica_BAD77932_IV N_tabacum_BAF44533_IV A_thaliana_CAA74930_IV V_vinifera_AAB65776_IV O sativa NP 001053186 IV D_carota_AAB08469_IV O sativa BAA23806 III Z_mays_NP_001140795_III V_vinifera_CAA92207_III A_thaliana_P19172_III N_tabacum_CAA77656_III G_max_AAK01734_I C_japonica_BAE43610_I C_japonica_BAD02536_I T distichum BAD02824 I P_abies_AAT09427_II P sitchensis ABK25320 II P storbus U57410 II O_sativa_AAL34317_II N tabacum BAA33971 II V_vinifera_CAC14015_II V_vinifera_CAC14014 I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S_bicolor_XP_002457689_VII O_sativa_EAY73581_VII P sitchensis ABK22545 II P_menziesii_GU063812_II

P abies AAQ17050 IV P glauca AAA85364 IV P menziesii GU063815 IV P_monticola_AAS83984_IV P_sitchensis_ABK22417_IV C_japonica_BAD77932_IV N_tabacum_BAF44533_IV A_thaliana_CAA74930_IV V_vinifera_AAB65776_IV O_sativa_NP_001053186_IV D_carota_AAB08469_IV O sativa BAA23806 III Z_mays_NP_001140795_III V_vinifera_CAA92207_III A thaliana P19172 III N_tabacum_CAA77656 III G max AAK01734 I

C_japonica_BAE43610_I C_japonica_BAD02536_I T_distichum_BAD02824_I P_abies_AAT09427_II P_sitchensis_ABK25320_II P_storbus_U57410_II O_sativa_AAL34317_II

N_tabacum_BAA33971_II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S_bicolor_XP_002457689_VII O_sativa_EAY73581_VII P_sitchensis_ABK22545_II P_menziesii_GU063812_II P_abies_AAQ17050_IV P_glauca_AAA85364_IV P_monticola_AAS83984_IV P_sitchensis_ABK22417_IV C_japonica_BAD77932_IV N_tabacum_BAF44533_IV A_thaliana_CAA74930_IV V_vinifera_AAB65776_IV O_sativa_BAA23806_III D_carota_AAB8469_IV O_sativa_BAA23806_III
V_vinifera_CAA92207_III A_thaliana_P19172_III N_tabacum_CAA77656_III G_max_AAK01734_I
C_japonica_BAE43610_I C_japonica_BAD02536_I T_distichum_BAD02824_I P_abies_AAT09427_II P_sitchensis_ABK25320_II P_storbus_U57410_II O_sativa_AAL34317_II N_tabacum_BAA33971_II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S_bicolor_XP_002457689_VII O_sativa_EAY73581_VII P_sitchensis_ABK22545_II P_menziesii_GU063812_II P_abies_AAQ17050_IV P_glauca_AAA85364_IV P_monticola_AAS83884_IV P_monticola_AAS8384_IV P_sitchensis_ABK22417_IV C_japonica_BAD77932_IV N_tabacum_BAF44533_IV A_thaliana_CAA74930_IV V_vinifera_AAB65776_IV O_sativa_BAA23806_III Z_mays_NP_001140795_III V_vinifera_CAA92207_III A_thaliana_P19172_III N_tabacum_CAA77656_III G_max_AAK01734_I
C_japonica_BAE43010_1 C_japonica_BAD02536_I T_distichum_BAD02824_I P_abies_AAT09427_II P_sitchensis_ABK25320_II P_storbus_U57410_II O_sativa_AAL34317_II N_tabacum_BAA33971_II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S_bicolor_XP_002457689_VII O_sativa_EAY73581_VII

