### Synthesis, processing and export of cytoplasmic endo-β-1,4xylanase from barley aleurone during germination

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Received 21 December 2000; accepted 9 February 2001.

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#### Summary

We have identified the major endo- $\beta$ -1,4-xylanase (XYN-1) in the aleurone of germinating barley grain, and show that it is expressed as a precursor of  $M_r$  61 500 with both N- and C-terminal propeptides. XYN-1 is synthesized as an inactive enzyme in the cytoplasm, and only becomes active at a late stage of germination when the aleurone ceases to secrete hydrolases. A series of processing steps, mediated in part by aleurone cysteine endoproteases, yields a mature active enzyme of  $M_r$  34 000. Processing and extracellular release of the mature enzyme coincide with the programmed cell death (PCD)-regulated disintegration of aleurone cells. We discuss the significance of delayed aleurone cell-wall degradation by endoxylanases in relation to the secretory capacity of the aleurone, and propose a novel role for aleurone PCD in facilitating the export of hydrolases.

Keywords: programmed cell death, xylanase, barley, aleurone, germination, secretion.

#### Introduction

In germinating cereal grains, the aleurone tissue secretes hydrolytic enzymes into the endosperm storage tissue that bring about the degradation of stored starch, protein and residual nucleic acids, providing a supply of nutrients for the growing embryo. Depolymerization of endosperm cell walls is essential for the mobilization of endosperm reserves, as it facilitates diffusion of hydrolases into the endosperm tissue, as well as itself providing a source of nutrients. The chemical composition of the aleurone and endosperm cell walls has been defined in detail, where arabinoxylans and (1,3-1,4)-β-glucans together account for 95% of wall polysaccharides with approximately 2% each of cellulose and glucomannans (Fincher, 1992). Their molecular organization has been likened to a cellulosereinforced multicomponent gel, which provides the necessary strength required to maintain tissue integrity while allowing free diffusion of water, phytohormones and low molecular-weight metabolites (Fincher and Stone, 1986). However, it is unlikely that the cell-wall matrix would be freely permeable to secreted proteins of more than 20 kDa, based on the calculated pore diameter (4 nm) of cell-wall microcapillaries (Carpita, 1979). It is thus not surprising that (1,3-1,4)- $\beta$ -glucanases capable of degrading the endosperm cell walls are among the first enzymes to be secreted by the aleurone of imbibed grain (Fincher, 1992). As de novo synthesized hydrolases secreted by the scutellum epithelium and aleurone move from the proximal to the distal end of the grain, the endosperm cell walls are progressively degraded, first with the loss of crystalline  $\beta$ -glucan, indicated by a loss of calcofluorbinding, and subsequently by their complete disintegration (Selvig et al., 1986). In this context it is relevant to consider how the aleurone tissue retains its structural integrity, while facilitating the export of hydrolases required for endosperm nutrient mobilization.

The aleurone cell walls differ in both structure and composition from the walls of the starchy endosperm. First, the aleurone walls are significantly thicker, comprising a thin inner wall and a thick outer wall; second, they show strong autofluorescence due to the abundance of ferulic acid esterified with arabinoxylan polymers in the wall (Bacic and Stone, 1981). The arabinoxylan content of the aleurone walls is, furthermore, significantly higher at 71% compared to 20% in the starchy endosperm (Fincher, 1992). Initially, secretion of hydrolases through the thick aleurone cell walls does not depend on extensive wall degradation, as  $\alpha$ -amylases appear to move through plasmodesmata and channels which may be created by limited cell-wall hydrolysis (Gubler et al., 1987). Depolymerization of the aleurone cell wall takes place after that of the  $\beta$ -glucan-rich endosperm cell walls (Schuurink *et al.*, 1997), consistent with the reported delay in the secretion/ release of endoxylanases in comparison to  $\beta$ -glucanase, xylosidase and arabinofuranosidase (Banik et al., 1997; Slade et al., 1989). The outer wall of the aleurone is degraded first, while the inner wall is retained around actively secreting aleurone cells, suggesting that the composition of the two layers may differ (Fincher, 1992; Schuurink et al., 1997). Hence the relatively resistant nature of the inner aleurone cell wall, in particular, and delayed release of hydrolases capable of degrading its component polymers may be critical for sustained enzyme secretion by aleurone tissue during germination. If endoxylanases were required for aleurone cell-wall degradation, the regulation of their synthesis and secretion should reflect this specific role.

