

Genetic Determinants of Textural Modifications in Fruits and Role of Cell Wall Polysaccharides and Defense Proteins in the Protection Against Pathogens

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ABSTRACT

Plant cell wall metabolism has been suggested to play a major role in the textural changes associated with fruit ripening. The significance of cell wall degrading agents such as polygalacturonase (PG), pectin methylesterase (PME), β -galactosidase (β -gal), endo-1,4- β -glucanase (EGase) and pectate lyase (PL) has led to important advances in our understanding of cell wall disassembly but studies looking at the way these agents may interact and work in concert as 'a cell wall disassembly line' will increase our understanding of fruit softening. In addition, the *in vivo* contribution of other cell wall degrading agents such as α -arabinofuranosidase (α -ara), rhamnogalacturonase (RGase), acetylesterase (AE) and xyloglucan transglycosylase hydrolase (XTH) to fruit softening remains to be evaluated. The role of the cell walls in the resistance against pathogens is another area of great interest from a postharvest perspective. Cell wall modifications that could reduce fruit susceptibility to decay would be of great value because of the potential to reduce pathological problems occurring during storage, handling and distribution. Interestingly it has been recently shown in *Arabidopsis* that the over-expression of a plant pectin methylesterase inhibitor can restrict fungal infection. It would be interesting to test whether or not this approach might be useful to control fruit postharvest diseases. Another aspect to explore further includes the determination of the potential applications of proteins influencing the ability of pathogen glycosidases to cleave plant cell wall polysaccharides such as polygalaturonases, pectin or pectate lyases and xyloglucanase inhibiting proteins. The present work describes some of the genetic determinants of the textural applications in horticultural commodities and discusses the role of plant cell wall polysaccharides and defense proteins as barriers against postharvest pathogens.

Keywords: cell wall, softening, fruit, decay, resistance against pathogens

Abbreviations: α -afs, α -arabinofuranosidase; AE, acetyl esterase; β -gal, β -galactosidase; CWDPs, cell wall degrading proteins; EGase, endo-1,4- β -D-glucanase; Exp, expansin; PG, polygalacturonase; PGIP, polygalacturonase inhibiting protein; PL, pectate lyase; PME, pectin methyl esterase; PR, pathogenesis related protein; RG I, rhamnogalacturonan I; RG II, rhamnogalacturonan II; RGase, rhamnogalacturonase; TILLING, targeting induced local lesions in genomes; XET, xyloglucan endo-transglycosylase; XTH, xyloglucan transglycosylase hydrolase

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INTRODUCTION

Fruit quality is associated with parameters that include appearance, shape, size, color flavor, aroma, nutritional value and texture (Kader 1992) which ultimately determine acceptability to the consumer. While controlled textural modifications occurring during ripening are desired from a consumer's perspective, excessive loss of firmness is a significant problem in postharvest management of horticultural crops, since this loss limits long distance transportation and reduces shelf life (Brummell and Harpster 2001). Textural modifications in plant tissues have been associated with changes in turgor pressure, tissue structure and integrity of cell wall polysaccharides (Shackel *et al.* 1991; Sexton *et al.* 1997; Lashbrook 2005). Although the contribution of tissue architecture and cell turgor changes to fruit firmness could be substantial, research has not identified specific targets on which further studies might focus. In contrast, several research groups have carried out detailed examinations of fruit cell wall polysaccharide disassembly in attempts to identify genes whose expression is associated for this process such as polygalacturonases, pectin methylesterases, β galactosidases, endo-1,4-β-D-glucanases, expansins and pectato lyases among others (reviewed in Brummell and Harpster 2001; Brummell 2006, Vicente et al. 2007b).

Besides their role in determining cell shape and tissue mechanical properties (Carpita and McCann 2000; Willats et al. 2001), plant cell walls also are a mechanical barrier against pathogens. It has been suggested that wall polymer disassembly events that are associated with programmed plant developmental processes could contribute to increase the susceptibility of plant tissues to pathogens (Vorwerk et al. 2004). Thus, in ripening fruits the necessity of maintaining a balance between softening and keeping a strong barrier for pathogen attack is a postharvest biology challenge that must be addressed. Whether it is possible to achieve the goal of generating commodities having the textural properties that consumers prefer while simultaneously maintaining cell walls as a barrier to fungal penetration and development is currently not clear. In any case, achieving this goal will require a clear understanding of the individual and collaborative roles of the cell wall degrading proteins (CWDPs) in cell wall disassembly (Fisher and Bennett 1991; Owino et al. 2005), as well as the recognition that fruit CWDPs action may have consequences vis à vis the pathogen susceptibility of ripening fruits.

In addition to the 'physical barrier' role of plant cell walls in limiting pathogen growth, there are several plant apoplast-localized proteins that could contribute to plant defenses. The best known of these are proteins that inhibit pathogen-produced cell wall degrading enzymes. Most notable are the polygalacturonase- (Albersheim and Anderson 1971; Abu-Goukh et al. 1983; de Lorenzo et al. 2001), pectin lyase- (Bugbee et al. 1993) and endoxylanase-inhibiting proteins (Debyser et al. 1997) that have been characterized in terms of their ability to provide protection against pathogens by limiting the contributions to penetration and infection of the pathogen's arsenal of CWDPs. Because the pathogen's cell wall plays crucial roles in its own vegetative development (Lorito et al. 1993, 1998), an additional defense strategy that targets the pathogen's extracellular matrix may have value for protection against pathogens. Along this line, plant genes encoding chitinases and β -1,3-glucanases, proteins capable of degrading fungal wall structural polymers, have been identified as pathogenesis-related (PR) proteins. In this review we describe our current understanding on the different genetic determinants of textural modifications in fruits and the role of cell wall polysaccharides and defense proteins in the protection against pathogens.