DWGALVSKNLEERILLHRNDANCPAKCEYTYEADVTATRSFG-AFG GGGGDISSLISKSLEDEMLKHRNDAACPCKCEYTHEADISAVKSFG-CFG DIGQLITRSMENDMLKHRNEGSCPCKCEYTYDADIAAAKAFP-CFG GPTSDLSGIISSSQEDDMLKHRNDAACPARCEYTYNADITAAKSFP-GFG
VATLVSEQLYNSLFLHKDDAAGPAKGFYTYASFIQAARTFP-KFA VATLVSEQLYNSLFLHKDDAAGPAKGFYTYASFIQAARTFP-KFA VSSIVSEQLYASLFLHKDDAAGPARGFYTYASFVRAATRFP-RFA GAVSDIATQDFFNG-ILSAATDGCAGKTFYTYTDFINAANSFS-SFG
AAVGDIATQSFFNG-ILSTAADSCACKTFYTYSDFINAANAFS-AFG AGGGSVGGIISQSFFNG-LAGGAGSSCECKGFYTYNAFIAAANAYS-GFG AGGGSVGGIISQSFFNG-LAGGAGSSCECKGFYTYNAFIAAANAFS-GFG GGGGSVGTIISESVFNG-LAGGAASSCECKGFYTYNAFIAAASAYS-GFG
GGGGNVGTIISONFFNG-LASGAGGSGEGKGFYTYNAFIAAANAIS GFG TGTG-VGSIVSSDVFNS-IVGGAASGCAGNGFYTYDSFISAANAFN-CFG SNGGSVADVVSNAFFNG-ITDQAASTCECKGFYTRANFLEALQSYP-NFG ANGVSVAFIVTQEFFNG-IISQAASSCAGNRFYSRGAFLEALDSYS-RFG
-SGSSWSDIVTQSFEDG-IISQAASSCAGKNFYTRAABISALNSYS-CFG GSGVSWESVVTEAFENG-IKNQAPNGCAGKNFYTRQSELNAAHSYS-GEA GNGVSWADIVTDDFFNG-IISQATGDCDGKNFYTRSAFLNALQSYS-SFG RYSLDLSCHDVSAVGADIKHCQSKYIPVLLSIGGQGC
YYSLDLSCHPLAGVGADVKHCQAKGILVLLSIGGPPNTNTGAGA TPEINLAGHCNPASNGCTSVSTGIRNCQNRGIKVMLSIGGGAG TPELNLAGHCNPAANTCTHFGSQVKDCQSRGIKVMLSLGGGIG NPVLNLAGHCDPNAGACTGLSNDIRACQNQGIKVMLSLGGGAG LAELYKCIEDLLKLPLTOOAIGOHONEKWVNELLDCPVGFLDLLG
TTG-DITARKRELAAFLAQTSHETTGGWASAPDGPYAW-GYCYLKENG TTG-DITARKRELAAFLAQTSHETTGGWASAPDGPYAW-GYCYLKENG TTG-DITTQKRELAAFLAQTSHETTGGWATAPDGPYAW-GYCFLRENG
NNG-DLETSKRELAAFFGQTAQETTGGWATAPDGPYAW-GYGFKEE NNG-DLETSKRELAAFFGQTSQETTGGWATAPDGPYAW-GYGFKEE NIG-DQDSRKRELAAFFGHTSQETTGGWPTAPDGPYAW-GYGFKDQV TSGGSAELIRRELAAFFGQTSHETTGGTRGSSD-QFQW-GYGFKEEI TTG-DTNTRKKEIAAFLAOTSHETTGGWATAPDGPYSW-GYGFKOEOG-S
TTG-DTNTRKREIAAFLAQTSHETTGGWATAPDGPYAW-GYGFLREQG-N TTG-DTTTRKREIAAFLAQTSHETTGGWASAPDGPYAW-GYCYLREQG-S TTG-DTATRKKEVAAFFQQTSHETTGGWATAPDGPYSW-GYCFKQEQN-P GTG-DLATRKRELAAFFAQISHETTGGWATAPDGPYSW-GLCYKEEIS-P
ATG-DLSTRKREVAAFFAQISHETTGGWATAPDGQYAW-GLGYKEEIS-P ATG-CADARKREVAAFLAQISHETTGGWATAPDGPYAW-GLGYKEEIN-P TTG-TSDDNKREIAAFFANVAHETTNLGYVEEIA-K TTG-TSDDQKREIAAFFANVAHET-GSLGYVEEIA-K
TTG-SNDVKKRBLAAFFANVMHET-GCLQYINEKN-P TTG-SNDVKKRELAAFFANVMHET-GCLQYINEKN-P TTG-SSDVQKRELAAFFANVMHES-GCLQYINEIN-P TTG-SADVTKRELAAFLANVMHET-GCMQYINERT-P TTG-ANDVOKRELAAFLANVMHET-GCLQYINEIS-P
TSG-SSDVNKREIAAFFANAAHDT-GGFGYIEBQN-P TMG-STDDSKREIAAFFAHVTHET-GHMGFINBINGP RVG-STDDSRREIAAFFAHVTHET-GRNFGYIEBIDGA NDG-STDANKREIAAFFAHVTHET-GHFGYIEBINGA
RDR-TNDDSKREIAAFFAHVTHET-GHMGYINEINGA ISG-SADDSKREIAAFFAHATHET-GYFGHKEETNGR AYSLPTNASAADVADHLWDSFLGGGRAGVPREFGDAVVDGVDLFIDQGGA GYSLPSARAAADLAAYLWDAYLGGSRAGLRREFGDAALDGVDLYIDQGGV SYSLSSSNDAONVANYLWNNELGOSS-SEDLGDAVVGTDEDTELGST
SISLSSSNDAQNVANILMNNE BGQSS-SKELGDAVIDG DEFILEGSI NYSIGSREDAKVIADYLWNNELGGKSS-SRELGDAVIDG IDEFILEGSE SYFLSSADDARNVANYLWNNYLGGQSN-TRELGDAVIDG IDEFILEGST KIRDSILLMKGSVGELQSALRRKRVGDLYMESYLSTYWRLRRN
GGDYCNSQQAPCASGKQYYGRGEIQLSWNYNYIAAGKAIGFDG GGDYCNSQQAPCASGKQYYGRGEIQLSWNYNYIAAGKAIGFDG GGDYCNSQQGPCASGKQYYGRGEIQLSWNYNYIAAGKAIGFDG NSADRYHGRGEIQLTGDYNYKAAGDALGYDL NGEDD
NSTDRMHGKGFIQLTGDINYKAAGALGYDL NSTDRYRGRGFIQLTGDYNYKAAGNALGYDL NKATSPPYYGRGFIQLTGQSNYQAAGNALGIDL PPNYCVAN-QQWPCAPGKTYFGRGFIQISYNYNYGPAGRAIGSDL PGDYCVAN-QQWPCAPGKKYYGRGFIQISYNYNYGPAGKAINYDL
PGAYCVPS-AQWPCAAGRKYYGRGEIQISYNYNYGQAGKAIGVDL ASDYCEPS-ATWPCASGKRYYGRGEMQLSWNYNYGLCGRAIGVDL ASNYCDATDKQWPCYPGKSYHGRGEIQLSWNFNYGPAGQALGFDG ASSYCDATDKQWPCYPGKSYHGRGEIQLSWNFNYGPAGQALGFDG QSSYCDATDKQWPCYPGKSYHGRGEIQISWNFNYGPAGQALGFDG

P sitchensis ABK22545 II P menziesii GU063812 II P_abies_AAQ17050 IV P glauca AAA85364 IV P menziesii GU063815 IV P monticola AAS83984 IV P sitchensis ABK22417 IV C_japonica_BAD77932_IV N_tabacum_BAF44533_IV A_thaliana_CAA74930_IV V_vinifera_AAB65776_IV 0 sativa NP 001053186 IV D_carota_AAB08469_IV O_sativa_BAA23806_III Z mays NP 001140795 III V_vinifera_CAA92207_III A thaliana P19172 III N tabacum CAA77656 III G max AAK01734 I C_japonica_BAE43610_I C_japonica_BAD02536_I T distichum BAD02824 I P abies AAT09427 II P sitchensis ABK25320 II P storbus U57410 II O sativa AAL34317 II N tabacum BAA33971 II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A_thaliana_AAA32769_I C_dactylon_AAC95375_VII S bicolor XP 002457689 VII O_sativa_EAY73581_VII P sitchensis ABK22545 II P_menziesii_GU063812_II P abies AAQ17050 IV P_glauca_AAA85364_IV P menziesii GU063815 IV P monticola AAS83984 IV P sitchensis ABK22417 IV C japonica BAD77932 IV N_tabacum_BAF44533_IV A thaliana CAA74930 IV V_vinifera_AAB65776_IV O_sativa_NP_001053186_IV D_carota_AAB08469_IV O sativa BAA23806 III Z mays NP 001140795 III V_vinifera_CAA92207_III A thaliana P19172 III N tabacum CAA77656 III G max AAK01734 I C_japonica_BAE43610_I C_japonica_BAD02536_I T_distichum_BAD02824_I P abies AAT09427 II P_sitchensis_ABK25320_II P storbus U57410 II O_sativa_AAL34317_II N tabacum BAA33971 II V_vinifera_CAC14015_II V_vinifera_CAC14014_I A thaliana AAA32769 I C_dactylon_AAC95375_VII S bicolor XP 002457689 VII O_sativa_EAY73581_VII P_sitchensis_ABK22545_II P_menziesii_GU063812_II P abies AAQ17050 IV P_glauca_AAA85364_IV P_menziesii_GU063815 IV P monticola AAS83984 IV P_sitchensis_ABK22417_IV