Three endo- $\beta$ -1,4-xylanase isoenzymes with an apparent  $M_{\rm r}$  of 41 000 have been purified from germinating barley and shown to be endohydrolases on the basis of product analysis (Slade et al., 1989). A cDNA and genomic clone encoding the endo- $\beta$ -1,4-xylanase of  $M_r$  41 000 have been characterized (Banik et al., 1996, Banik et al., 1997). The authors proposed that the enzyme was expressed with a 32-amino-acid presequence having characteristics of a signal peptide, based on a comparison of the deduced sequence of the encoded protein and the determined N-terminal sequence of the enzyme. However, the secretion of this  $M_r$  41 000 enzyme and its contribution to aleurone cell-wall degradation has not been examined. Two previous reports describe secreted barley xylanases of apparent  $M_r$  29 000 and 34 000, which were detected in the culture medium of gibberellic acid-induced aleurone layers after 28-32 h incubation (Benjavongkulchai and Spencer, 1986; Dashek and Chrispeels, 1977). It was suggested that the secreted xylanase remained bound to the aleurone cell wall during channel formation, and was only released following complete degradation of the outer wall. The enzymatic properties and structural similarity between these different barley xylanases have never been investigated. Furthermore, it is not possible from these studies to conclude if the viability and secretory role of the aleurone tissue during germination is due to its unique cell-wall composition and/or the regulated secretion and release of xylanases involved in cell-wall degradation.

In this study we have set out to identify the major endo- $\beta$ -1,4-xylanase activity expressed in germinating barley grain, and to study in detail the timing of its synthesis and export in relationship to the physiological role of the aleurone tissue. Our investigations reveal that endo- $\beta$ -1,4xylanase is expressed later than the majority of hydrolases in the aleurone tissue during germination, and is synthesized as an inactive  $M_r$  61 500 precursor in the cytoplasm. We demonstrate that both processing of the precursor, which involves removal of both N- and C-terminal peptides, and export of the mature, active  $M_r$  34 000 enzyme from the aleurone cells, is regulated by aleurone programmed cell death (PCD).

#### Results

## Characterization of a barley endo- $\beta$ -1,4-xylanase purified from germinating barley

In order to identify and purify the major endo- $\beta$ -1,4xylanase activity in the germinating barley grain (Hordeum vulgare cv. Triumph), the activity of this enzyme was followed during germination at 15°C over a period of 16 days. The shoots and roots were removed in order to focus specifically on enzyme activity involved in endosperm metabolism. While endoxylanase activity was first detectable after 4 days of germination and started to increase significantly after 6 days, the activity level reached a peak only after 15 days (Figure 1a). The late accumulation of endoxylanase activity is in sharp contrast to  $\alpha$ -amylase, whose synthesis is known to be initiated in the aleurone and scutellum epithelium shortly after imbibition (Figure 1a). Barley grain germinated for 14 days at 15°C was therefore used as the starting material for endoxylanase purification. A single endoxylanase activity was detected and purified to homogeneity by column chromatography (see Experimental procedures), and corresponded to a protein of apparent  $M_r$  of 34 000 on SDS-PAGE (Figure 1c, track 3). The purified protein had properties very similar to those of the  $M_r$  34 000 barley xylanase purified by Benjavongkulchai and Spencer (1986) in terms of its pl of 4.6, optimum activity at pH 6.0, and sensitivity to inhibitors (not shown). The amino-terminal sequence of the  $M_r$  34 000 protein was determined to be LDNAFPFGTCINTSVIQKPAFLDFFTNH. The sequences of several internal peptides, obtained by cleavage of the purified  $M_r$  34 000 protein, were determined, and the C-terminal peptide sequence was found to be FLNLQKEWK. These peptide sequences were aligned with identity to the deduced sequence of the  $M_r$  41 000 barley 1,4-β-D-xylan xylanohydrolase (EC 3.2.1.8) iso-



Figure 1. Expression of endo- $\beta$ -1,4-xylanase and  $\alpha$ -amylase in germinating barley grain.

(a) Endo- $\beta$ -1,4-xylanase ( $\blacksquare$ ) and  $\alpha$ -amylase ( $\bigcirc$ ) activity detected in extracts of grains of cv. Triumph (minus shoots and roots) from 0 to 16 days after germination (DAG) at 15°C.

(b) Western blot analysis of the grain extracts from (a) probed with anti- $M_r$  34 000 (XyI) and anti- $\alpha$ -amylase (Amy).