GENERAL FEATURES OF PLANT CELL WALL COMPOSITION AND STRUCTURE

Cell wall structure

Plant cells are surrounded by a complex, dynamic and organized structure composed of polysaccharides, proteins and phenolic compounds (Carpita and Gibeaut 1993). Approximately 90% of the plant cell walls on a dry weight basis are comprised by three major groups of polysaccharides: cellulose, hemicelluloses and pectins (Brett and Waldron 1996). In cereals, the pectins are a minor cell wall constituent but in fruits, pectins represent a high proportion of the wall polysaccharide complement.

Cellulose

Cellulose is a polymer of β -1,4 linked glucose (Brett and Waldron 1996). The individual glucan chains are held together by hydrogen bonds forming a supramolecular structure in which approximately 36 individual glucan chains are associated. These assemblages of glucans are the cellulose microfibrils (Carpita and McCann 2000). Cellulose organization leads to a structure that is highly resistant to enzymatic degradation. In addition cellulose microfibrils have a tensile strength that is comparable to that of steel of the same thickness (Alberts et al. 2002). The microfibrils play a major role in determining cell shape and providing loadbearing capacity to plant tissues (Bacic et al. 1988). However, as ripening-associated fruit softening occurs, there is little change in cellulosic glucan integrity or microfibrils (Brummell 2006). One exception to this is avocado in which as softening proceeds the cell walls appear to be completely disassembled (Platt-Aloia et al. 1980; O'Donoghue et al. 1994).

Hemicelluloses

Several different polymers soluble in alkalis are classified as hemicelluloses or cross-linking glycans (Brummell and Harpster 2001). The proportion of hemicellulosic compounds present in fruits usually ranges from 25 to 35% (Carpita and McCann 2000). Xyloglucan is the most abundant hemicellulosic compound in dicot species (Williats et al. 2001). It is composed of a backbone of β -1,4-linked glucose with lateral chains of α -1,6 linked xylose which could also be decorated with galactose, arabinose and fucose. Xyloglucan depolymerization accompanying fruit ripening has been observed in most species analyzed so far (Brummell 2006). Although a decrease in the apparent molecular weight of xyloglucan is observed as fruit ripen, relatively large xyloglucan molecules are still observed at advanced stages of development (Brummell 2006). Xylans are a second kind of hemicellulosic compounds found in plant cell walls. They have a backbone of β -1,4-linked xylose and could contain lateral chains rich in arabinose and or glucuronic acid. They are usually highly abundant cross linkingglycans in monocots species, however some studies in berry fruits suggest that these species could have a significant amount of xylose-rich polymers (Vicente et al. 2007a). Work in tomato (Lycopersicon esculentum) also showed that xyloglucomannan are abundant among hemicellulosic polysaccharides (Seymour et al. 1990). In banana the hemicellulosic fractions showed a high proportion of xylose (Xyl) and only traces of glucose (Glc) suggesting that xylans might be also abundant. Interestingly, increased solubilization of Xyl in the water fractions concomitant with a reduction of this sugar in the KOH-soluble fractions during ripening suggests extensive degradation of xylans (Prabha and Bhagyalakshmi 1998). Other hemicellulosic compounds usually less abundant and that have received less attention include glucomannans, galactomannans and galactoglucomannans (Carpita and McCann 2000).

Pectins

Fruit tissues are particularly rich in pectins which can account for 40% of the total cell wall polysaccharides. Particularly rich in polyuronides is the middle lamella, the region in between individual cells. Pectins include very diverse types of galacturonic acid-rich polymers; the different wall pectins contain as many as 17 different monosaccharide building blocks as constituents of polymer backbones and elaborate side chains (Ridley et al. 2001). The most abundant polyuronide present in plant cell walls is homogalacturonan, a polymer of α -1,4-linked galacturonic acid residues which can have different degrees of methyl ester-ification (Williats *et al.* 2001). In addition to the methyl esters at the C6 carboxyl group of galacturonic acid residues, acetyl esters can be found at C2 and C3 (Ishii 1997; Williats et al. 2001). Acetyl esterification has been also found in other cell wall components such as xylans. While methyl esters affect the capacity of pectin molecules to interact with each other by calcium bridges, acetyl esters might affect the physicochemical properties of the polymers (e.g. solubility) and could also reduce the action of pectindigesting enzymes to cleave the polymers. Reduction in pectin polymer size during ripening has been reported in several species (reviewed in Brummell 2006). Some fruits such as avocado (Persea americana) show a dramatic downshift in polyuronide size (Huber and O'Donoghue 1993). On the other hand almost no pectin depolymerization is detected in peppers (Capsicum annum) and only moderate changes are found in banana (Musa paradisiaca), apple (Malus domestica) and blueberry (Vaccinium corymbosum) (Brummell 2006; Vicente et al. 2007a).