SD-	YCD	STN	ΓQΥΡ	CASO	;QQ <mark>y</mark> y	GRGPI	QLT(GNAN	YGAA	TYLC	ADL	-
SDS	YCD	STN	ΓQΥ <mark>Ρ</mark>	CVSC	KQYY	GRGPI	Ľ Q LTV	WNY <mark>n</mark>	YGAA	DYLC	SDL	-
PIN	YCQ	SS-	STWP	CTSG	GKSYH	GRGPI	QLSV	VNY <mark>n</mark>	YGAA	KSIC	FDG	-
PMK	YCQ	SS-	STWP	CTSC	GKSYH	GRGP	l <mark>q</mark> lsv	VNY <mark>n</mark>	YGAV	KSIC	FDG	-
PII	YCQ	SS-	STWP	CTSC	GKSYH	GRGP	1 <mark>0</mark> lsv	VNY <mark>n</mark>	YGAA	QSIC	FDG	-
PMI	ΥСМ	SS-	ATWP	CASC	KSYH	GRGPI	1 <mark>0</mark> lsv	WNY <mark>n</mark>	YGAA	QSIG	FDG	-
SSN	YCQ	ss-	STWP	CTSG	GKSYH	GRGPI	1 <mark>0</mark> lsv	VNY <mark>n</mark>	YGAA	QSIC	FDG	-
TSI	YCD	ASN	ΓQΥ <mark>Ρ</mark>	CASC	GKTYH	GRGP	1 <mark>0</mark> lsv	NNY <mark>n</mark>	YGAAC	SYIÇ	FDG	-
SLE	YCD	ENN	TEYP	CVSC	KNYY	GRGP:	I QLSV	VNFN	YGPAC	KSIC	FDG	-
SKE	YCD	ENA	ΓQΥΡ	CNPN	IKGYY	GRGP	[QLS]	VN F N	YGPAC	TAIC	FDG	-
SHN	YCD	SSN	ΓQΥ <mark>Ρ</mark>	CVSC	QNYY	GRGP	QLTV	VNY <mark>n</mark>	YGAAC	NSIC	FNG	-
SME	YCD	KNN	KQWP	CQPC	KKYY	GRGPI	QISV	VNY <mark>n</mark>	YGPAC	QNIC	FDG	-
DKS	YCE	SKA	G−YP	CNAN	IVKYF	GRGPI	lQLTV	WNYN	YIDAC	KSNE	FDG	-
E-H	IYDE	LAR	RLFS	HYK-		FEML	LTAT 1	[RCS]	YPDHF	rldma	LATGLFT	H
DGH	IYDE	LAR	RLYA	YNRS	SYRGR	LGVT	TAT	/RCA	YPDPF	RAQAA	LATGLVS	R
L-H	IWDD	LAR.	ALSR	IEFÇ	QERG	RKVY.	JTAAI	PQCPI	FPDKV	/PGTA	LNTGLFD	Y
Q-H	IWDD	LAR	flsk	FSH-	RG	RKIY.	JTGAI	PQCPI	FPDRI	LMGSA	LNTKRFD	Y
Q-H	IWDE	LAK	TLSQ	FSQ-	·Ç	RKVY.	TAAI	PQCPI	FPDTV	VLNGA	LSTGLFD	Y
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	ц т			NCST					DKD		HEMMACE.	v
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	T.	RNP	ETVA	NCSI	TARC		- WM		TKP		HOVMVGE.	Υ
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	T.	NNP	ETVA		TSWK	TALWI		INTG	SVG		HAATTS-	_
	L	NNP	EKVG	ODSI	ISFK	TAV	- W MF	KNS-		NC	HSAITS-	_
	L	NNP	EKVG	KDPI	TSSK	TAVW	- W MF	KNR-		NC	HSAITS-	_
	L	NNP	EKVG	QDAI	ISFK	TAVVI	r – M me	KNS-		NC	HSAITG-	_
	v	NNP	ek <mark>v</mark> g	QDSI	ISFK	TAV	- W MF	KNS-		NC	HSAITS-	_
	L	NNP	ek <mark>v</mark> g	QDAI	ISFK	TAV	r – W mf	KNS-		NC	HSAITS-	_
	L	NNP	EI <mark>V</mark> G	TDSI	ISFK	TAVW	r – WMN	/NS-·		NC	HTAITS-	_
	L	NDP	di <mark>v</mark> a	RDAV	/ISFK	TALW	Z – <mark>W</mark> MI	NN		C	HSLITS-	_
	L	NAP	et <mark>v</mark> a	TDPV	/ISFK	TALW	(− 0 11	NR		V	QPVIS	-
	L	SNP	GIVA	TDVV	TSFK	TALW	r – W Mì	NN		V	HSVIG	-
	L	RDP	dr <mark>v</mark> a	QDPI	ISFK	TALW	r – WMP	NN		V	HQVML	-
	L	NNP	di <mark>v</mark> a	SDAV	VSFR	TALW	∠– M KV	/K·		V	QSVTT	-
IHV	RVF	GG-	GG	DAGC	TTRH	IRASWI	ER W A <i>I</i>	AAYP	GS	LVY	LGVVAS-	-
VHV	RLY	G		DLKC	TWSE	REAW	EK W A <i>I</i>	AAYP	AS	RVF	VGVVAS-	-
VWV	QFY	NNP	PCQY	SSGN	ITNNI	LNSWI	JRWTS	SSIN	ST	GSF	MGLPAS-	-
VWI	QFY	NNP	PCSY	SSGN	ITQNI	FDSWN	IKWT:	FSIA	AQ	KFF	'LGLPAA-	-
VWV	'QF'Y	NNP	PCQY	SGGS	SADNL	KNYWI	1Q <mark>w</mark> n-	-AIQ	AG	KIF	'LGLPAA-	_
	SIF	ESL	VVFL	SSPI	LKLK	PNKW	ALVVS	SRLM	QKGVE	FAYNN	HQEDINE:	L
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NPS VDC	GSD	SAA	GRIA			TNGGI			DSKVÇ	DRIC	FIRRICD	⊥ т
CDC			JR DA	GIGV		TNGGI					FTARIOD.	T V
ore	עדעי חידתי		CDUD	GIGN		TNCC			SAIQÇ	JGRIG DCDIC	T IQIION. TVOTTONI	n. vz
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						TNGG	FCC3		ND V QÇ		AAKDAGUI	
TPS		SAA	RRVP	GEGU	TTNT	TNGG	FCNF			SBIG	FYRRYCO	Т
TPS	SSD	TSA	GRVP	GYGT	TTNT	TNGG	FCGF	KGS-1	NPOMF	DRIG	FYKRYCD	T.
TPS	GAD	RSA	GRI.P	GFG	TNT	INGG	/ECGF	KGV-Y	VPOM		FYKRYCD	I
OPS	DAD	RAA	GRLP	GYGU	ITNT	INGGI	ECGF		DGRVA	DRIG	FYORYCN	I
RPI	'ATD	VAG	NRMP	GFGI	VTNI	VNGGI	ECNE	RTD-1	DARVN	INRIG	FYRRYCO	Ι
RPI	'AAD	AAA	NRTA	GFGI	VTNI	VNGGI	ECNE	RTD-1	DARVN	INRIG	FYQRYCO	Ι
RPG	PAD	VAA	NRTA	GFGI	VTNI	VNGGI	ECNE	RAG-1	DARVN	INRIG	FYRRYCO	V
			GQ	GFGZ	TIQA	INGA	ECNO	GGK-1	PDQVN	IDRIS	HYTNYCS	Q
			GQ	GFGF	TIRI	INGG	/ECDO	GKS-1	pssvç) D rv s	LYTNYCS	2
			GQ	GFG	TIKA	IN-SI	4 <mark>EC</mark> NC	GGN-S	SGEVS	SSRVN	YYKKICS	Q
			GK	GLG	TIKA	IN-SI	4 <mark>EC</mark> NO	GGN-S	SGEVN	IS <mark>R</mark> VN	YYKKICS	Q
			GQ	GFGZ	TIKA	IN-SC	G <mark>EC</mark> NO	GGN-S	SGEVS	SS <mark>R</mark> VN	YYKKICS	2
			GQ	GFG	TIKA	IN-SĢ	Q <mark>EC</mark> NO	GGN-	SGEVN	ISRVN	YYKNICS	2
			GQ	GFG	TIKA	IN-SC	GECNO	GGN-S	SGQVN	IS <mark>R</mark> VI	YYKKFCS	2