(c) Extracts from (a) of grains germinated for 8 (tracks 1, 4, 7) and 14 days (tracks 2, 5, 8) analysed by SDS–PAGE/silver staining and Western blot analysis, probed with anti- $M_r$  34 000 (XyI) or anti-N-peptide/ $M_r$  41 000 (N-XyI). Purified  $M_r$  34 000 endo- $\beta$ -1,4-xylanase analysed by silver-stained SDS–PAGE (track 3) and Western blot (track 6 and 9).

(d) Northern blot of RNA extracts of cv. Triumph grains from (a) probed with a partial *XYN*-1 cDNA, pFL0083 (XyI) and  $\alpha$ -amylase cDNA [790 bp *Sac*1 fragment of pM/C; Rogers (1985)] (Amy). Estimated mRNA size is indicated (nt = nucleotides).

enzyme X-1 (Slade *et al.*, 1989) encoded by the cDNA pMX1(1.6A) (Banik *et al.*, 1996).

## Primary structure of barley endo- $\beta$ -1,4-xylanase and its corresponding gene

A genomic clone (Hv:XYN-1) was isolated from a barley cv. Igri genomic library by hybridization to a partial cDNA clone encoding the  $M_r$  34 000 endoxylanase (pFL400). The Hv:XYN-1 gene was identified on a 5529 bp Xbal fragment whose nucleotide sequence (EMBL accession number AF287726) was scanned for ORFs using the GCG program. The first exon, initiated by an ATG codon, was predicted 126 nt 3' downstream of the TATAA box, while two introns were predicted to interrupt the ORF (nucleotides +19/+101, +624/714) (Figure 2a). The predicted ORF sequence and introns in the Hv:XYN-1 gene were confirmed by alignment with a full-length XYN-1 cDNA sequence, obtained from overlapping 5' RACE and the 3' cDNA (pFL400) sequences (see Experimental procedures).

The Hv:XYN-1 gene encodes an unexpectedly large polypeptide of  $M_r$  61 500 with a predicted pl of 5.6. The determined N-terminal and internal peptide sequences of both the  $M_r$  34 000 and the  $M_r$  41 000 endoxylanase purified by Slade et al. (1989) show almost complete identity to the amino-acid sequence encoded by the Hv:XYN-1 gene. The position of the peptide sequences (underlined residues shown in bold) of the  $M_r$  34 000 protein with respect to the  $M_r$  41 000 barley 1,4- $\beta$ -D-xylan xylanohydrolase and the  $M_r$  61 500 deduced translation product is shown in Figure 2(b). The  $M_r$  41 000 enzyme, with the N-terminal sequence VYP...KLG (double underlined residues in Figure 2b), extends beyond the Nterminus of the  $M_r$  34 000 protein. On the basis of these data it is proposed that the Hv:XYN-1 gene encodes an  $M_r$ 61 500 polypeptide which subsequently undergoes a series of processing steps to yield the mature  $M_r$  34 000 enzyme.

## Synthesis and activity of barley endo- $\beta$ -1,4-xylanase in germinating grain

To facilitate a detailed study of the synthesis of the  $M_r$  34 000 endoxylanase, polyclonal antibodies were raised against the purified protein (Figure 1c, track 3) that recognize the enzyme in Western blots (Figure 1c, track 6). Additionally, polyclonal antibodies were raised against a 30-residue synthetic peptide (VYPVDHKARFRQLKD-KTDKARKRDVILKLG) homologous to the amino-terminus of the  $M_r$  41 000 endoxylanase (Figure 2b; Slade *et al.*, 1989), to establish the relationship between the predicted precursor, intermediate and mature forms of barley endoxylanase.



**Figure 2.** Structure of the endo- $\beta$ -1,4-xylanase *Hv:XYN-1* gene and encoded protein.

(a) Hv:XYN-1 gene structure, showing exons (shaded boxes) with nucleotide numbering, and PXYN-1 cDNA (given beneath) with amino-acid numbering.

(b) Deduced amino-acid sequence of XYN-1 endo- $\beta$ -1,4-xylanase, showing processing sites (arrows) at the N-terminus of the  $M_r$ 41 000 (VYP.) and N- and C-terminus of the  $M_r$  34 000 mature protein (residues in bold). Peptide sequences determined by authors (underlined) or by Slade *et al.* (1989) (double underlined) are indicated.

The activity profiles of endoxylanase and  $\alpha$ -amylase in extracts of barley grain germinated at 15°C (Figure 1a) were compared with the relative levels of endoxylanase and  $\alpha$ -amylase found by immunodetection, using antibodies raised against  $\alpha$ -amylase (Juge *et al.*, 1993) and the  $M_r$  34 000 endoxylanase (Figure 1b). The synthesis and accumulation of immunodetectable  $\alpha$ -amylase mirrored the early detection and rise in  $\alpha$ -amylase activity following the onset of germination.