Other polyuronides present in plant cell walls are rhamnogalacturonan I (RGI) and rhamnogalacturonan II (RGII). RGI consists of a backbone of alternating α -1,2-rhamnosyl and α -1,4-galacturonosyl residues (Willats *et al.* 2001). The rhamnosyl residues also can have lateral chains of arabinans, galactans or arabinogalactans (Carpita and McCann 2000). Homogalacturonan has also been suggested to be a side chain of RGI (Vincken et al. 2003). Loss in RGI arabinose and galactose by hydrolytic cleavage of the lateral chains of the polymer is a significant feature accompanying fruit ripening (Gross and Sams 1984). In some fruit, such as pears and berry fruits, arabinose is highly abundant and a marked decrease in this sugar (up to 80%) is observed as ripening proceeds. In other commodities such as apple, melon, squash, muskmelon and tomato, the reduction in cell wall galactose content (up to 70%) is a prominent feature of ripening-associated wall compositional change (Gross and Sams 1984). In many cases, these changes are associated with an increase in pectin solubility that precedes pectin depolymerization. It has been speculated that arabinose and galactose side chain removal could have an impact on overall cell wall porosity, increasing the cross-sectional area of the spaces between wall polymers and enhancing access of larger CWDPs to their wall polysaccharide substrates. However, changes in wall porosity accompanying fruit ripening have not been specifically reported although increased cell wall swelling has been described for many ripening fruits (Redgwell et al. 1997). Finally, a pectic polymer that has received much attention recently is rhamnogalacturonan II (RGII). RGII is the most complex polysaccharide present in the cell wall with 12 different kinds of sugars on its structure (O'Neill et al. 2004). Interestingly, RGII molecules can associate by borate diester bonds to form dimers (Kobayashi et al. 1996) and changes in the RG II monomer to dimer ratio affect cell wall mechanical properties, and plant growth (Ishii et al. 2001; O'Neill et al. 2001, 2004). For instance a reduction in RGII occurring as dimers from 90% in wild type plants to 50% in mutants defective in Arabidopsis mur1-2 mutants decreased leaf growth five times (O'Neill et al. 2004). Hypocotyls from Arabidopsis mutants affected in RGII structure also showed reduced tissue tensyl resistance (Ryden et al. 2003) leading the authors to conclude that borate-complexed rhamnogalacturonan II contributes to the strength of cell walls. Whether changes in RGII structure or dimerization occur during fruit ripening and exert direct or indirect effects on wall properties (by altering cell wall pore size and mobility of cell wall degrading proteins through the apoplast) has not been characterized.

Cell wall architecture

All the polysaccharides described above together with several groups of structural proteins are responsible for the architecture of the plant cell walls. Hemicelluloses are thought to be associated with the microfibril's surface via the formation of hydrogen bonds. The resulting cellulosehemicellulose matrix (CHM) is composed of microfibrils and hemicelluloses that both coat and cross-link them (Carpita and McCann 2000) while pectins are thought to fill the spaces between the CHM. The free carboxylic groups of unesterified pectin residues have been shown to ionically interact with calcium ions also present in the apoplast (Williats et al. 2001). Consequently a higher degree of methylesterification of pectin would decrease the level of interpectate calcium cross bridges. Another kind of association of cell wall polymers includes the formation of RG II dimers via borate diester bonds (O'Neill et al. 2004). There is general acceptance of the overall structural plan of the pectin network and CHM in primary cell walls and of the kinds of polymers that these walls contain. However, more controversy has arisen in relation to the nature of the interactions between the different wall components and their distribution within the wall. Several cell wall models have been proposed to date:

Covalently-bridged matrix: Early work by the Albersheim group suggested that the primary cell wall can be considered a single macromolecule in which the different components (with the exception of the connection between xyloglucan (XyG) and cellulose) are associated by covalent bonds (Keegstra *et al.* 1973).

Sticky network model: Failure to find further evidence of the covalent associations between cell wall components, led to an alternative, the 'sticky network' model (Cosgrove 2001). In this model XyG binds to additional hemicellulose by hydrogen bonds and interconnects the cellulose micro-fibrils forming the CHM, while pectic polysaccharides form a second coextensive but independent network.

Multicoat model: This model suggests that hemicelluloses coating the micro-fibrils are not seen as direct bridges between microfibrils, but instead interact with other hemicelluloses and pectins in the space between them (Talbott and Ray 1992).

Stratified model: Ha *et al.* (1997) proposed a stratified model in which cellulose is proposed to be directly cross-linked by XyG, as in the sticky network model. However, in the stratified model, cross-links occur within single micro-fibril-XyG layers while layers of pectin polymers are located in strata that separate the distinct microfibril-XyG layers.

In the past few years there has been new evidence for covalent interactions between XyG and pectins. This was first described in rose suspension cells (Thompson and Fry 2000) and further work showed that covalent linkages between XyG and pectic polysaccharides are present in several species (Popper and Fry 2005). Recently it was also reported that pectin lateral chains also can bind to cellulose microfibrils (Zykwinska *et al.* 2005) and this interaction may prove to be also of considerable significance in the modeling of plant cell walls.

GENES CODING FOR PROTEINS INVOLVED IN CELL WALL DEGRADATION

Several cell wall degrading enzymes and proteins involved in cell wall disassembly have been characterized (Fisher and Bennett 1991; Hadfield and Bennett 1998; Brummell and Harpster 2001; Cosgrove *et al.* 2002).

Pectin degrading proteins

Polygalacturonase (PG)

PGs, poly $(1 \rightarrow 4 - \alpha$ -galacturonide) glycanohydrolases, are involved in the hydrolytic cleavage of homogalacturonan (Hadfield and Bennett 1998). PG has been described in several fruit species and its activity usually increases during fruit ripening. Exo-polygalacturonases (EC 3.2.1.67) cleave pectin form the non reducing end removing one sugar residue at a time while endo acting polygalacturanases (EC 3.2.1.15) can hydrolyze the polymer at internal sites. For a long time it was thought that PG played a central role in polyuronide degradation and fruit softening. However, antisense suppression of PG in tomato did not lead to fruit with dramatically reduced softening (Brummell and Harpster 2001) and transgenic lines suppressed in PG activity remained slightly firmer than the untransformed controls only late in ripening. These results suggested that tomato fruit softening could be independent from PG activity. However, it is not clear if this finding holds true for other fruits.

