Antifungal Proteins

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Fungi are amazing organisms, being able to use almost any surface (e.g., bathroom tile, skin, or leaves) for growth. Unfortunately, they also are proficient at colonizing and using plants, humans, and animals as substrates. During the last two decades, the incidence of human fungal infections, especially involving immunocompromised patients, has dramatically increased (27, 41, 57). This is in part due to the tremendous advances in medicine that permit the saving of patients with neoplastic and immunocompromising diseases who would otherwise not have survived. It is ironic that many of these patients succumb to fungal infections for which there are few or no drugs available for treatment. Encouragingly, naturally occurring antifungal proteins and peptides, as well as synthetic derivatives, have the potential to be very interesting clinical leads.

Fungi are an extremely diverse group of organisms, with about 250,000 species widely distributed in essentially every ecosystem. Muller and Loeffler (124) estimate that the weight of fungi on Earth exceeds that of humans; Armillaria bulbosa, a tree root pathogen, is reported to be among the largest and oldest organisms on the planet (162). Humans and other animals are exposed to fungi from the moment of birth. Fortunately, only 200 or so species are pathogenic to mammals, although many nonpathogenic fungi cause allergy symptoms (3). The majority of fungal exposures and infections are selflimiting in intact animal hosts (76). However, in patients with compromised immune systems, infections even by fungal organisms with low virulence can be life threatening; for example, systemic fungal infections of leukemia patients account for 50% of fatalities (101, 141). Nosocomial bloodstream infections have a similar fatality rate (107).

Plants are also exposed to a large number of pathogenic fungi; although they do not have an immune system, plants have evolved a variety of potent defense mechanisms, including the synthesis of low-molecular-weight compounds, proteins, and peptides that have antifungal activity (16, 18, 47, 80, 104, 127, 151, 159, 177). Similarly, bacteria, insects, mollusks, fungi, and mammals synthesize a number of proteins and peptides that are antifungal (13, 19, 20, 30, 49, 51–54, 58, 68, 69, 79, 83, 109–111, 122, 126, 128, 153, 188, 189, 192). These proteins appear to be involved in either constitutive or induced resistance to fungal attack. It is a testament to the efficacy of these defenses that plants and animals, including humans, do so well against pathogenic fungi.

There are hundreds of antifungal peptides and proteins known, with more being discovered almost daily. This brief review will focus on proteins with molecular masses of greater than \sim 5 kDa, about 50 amino acids in length; this choice is somewhat arbitrary, for there is not consensus concerning where a peptide ends and a protein begins. Even eliminating the small proteins (peptides), the list of antifungal proteins is large and daunting. The reader is directed to a review concerning antifungal peptides and proteins of less than 5 kDa (30). Given the diverse and varied types of proteins, this review will be an overview of the primary classes of antifungal proteins. Thirteen classes of antifungal proteins will be described: PR-1 proteins, $(1,3)\beta$ -glucanases, chitinases, chitin-binding proteins, thaumatin-like (TL) proteins, defensins, cyclophilin-like protein, glycine/histidine-rich proteins, ribosome-inactivating proteins (RIPs), lipid-transfer proteins (LTPs), killer proteins (killer toxins), protease inhibitors, and other proteins. These proteins have been named primarily on the basis of either their mechanism of action, (e.g., glucanases), their structure (e.g., cysteine rich), or their similarity to a known "type" protein. To confuse the nomenclature further is the fact that several proteins can be and have been classified into more than one group. It is unfortunate that a standard nomenclature based on structure or some other unifying property(ies) of these proteins has not been proposed or adopted.

FUNGAL CELL WALL STRUCTURE

The fungal cell wall protects the organism against a hostile environment and relays signals for invasion and infection of a likely plant, animal, or human host. The cell wall of fungi and yeasts is synthesized at each hyphal apex in a complex assembly sequence (45, 105, 149). For example, the walls of *Neurospora crassa* and *Candida albicans* are composed of chitin, $(1-3)\beta$ -Dglucan, $(1,6)\beta$ -glucans, lipids, and peptides embedded in a protein matrix. The fungal wall affords a clear and discernible difference between fungi and their plant and animal hosts, providing an experimental target for antifungal antibiotics. A schematic of a typical fungal cell wall is shown in Fig. 1. It is important to note that fungi have significant internal turgor pressure so that even slight perturbation of the cell wall results in fungal cell lysis (54, 73, 118–120).

Several classes of antifungal proteins involve inhibition of the synthesis of the fungal cell wall or disrupt cell wall structure and/or function; others perturb fungal membrane structure, resulting in fungal cell lysis. The assays for antifungal activity include microtiter broth assays, agar diffusion assays, broth microdilution assays (43), and in planta assays (the determination of resistance of transgenic plants overexpressing a protein of interest). Most of the antifungal proteins described below are quite potent, with MICs in the micromolar or microgramper-milliliter range, equivalent to MICs of many of the currently used agricultural and pharmaceutical antifungal compounds.

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FIG. 1. Schematic of fungal cell wall. GPI, glycophosphatidylinosi-tol.

ANTIFUNGAL PROTEINS

PR proteins. Plants when exposed to pathogens such as fungi and viruses produce low-molecular-weight antimicrobial compounds called phytoalexins, antimicrobial peptides, and small proteins (e.g., thionins [11, 40], defensins [14], hevein-like proteins, and knottin-like peptides [154]) and up-regulate a number of antimicrobial proteins. These plant proteins, called pathogenesis-related (PR) proteins, have been classically divided into five groups, PR-1, -2, -3, -4, and -5, based on serological and amino acid sequence analyses (180). Recently, another 6 groups of proteins have been suggested for inclusion as PR proteins, bringing the total to 11 groups. The reader is directed to a number of reviews concerning PR proteins, their regulation, and possible roles in plant defense (80, 163, 180, 194).