C japonica BAD77932 IV	GOCFCATTRAIN-SMECDGGN-AATVASEVNYYOKFCOO
N tabacum BAF44533 IV	
A thaliana CAA74930 IV	
V vinifera AAB65776 IV	
0 sativa NP 001053186 TV	O-CFCATTRATNGALEONGKN-PGAVNARVNYVKDYCRO
D carota AAB08469 IV	O-CFCATTRAIN-SIDONGGS-PDAVNSBVSINNSVOSK
O sativa BAA23806 III	PEODANAYLPRKVLFSDVLSHIVEKPNYGGLMIWDRYYDK
Z mays NP 001140795 III	PEADKDAYMFOKDLYYNVLOFAOKAPNYGGLMIWDRYYDK
V vinifera CAA92207 III	SAAAGRGFIPANVLTSOILPVIKRSPKYGGVMLWSKYYDD
A thaliana P19172 III	PEAAGSGYIPPDVLTSQILPTLKKSRKYGGVMLWSKFWDD
N tabacum CAA77656 III	QGAAGSGFIPSDVLVSQVLPLINGSPKYGGVMLWSKFYDN
	EKVDFALNSLILDNLNKDAEAEAEKIQSAHGRLEALVVAIEEIESGLECL
C japonica BAE43610 I	LGVSY <mark>G</mark> P <mark>N</mark> LD <mark>C</mark> FN <mark>Q</mark> RPFGFAL
C japonica BAD02536 I	LGVSYGPNLDCFNQRPFGFAL
T distichum BAD02824 I	LGVSY <mark>G</mark> PNLD <mark>O</mark> FN O RPFGFAL
P abies AAT09427 II	LGVDSCSNLDCNNQKHFGN
P sitchensis ABK25320 II	LGVDSCSNLDCNNQKHFGN
P storbus U57410 II	LGVDV <mark>C</mark> SNLDYKN <mark>Q</mark> KPYGT
O sativa AAL34317 II	LGTGY <mark>G</mark> SNLD <mark>C</mark> YN <mark>C</mark> RNFAS
N tabacum BAA33971 II	LGVDP <mark>G</mark> N <mark>NLD</mark> GAN <mark>Q</mark> KPFGQ
V_vinifera_CAC14015_II	MGIGY <mark>G</mark> SNLD <mark>C</mark> NNQRPFS
V_vinifera_CAC14014_I	LRVSY <mark>G</mark> NNLD <mark>C</mark> NN <mark>C</mark> RPFGSGLLLDTI
A thaliana AAA32769 I	FGVNP <mark>G</mark> GNLD <mark>C</mark> YN C RSFVNGLLEAAI
C_dactylon_AAC95375_VII	FNVDT <mark>G</mark> P <mark>NLDC</mark> AHQQPY
S_bicolor_XP_002457689_VII	FNVDA <mark>G</mark> ANLD <mark>C</mark> AHQQPY
O_sativa_EAY73581_VII	LGVDVGPNLDCEHQQPF
P_sitchensis_ABK22545_II	FGVDP <mark>G</mark> SNLSC
P_menziesii_GU063812_II	LGVDPGSNPSC
P_abies_AAQ17050_IV	LGVDPGANVSC
P_glauca_AAA85364_IV	LGVDPGANVSC
P_menziesii_GU063815_IV	LGVDPGANVSC
P_monticola_AAS83984_IV	LGVDP <mark>G</mark> ANLSC
P_sitchensis_ABK22417_IV	LGVDA <mark>G</mark> TNVSC
C_japonica_BAD77932_IV	LNVDT <mark>G</mark> S <mark>N</mark> LQ <mark>C</mark>
N_tabacum_BAF44533_IV	LGVETGDNLTC
A_thaliana_CAA74930_IV	LGVDP G NNLTC
V_vinifera_AAB65776_IV	LGASPGDNLTC
O_sativa_NP_001053186_IV	FGVDP G GNLYC
D_carota_AAB08469_IV	FGVAPGDNQRC
O_sativa_BAA23806_III	KTGYSAGKVF
Z_mays_NP_001140795_III	MNHYISSS
V_vinifera_CAA92207_III	QSGYSSSIKSSV
A_thaliana_P19172_III	KNGYSSSILASV
N_tabacum_CAA77656_III	GYSSAIKANV
G max AAKU1734 T	FKRLINTRVSFLNTFSP

Fig. 3 Alignment of amino acid sequences for selected conifers and angiosperms chitinases. Each of the clones' ID include species name, NCBI accession number and the designated class number as I, II, III, IV and VII. Hyphens show gaps in sequences for the best alignment. Letters with black and gray background indicate amino acid residues that are identical in a wide (black) and a restricted (grey) range of chitinase classes and plant species, respectively. Plant chitinases are selected from the following species *Arabidopsis thaliana*, *Cryptomeria japonica*, *Cynodon dactylon*, *Daucus carota*, *Glycine max*, *Nicotiana tabacum*, *Oryza sativa*, *Picea abies*, *Picea glauca*, *Picea sitchensis*, *Pinus monticola*, *Pinus storbus*, *Pseudotsuga menziesii*, *Sorghum bicolor*, *Taxodium distichum*, *Vitis vinifera* and *Zea mays*.

Constitutive regulation of conifer chitinases

In healthy plants, some forms of chitinases, both vacuolar and apoplastic, are synthesized constitutively. Constitutive defense consists of a suite of stable defense products of varying properties that provide a generalized capacity for resistance to a broad range of organisms (Franceschi et al. 2005). Each of the constitutive defenses is determined by genetics and by the prior history of an organism. Constitutive regulation is also the first line of defense of all organisms, including plants, and it comprises a number of physical and chemical barriers (Bonello et al. 2006). Although morphological, anatomical and chemical structures are the major components of the constitutive defense of conifers, there are many defense-related proteins including chitinases that are constitutively regulated. Constitutive expression of chitinases is evident in many conifers including P. menziesii (Robinson et al. 2000; Zamani et al. 2003; Sturrock et al. 2007; Islam et al. 2009), Pinus monticola Doug. ex D. Don (Liu et al. 2005), P. abies (Wiweger et al. 2003; Hietala et

al. 2004; Fossdal *et al.* 2006, 2007), *Picea glauca* (Moen.) Voss (Dong and Dunstan 1997), *Pinus sylvestris* L. (Pirttilä *et al.* 2002), *Taxus baccata* L. (Uzal *et al.* 2009), and *C. japonica* (Kusimi *et al.* 2002; Fujimura *et al.* 2005, 2007).