The interaction between the different cell wall degrading agents is not clearly understood yet, but we have recently found that the simultaneous over-expression of PGand Exp1 resulted in tomato fruits that softened faster than control fruit (Vicente *et al.* unpublished results). It would be interesting to evaluate if the combined suppression of PG and other cell wall degrading proteins with potential functional redundancy, such as pectate lyase (Marín Rodríguez *et al.* 2002) also could delay fruit softening.

Pectate lyase (PL; EC 4.2.2.2)

Lyases cleave glycosidic bonds by β -elimination, giving rise to unsaturated products. Among these enzymes, pectin lyases show specificity for methyl esterified substrates (pectin), while pectate lyases catalyze the eliminative cleavage of de-esterified pectin (Medina-Escobar et al. 1997). Pectate lyases are widely distributed among microbial plant pathogens (Searle-van Leeuwen et al. 1992; Shvchik et al. 1997). In the case of fruits they have been identified in banana (Dominguez-Puigjaner et al. 1997; Pua et al. 2001), grape (Vitis vinifera) (Nunan et al. 2001) and strawberry (Fragaria × anannasa) (Medina-Escobar et al. 1997) and although PL activity was previously thought to be absent in tomato fruit (Besford and Hobson 1972), the unsaturated oligosaccharides diagnostic of PL action have been detected (An et al. 2005). Suppression of a strawberry pectate lyase (pl) genes resulted in significantly firmer fruit and a reduction in both ripening-related in vitro wall swelling and in the normal shift of covalently bound wall pectins to chelator-soluble form (Jiménez-Bermúdez et al. 2002), suggesting that the enzyme might have a significant role in controlling pectin disassembly and fruit softening.

Pectin methylesterase (PME; EC 3.1.1.11)

Pectin degradation requires the combined action of hydrolases and lyases, which cleave the bonds between the galacturonosyl residues of homogalacturonans and methylesterases, which remove methoxyl groups from pectin (Tieman et al. 1992). Pectins are synthesized and secreted to the cell wall with a high degree of methyl esterification (Williats et al. 2001). PME-mediated methyl ester removal has several impacts on cell wall properties and metabolism. The liberation of carboxylic groups might increase the capacity of pectins to interact by calcium bridges (Tieman et al. 1992). However, demethylated pectin is a preferred substrate for PG. Consequently a reduction in the degree of esterification of the pectin fraction could potentially favor the hydrolysis of homogalacturonan. Tieman and Handa (1994) reported that tomato fruits from transgenic plants with down-regulated PME gene expression showed complete loss of tissue integrity during fruit senescence but this genetic manipulation had little effect on fruit firmness during ripening.

β-galactosidase (β-gal; EC 3.2.1.23)

Galactose loss from the cell wall fraction is also a common feature observed during fruit ripening in several fruits including tomato, pepper, peach, apple, melon and squash (Gross and Sams 1984). β -gal activity has been detected in several fruits. In the case of tomato, seven different β -galencoding genes have been identified (Smith and Gross 2000), and lines in which β -gal4 expression was suppressed showed reduced softening (Smith *et al.* 2002). Interestingly, the effect on fruit firmness was observed in lines in which the gene was suppressed early in development suggesting that the removal of galactose from pectin side chains might be a prerequisite for late ripening softening.

α-arabinofuranosidase (α-Afs; 3.2.1.55)

α-L-arabinofuranosidases are plant enzymes capable of releasing terminal arabinofuranosyl residues from cell wall matrix polymers (Saha et al. 2000). Three different α-Af isoforms have been identified in tomato fruit (Sozzi et al. 2002). While the activity of isoforms I and II was reduced or showed no changes during ripening, isoform III markedly increased as ripening progressed, identifying it as a candidate for a role in softening-related depolymerization. However, whether or not α -Afs have an important role in fruit textural modifications during ripening has not been determined yet. Recently, a full-length cDNA clone encoding a α -Af (PpARF2) was cloned from pear, a fruit which shows extensive loss of arabinose during ripening (Tateishi et al. 2005). It would be interesting to determine the impact of suppressing *PpARF2* in pear fruit cell wall metabolism and softening.

Other pectin-degrading enzymes

Other pectin-degrading enzymes have received less attention. These include rhamnogalacturonases (RGases) and acetyl esterases (EC 3.1.1.6). RGases are involved in the cleavage of rhamnogalacturonan I backbones and were initially identified in microorganisms (Mutter et al. 1998). The presence of RGases in plants has been reported in some fruits (Gross et al. 1995). However, RGase activity in fruit extracts has not been widely tested and so the significance of these enzymes in fruit softening has not been determined. Another set of enzymes that has not received much attention includes acetyl esterases (AEs). Several cell wall components, including pectins and xylans have been shown to be acetylated (Ishii 1997; Dea and Madden 1986). For pectins, the degree of acetylation is variable depending on the species considered. Sugar beet RGI could present high degree of acetylation (DAc 60%), while other fruits such as Japanese quince the DAc is much lower (3%) (Thomas and Thibault 2002). Unfortunately the DAc in different fruit species remains uncharacterized. Despite of it could be hypothesized that acetylation of pectins would affect their physicochemical properties and reduce their susceptibility to degradation by other cell wall degrading enzymes such as PGs, PLs and/or RGases. For instance, pectate lyase secreted by Erwinia sp. cleaves only those galacturonic acid residues that are not acetyl-esterified (Davis et al. 1984; Shvchik et al. 1997). AEs have been identified in tomato (Savary 2001) and purified orange (Williamson 1991). It would be interesting to determine the influence of these enzymes on fruit cell wall integrity.