In the first 4–7 days of germination, the polypeptides recognized by the  $M_r$  34 000 antiserum had apparent  $M_r$  of approximately 60 000 and 50 000 (the presence of an approximately  $M_r$  38 000 doublet in this 3-day sample was not reproducible and is considered an artefact). In 8-day-germinated grain, additional immunoreactive polypeptides of  $M_r$  approximately 40 000 appeared, and a polypeptide of  $M_r$  34 000 was only detected after 10 days. The larger size and sequential appearance of the polypeptides in germinating grain, which share epitopes with the  $M_r$  34 000 enzyme, suggest that they are the precursor and intermediate forms of the  $M_r$  34 000 endoxylanase.

The level of detectable endoxylanase activity in grain remained low over the first 6 days, then steadily increased from 7 to 15 days germination. This suggests that barley endoxylanase may be synthesized as an inactive precursor which is activated during processing. From our sequence alignments it is likely that the  $M_r$  41 000 endoxylanase is a processing intermediate of the mature  $M_r$  34 000 endoxylanase. Since the  $M_r$  41 000 endoxylanase was purified as an active enzyme from germinating grain (Slade *et al.*, 1989), we deduce that partial processing is sufficient to activate this enzyme. The rise in endoxylanase activity in germinated grain at 8 days coincides with the appearance of an immunodetectable approximately  $M_r$  40 000 polypeptide.

Western blots of the grain extracts germinated for 8 and 14 days were then probed with either the  $M_r$  41 000

endoxylanase N-terminal peptide antiserum or the  $M_r$ 34 000 antiserum. A major immunodetected polypeptide of approximately  $M_r$  60 000 and minor amounts of polypeptides of  $M_r$  40 000-60 000 in the 8-day extract were recognized by both antisera (Figure 1c, tracks 4 and 7). In the 14-day extract, a single polypeptide was detected with the  $M_r$  34 000 antiserum (Figure 1c, track 5), that comigrated with the purified and immunodetectable  $M_r$ 34 000 endoxylanase (track 6). The antiserum to the  $M_r$ 41 000 N-terminal peptide detected only trace amounts of a putative  $M_r$  52 000 intermediate in the 14 day extract, but not the mature  $M_r$  34 000 enzyme (Figure 1c, track 8). These data support the hypothesis that the major endoxylanase in barley grain is synthesized during germination as a precursor of  $M_r$  61 500, and undergoes a series of processing steps to yield a mature enzyme of  $M_r$  34 000. Furthermore, recognition of the larger precursor forms ( $M_r$ 40 000-60 000) by the antisera to both the  $M_r$  41 000 N-terminal peptide and the  $M_r$  34 000 confirms that the  $M_r$ 41 000 endoxylanase, purified by Slade et al. (1989), is a processing intermediate.

In order to provide additional evidence for the timing and regulation of endoxylanase synthesis during germination, Northern blot analysis was performed on total RNA extracted from the germinating grain samples. The blot was probed with a partial 3' cDNA clone (pFL0083) encoding the C-terminal portion of the  $M_r$  34 000 endoxylanase, identified in a barley aleurone cDNA library (see Experimental procedures), and with an  $\alpha$ -amylase cDNA (Rogers, 1985) (Figure 1d). Transcripts of 1900 nucleotides that hybridized to the pFL0083 cDNA were detected after 4 days germination, coinciding with the appearance of  $M_r$  55 000-60 000 polypeptides immunodetected by the  $M_r$  34 000 antiserum (Figure 1b). Thus, compared with the AMY gene family, the Hv:XYN-1 gene is transcriptionally upregulated relatively late in the germination programme.



Figure 3. Expression of endo- $\beta$ -1,4-xylanase and  $\alpha\text{-amylase}$  in isolated aleurone layers.

Enzymatic activities (I) of endo- $\beta$ -1,4-xylanase (Xyl) and  $\alpha$ -amylase (Amy) and immunodetection (II) of endo- $\beta$ -1,4-xylanase detected in extracts of GA<sub>3</sub>-induced barley cv. Triumph aleurone layers (L) and incubation media (M) over a 5-day period.