In *P. abies* a high level of constitutive chitinase expression has been reported. Differential regulation of a chitinase (PaChi1) was also observed after wounding and pathogen inoculation in the same plant. These data suggest that some chitinases may not have a major defense role, but may play an important role in plant growth and development (Hietala *et al.* 2004). Constitutively expressed chitinases may regulate plant development by generating signal molecules from endogenous substrates such as arabinogalactan proteins containing *N*-acetylglucosamine (Collinge *et al.* 1993; van Hengel *et al.* 2001). Specifically, constitutively expressed conifer chitinases may play a major role in somatic embryogenesis and seed development (Wiweger *et al.* 2003; dos Santos *et al.* 2006, 2008).



Fig. 4 Phylogenetic tree constructed using amino acid sequences of different classes of chitinases from gymnosperms and angiosperms. Using MEGA 4.0, construction of this tree was based on the full length coding regions of the amino acid sequences. Each of the clones' ID includes species name, NCBI accession number and the designated class number as I, II, III, IV and VII.

Inducible regulation of conifer chitinases

Inducible defense in planta is achieved through different PR proteins, signal chemicals and elicitors that respond under stress conditions to degrade components of invasive organisms, toxic proteins like porins and lectins, and inhibitors of enzymes such as proteinase and amylase inhibitors. PR protein-based inducible defenses can be highly specific to a particular organism (Franceschi *et al.* 2005). For instance, in *P. abies*, chitinases exist as a fairly large family of proteins, but only a small subset of this group may be upregulated during infection of a specific fungal pathogen (Hietala *et al.* 2004; Nagy *et al.* 2004).

The plant chitinase family appears to be a prominent component of the inducible defense of conifer species. Biotic and abiotic stress factors such as pathogens and pests (Hietala *et al.* 2004; Nagy *et al.* 2004; Liu *et al.* 2005; Sturrock *et al.* 2007; Islam *et al.* 2010), wounding (Fossdal *et al.* 2006; Ralph *et al.* 2006; Lippert *et al.* 2007), drought (Sathyan 2004; Lorenz *et al.* 2006) overwintering (Zamani *et al.* 2003; Jarząbek *et al.* 2009), elicitors (Wu *et al.* 1997; Mason and Davis 1997), inhibitors (Liu *et al.* 2005), and exogenous applications of signal chemicals (Kozlowski and Métraux 1998; Davis *et al.* 2002; Liu *et al.* 2005) may induce diverse chitinase isoforms in conifers.



Fig. 5 Immunolocalization of a Douglas-fir endochitinase-like protein (ECP). (A) Transmission electron micrograph showing the localization of ECP in *Phellinus sulphurascens*-infected DF root tissues at 3200X magnification. **(B)** Higher magnification (5500X) of **(A)**, showing distribution pattern of immuno-gold labelled ECP. HC – host cell, HCM – host cell membrane, HCW – host cell wall, HICS – host intercellular space, HP – host papillae, ECP – endochitinase protein, numerical legends show magnification for each micrograph (modified from Islam *et al.* 2009).

BIOLOGICAL FUNCTIONS

Available data indicate that conifer chitinases play important roles in plant defense, growth and development, and other physiological processes. Several investigators have reported on the biological functions and physiological processes of conifer chitinases; these are documented in **Table 1**. Important functional categories of conifer chitinases are presented below.

Conifer chitinases in defense against pathogens

Many previously mentioned studies suggest that conifer chitinases play their most significant roles in defense against pathogens. The antifungal activity of a class IV chitinase from P. abies was tested recently by Ubhayasekera et al. (2009) who confirmed that this conifer chitinase strongly inhibits H. annosum growth. In the same P. abies-*H. annosum* pathosystem, expression of chitinase genes was found to be higher in resistant P. abies clones than in susceptible clones a few days after infection with H. annosum (Hietala et al. 2004; Fossdal et al. 2006, 2007). Hietala et al. (2004) monitored H. annosum colonization and chitinase transcript levels in P. abies clones differing in disease resistance and concluded that chitinase gene expression is correlated with the resistance mechanism of P. abies. The high constitutive levels of chitinases in P. abies may signify a role in releasing fungal cell wall elicitors at the onset of infection (Fossdal et al. 2006, 2007).

Sequencing of a cDNA library constructed from *P. sulphurascens*-infected DF seedling roots showed that the chitinase gene family is one of the largest constituents of the DF cDNA library (Islam *et al.* 2010). At least three class II and six class IV chitinase genes were identified from DF seedlings. Real-time PCR analyses showed significant differential expression patterns of these genes locally in root tissues and systemically in needle tissues after fungal inva-