Each of the five classical groups of PR proteins has two subclasses: a basic subclass found in the plant cell vacuole and an acidic subclass usually found in the extracellular space (reference 80 and references therein). Each group has members with antifungal activity, and cognates of most groups have been found in a diversity of other organisms. The mechanisms of antifungal action of only the PR-2 and PR-3 groups of proteins have been clearly identified.

(i) **PR-1 proteins.** PR-1 proteins are accumulated to high levels after pathogen infection and are antifungal both in planta (transgenic plants overexpressing tobacco PR-1) and in vitro (129, 165). PR-1 proteins have been found in rice, wheat, maize, tobacco, *Arabidopsis thaliana* barley, and many other plants (1, 15, 117, 125, 145); an alignment of seven PR-1 proteins is shown in Fig. 2. Note that although these proteins are from diverse sources, they are remarkably similar (at least 35% identity). PR-1 proteins have antifungal activity at the micromolar level against a number of plant pathogenic fungi, including *Uromyces fabae, Phytophthora infestans*, and *Erysiphe*

graminis (129). PR-1 proteins have molecular masses of ~15 to 17 kDa and have homology to the superfamily of cysteine-rich proteins. Although the precise mechanism of antifungal activity is not understood for plant PR-1 proteins, a PR-1-like protein, helothermine, from the Mexican banded lizard interacted with membrane-channel proteins of target cells, inhibiting the release of Ca²⁺ (123). Whether antifungal plant PR-1 proteins act by this mechanism is not known but is suspected.

(ii) PR-2 proteins (β -glucanses). PR-2 proteins have (1,3) β endoglucanase activity in vitro and have been grouped into three classes on the basis of amino acid sequence analysis (8, 25, 95, 103, 113, 131, 140). Class I glucanases are basic proteins of \sim 33 kDa and are found in the plant vacuole. Classes II and III include acidic, extracellular proteins of about 36 kDa. The major structural difference between class I proteins and the other two classes is that class I proteins are synthesized as preproproteins that are processed prior to being enzymatically active. PR-2 proteins have been found in a wide variety of plants, including tobacco, A. thaliana, peas, grains, and fruits (25, 77, 146); the proteins are active in vitro at micromolar levels (\sim 50 µg/ml) against a wide number of fungi, including human and plant pathogens (e.g., Rhizoctonia solani, C. albicans, and Aspergillus fumigatus). The antifungal activity of PR-2 proteins has been convincingly demonstrated by a number of in vitro enzyme and whole-cell assays (163) as well as in planta using transgenic plants overexpressing a PR-2 protein (71).

The antifungal activity of plant $(1,3)\beta$ -glucanases is thought to occur by PR-2 proteins hydrolyzing the structural $(1,3)\beta$ glucan present in the fungal cell wall, particularly at the hyphal apex of filamentous molds where glucan is most exposed, resulting in a cell wall that is weak. This weakened cell wall results in cell lysis and cell death.

(iii) PR-3 proteins (chitinases). A number of enzymatic assays have shown PR-3 proteins to have in vitro chitinase activity. Most PR-3 proteins have molecular masses of between 26 and 43 kDa (131, 187). Chitinases (both plant PR-3 chitinases and chitinases from other sources) have been divided into five groups. class I chitinases contain an N-terminal cysteine-rich domain of \sim 40 amino acids (also known as the wheat germ agglutinin domain), a chitin-binding hevein-like domain, a highly conserved central portion, and a hinge region; most class I proteins have molecular masses of ~32 kDa. Class II proteins are similar in amino acid sequence to class I proteins, but they lack the N-terminal cysteine-rich domain and have molecular masses of 27 to 28 kDa. Class IV proteins resemble class I chitinases but are significantly smaller due to four major deletions. Class III proteins do not share amino acid sequence homology to any other class and have molecular masses of ~ 28 to 30 kDa. Class V chitinases show sequence similarities to bacterial exochitinases and have molecular masses of 41 to 43 kDa. In addition to chitinases, a chitosanase (chitosan is deacetylated chitin) from Streptomyces strain N174 with antifungal activity has been isolated (119), and its X-ray structure has been determined.

Chitinases have been isolated from fungi (74, 112), plants (tobacco [114], cucumber, beans [198], peas, grains [63], and many others [37, 96, 112, 121, 150, 193]), and bacteria (22) and have potent antifungal activity against a wide variety of human and plant pathogens, including *Trichoderma reesei*, *Alternaria*