## Synthesis and activity of barley endo- $\beta$ -1,4-xylanase in GA-induced aleurone layers

Isolated aleurone tissue is a valuable system to follow the temporal regulation of hydrolase synthesis as well as the fate of *de novo* synthesized proteins. Aleurone tissue isolated from Hordeum vulgare cv. Triumph was incubated at 25°C in the presence of gibberellic acid (GA<sub>3</sub>). α-Amylase activity was secreted into the medium, reaching a maximum after 2 days, while endoxylanase activity was initially detected in extracts of aleurone tissue after 2 days incubation and rose to a maximum by 3 days (Figure 3, I). The appearance of endoxylanase activity in the medium was delayed by 2 days, suggesting that de novo synthesized endoxylanase is not immediately released. The proteins in the aleurone tissue and incubation medium were separated by SDS-PAGE, blotted and probed with  $M_r$  34 000 antiserum (Figure 3, II). Immunodetectable polypeptides of  $M_r$  60 000 were present in the aleurone after 1 days incubation, although endoxylanase activity was barely detectable. After 2 and 3 days incubation, immunodetectable polypeptides of  $M_r$  40 000 and below were prominent within the tissue, concomitant with a sharp rise in endoxylanase activity. Release of endoxylanase activity into the medium was associated with the immunodetection of an  $M_r$  34 000 polypeptide in the tissue and medium.

These data are consistent with the hypothesis that barley endoxylanase is expressed as an inactive  $M_r$  61 500 precursor within the aleurone, which is activated during processing to the  $M_r$  41 000 intermediate and is subsequently processed to the mature  $M_r$  34 000 endoxylanase and simultaneously released. The synthesis of the barley endoxylanase as a precursor then raises the question of the function of the 213 N-terminal and 55 C-terminal amino-acid residues that are removed by post-translational processing.

#### Cellular localization of the Hv:XYN-1 gene product

As barley endoxylanase is synthesized in aleurone tissue, aleurone protoplasts provide a homologous model system for examining its synthesis and localization. Isolated protoplasts were co-transfected with plasmids pAMY6-4/ XYN [1-556], comprising the Hv:XYN-1 coding region (nt +1/+1845) translationally fused to the aleuronespecific AMY6-4 α-amylase promoter, and pAMY/IH(A12-M) AY13] GC-NOS encoding the cytoplasmic form of a heterologous thermostable (1,3–1,4)-β-glucanase (Jensen et al., 1996). After 1 day of incubation, GA<sub>3</sub>-induced transfected protoplasts over-expressed the  $M_r$  61 500 endoxylanase precursor (Figure 4a, L), which co-migrated with endogenously expressed endoxylanase precursor detected in mock-transfected protoplasts (Figure 4a, track 5b). The immunodetection of lower  $M_r$  endoxylanase forms that accumulated in the protoplasts during the 5-day incubation indicates partial processing of the precursor. Transient expression of pAMY6-4/XYN [1-556] led to a progressive rise in endoxylanase activity within the protoplasts, which paralleled the appearance of processed intermediates. Endoxylanase activity first appeared in the medium at 3 days (Figure 4b), concomitant with the immunodetection of  $M_r$  40 000 processing intermediates and the  $M_r$  34 000 endoxylanase (Figure 4a, M).

The localization of co-expressed thermostable cytoplasmic (1,3-1,4)- $\beta$ -glucanase was used to monitor the viability of the protoplasts during transient expression incubation. During the first 4 days,  $\beta$ -glucanase activity accumulated in the protoplasts (Figure 4c).  $\beta$ -Glucanase activity was detected in the medium from 3 days, and comprised 14% of the total  $\beta$ -glucanase activity by 4 days, indicating the onset of protoplast death and the release of intracellular proteins. As endoxylanase was released from protoplasts simultaneously with cytoplasmic β-glucanase, we conclude that its extracellular release was due to protoplast death rather than secretion. The percentage of endoxylanase activity found in the medium at 4 days (24% of total activity) was higher than that of  $\beta$ -glucanase. The predominance of the enzymatically active  $M_r$  40 000 and 34 000 endoxylanases in the medium, in comparison to the protoplasts, indicates that processing and activation of the precursor coincides with extracellular release, leading to an increase in specific activity.

Parallel transfections were performed with plasmid pAMY/[ $\alpha$ H(A12-M) $\Delta$ Y13]GC-NOS encoding the thermostable (1,3–1,4)- $\beta$ -glucanase fused to the  $\alpha$ -amylase signal peptide. After 2 days incubation, the distribution of  $\beta$ -glucanase activity between the protoplasts and medium was 44 and 126 mU per 10<sup>6</sup> protoplasts, respect-



Figure 4. Transient expression of the barley endo-β-1,4-xylanase and heterologous thermostable β-glucanase in barley aleurone protoplasts. Protoplasts were co-transfected with pAMY6-4/XYN [1–556] and pAMY/ [H(A12-M)ΔY13]GC-NOS in a DNA ratio of 5 : 1.