Glycan-degrading proteins

endo-1,4-β-glucanase (EGases; EC 3.2.1.4)

EGases hydrolyze internal linkages of $(1\rightarrow 4)$ - β -D-linked glucan chains (Brummell and Harpster 2001). The enzyme's *in vivo* substrates are thought to include hemicelluloses

(xyloglucan, glucomannan) and non-crystalline cellulose. EGases have been identified in all fruit species tested (Brummell and Harpster 2001). The suppression of EGaseencoding genes in tomatoes and sweet peppers had no impact on fruit softening and the anticipated reduction of hemicellulose depolymerization in ripening peppers was not detected (Brummell et al. 1999a; Harpster et al. 2002a). Over-expression of a ripening-related EGase in transgenic tomato fruit did not result in modified fruit softening or XyG depolymerization (Harpster et al. 2002b). These results suggest that the enzyme is not a limiting factor for fruit softening or hemicellulose degradation, although the expression of multiple EGase isoforms in some fruits makes this conclusion somewhat uncertain. Whether this is true in other fruits is not clear yet. The interpretation of the roles of EGases in fruit ripening becomes even more complex considering that while some EGases have been shown to be involved in cell wall degradation others are thought to be primarily located in the plasma membrane and involved in polymer synthesis (Nicol et al. 1998).

Xyloglucan endotransglucosylase/hydrolases (XTHs; 2.4.1.207)

XTHs are identified by their in vitro action as transglucosylases, catalyzing the endo-cleavage of a XyG polymer backbone and subsequent transfer of the newly generated reducing end to the non-reducing terminus of an acceptor XyG. However, some proteins with in vitro transferase activity act preferentially as hydrolases (Rose et al. 2002a). XTHs have been shown to act on the XyGs attached to cellulose microfibrils (Vissenberg et al. 2005). Interestingly, it has been recently shown that the barley XyG xyloglucosyl transferase (HvXET5), can catalyze the formation of covalent linkages between XyGs and cellulosic substrates in vitro (Hrmova et al. 2007), suggesting a role of the enzyme in cell wall assembly, determining the interactions between different cell wall polymers. XTH expression and activity have been correlated with cell growth rate (Potter and Fry 1994; Catala et al. 1997). Increased XTH activity has been observed in some fruits during ripening (Redgwell and Fry 1993; Percy et al. 1996). Several XTHs have been isolated from ripe tomato fruit (de Silva et al. 1994; Saladie et al. 2006) and the potential role of these enzymes in fruit softening is still under study.

Expansin (Exp)

Expansins are relatively small proteins (25-27 kDa) which are able to increase the relaxation of plant cell walls (Cosgrove 2001). They were first identified due to their ability to promote the loosening of the cell wall of cucumber seedlings in vitro (McQueen-Mason et al. 1995; Cosgrove 2001). Extensive work has been done in the last 15 years to show that expansins are involved in several developmental processes such as growth, abscission, and softening (Cosgrove et al. 2002). Expansins have a cellulose binding domain and an endoglucanase-like domain. However, no hydrolytic activity has been demonstrated, and it has been suggested that they may act by disrupting hydrogen bonds between hemicelluloses like XyG and cellulose and consequently increase cell wall relaxation. The suppression of the fruit ripening-associated Exp1 in tomato fruit decreased fruit softening relative to unmodified controls (Brummell et al. 1999b).

Other cell wall degrading enzymes such as glucosidases (3.2.1.21), xylosidases (EC 3.2.1.37-3.2.1.72) xylanases (EC, 3.2.1.8) and mannanases (3.2.1.78) have been identified in ripening fruits but have received less attention and their contribution to fruit softening and cell wall disassembly is not clear.

ROLE OF PLANT CELL WALLS AS A BARRIER AGAINST PATHOGENS

Fleshy fruit, such as peaches, apples, pears and tomatoes are particularly susceptible to rotting organisms and postharvest diseases account for millions of dollars in losses every year (Narayanasamy 2006). Plant cell walls represent a physical barrier to pathogen infection. While some pathogens rely on natural surface breaks to penetrate host tissues, most pathogens develop within the apoplast as they colonize and infect their hosts (Vorwerk *et al.* 2004). Pathogenic fungi and bacteria utilize secreted CWDPs to digest host cell walls, a process that permits them to extend the zone of infection while they harvest sugar substrates from cell wall polysaccharides.

Among the CWDPs produced by microorganisms are endo- and exo-polygalacturonases, pectate lyases, and endo-1,4 β-glucanases (Colmer and Keen 1986), enzymes that target the key non-cellulosic networks of the host's primary cell walls. The secretion of enzymes that target plant cell walls usually characterizes necrotrophic pathogens, either fungi, such as Botrytis spp., or bacteria, such as Erwinia spp. However, utilization of CWDPs as a component of the pathogen's infection strategy is not exclusive to necrotrophs. For example, Claviceps purpurea, a fungal biotrophic pathogen of cereals and causal agent of the ergot disease, actively digests pectin polymers during its infection of young ovaries. The importance of CWDP production to C. purpurea's pathogenicity is demonstrated by the fact that mutants lacking functional endoPGs are unable to infect compatible rye hosts (Oeser et al. 2002).