A. B. S. L. S. N. H. Z.	thaliana napus tuberosum esculentum nigra tabacum vulgare mays	10 MNFTGY MKVIYC MGLFNI MGLFNM MAHNHWCN MGFVLFSQME MQTE MAF	20 SRFLIVFVA SRLLLILAA SLLLTCL MSL-LLMTCL MLFSVALVCV SFFLVSTLL PRLACLLALA PRLACLLALA	LVGALVLP LVGALVHP MVLAIFHS MVLAIFHS VALVMVQY LFLIISLS MAAAMVNL MAAIVVAP	30 SKAQDSPQ SRAQNSPQ CDAQNSPQ CDAQNSPQ SVAQNSPQ CGAQNSPQ SQAQNSPQ CTAQNSPQ	40 DYLRVHNQ DYVNAHNQ DYLAVHND DYLEVHND DYVDAHNA DYLDAHNT DYVSPHNA DYVDPHNA	50 ARGAVGVGP ARQQVGVGP ARAQVGVGP ARAQVGVGP ARADVGVEP ARADVGVGP ARADVGVGP	60 MQWDERVAA VQWDGTLAA MSWDAGLAS MSWDADLES VTWDESVAA LTWDDQVAA VSWSTKLQA VSWSTKLQA	YARSYAEQ FAQSYADR RAQNYANS RAQSYANS FARQYAQS YAQNYASQ FAQNYANQ YAQSYAAQ
A. B. S. L. S. N. H. Z.	thaliana napus tuberosum esculentum nigra tabacum vulgare mays	70 LRGNCRLIHS LRGDCRLVHS RTGDCNLIHS RAGDCNLIHS RAGDCRLVHS LAADCMLVHS RINDCKLQHS RQGDCKLIHS * * **	80 GGP-YGENI GGP-YGENI GGSGENI GDPRYGENI GGP-YGENI GGP-YGENI GGP-YGENI	90 AWGSGD AWSSAD AKGSGD AKGGGD AFGSGF-E AWGSGD-F FWGSAGAD FWGSAGAD	100 LSGVSAVN FSGVSAVN FTGRAAVQ FTGRAAVE LTGRNAVD MTAAKAVE WKASDAVN WSASDAVG **	11 MWVSEKAN LWVNEKAN LWVSEKPN MWVAERND MWVNEKQY SWVSEKKD SWVSEKQY ** *	0 1 YNYAANTCN YNYASNTCI YNYGTNQCA YNYDTNECV YNPNTNTCA YDHDSNTCA YDYGSNTCA YDHDTNSCA * * *	20 GVCGHYT SGQVCGHYT SGKMCGHYT PGKVCGHYT QGQVCGHYT AGKVCGHYT EGQVCGHYT * ***	130 QVVWRKSV QVVWRNSV QVVWRDSV QVVWRNSV QVVWRNSV QVVWRAST QVVWRDST ***** *
A. B. S. L. S. H. Z.	thaliana napus tuberosum esculentum nigra tabacum vulgare mays	140 RLGCAKVRCN RIGCGKARCN RLGCGRARCN RIGCARVRCN RVGCARAQCN SIGCARVVCN AIGCARVVCL ** *	150 ING-GTIISC ING-WWFISC IDG-WWFISC ING-AWFISC ISG-GYVVSC INNRGVFITC INNRGVFITC	160 CNYDPRGNY CNYDPVGNW CNYDPVGNW CNYSPPGNY CNYSPPGNY CNYEPRGNI CNYEPRGNI CSYNPPGNV * * **	170 VNEKPY VNEKPY VGQRPY VGQRPY VGQSPYEL IGQKPY VGESPY **	18 KRRPFHVI	0 YVRTSA		

FIG. 2. Amino acid sequence alignment of representative PR-1 proteins from *Arabidopsis thaliana* (accession no. P33154), *Brassica napus* (rape, accession no. T08154), *Solanum tuberosum* (potato, accession no. CAB58263), *Lycopersicon esculentum* (tomato, accession no. CAA04881), *Sambucus nigra* (elder, accession no. Q41359), *Nicotiana tabacum* (tobacco, accession no. S10205), *Hordeum vulgare* (barley, accession no. Q05968), and *Zea mays* (maize, accession no. T02054). Alignments were performed with the ClustalW program (http://clustalw.genome.ad.jp/); * indicates amino acid identity.

solani, A. radicina, Fusarium oxysporum, R. solani, Guignardia bidwellii, Botrytis cinerea, and Coprinus comatus. By analogy with β -glucanases, the mode of action of PR-3 proteins is relatively straightforward: PR-3 proteins are endochitinases that cleave cell wall chitin polymers in situ, resulting in a weakened cell wall and rendering fungal cells osmotically sensitive. Not surprisingly, PR-2 (β -glucanases) and PR-3 (chitinases) proteins act synergistically in inhibiting fungal growth, both in vitro and in planta (71).

(iv) PR-4 (chitin-binding) proteins. PR-4 proteins are chitin-binding proteins, have molecular masses of 13-14.5 kDa, and have been classified into two groups (42, 56, 143, 179). Class I proteins have amino acid sequence similarities to hevein (a chitin-binding polypeptide [42, 85, 179]) and belong to the superfamily of chitin-binding lectins. Class II proteins lack the chitin-binding domain. PR-4 proteins have been isolated from potato, tobacco, barley, tomato, and many other plants (42, 56, 85, 143, 179); an alignment of six PR-4 proteins is shown in Fig. 3. Note that the PR-4 proteins from the diverse sources share common sequences. Both classes of proteins

have potent antifungal activity against a wide variety of human and plant pathogens (e.g., *Trichoderma harzianum, Fusarium culmorum, F. graminearum*, and *B. cinerea*). The antifungal activity of class I proteins is likely the result of protein binding to nascent fungal cell wall β -chitin. By mechanisms not understood, this results in disrupted cell polarity, with concomitant inhibition of growth (13). The mechanism of action of class II proteins (which lack the chitin-binding hevein domain but are antifungal nonetheless) is not understood.