(a) Western blot analysis of endo- $\beta$ -1,4-xylanase in cell (L) and media (M) fractions of transfected protoplasts during 5 days incubation (5b: 5 days mock-transfected protoplasts), probed with anti-M, 34 000.

(b) Endo- $\beta$ -1,4-xylanase activity in cell (L) and media (M) fractions of transfected (solid lines) and mock-transfected (dashed lines) protoplasts from (a).

(c) Co-expressed (1,3–1,4)- $\beta$ -glucanase activity in cell (L) and media (M) fractions of transfected (solid lines) and mock-transfected (dashed lines) protoplasts from (a).

ively. The secretion of 74% of the transiently expressed  $\beta$ -glucanase activity confirmed the secretory capacity of the protoplast preparation. In summary, these data support the conclusion that the *Hv:XYN-1* gene expresses an  $M_r$  61 500 endoxylanase precursor, which is not targeted for extracellular secretion.

To reveal the intracellular localization of the *Hv:XYN-1* gene products, advantage was taken of green fluorescent protein (GFP) fusions expressed in aleurone protoplasts. As the location of an intracellular targeting signal within a polypeptide may be functionally important (Matsuoka and



Figure 5. Transient expression of GFP fusion proteins in barley aleurone protoplasts.

Confocal images of aleurone protoplasts, incubated for 24 h with GA<sub>3</sub>, following transfection with the chimeric GFP gene constructs (a) pXYN/ [XYN1-556/L/GFP]; (b) pAMY6-4/[AMY/L/GFP]; (c) pXYN/[XYN1-213/GFP/ XYN502-556]; (d) pAMY6-4/[AMY1-29/GFP/AMY419-423]. V, storage protein vacuoles; scale bar = 10  $\mu$ m.

Neuhaus, 1999), two types of fusion were tested. The GFPcoding sequence was either fused 3' to the Hv:XYN-1 coding sequence via a spacer sequence from an Erwinia carotovora CelN cellulase gene (Olsen et al., 1996), such that the two functional domains were separated by a 19residue Thr/Pro-rich linker; or alternatively the GFP coding sequence was substituted for the mature  $M_r$  34 000 coding sequence within the Hv:XYN-1 gene. Aleurone protoplasts transfected with the GFP fusions were cultured with GA<sub>3</sub>, harvested after 24 h and GFP expression was analysed by confocal microscopy. The recorded images (Figure 5a,c) reveal that both endoxylanase-GFP fusion proteins were located in the cytoplasm.  $\alpha$ -Amylase-GFP fusions were similarly expressed as an α-amylase-linker-GFP fusion or as a GFP substitution, flanked by the signal peptide and five C-terminal residues of  $\alpha$ -amylase. The confocal images (Figure 5b,d) show that both  $\alpha$ -amylase-GFP fusions were located in subcellular compartments, characteristic of ER. As the  $M_r$  61 500 endoxylanase precursor polypeptide is shown to be a cytoplasmic protein, alternative functions must be sought for the N- and C-terminal propeptides.

# Functional analysis of the barley $M_{\rm r}$ 61 500 endo- $\beta$ -1,4-xylanase propeptides

To investigate the functional importance of the propeptide domains, a series of *Hv:XYN-1* gene mutants (fused to the

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Figure 6. Transient expression of full-length and truncated barley endo- $\beta$ -1,4-xylanase in barley aleurone protoplasts.

(a) Western blot analysis of endo- $\beta$ -1,4-xylanase in cell (L) and media (M) fractions of protoplasts, mock-transfected (b) or transfected with pAMY6-4/XYN plasmids encoding full-length XYN (1–556, 61.5 kDa), and truncated 1–551 (60.9 kDa), 1–546 (60.4 kDa), 1–536 (59.4 kDa), 1–501 (55.4 kDa), 130–556 (48.0 kDa), 209–501(33.4 kDa) endo- $\beta$ -1,4-xylanase, and incubated for 2 days in the presence of GA<sub>3</sub>. Analysis of the cell fraction includes the cell pellet (P) and supernatant (S) of protoplasts after sonication and centrifugation at 1000 g for 5 min. Western probe: anti- $M_r$  34 000.