For many years, the ability to digest plant cell walls has been associated with the virulence of rotting organisms. For example, when one of the six endoPGs secreted by B. cinerea was knocked out by partial gene replacement, the mutants retained the pathogenicity on tomato leaves and on apple and tomato fruits, but showed a decrease in their ability to develop expanding macerated lesions (ten Have et al. 1998). Black rot symptoms on citrus fruit were also significantly reduced when an endoPG of the fungal pathogen Alternaria citri was mutated (Isshiki et al. 2001) and PG activity is required for full virulence of Aspergillus flavus on cotton bolls. However, probably due to the functional redundancy of the secreted CWDPs, targeted knock outs of these proteins have resulted in a decreased virulence of only a few pathogens (Rogers et al. 2000; Valette-Collet et al. 2003; Kars et al. 2005; Reis et al. 2005).

Fruit ripening is typically associated with increased susceptibility to opportunistic pathogens (Giovannoni 2004). In many cases, unripe fruit show high tolerance to fungal infection, whereas these same fruit become increasingly pathogen-susceptible as ripening occurs. Rotting organisms fail to develop on mature green tomato fruit, whereas red ripe fruit are colonized rapidly with extensive tissue maceration (Prusky 2003). Strawberries, blueberries, raspberries and blackberries suffer severe rotting caused by B. cinerea and Rhizopus stolonifer at ripe stage (Vicente et al. 2005). Although infection occurs at early developmental stages, only ripe peaches and grapes show high disease severity form Monilinia fruticola (Lee and Bostock 1996) and B. cinerea infections (Hill et al. 1981); both brown and gray rots are extremely serious diseases of these commodities. In avocado fruit, ripening is accompanied by a dramatic increased susceptibility to Colletotrichum gloeosporioides, the causal agent of anthracnose, a major cause of decay during storage of the fruit (Prusky et al. 1993).

During fruit ripening cell walls undergo extensive disassembly, a process that is particularly interesting in the context of the relationship of ripening and increased susceptibility because many of the CWDP types produced by ripening fruits are the same as the CWDPs secreted by invading pathogens. Although cell wall metabolism in the context of ripening of many edible fruit has been extensively studied, the contribution of that self-disassembly of cell wall to the susceptibility of the ripening fruit is still a matter of debate.

The outcome of fruit interactions with necrotrophic pathogens depends on many factors that are unrelated to the ripening-associated disassembly of the host's cell walls. Several authors have reviewed aspects of the preformed factors and induced responses that are related to an effective defense (Elad 1997; Labavitch 1998; Prusky 2003). We will not comment on these aspects of pathogen defenses in this short review. Several observations support the idea that fruit wall metabolism is also important factor in determining susceptibility. For instance, calcium treatments delay cell wall disassembly and have been used to reduce the rate of softening and spoilage of fruits (Poovaiah 1986; Mignani et al. 1995). Tomato fruit mutations, such as the nonripening (nor) and the never ripe (nr) with reduced ripening-associated softening show decreased susceptibility to rotting (Lavy-Meir et al. 1989; Kramer et al. 1992). Furthermore, tomato fruit with reduced levels of PG (Smith et al. 1990; Kramer et al. 1992) are less susceptible to Geotrichum candidum and R. stolonifer. It is not clear whether other proteins involved in ripening-related wall change also affect a fruit's pathogen susceptibility, but this point has not been widely addressed. Suppression of the expression of the tomato fruit expansin gene LeExp1 resulted in firmer fruit with prolonged shelf-life, but did not reduce the ripened fruit's susceptibility to B. cinerea and Alternaria alternata (Brummell et al. 2002). Interestingly, recombinant nr tomato mutants constitutively expressing a full-length PG cDNA are only partially more susceptible to G. candidum than control nr tomatoes (Kramer et al. 1992) suggesting that PG activity is not sufficient to cause all the biochemical modifications of the cell walls thought to lead to the increased susceptibility of the ripening wild-type tomato fruit. These observations suggest that the suppression of genes encoding proteins involved in cell wall disassembly during ripening may be a valid approach for developing novel horticultural commodities with reduced susceptibility to microbial spoilage. However, they also make clear that focusing on a single CWDP-encoding gene might not be sufficient to limit the increase in susceptibility that normally accompanies ripening. The simultaneous suppression of multiple fruit CWDP genes could prove to be more useful. For instance, we have recently produced transgenic tomato lines with suppressed expression of both PG and Exp1, two proteins whose independent suppression leads to reduced wall disassembly and firmer fruit (Powell et al. 2003). Will these lines produce ripe fruit that are less susceptible to pathogens? While such a strategy might reduce concerns about postharvest treatments of fruits with fungicidal chemicals, it is likely that public reluctance to accept genetically modified horticultural products will remain an issue, at least in the short term. This concern may be overcome using knockout lines developed through chemical mutagenesis and subsequent TILLING (targeting induced local lesions in genomes) to identify fruit lines with altered ability to disassemble wall polysaccharide networks and, potentially, enhanced pathogen tolerance (Henikoff et al. 2004). Such efforts would be strengthened by success in identifying which aspects of ripening-associated cell wall metabolism are linked to the increased susceptibility of ripening fruits and development of an efficient phenotyping protocol to efficiently and accurately quantify fruit susceptibility to pathogens and obtain results that are consistent and comparable between different research laboratories. The latter will require the identification of biologically relevant, standard inoculation procedures and also techniques for disease quantitation and measurement of accumulated pathogen biomass (Benito et al. 1998; Dewey and Yohalem 2004).