Table 1 Functions and biological processes of conifer chitinases

Origin	Chitinase type	Functions/biological processes	References
Pseudotsuga menziesii	Class IV and II	Defense against pathogen	Islam et al. 2010a
Pseudotsuga menziesii	Endochitinase		Robinson et al. 2000; Zamani et al. 2003; Sturrock et al.
			2007; Islam et al. 2009
Pinus monticola	Class IV		Liu et al. 2005
Pinus taeda	Class II		Davis et al. 2002
Picea abies	Class II		Jøhnk et al. 2005
Picea abies	Class I, II, IV		Hietala et al. 2004
Picea glauca	Chitinase		Nagy et al. 2004
Picea abies	Chitinase		Asiegbu <i>et al.</i> 1993; Sharma <i>et al.</i> 1993; Fossdal <i>et al.</i> 2006, 2007
Pinus sylvestris	Chitinase		Hodge et al. 1995
Pinus contorta	Chitinase		Nsolomo and Woodward 2007
Pinus sylvestris	Chitinase		Asiegbu et al. 1995, 2005; Nsolomo and Woodward 2007
Pinus nigra	Chitinase		Nsolomo and Woodward 2007
Picea abies	Chitinase		Kozlowski and Métraux 1998; Kozlowski et al. 1999
Pinus sylvestris	Chitinase IV		Adomas et al. 2007, 2008
Pinus taeda	Chitinase		Popp <i>et al.</i> 1997
Pinus strobes	Class II	Defense against wounding	Wu et al. 1999
Picea abies	Class II, IV		Hietala et al. 2004; Fossdal et al. 2006, 2007
Picea glauca	Class IV		Dong and Dunstan 1997
Picea sitchensis	Class IV, chitinase		Ralph et al. 2006; Lippert et al. 2007
Pinus taeda	Class IV, chitinase	Defense against drought	Chang et al. 1996; Lorenz et al. 2006
Pinus halepensis	Class I		Sathyan 2004
Pinus taeda	Class I		Sathyan 2004
Picea abies	Chitinase		Nagy et al. 2004
Picea glauca	Class IV		Dong and Dunstan 1997
Picea abies	Class II, IV	Defense against overwintering	Jarzabek et al. 2009
Picea pungens	Class II, IV	5 5	Jarzabek et al. 2009
Pseudotsuga menziesii	Endochitinase		Zamani et al. 2003
Picea sitchensis	Class IV	Defense against insects	Lippert et al. 2007
Picea sitchensis	Class IV, chitinase	e e e e e e e e e e e e e e e e e e e	Ralph <i>et al.</i> 2006
Pinus densiflora	Endochitinase	Defense against nematodes	Shin <i>et al.</i> 2009
Picea abies	Class I	Mycorrhizal symbiosis	Salzer et al. 1997a. 1997b
Pinus svlvestris	Chitinase	<u> </u>	Hodge et al. 1995
Crvptomeria iaponica	Class IV	Pollen allergen	Fujimura <i>et al.</i> 2005. 2007
Picea ahies	Class IV	Growth and development	Wiweger <i>et al.</i> 2003
Picea glauca	Class IV	FFFF	Dong and Dunstan 1997
Araucaria angustifolia	Class IV		dos Santos $et al 2006 2008$
Pinus sylvestris	Chitinase	Program cell death	Pirttilä <i>et al.</i> 2002
Picea ahies	Class IV		Wiweger et al. 2003
Pinus storbus	Class II	Chitosan-induced	Wn <i>et al</i> 1997
Pinus elliottii	Class II		Mason and Davis 1997
Pinus taeda	Chitinase		Popp <i>et al.</i> 1997: Davis <i>et al.</i> 2002
Pinus taeda	Class L II IV	Salicylic acid-induced	Davis et al. 2002
Picea ahies	Chitinase	Sundyne uela madeed	Kozlowski and Métraux 1998
Pinus taeda	Class L IV	Jasmonic acid-induced	Davis et al. 2002
Pinus monticola	Class IV	Methyl jasmonate-induced	Lin et al. 2002
Picea ahies	Chitinase	manuel jusificitate-induced	Kozlowski <i>et al.</i> 1999
Picea ahies	Class I	Chitotetraose/chitin-induced	Salzer <i>et al.</i> 1997a 1997b
Pinus monticola	Class IV	Inhibitor_induced	Lin et al. 2005
1 mus monucolu Cveus revolute	Class V	Transalvoosylation activity	Taira et al. 2009
Cycus revoluia	CidSS V	Transgrycosylation activity	1alla el Ul. 2007

sion. Western immunoblot data also showed significant accumulation of a class IV chitinase in *P. sulphurascens*infected DF seedlings (Islam *et al.* 2010). Previously, an endochitinase-like protein was reported as occurring in the roots of 11- and 25-year-old DF trees that were naturally infected with *Armillaria ostoyae*. This protein was also found to be upregulated in DF plants infected with *P. sulphurascens* (formerly *P. weirii*) (Robinson *et al.* 2000; Zamani *et al.* 2003). Western immunoblots also revealed that the apoplastic fluid of DF roots and needles contained multiple ECP isoforms with isoelectric points ranging from 5.3 to 5.8 and molecular masses of 27–30 kDa (Zamani *et al.* 2003). Sturrock *et al.* (2007) demonstrated that this ECP protein was significantly upregulated in *P. sulphurascens*infected DF seedling roots (**Fig. 6**).

In *P. elliottii* seedlings, multiple chitinase homologs accumulated after challenge by the fungal pathogen *Fusarium subglutinans* Woll. & Rein. These chitinase isoforms were also induced by potential signaling molecules identified from angiosperms (Davis *et al.* 2002). In *P. abies* seedling roots, chitinase accumulation was increased three days after inoculation with *Pythium* sp. (Sharma *et al.* 1993).



Fig. 6 Western immunoblot showing the accumulation of an endochitinase protein in DF seedlings. The root (lanes 1 to 4) and needle (lanes 5 to 8) samples of young Douglas-fir seedlings collected from uninfected controls at 12 days post inoculation (dpi) and from *Phellinus sulphurascens*-infected plants at 2, 7, and 12 dpi. PC-positive controls obtained from Douglas-fir needles for ECP. Lanes 1 and 5, uninfected controls; lanes 2 and 6, 2 dpi; lanes 3 and 7, 7 dpi; and lanes 4 and 8, 12 dpi (modified from Sturrock *et al.* 2007).

Chitinase activity was also increased in P. abies seedlings infected with pathogenic oomycetes (Kozlowski and Métraux 1998) and both local and systemic increases in chitinase activity were recorded after inoculation with the root die-back fungus Rhizoctonia (Nagy et al. 2004). Asiegbu et al. (1999) reported that following adhesion and cellular penetration by the pathogen, several pathogenesis-related proteins, including chitinase and glucanase, are induced in roots of P. abies inoculated with Fusarium avenaceum (Corda ex Fries) Sacc. Liu et al. (2005) reported that two isoforms of a class IV chitinase were differentially regulated in slow-canker-growth resistant and susceptible seed families of P. monticola. A 27-kDa chitinase isozyme (PmCh4A) accumulated in both susceptible and slow-canker-growth resistant seedlings after infection by Cronartium ribicola J. C. Fisch., while a 26-kDa chitinase isozyme was expressed specifically in slow-canker-growth resistant seedlings. Wounding treatment also induced expression of this protein suggesting that P. monticola chitinases play important defense roles and can be used in marker-assisted selection in forest breeding (Liu et al. 2005).

Recent work by Štefani *et al.* (2010), which considered the environmental impact of transformed trees, showed that an endochitinase-transformed white spruce had no negative effect on soil fungal biomass and ectendomycorrhizal symbiosis. While these results are encouraging, further research on transformed trees, including the use of large-scale field trials, is needed.

Conifer chitinases in defense against insects

Insect feeding can have major ecological and economic impacts on both natural and planted conifer forests. Resistance to insect attack in conifers is a major focus of current forest health research programs. Chitinases may perform numerous roles in the defense against insect pests or against insect-associated fungi. There is evidence that a class IV chitinase was differentially induced in white pine weevil (*Pissodes strobe* W. D. Peck)-infested *Picea sitchensis* (Bong.) Carr. bark (Lippert *et al.* 2007). A poplar chitinase is also induced during infestation by gypsy moth (*Lymantria dispar* L.) larvae (Lawrence and Novak 2006). These data suggest that chitinases play a role in defense against insects. Plant-derived chitinase enzyme can be active in the insect gut and can have detrimental effects in the development of insect herbivores (Chen *et al.* 2008; Howe and Jander 2008).