Chitin-binding proteins and peptides that have antifungal activity but are not PR proteins have been isolated from a number of sources, including bacteria (13), plants, insects, and crustaceans (19, 29, 61, 76, 83, 131, 136). These non-PR-4 chitin-binding proteins include the tachystatins (75, 135) (horse-shoe crab, 6.8 to 7.4 kDa), the penaeidins (31–33) (penaeid shrimp, 5.5 to 6.6 kDa), antifungal protein 1 (AFP1) (13) (*Streptomyces tendae*, 9.8 kDa), and others. Fungi inhibited by these proteins include plant and human pathogens, e.g., *Paecilomyces variotii, Aspergillus spp., F. oxysporum, N. crassa, B. cinerea*, and *Alternaria brassicola*. It is likely that these proteins

Vitis vinifera N. tabacum Arabidopsis Hordeum vulgare Lycopersicon A Lycopersicon B	MERRGICKVVVLLSLV							
Vitis vinifera N. tabacum Hordeum vulgare Arabidopsis Lycopersicon A Lycopersicon B	20 ACAAAQ AMAAAQ Q NCWGSGPSGPGE HSCEAQ HSCEAQ	30 2SASNVRATYHY 2SATNVRSTYHI 2QANDVRATYHY 2SASNVRATYHY 2NSPQDYLAVHN 2NSPQDYLAVHN *	40 YNPEQN YNPQNI YRPAQN IDARAQVGVGI IDARAQVGVGI	50 Gwdlnavsa Nwdlgapav Nwdlgapav -Nwdlravsa PMSWdanlasr PMSWdanlasr **	60 YCSTWDASQ FCATWDADK SAYCATWDA YCSTWDADK AQNYANSRA AQNYANSRA	70 PLAWRS PLAWRQ SKPLSWRS PYAWRS GDCNL GDCNL		
Vitis vinifera N. tabacum Arabidopsis Hordeum vulgare Lycopersicon A Lycopersicon B	80 KYGWTAFCGPSG KYGWTAFCGPAG KYGWTAFCGPAG IHSGAGENLAKG IHSGAGENLAKG	90 SPTGQAACGKCI SPRGQVSCGRCI SPRGQASCGKCI SPRGQAACGKCI SGGDFTGR-F GGGDFTGR-F SGGDFTGR-F	100 SVTNTATGT(RVTNTGTGT(RVKNTRTNAA RVTNPATGA(AVQLWVSERI AVQLWVSERI *	110 DATVRIVDQCS DTVRIVDQCS AVTVRIVDQCS DITARIVDQCA PDYNYATNQCV SYNYATNQCV **	120 NGGLDLDSG NGGLDLDVN NGGLDLDVA NGGLDLDWD GGKMCGHYT GGKKCRHYT *	130 -VFNKLDT -VFNQLDT -MFNQIDT TVFTKIDT -QVVWRNS -QVVWRNS		
Vitis vinifera N. tabacum Arabidopsis Hordeum vulgare Lycopersicon A Lycopersicon B	140 NGAGYNQGHLIV NGVGYQQGHLIV DGFGYQQGHLIV NGIGYQQGHLNV VRLGCGRARCNN VRLGCGRARCNN	150 YNYEFVDCGD YDYEFVNCND YDYQFVDCGNEI YNYQFVDCRD IGWWFISCNYDE K *	160 JGQPDSRNMI VGNWVGERPY VGNWIGQRPY	170 LVSAIDRV K				

FIG. 3. Amino acid sequence alignment of selected PR-4 proteins from *Vitis vinifera* (accession no. AAC33732), *Nicotiana tabacum* (common tobacco, accession no. S23799), *Arabidopsis thaliana* (accession no. P43082), *Hordeum vulgare* (barley-barwin, accession no. A43474), and *Lycopersicon esculentum* (tomato, accession no. P04284 and Q04108). Alignments were performed with the ClustalW program; * indicates amino acid identity.

act by a mechanism similar to that of the class I PR-4 proteins, namely, binding to cell wall chitin and disrupting cell polarity, thus leading to inhibition of fungal growth.

(v) **PR-5** (TL) proteins. PR-5 proteins share significant amino acid homology to thaumatin (a sweet-tasting [to humans] protein from the South African ketemfe berry bush) and are known as TL proteins. TL proteins have been isolated from *A. thaliana* (59, 60), corn (62, 148), soybeans, rice, wheat, tobacco (81), tomato (161), pumpkin (21), beans (196), barley (55), flax (12), and many other plants (122, 182, 184). The majority of PR-5 proteins have molecular masses of \sim 22 kDa and are stabilized by eight disulfide bonds. This highly stabilized structure allows PR-5 proteins to be very resistant to protease degradation (148). The X-ray structures have been determined for two PR-5 proteins and thaumatin (82, 134).

Although the precise mechanism of action of PR-5 proteins is not completely understood, there are a number of interesting observations that may eventually lead to a unified hypothesis for how these proteins function to kill fungi (24, 66, 147, 158,

186). First, several TL proteins cause cell permeability changes in fungal cells with a cell wall but have no or little effect on protoplasts (148). For example, zeamatin (a TL protein from corn) caused very rapid cell lysis of N. crassa, even at 4°C; lysis occurred primarily at subapical regions (148). Second, a number of PR-5 proteins bind $(1,3)\beta$ -glucan and have detectable in vitro $(1,3)\beta$ -glucanase activity (47, 176). Third, zeamatin inhibits insect α -amylase and mammalian trypsin activities in vitro (152a). Fourth, osmotin, a TL protein from tobacco, causes perturbations in the regulation of fungal cell wall assembly (200, 201). Fifth, zeamatin and nikkomycin act in synergy, reducing the amount of zeamatin required for cell killing up to 1,000-fold (148). These disparate observations are difficult to assimilate into one mechanism of action. Regardless of the precise mode of action of TL proteins, they are fungicidal against a wide number of plant and human pathogens in vitro. Importantly, one protein, zeamatin, has shown efficacy in a murine vaginal model of C. albicans infection (D. A. Stevens et

al., submitted for publication). It may be that certain PR-5 proteins can be developed into human therapeutics.