IN DEFENSE OF THE PLANT CELL WALL

Over the eons of interactions with pathogens, plants have evolved strategies to counteract pathogen virulence mechanisms. These include the secretion to the apoplast of proteins that inhibit several of the microbial CWDPs that target the plant cell wall barrier during penetration and infection. Polygalacturonase-inhibiting proteins (PGIPs) have received considerable research attention over the last 3 decades (Albersheim and Anderson 1971; Abu-Goukh et al. 1983; Bergmann et al. 1994; reviewed in de Lorenzo et al. 2001; Gomathi et al. 2006), but the involvement in defense of plant proteins that inhibit pathogen pectin lyases (Bugbee et al. 1993) and endoxylanases (Debyser et al. 1997; Rouau and Surget 1998; McLauchlan et al. 1999) has also been described. PGIPs have been identified in several important horticultural commodities, including tomatoes, pears, apples, raspberries and strawberries (Stotz et al. 1993, 1994; Yao et al. 1995; Mehli et al. 2004). PGIPs are selective inhibitors of pathogen PGs, but do not affect plant PGs. Interestingly, transcripts of the tomato fruit PGIP (LePGIP1) accumulate during the early stages of fruit development and decline with ripening, suggesting a role in the general resistance of green fruit to pathogen infection (Powell et al. 2000). Furthermore, transgenic tomato and grape tissues expressing the PGIP from pear fruit (pPGIP) driven by the constitutive promoter CaMV35S display reduced susceptibility to B. cinerea (Powell et al. 2000; Agüero et al. 2005). However, to date field tests of recombinant lines over-expressing PGIP gene(s) have not provided data demonstrating a PGIP role in defense. This likely supports the idea that PGIPs are only one component of a fruit's basal pathogen defenses and that, in many situations, other elements of basal defense systems play the more important roles in successful defenses (Stotz et al. 2004). Earlier in this review we discussed a few tests of the pathogen susceptibility of transgenic tomato fruits with suppressed expression of the ripening-associated fruit PG genes. These findings support the idea that the infection of fruit tissues by necrotrophic pathogens is assisted by the cell wall disassembly that accompanies ripening. This general idea is further supported by a recent report by Lionetti et al. (2007). Earlier work (Wolf et al. 2003; Raiola et al. 2004) had identified Arabidopsis genes encoding proteins that were potent inhibitors of PME. However, in this case the PME-inhibiting protein (PMEI) inhibited the PMEs of Arabidopsis, not the PMEs of potential pathogens. Transgenic Arabidopsis lines overexpressing the PMEI-encoding sequences displayed reduced endogenous PME activity and were less susceptible to infection by B. cinerea (Lionetti et al. 2007). Thus, if ripening-associated cell wall disassembly does contribute to ripening-associated increases in pathogen susceptibility, combining in a single transgenic fruit reduced capacity to disassemble cell wall networks during ripening with overexpression of PGIP or another protein inhibitor of pathogen CWDPs might lead to a substantial decrease in ripened fruit pathogen susceptibility and, consequently, substantially reduced use of fungicidal chemicals in the postharvest environment.

THE BEST DEFENSE MAY BE A GOOD OFFENSE: HOST DEFENSES THAT TARGET THE PATHOGEN'S CELL WALLS

Fungal cells also have cell walls. Fungal cell walls are rigid multilayered structures whose principal components, at least for true fungi, are a linear polymer of β -1,4-*N*-acetylglucosamine (chitin), 1,3- and 1,6-β-linked glucans, mannan and proteins, with extensive cross-linking between the components (Adams 2004). This protective shell is fundamental for fungal viability and pathogenicity, not only determining fungal morphology and providing an osmotic protection, but also regulating material exchange with the external environment, adhesion with the substrate, host penetration and cell-to-cell communication. Because of the importance of cell wall in fungal development and pathogenicity, several drugs and fungicides have been designed to target the biogenesis of cell wall components. Polyoxins, naturally occurring molecules that inhibit fungal chitin synthase, are used to control many fungal pathogens of plants (Gooday 1989; Asano 2003). Echinocandins, synthetically modified lipopeptides, inhibit the biosynthesis of β -glucans of *Candida* spp. and are used to control these important human pathogens (Denning 2002). Furthermore, the antifungal proprieties of *Trichoderma* spp., which are well known mycoparasitic and antagonistic fungi that are exploited as biocontrol agents of root rotting pathogens, are largely due to their secretion of a set of fungal cell wall-degrading enzymes (Lorito *et al.* 1993). Interestingly, transgenic potato and to-bacco plants over-expressing a chitinase gene from *T. harzianum* were highly tolerant to *Rhizoctonia solani*, *Alternaria alternata*, *A. solani* and *B. cinerea* (Lorito *et al.* 1998).