Conifer chitinases in wound stress

Conifer chitinases can be induced subsequent to wound or mechanical damage. For example, in *P. abies* wounding alone resulted in a clear gradient in the expression of chitinases (PaChi4 and PaChi2) with the highest levels immediately adjacent to the inoculation point (Hietala *et al.* 2004). In contrast to inoculation, the maximum induction levels of the two genes were observed three days after wounding. Chitinase PaChi2 has high similarity to an extracellular class II chitinase, Pschi4, of *Pinus strobus* that is induced by chitosan and wounding (Wu *et al.* 1997, 1999). Dong and Dunstan (1997) also reported that wounding enhanced chitinase- and glucanase-related gene expression in *P. glauca.*

Conifer chitinases in drought stress

Drought has been demonstrated to induce multiple chitinases in *P. taeda* (Lorenz *et al.* 2006). Sathyan (2004) also reported that water stress induced chitinases in *P. taeda* and *P. halepensis*, while Nagy *et al.* (2004) reported that several isoforms of peroxidase and chitinase were differentially accumulated in *Picea abies* after exposure to drought and the fungal pathogen *Rhizoctonia*. In a contrary finding, a chitinase isoform was observed to be down-regulated in *P. taeda* in response to water-deficit stress (Chang *et al.* 1996); however, this protein-coding gene is not the same one reported by the previous authors. Fossdal *et al.* (2006, 2007) found that a combination of pathogen infection and drought stress lead to a specific elevation of chitinases in *P. abies*. Similar to gymnosperms, angiosperm chitinases have also been found to be expressed under drought stress (Bray 2004).

Conifer chitinases in frost/overwintering stresses

Antifreeze proteins (AFPs) refer to a class of polypeptides that enhance the ability of certain organisms including vertebrates, plants, fungi and bacteria to endure freezing environments. These proteins permit the survival of cells in subzero environments. AFPs bind to small ice crystals to inhibit expansion, protrusion, and recrystallization of ice that would otherwise be fatal (Kuiper 2001; Jorov et al. 2004). In most plants, freezing tolerance varies among plant organs, and is strongly correlated with seasons of the year, thereby changing in the course of plant development (Larcher 2003). Conifer chitinases possess potent antifreeze and cryoprotective properties. For example, a 27-kDa apoplastic chitinaselike protein (AP27) was identified from *P. abies* and *Picea* pungens Engelm. Needles that was shown to modify the growth of ice and thermal hysteresis. The key feature of the N-terminal sequence of this protein is the presence of many hydrophilic residues, including serine, threonine, aspartic acid and glutamine (Jarząbek et al. 2009). These N-terminal amino acid residues can directly bind ice crystals and, as a result, limit ice growth in living tissues (Davies et al. 2002; Leinala et al. 2002). A similar type of apoplastic endochitinase protein collected from P. sulphurascens-infected winter P. menziesii needles showed evidence of its higher accumulation in winter months (Zamani et al. 2003). The Nterminal sequences of this protein revealed high sequence homology to class II and/or class IV chitinases from other conifer species including *P. abies*, *P. glauca*, and *P. monti*cola. As with conifer chitinases, a number of other PR proteins secreted into the apoplast during cold acclimation are thought to be responsible for disease resistance (Ekramoddoullah et al. 1995, 2001; Matheus et al. 2003). Interestingly, some cold-induced PR proteins, including chitinases, display both antifungal and antifreeze activities, suggesting a dual function of these proteins in protecting plants from overwintering and other biotic and abiotic stresses (Hon et al. 1995; Kuwabara and Imai 2009). However, the signaling pathway for cold-induced disease resistance is currently unknown but can be independent of pathogen-induced defense mechanisms (Kuwabara and Imai 2009).

Conifer chitinases in other stresses

The available data suggest that plant chitinases play a role in combating a variety of stresses. For example, a basic chitinase (ChitiWb1) encoding gene significantly increased in leaves and cultured cells of wing bean treated with NaCl, KCl, CaCl₂, mannitol or saccharose (Tateishi *et al.* 2001). In tobacco, extracellular chitinases were also increased significantly under salt stress (Dani *et al.* 2005). Dong and Dunstan (1997) reported that wounding and other stresses such as drying and flooding enhanced chitinase- and glucanase-related gene expression in *P. glauca*. These data infer that conifer chitinases may play important defensive roles against most abiotic stresses, aside from their major roles in pathogen defense and plant development.

Conifer chitinases in programmed cell death

Several studies have demonstrated that in *P. glauca* and *P. abies*, class IV chitinases are expressed during embryo development and have been associated with programmed cell death (PCD; Dong and Dunstan 1997; Dyachok *et al.* 2000, 2002; Wiweger *et al.* 2003), possibly through hydrolyzing or releasing oligosaccharides related to cell-to-cell signaling. Class IV chitinase genes have also been impli-

cated in PCD in other plants such as carrot and *Arabidopsis*, possibly by acting on arabinogalactan proteins (van Hengel *et al.* 1998; Passarinho *et al.* 2001), and might also be involved in transition from polyembryonal masses to somatic embryos by direct or indirect activation of PCD (Wiweger *et al.* 2003). The question is whether the involvement of conifer chitinases in PCD is only related to growth and development of embryos or whether they activate some hypersensitive responses associated with plant defense at the early stage of plant development. Further investigation is required to better understand the association of conifer chitinases in PCD.

Conifer chitinases in pollen allergens

A class IV chitinase (CJP-4) has been isolated from C. japonica pollen. The purified protein displayed the ability to bind IgE from all patients tested. The CJP-4 is a 34-kDa protein, displaying endochitinase activity that cross-reacts with latex allergens (Fujimura et al. 2005, 2007). Similarly, there are some other conifer PR proteins that also display allergic behavior, including thaumatin-like proteins and PR10 proteins (Futamura et al. 2002; Liu et al. 2003; Fujimura et al. 2005, 2007). According to Fujimura et al. (2005), the CJP-4 and other chitinases may act as causative allergens of the cross-reactivity in C. japonica pollinosis and oral allergy syndrome. There is evidence that angiosperm pollen chitinases are also involved in allergic reactions. For example, a 32-kDa IgE-binding green bean protein was strongly induced by ethylene treatment. The protein, designated as PvChI, was identified as a class I chitinase closely related to the major avocado allergen Prs a 1 (Sánchez-Monge et al. 2000).

Conifer chitinases in growth and development

Chitinase-like proteins have long been proposed to play roles in normal plant growth and development (De Jong et al. 1992; Collinge et al. 1993; Dong and Dunstan et al. 1997; Zhong et al. 2002). The expression of plant chitinase genes in the absence of pathogen attack or other stress conditions has been studied in many plant tissues, including those of conifers (Collinge et al. 1993; Høj and Fincher 1995; Dong and Dunstan 1997; Dyachok et al. 2002; Wiweger et al. 2003; dos Santos et al. 2008). This expression suggests that chitinases are involved in plant growth and development. The non-defensive role of plant chitinases was initially proposed from a study of somatic embryo development in carrot plant (De Jong et al. 1992; Kragh et al. 1996). In recent years, embryogenic cultures of P. abies have been used extensively for studying the regulation of embryo development (von Arnold et al. 2002). The developmental pathway of somatic embryogenesis of P. abies involves proliferation of proembryogenic masses, somatic embryo transition and further development of somatic embryos (Wiweger et al. 2003). The importance of chitinases in P. abies embryogenesis in vitro was demonstrated by stimulating early somatic embryo development in the presence of exogenously supplied chitinase which was derived from Streptomyces griseus Waks. & Henr. (Egertsdotter and von Arnold 1995, 1998; Dyachok et al. 2002) or from a preconditioned medium of embryogenic cultures (Egertsdotter et al. 1993). Furthermore, the expression of chitinase-like proteins appears to be developmentally regulated during growth and development in other conifers. For example, in P. glauca the transcript of a chitinase (PgChi-1) is highly abundant in embryogenic tissues. The expression level was further increased between the filamentous stage of development and in fully developed cotyledonary embryos (Dong and Dunstan 1997). It has been suggested that during in vitro somatic embryogenesis extracellular chitinases are able to cleave the glycosidic bonds of glucosamine and Nacetylglucosamine residues in the sugar moiety of arabinogalactan proteins (AGPs; van Hengel et al. 2001) generating oligosaccharide signal molecules essential for early