Defensins. Defensins are a diverse group of low-molecularmass cysteine-rich proteins found in mammals, fungi (89), insects (91), and plants (14, 16). The insect and mammalian defensins are quite small (3 to 5 kDa) and form voltage-dependent ion channels in plasma membranes (92, 93, 171). Thionins are also small (3 to 5 kDa) cysteine-rich peptides that are toxic to fungi (171). Neither the mammalian defensins, insect defensins, nor thionins will be described in this review, for they are generally smaller than 5 kDa.

Plant and fungal defensins are cysteine-rich proteins ranging from 45 to 54 amino acids, are positively charged, and in most cases contain four disulfide bonds that stabilize each protein in solution (4, 5, 38, 49, 87, 88, 106, 110, 135, 155, 168, 169, 170, 181). In addition, most defensins are highly oligomeric (many subunits of 4 to 5 kDa) in situ (168, 169). Defensins are classified into four groups. Group I defensins cause morphological changes in susceptible fungi and are known as morphogenic defensins, group II proteins inhibit fungal growth but do not cause morphological changes (nonmorphogenic group), group III are inactive against test fungi but inhibit α-amylases in vitro, and group IV are unique in terms of antifungal specificity and structure (155). An amino acid alignment of a number of plant and fungal defensins is shown in Fig. 4. Note the high degree of similarity within each group. In addition, the positions of the cysteine residues are conserved in group I, II, and III proteins. No other significant homology exists between groups.

In contrast to mammalian and insect defensins, plant defensins do not form channels either in artificial bilayers or in artificial liposomes (38), and they do not show significant hyphal permeabilization activity (171). In studies using *N. crassa*, Theviseen and coworkers have shown that treatment of hyphae with the defensins from radish (Rs-AFP2) or dahlia (DM-AMP1) caused K⁺ efflux and Ca²⁺ uptake through binding to specific cell membrane receptors (171–174). Although not tested with other fungi, it is likely that fungal inhibition occurs through this mechanism, i.e., ion efflux. Defensins are broadly active, inhibiting a large number of human and plant fungal pathogens, including *B. cinerea, Alternaria brassicola, F. culmorum, F. oxysporum, F. solani*, and *C. albicans* at micromolar levels.

Cyclophilin-like protein. Cyclophilins are a highly conserved group of proteins that are the intracellular receptors for cyclosporin; they have been found in a wide variety of organisms, including bacteria, plants, animals, and fungi (137). Recently an 18-kDa protein was isolated from mung bean (*Phaseolus mungo*) with activity against *R. solani, F. oxysporum, B. cinerea*, and *Coprinus comatus* (199). This protein, called mungin, showed significant homology to cyclophilins and inhibited α - and β -glucosidases in vitro. However, the antifungal mechanism of action of mungin is not known.

Glycine/histidine-rich proteins. Insects synthesize a number of glycine/histidine-rich antifungal proteins and polypeptides, including those from *Holotrichia diomphalia* larvae (holotrichin, 84 amino acids [97]), *Sarcophaga peregrina* (flesh fly, AFP, 67 amino acids [68]), and *Tenebrio molitor* (tenecin, 49 amino acids [28, 96, 98, 99]). An alignment of these proteins is

shown in Fig. 5. Note that they are extremely rich in glycine and histidine, which comprise as much as 80% of the amino acids. Importantly, fungi inhibited included *C. albicans*, the most common human pathogen (e.g., the 50% inhibitory concentration of tenecin is $\sim 8 \mu g/ml$ [28]). The mechanism of action of these proteins is not understood.

RIPs. RIPs are RNA *N*-glycosidases that depurinate rRNA, resulting in the arrest of protein synthesis due to ribosome damage (7, 39, 65, 94, 144, 167). Plant RIPs inhibit mammalian, bacterial, fungal, and plant protein syntheses in vitro and in vivo (67). As an aside, how plants protect themselves from the action of their own RIPs is a subject of very interesting research. RIPs have been classified into three groups. Type 1 RIPs are single-chain N-glycosidases with molecular masses of 11 to 30 kDa. Type 2 RIPs contain two chains, a cell-binding lectin (B chain) and an N-glycosidase (A chain), with molecular masses of ~ 60 kDa (202); type 2 RIPs include toxic members such as ricin and nontoxic members such as ebulin 1 (44) and nigrin b. Type 3 RIPs consist of four chains organized as two dimers of type 2 RIPs. RIPs have been isolated from a number of plants (Mirabilis expansa [183], Pisum sativum [90, 197] Momordica charantia [100], Ricinus communis [6], Viscum *album*, and many others [35, 50, 102, 138, 178, 185, 190, 195]) as well as from fungi, e.g., Aspergillus giganteus (a-sarcin [51, 188]) Unfortunately, the antifungal activities of only a few of the many RIPs have been described.

RIPs have intrinsic antifungal activity due to their ability to inactive fungal ribosomes in vitro and, presumably, in situ. Recent studies with a type 2 RIP showed that the cell-binding B chain (lectin) binds to fungal cells, forming a channel allowing the *N*-glycosidase A-chain entry into cells, resulting in RNA damage (191, 202). Precisely how type I RIPs which do not have a cell-binding chain inhibit fungi, i.e., how are they internalized, is not known. Both type I and type 2 RIPs show broad activity against a number of plant and human pathogenic fungi as well as toxicity against mammalian cells (some type 2 RIPs are highly toxic to animals, likely because of the presence of the cell-binding B chain) (132, 142, 146).