In their defense, plants make use of some of the strategies used by invading pathogens. Many plants produce chitinases and β -1,3-glucanases, hydrolases that can digest fungal cell wall components. These fungal wall-digesting enzymes are considered pathogenesis-related (PR) proteins because their expression often is triggered by pathogen infection. Chitinases catalyze the random hydrolysis of the 1,4-β-linkages between the N-acetyl-glusosamine residues of chitin. Plant chitinases are organized in five different classes based on DNA sequences and structures (Neuhaus et al. 1996). In vitro experiments demonstrated that some plant chitinases degrade fungal cell walls and reduce fungal growth (Schlumbaum et al. 1986). The over-expression of a tobacco class I endochitinase gene in Nicotiana sylvestris plants did not result in increased resistance to Cercospora nicotianae infection (Neuhaus et al. 1991); however there is considerable evidence supporting a role of chitinases in plant defense. Chitinase gene expression generally is induced under biotic and abiotic stresses, although a developmental accumulation of chitinases occurs also. Roby et al. (1990) showed the localized activation of a bean chitinase promoter around fungal infection sites upon challenge with B. cinerea, R. solani and Sclerotium rofsii. A delay in disease symptom development and general tolerance to R. solani occurred when tobacco seedlings constitutively expressed the bean chitinase gene (Broglie et al. 1991). Because of the composite structure of the fungal cell walls, it is likely that the single hydrolytic activity of chitinases does not have a consistent dramatic effect on fungal growth because chitin is embedded in a matrix of glucan fibers. Leah (1991) and Mauch (1988) showed that the antifungal proprieties of plant chitinases are enhanced when β -1,3glucanases were added in combination with chitinases; the combination likely being more effective because of the added impact on the glucan polymers of fungal walls. In planta, susceptibility to fungal attack decreased when chitinase and glucanase genes were over-expressed in combination in transgenic tobacco plants (Zhu et al. 1994). Increased tolerance of tobacco plants to R. solani was achieved by constitutive co-expression of a class II chitinase, a β -1,3-glucanase and a ribosome inactivating protein from barley (Jach et al. 1995). An indirect effect of chitinases and β -1,3-glucanases is also supported by the observation that oligosaccharides, specific oligochitin and β -1,3-1,6-oligoglucan molecules released from the fungal cell wall by plant enzymes can elicit plant responses (Côté and Hahn 1994). Recently, Kaku et al. (2006) cloned a plasma membrane receptor of a chitin oligosaccharide elicitor. While plants have co-opted a pathogen strategy by using CWDPs against the invader, pathogens have used a plant strategy to counter this defense. Rose et al. (2002b) cloned Phytophthora sojae genes encoding proteins that inhibit the "defense" glucanases secreted by soybean.

Besides chitin and glucans, fungal cell wall mannans also appear to play an important role in fungal growth and interaction with different types of host organisms. In *C. albicans*, cell wall β -glucans are masked by mannoproteins that protect the infecting fungus from the inflammatory response of the human immune system that otherwise would be triggered by β -glucans (Wheeler and Fink 2006). Conidia of the fungal rice blast *Magnaporthe grisea* contain mannose as the only carbohydrate in their spore tip mucilage and the polysaccharide seems to be crucial for fungal adhesion to the host surface (Howard and Valent 1996). The toxicity of the PR5 protein osmotin on Saccharomyces cerevisiae depends on fungal wall phosphomannans (Ibeas et al. 2000). In spite of the evidence identifying mannans as important to the interaction of fungi with animal and plant hosts, so far there have been no studies identifying a plant defense strategy that specifically targets fungal wall mannans. Plants produce mannanases that appear to be involved in important developmental processes, such as seed germination (Nonogaki and Bradford 2000; Mo and Bewley 2002, 2003) and anther and pollen development (Filichkin et al. 2004). A tomato fruit mannanase activity that is localized primarily in the epidermis and in the outer pericarp cell layers increases during ripening (Bewley et al. 2000); intriguingly, tomato cultivars that do not produce mannanase activity ripen and soften normally, suggesting that these enzymes may not be involved in the disassembly of fruit cell wall mannans. Mannans are abundant polymers of the walls of pathogens like B. cinerea and it could be speculated that perhaps the mannanase expression at the fruit periphery represents another example of a plant defense strategy that targets the cell walls of potential pathogens. To date, there have been no tests of the relative pathogen susceptibility of tomato cultivars producing differing amounts of mannanase.

CONCLUSIONS

Recent work in cell wall biology has been fruitful in identifying some agents that seem to be important in determining fruit textural changes. However, understanding and controlling fruit softening seems to be harder than it had been once envisioned. Some of the factors that contribute to this complexity are: 1) the importance of changes different from cell wall polysaccharide degradation such as modifications of turgor pressure to fruit softening is still highly unknown; 2) extensive cell wall disassembly occurs in most fruits, but factors that could be limiting in determining polymer breakdown and softening in a certain species could not be as crucial in other fruits; 3) the presence of multiple forms for many enzymes might determine high redundancy and complicate genetic strategies for controlling fruit textural modifications ('many ways of going soft I'); 4) the presence of different enzymes targeting similar polysaccharides could determine functional redundancy which could also make more difficult to control softening by genetic approaches ('many ways of going soft II"); 5) we still have little understanding of the interaction among different CWDP in vivo.

Regarding the role of cell wall polysaccharides and defense proteins in the protection against pathogens there have been many advances such as 1) determining that the action of some but not all plant CWDP might facilitate pathogen colonization; 2) characterizing and identifying some plant secreted inhibitors which could reduce the activity of pathogen CWDP and be part of the defensive arsenal; 3) studying some plant proteins that can target fungal cell walls (chitinases and β -1,3-glucanases). Despite that, much work is still required to identify the whole repertoire of plant proteins involved in the interactions with pathogens at the apoplastic 'battle-front'. In addition while biotechnological approaches to suppress some of the factors enhancing susceptibility or over-express defense factors in the fruits seem to be a feasible, the ultimate practical applications of altering the level of these proteins still need to be determined.

In this scenario the question raised is again: will it be possible to achieve the goal of generating commodities having the textural properties that consumers prefer while simultaneously maintaining cell walls as a barrier to fungal penetration and development? This is difficult to know. In recent years several groups have identified and characterized several genetic determinants of textural modifications in fruits and proteins that could be considered in strategies aiming to increase defenses against pathogens. Research has gone far, but we it still needs to go farther.

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