stages of plant embryogenesis (Malinowski and Filipecki 2002). Another study also reported that the embryogenic tissues and nonembryogenic calli of *Pinus caribaea* Morel. produce proteins of 48 or 56 and 25 kDa, respectively. All of these proteins cross-react with several classes of tobacco chitinases. These chitinase-like proteins showed potential chitinase activity on SDS-PAGE gels overlaid with glycol chitin as a synthetic substrate. However, when an AGP fraction from embryogenic tissues substitutes for glycol chitin on gels, only the 48-kDa embryo-specific chitinase-like protein acts on this substrate suggesting that an interaction between this protein and a specific set of AGPs might exist within embryogenic tissues of P. caribaea (Domon et al. 2000). There is also evidence that extracellular chitinase protein expressed in the endosperm of carrot rescues somatic embryos of the carrot ts11 variant (van Hengel et al. 1998).

It is assumed that chitinases secreted in P. abies and carrot cultures can degrade lipo-chitooligosaccharides (LCOs). In both P. abies and carrot embryogenic systems, bacterial Nod factors can substitute for chitinases in their effect on early somatic embryo development (De Jong et al. 1992; Egertsdotter and von Arnold 1998), which can promote the development of pro-embryogenic masses (PEMs) from small cell aggregates in P. abies (Egertsdotter and von Arnold 1998; Dyachok et al. 2000). It is not yet confirmed that secreted chitinases can degrade LCOs in a similar way as plant chitinases hydrolyze the rhizobial Nod factors (Staehelin et al. 1994, 1995). However, data suggest that chitinases are involved in the production of plant signal molecules that are similar to the rhizobial Nod factors. For example, the promotion of somatic embryo development in carrot by endochitinase EP3 could be mimicked by rhizobial LCOs (De Jong et al. 1992). The EP3 chitinase colocalizes with AGPs in developing seeds, and it was shown to cleave AGPs in vitro (van Hengel et al. 2001). Furthermore, dos Santos et al. (2008) observed the somatic embryos of a superior genotype showed higher chitinase expression and concluded that chitinases can be used as an indicator of a genotypic superiority for the development of somatic embryogenesis in Araucaria angustifolia (Bertol.) Kuntz

Recently mutations in chitinase-like genes have been obtained in Arabidopsis to probe the developmental role of plant chitinases. A chitinase-like gene (AtCTL1) encoding protein AtCTL1 caused ectopic deposition of lignin and aberrant shapes of cells with incomplete cell walls in the pith of inflorescence stems. Consistent with its ubiquitous expression pattern, mutation of the AtCTL1 gene affected many aspects of plant growth and development, including exaggerated hook curvature, reduced length and increased diameter of hypocotyls in dark-grown seedlings, and reduced root length and increased number of root hairs in light-grown seedlings. These results suggest that AtCTL1 is essential for normal plant growth and development in Arabidopsis (Zhong et al. 2002). Taira et al. (2009) reported a class V chitinase from a Cycas revoluta which showed transglycosylation activity.

Conifer chitinases in biocontrol

Researchers interested in new biopesticides have given considerable attention to chitinases (Brown 1998; Goodday 1999; Herrera-Estrella and Chet 1999; Karasuda *et al.* 2003; Chung and Kim 2007). There is evidence that a class IV chitinase from a yam (*Dioscorea opposita* Thunb.) can effectively control the powdery mildew of strawberries (Karasuda *et al.* 2003). It is also suggested that *Escherichia coli* is able to produce recombinant chitinase in the soil that can control the pathogenesis by *F. oxysporum* without colonization (Chung and Kim 2007). Since chitinases are one of the dominant protein families in conifer systems, there is a great potential to explore chitinase-based products from conifers that could be commercially produced using recombinant protein technology. For example, *E. coli* expressing an endochitinase gene can effectively control *Fusarium* wilt of cucumber. Since insects are too expensive to be a commercial source of chitinase (Brown 1998), conifers could be an option as a source of chitinases. Biological control incorporating the use of a biodegradable enzyme like chitinase would be more environmentally sound than conventional pesticide applications.

Conifer chitinases in biofuel production

Many living organisms use complex networks of fibrous and crystalline polysaccharides to maintain their structural integrity. Enzymatic conversion of the most recalcitrant of these polysaccharides is of great biological and economic importance (Eijsink et al. 2008). In plants, the major structural polysaccharide is cellulose [$\beta(1\rightarrow 4)$ linked glucose], whereas non-plants such as insects, crustaceans and fungi employ chitin [$\beta(1\rightarrow 4)$ linked *N*-acetyl glucosamine], which occurs in two major forms, α -chitin and β -chitin. Cellulose and chitin are the most abundant biopolymers in the terrestrial and marine environments, respectively. In nature, degradation of cellulosic or chitinous biomass is achieved by mixtures of hydrolytic exo- and endo-acting enzymes that act in a synergistic manner (Horn et al. 2006; Merino and Cherry 2007). Eijsink et al. (2008) claimed that chitinase could be used for the future development of biomass conversion. In conifers, the abundance of different chitinases indicates potential for future biomass conversion research.

CONCLUSION

Our understanding of the role of conifer chitinases in defense against pests and pathogens lags behind that pertaining to chitinases involved in defense against pathogens affecting short-lived angiosperm crop plants. To date, a variety of studies have confirmed that conifer chitinases play a significant role in many aspects of plant protection against biotic and abiotic stresses. They also function in plant growth and development. Despite constitutive expression of chitinases in conifer plants, chitinases have also been found to be induced locally and systemically by different stressors. Signal molecules such as salicylic acid, jasmonic acid and ethylene play key roles in chitinase induction in conifer systems. Several studies have significantly contributed to our understanding of this ubiquitous protein family in conifer plants, providing more knowledge of chitinase structural properties, antifungal activities, substrate specificity and catalytic mechanisms. The available literature also reveals that conifer chitinases serve non-defensive functions during somatic embryogenesis, somatic embryo rescues and PCD. Several recent lines of evidence have substantiated the biotechnological potential of conifer chitinases to counter fungal diseases. Further chitinase genomics and proteomics research will enhance our understanding of structural diversity, substrate specificities, regulations and isoform specific functions of conifer chitinases. There is also a need to conduct research to realize the potential applications of conifer chitinases in biocontrol and biofuel production for future generations.

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