LTPs. LTPs have the ability to transfer phospholipids between membranes. LTPs are small proteins (\sim 8.7 kDa) of \sim 90 amino acids stabilized by four disulfide bonds with a central tunnel-like hydrophobic cavity. They have been isolated from a number of sources, including mammals, plants, fungi, and bacteria (17, 26, 115, 116, 130, 154, 166, 175), and may play several in vivo roles, including lipid exchange between cytoplasmic organelles and, importantly, defense against pathogens (48). An alignment of a number of LTPs is shown in Fig. 6. Note that although the proteins are from diverse sources, they have striking homologies (between 37 to 90% identity). LTPs are active in vitro against a number of bacteria and fungi; however, the mechanism of action is not known. It may be that these proteins insert themselves into the fungal cell membrane, and the central hydrophobic cavity forms a pore, allowing efflux of intracellular ions and thus leading to fungal cell death. How this is related to their lipid transfer function is not clear.

Killer proteins (killer toxins). A number of yeasts secrete proteins that are lethal to sensitive fungal cells. These proteins, called killer proteins or killer toxins, are encoded either by double-stranded RNA, linear double-stranded plasmid DNA, or nuclear genes (2, 23, 70, 108, 153). Fungal cells secreting a

GROUP I	1	10	20	30	40	50
Rs-AFP2	QKLCQRPSO	GTWSGVCGNNN	ACKNQCIRL	EKARHGSCNY	VFPAHKCI	CYFPC
AF2A SINAL	QKLCQRPSG	TWSGVCGNNN	ACRNQCINL	EKARHGSCNY	VFPAHKCI	CYFPC
Rs-AFP1	QKLCERPSO	GTWSGVCGNNN	ACKNQCINL	EKARHGSCNY	VFPAHKCI	CYFPC
AFP1 SINAL	QKLCERPSO	GTWSGVCGNNN	ACKNQCINL	EKARHGSCNY	VFPAHKCIC	CYFPC
At-AFP1	QKLCERPSO	TWSGVCGNSN	ACKNQCINL	EKARHGSCNY	VFPAHKCIC	CYFPC
At-AFP2	QKLCERPSG	TWSGVCGNSN	ACKNQCINL	EKARHGSCNY	VFPAHKCI	CYFPC
At-AFP3	QKLCEKPSO	TWSGVCGNSN	ACKNQCINL	EGAKHGSCNY	VFPAHKCI	CYVPC
Rs-AFP4	QKLCERSSO	GTWSGVCGNNN	ACKNQCINL	EGARHGSCNY	IFPYHRCIC	CYFPC
AFP1-BRARA	QKLCERPSO	GTWSGVCGNNN	ACKNQCIN			
AFP2-BRANA	QKLCERPSO	TWSGVCGNNN	ACKN			
AFP2-BRARA	QKLCERPSG	TXSGVCGNNN	ACKNQCIR			
Rs-AFP3	KLCERSSO	GTWSGVCGNNN	ACKNQCIRL	EGAQHGSCNY	VFPAHKCI	CYFPC
AFP3-BRANA	KLCERSSO	GTWSGVCGNNN	ACKNQCIRL	EGAQHGSCNY	VFPAHKCIC	CYFPC
	*** **	* ***** *	** **** *	* * *****	** * ***	** **
GROUP II	1	10 2	20	30	40	50
Ah-AMP1	LCNERPSQ	TWSGNCGNTA	HCDKQCQDW	EKASHGACHE	RENHWKCFO	CYFNC
Ct-AMP1	NLC-ERASI	JTWTGNCGNTG	HCDTQCRNW	IESAKHGACHK	(R-GNWKCFO	CYFNC
Dm-AMP1	ELC-EKASF	TWSGNCGNTG	HCDNQCKSW	IEGAAHGACHV	RNGKHMCF	CYFNC
	** * *	** *****	*** ** *	* * *****	* ***	****
	_		~ ~	.		
GROUP III	1	10 2	20	30	40	
St-PTH1	RHCESLSHF	RFKGPCTRDSN	CASVCETER	FSGGNCHGFF	RRCFCTKP	2
Siα2	RVCMKGSAG	GFKGLCMRDQN	CAQVCLQEG	WGGGNCDGVM	1RQCKCIRQ0	C
So-D1	XTCESPSHR	FKGPCATNRN	CRS			
	* *	*** * *	* ** *	**** *	* * * ``	*
GROUP IV	1	10 :	20	30	40	50
So-D2	GIFSSRKCF	TPSKTFKGIC	TRDSNCDTS	CRYEGYPAGE	CKGIRRRC	MCSKPC
So-D7	GIFSSRKCKTPSKTFKGYCTRDSNCDTSCRYEGYPAGD					
So-D4	MFFSSKKCKTVSKTFRGPCVRNA					
So-D5	MFFSSKKCKTVXKTFRGPCVRNAN					
So-D3	GIFSSRKCKTVSKTFRGICTRNANC					
So-D6	GIFSNMYXF	RTPAGYFRGPX	GYXXN			
	**	* * *	****	*******	f	

FIG. 4. Amino acid sequence alignment of selected group I to IV defensins. Rs-AFP 1 to 4 are from *Raphanus sativas* (radish, accession no. P30225, P30230, 024332, and 024331), At-AFP1 to 3 are from *Arabidopsis thaliana* (thale cress, accession no. P30224, 080995, and 080994), AFP2-BRANA (rape, accession no. P30226) and AFP3-BRANA (rape, accession no. Q39313) are from *Brassica napus*, AFP1-BRARA (accession no. P30227) and AFP2-BRARA (accession no. P30228) are from *B. rapa*, AFP1_SINAL (white mustard, accession no. P30231) and AF2A_SINAL (white mustard, accession no. P30232) are from *Sinapis alba*, Ct-AMP1 (accession no. S66219) is from *Clitoria ternate*, Ah-AMP1 (common horse chestnut, accession no. S66218) is from *Aesculus hippocastanum*, Dm-AMP1 (bedding dahlia seeds, accession no. AAB34972) is from *Dahlia merckii*, St-PTH1 (potato tubers, accession no. AAB 31351) is from *Solanum tuberosum*, Sio2 (sorghum, accession no. P21924) is from *Sorghum bicolor*, and So-D1- to -7 (spinach) are from *Spinacia oleracea*. Alignments were done with the ClustalW program;* indicates amino acid identity.