(b) Endo- $\beta$ -1,4-xylanase activity in cell (**I**) and media (**I**) fractions of the transfected protoplasts from (a) relative to mock-transfected protoplasts, whose activity is set to 1.

AMY6-4 promoter) encoding endoxylanase, truncated at either the N- and/or C-terminus, were expressed in GA<sub>3</sub>induced aleurone protoplasts. The transfected protoplasts were incubated for 2 days, sufficient for the partial processing and activation of barley endoxylanase when Over-expressed in protoplasts (Figure 4b). Expression of the full-length  $M_r$  61 500 endoxylanase, as well as each of the truncated polypeptides, was immunodetected and their migration on SDS–PAGE corresponded to their predicted  $M_r$  61 500 endoxylanase strongly enhanced

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endoxylanase activity compared to the mock-transfected control (Figures 4b, 6b). However, the step-wise truncation of the 55 amino-acid residue C-terminal propeptide strongly reduced endoxylanase activity (compare XYN with 1–551, 1–546, 1–536, 1–501 in Figure 6b). Similarly, a truncated endoxylanase lacking the first 129 amino acids of the N-terminal 213 residue propeptide (130–556) was inactive when expressed in protoplasts (Figure 6b). When the mature  $M_r$  34 000 enzyme was expressed, where both N- and C-terminal propeptides were deleted (209–501), the immunodetectable protein was also inactive (Figure 6b). The loss of endoxylanase activity could not be attributed to a failure to express the truncated hydrolase (Figure 6a, L), or to its secretion into the medium (Figure 6a, M).

As endoxylanase activity was only found in protoplasts over-expressing the full-length  $M_r$  61 500 endoxylanase, deletion of the propeptide domains may have impaired protein folding. To test this hypothesis, we examined the solubility of the full-length endoxylanase and the truncated forms expressed in barley protoplasts, on the grounds that insolubility is an indicator of misfolded proteins. The protoplasts expressing the different endoxylanase polypeptides were sonicated and centrifuged to yield a cell pellet and supernatant. The full-length endoxylanase expressed by the endogenous protoplast XYN-1 gene was immunodetected in all the supernatant fractions, consistent with its being a soluble enzyme (Figure 6a, S versus P). While the majority of over-expressed full-length endoxylanase was also found in the supernatant, a significant proportion of the truncated endoxylanases were immunodetected in the pellet fraction, indicating that the propeptide domains may be required for protein folding (Figure 6a, P versus S).

## Processing, activation and release of barley endo- $\beta$ -1,4-xylanase

The events that bring about the processing of the  $M_r$  61 500 precursor and release of the mature  $M_r$  34 000 endoxylanase in aleurone tissue (Figures 1b, 3) may depend on GA-induced PCD seen in this tissue during germination (Wang *et al.*, 1998). The morphological and biochemical events resulting in aleurone PCD have been convincingly demonstrated in isolated aleurone protoplasts in response to GA (Bethke *et al.*, 1999; Fath *et al.*, 1999). The association of these events with the processing and release of endogenously expressed endoxylanase was thus examined.

Aleurone protoplasts incubated for 2 days in the presence of GA<sub>3</sub>, at a plating density of  $2.5 \times 10^4$  protoplasts per well, contained numerous small protein storage vacuoles (PSVs; Figure 7a, 1) characteristic of protoplasts at an early developmental stage in the progression to PCD (Bethke *et al.*, 1998). Extracellular acidification, used as a



Figure 7. Release, processing and activity of endo- $\beta$ -1,4-xylanase synthesized by GA<sub>3</sub>-induced barley aleurone protoplasts.

(a) Light microscope image of protoplasts after 2 days culture at a plating density of  $2.5 \cdot 10^4$  protoplasts per well (1) or  $1.25 \cdot 10^4$  protoplasts per well ( $\frac{1}{2}$ ) (bar = 20  $\mu$ m).

(b) Western blot analysis of endo- $\beta$ -1,4-xylanase in cell (L) and media (M) fractions of protoplasts cultured at 1 or 0.5 plating density over 3 days, using anti- $M_r$  34 000 X-1 (Xyl). Cell fractions were also probed with anti-RPL60 (RPL).

(c) Endo- $\beta$ -1,4-xylanase activity detected in cell (L) and media (M) fractions of protoplasts from (b).