killer toxin are resistant to their own toxin but are sensitive to other toxins. Saccharomyces cerevisiae, Ustilago maydis, Hanseniaspora uvarum, Zygosaccharomyces bailii, Phaffia rhodozyma, Kluveromyces lactis, and several Pichia species secrete a number of killer proteins (reviewed in reference 108). Over 20 individual killer toxins have been identified, varying in molecular mass from 10.7 to 156.5 kDa (58, 84). The killer toxins have broad, potent antifungal activity against a number of human and plant pathogens (including *Pneumocystis carinii* [157])—MICs vary from 20 μ g/ml to far less. Although they have varied mechanisms of action, the first step of killer protein activity involves binding of the protein to specific cell surface receptors. Once bound, killer proteins are internalized and can disrupt cell wall synthesis, DNA synthesis, and K^+ channel activity, inhibit (1,3) β -glucan synthesis, or arrest the cell cycle (2, 36, 78, 79, 164). Any one of these effects leads to inhibition of fungal growth and to fungal cell death.

Protease inhibitors. Protein inhibitors of serine (e.g., trypsin and chymotrypsin) and cysteine proteases have emerged as a class of antifungal proteins that have potent activity against plant and animal pathogens. Cysteine protease inhibitors have been isolated from a number of plants and form a fourth group of cystatins, the phytocystatins (10, 72, 86, 139). The phytocystatins are single polypeptides of 10 to 12 kDa and share common structural motifs. Although

	1	10	20	30	40		50	
Tenecin 3	MKTFVIC	LILVVAVSAA	PDHHDGHLO	GHQTGHQGG	QQGGHL	GGQQGGH	ILGGHQGGQPGG	
AFP	MVKLFVIV	ILALIAVAFG-		QHGHGGQI	DQHGYG	HGQQAVY	GKGHEG-HGVN	
Holocitrin 3		YGPGDG-	HGGGHGC	GHGGGHGNG	QGGGHG.	HGPGGGF	'GGGHGGGHGGG	
	* ***			* *	*	*	** *	
	60	70	80	90				
Tenecin 3	HLGGHQGGIGG-TGGQQHGQHGPGTGAGHQGGYKTHGH							
AFP	NLGQDGHGQHG-YAHGHSDQHGHGGQHGQHDGYK							
Holocitrin 3	GRGGGGSGGGSPGHGAGGGYPGGHGGGHHGGYQTHGY							
	* *	*	*	* ** ;	*			

FIG. 5. Amino acid sequence alignment of selected glycine/histidine-rich proteins. Tenecin 3 (yellow mealworm, accession no. AAA97579.1) is from *Tenebrio molitor*, AFP (flesh fly, accession no. BAA02954.1) is from *Sarcophaga peregrina*, and holotricin 3 (accession no. BAA02889) is from *Holotrichia diomphalia*. Alignments were done with the ClustalW program, * indicates amino acid identity.

phytocystatins are active against plant pathogens such as *F*. *solani* (MIC of 20 μ g/disk in an disk agar diffusion assay) and *Trichoderma reesei* (250 ng/disk) (72), the mechanism of antifungal activity is not understood.

Serine protease inhibitors that have antifungal activity also have the interesting property of inhibiting α -amylase activity from insects but not from bacterial or mammalian sources (152a). These proteins are bifunctional, inhibiting enzymes as well as inhibiting insect and fungal growth. Blanco-Labra and Iturbe-Chinas identified a bifunctional α -amlyase/trypsin inhibitor from corn (10); later it was found that this protein was identical to zeamatin (147, 148). We have recently confirmed that at high trypsin/zeamatin and α -amylase/zeamatin molar ratios, zeamatin inhibits trypsin and insect α -amylase activities in vitro (152a). Other bifunctional proteins from ragi (*Eleusine coracana*), wheat, and barley have been isolated and characterized (9, 46, 133, 152, 160). Only a few of these proteins have been tested for in vitro antifungal activity, with zeamatin being

	1	10	20	30	40	50
NLTP BETVU	MASSAFVKF	TCALVMCM	IMVAAPLAE-	AITCGLVASKI	LAPCIGYLQG·	APGPSAACCGGI
LTP_SPIN				GITCGMVSSKI	LAPCIGYLKG	GP-LGGGSSGGI
NLT1 LYCES	MEMFGKI	ACFVVFCM	IVVVAPHAE-	SLSCGEVTSG	LAPCLPYLEGI	R-GPLGGCCGGV
LTP1	MEMVSKI	ACFVLLCM	IVVVAPHAE-	ALTCGQVTAGI	LAPCLPYLQGI	R-GPLGGCCGGV
NLT1_TOBAC	MEIAGKI	ACFVVLCM	IVVAAPCAE-	AITCGQVTSNI	LAPCLAYLRN	F-GPLGRCCGGV
NLT1_GOSHI	MSLKL	ACVVVLCM	IVVGAPLAQG.	AVTSGQVTNSI	LAPCINYLRG	SGAGAVPPGCCTGI
NLT1_PRUDU	MAYSAMTKL	ALVVALCM	IVVSVPIAQ-	AITCGQVSSNI	LAPCIPYVRG	GGAVPPACCNGI
NLTP_HELAN	MAKMAMMV	LCAGVTCM	IVVGAPYTE	ALSCGQVSSSI	LAPCISYLTK	GGAVPPACCSGV
NLT1-RICE	MARAQLI	LLVALVAA	LLLAAQAMA	AISCGQVNSAV	VSPCLSYARG	GSGPSAACCSGV
NLTP_CICAR	MASMKV	VCVALIMC	IVIAPMAES.	AITCGRVDTAI	LAPCLGYLQG	GPGPSAQCCGGV
				* *	** *	*
	60	70	80	90	100	110
NLTP_BETVU	KSLNSAAASI	PADRKTAC	TCLKSAATS	IKGINYGKAAS	SLPRQCGVSVI	PYAISPNTNCNAIH
LTP_SPIN	KALNAAAAT	IPDRKTAC	NCLKSAANA	IKGINYGKAAG	GLPGMCGVHI	PYAISPSTNCNAVH
NLT1_LYCES	KGLLGAAKTI	PEDRKTAC	TCLKSAANS	IKGIDTGKAAG	GLPGVCGVNI	PYKISPSTDCSTVQ
LTP1	KGLLGSAKT	FADRKTAC	TCLKSAANA	IKGIDLNKAAC	GIPSVCKVNI	PYKISPSTDCSTVQ
NLT1_TOBAC	KALVNSART	FEDRQIAC	TCLKSAAGA	ISGINLGKAAC	GLPSTCGVNI	PYKISPSTDCSKVQ
NLT1_GOSHI	KSLNSAAQT	ſPVRQAAC	RCIKSAAAG	ITGINFGLASC	GLPGKCGVNI	PYKISPSTDCNSVK
NLT1_PRUDU	RNVNNLART	[PDRQAAC	NCLKQLSAS	VPGVNPNNAAA	ALPGKCGVNI	PYQISPSTNCANVK
NLTP_HELAN	KSLNSAAKT	FPDRQAAC	GCLKSAYNS	ISGVNAGNAAS	SFPGKCGVSI	YKISPSTDCSKVQ
NLT1-RICE	RNLNSAATT	FADRRTAC	NCLKNVAGS	ISGLNAGNAAS	SIPSKCGVSI	PYTISPSVYCSSVN
NLTP_CICAR	RNLNSAAVT	I PDRQAAC	NCLKSAAGS	ISRLNANNAAA	ALPGKCVVNII	YKISTSTNCATIRV
	*	* **	* *	*	* * * *	** ** *

FIG. 6. Amino acid sequence alignment of selected LTPs. NLTP_BETVU (beet, accession no. Q43748) is from *Beta vulgaris*, LTP_SPIN (common spinach, accession no. S00060) is from *Spinacia oleracea*, NLT1_LYCES (tomato, accession no. P93224) is from *Lycopersicon esculentum*, LTP1 (tomato, accession no. AAB07486) is from *L. pennellii*, NLT1_TOBAC (common tobacco, accession Q42952) is from *Nicotiana tabacum*, NLT1_GOSHI (upland cotton, accession no. 42762) is from *Gossypium hirsutum*, NLT1_PRUDU (almond, accession no. Q43017) is from *Prunus dulcis*, NLTP_HELAN (common sunflower, accession no. Q39950) is from *Helianthus annuus*, NLT1-RICE (rice, accession no. T02038) is from *Oryza sativa*, and NLTP_CICAR (chickpea, accession no. 023758) is from *Cicer arietinum*. Alignments were done with the ClustalW program; * indicates amino acid identity.

the most extensively characterized. The mechanism of antifungal activity of these proteins is not fully understood.

Other proteins. New proteins that have antifungal activity but do not neatly fall into any of the above classes are being discovered at a rapid pace. Only a few can be mentioned here. Viridin, a novel protein isolated from the culture medium of *Trichoderma viride*, has a molecular mass of 65 kDa and is active against sensitive fungi at 6 μ M (52, 53). Snakin-1 isolated from potato has a molecular mass of 6.9 kDa and is active at 10 μ M (156). A 30-kDa protein with very potent antifungal activity (50 ng/disk in an agar diffusion assay) was isolated from Engelmann's daisy (*Engelmannia pinnatifida*); this protein showed 35 to 50% identity to self-incompatibility glycoproteins, not previously known to be antifungal (64). The mechanism of action of none of these proteins is known.

CONCLUSIONS

Antifungal proteins and polypeptides have been isolated from diverse groups of organisms, including plants, fungi, bacteria, insects, and animals (both vertebrates and invertebrates). The mechanisms of action of these proteins are as varied as their sources and include fungal cell wall polymer degradation, membrane channel and pore formation, damage to cellular ribosomes, inhibition of DNA synthesis, and inhibition of the cell cycle. The mode of action of many proteins remains unknown and is the subject of active research. The range of fungi inhibited by antifungal proteins is extremely broad, with plant pathogens and humans pathogens being sensitive at micromolar levels; in some cases, even more potent inhibition was found.

The genes encoding many antifungal proteins are currently being used by agribusiness to create genetically modified plants that have increased fungal resistance in the field. Whether these transgenic plants and the crops derived from them gain acceptance in the marketplace remains to be seen. Equally important, antifungal proteins and peptides are being tested for use as pharmaceutical agents for the treatment of human and animal fungal diseases. This is particularly exciting since the modes of action of these proteins are vastly different from the currently used therapeutics, resistance to which is becoming a clinical problem. There are a number of antifungal proteins in various stages of preclinical development, and the results of these experiments and of the subsequent human clinical trials are eagerly anticipated.

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