(d) pH of protoplasts incubation medium from (b).

monitor of GA-induced aleurone development, was also limited in protoplasts incubated for 3 days at this plating density (Figure 7d, 1). The precursor endoxylanase accumulated in these protoplasts over the 3 days, but processing to the  $M_r$  34 000 enzyme was not detected and endoxylanase activity remained low (Figure 7b,c, 1). This expression pattern mirrors that seen in Figure 4, where GA-induced protoplasts accumulated the over-expressed endoxylanase over 3 days, but precursor processing remained minimal and the activity of the endogenously expressed gene (in mock-transformants) was barely detectable.

GA<sub>3</sub>-induced aleurone protoplasts incubated at half plating density ( $1.25 \times 10^4$  protoplasts per well) were highly vacuolated after 2 days (Figure 7a) characteristic of protoplasts just prior to PCD (Bethke et al., 1999). Furthermore, acidification of the medium was significantly greater in these protoplasts (Figure 7d), indicating a more rapid progression of the developmental events leading to PCD. Endogenously expressed endoxylanase was also immunodetected in these protoplasts (Figure 7b). However, after 2-3 days incubation, when the protoplasts were highly vacuolated, the endoxylanase precursor was both processed to the mature  $M_r$  34 000 enzyme and released into the medium, suggesting that maturation of this enzyme coincides with the final stage of aleurone protoplast PCD. Endoxylanase activity rose sharply in parallel with maturation and release of the hydrolase (Figure 7b,c), further indicating that this enzyme is synthesized as an inactive precursor that is activated during processing.

Cell death, the final event in aleurone protoplast PCD, follows the loss of protoplast membrane integrity (Bethke *et al.*, 1999). The occurrence and timing of cell death in our two protoplast incubations was monitored by measuring retention of the resident protein, calreticulin (RPL), in the protoplasts. Calreticulin was lost from protoplasts within 24 h of their reaching the highly vacuolate stage after 2 days' incubation at half plating density (Figure 7b). Protoplasts delayed in the developmental progression of PCD by higher plating density (1), showed no evidence of calreticulin loss. Cell death is thus implicated as the mechanism for endoxylanase release from aleurone protoplasts, as this process coincided with the loss of protoplast membrane integrity.

## Endo- $\beta$ -1,4-xylanase maturation is mediated by cysteine endoproteases

A series of proteolytic cleavages brings about the progressive maturation of the endoxylanase synthesized in the aleurone of germinating grain (Figure 1b). We investigated the conditions required for processing of the  $M_r$  61 500 precursor present in extracts of aleurone tissue of 3-day imbibed, embryo-less cv. Himalaya grain (Figure 8). When the aleurone extract was incubated at pH 5.4, the precursor was partially processed to an approximately  $M_r$  50 000 intermediate, while at pH 4.2 a circa  $M_r$  40 000 protein was

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Figure 8. In vitro processing of the  $M_{\rm r}$  61 500 endo- $\beta$ -1,4-xylanase precursor.

Western blot analysis of endo- $\beta$ -1,4-xylanase in: (a) extracts of cv. Himalaya aleurone (L) incubated for 0 or 16 h at 25°C in APM buffer adjusted to pH 5.4 (5) or 4.2 (4), and with 4 mM DTT (4D, 5D), Western blot probe, anti- $M_r$  34 000; (b) extracts of cv. Himalaya aleurone incubated as in (a) in the presence of protease inhibitors: E-64 (I), leupeptin (II), PMSF (III), EDTA (IV) or pepstatin (V).

the major processing intermediate detected in Western blots (Figure 8a). The processing steps yielding the mature  $M_r$  34 000 enzyme were strongly enhanced by the presence of a reducing agent (DTT). This implies that protease(s) capable of processing the  $M_r$  61 500 precursor were present in the tissue, but in an inactive form and/or in a separate cell compartment.

Although several different types of endoproteases may contribute to the observed processing of endoxylanase, yielding various processed forms, maturation to the  $M_r$ 34 000 enzyme was found to be sensitive to inhibitors of cysteine proteases (E-64) and serine/cysteine proteases (leupeptin), and less sensitive to inhibitors of serine proteases (PMSF), metallo-proteases (EDTA) and aspartate proteases (pepstatin) (Figure 8b). Thus the major protease activity in germinating aleurone which is required for processing and activation of endoxylanase has the properties of cysteine endoproteases, because the observed protease activity was dependent on acidic pH, enhanced by reducing conditions, and sensitive to cysteine protease inhibitors.

#### Discussion

# The major barley endo- $\beta$ -1,4-xylanase in germinating barley grain has an apparent M<sub>r</sub> of 61 500 and is processed to a mature enzyme of M<sub>r</sub> 34 000

Endo- $\beta$ -1,4-xylanase activity was barely detectable in barley grains during the early stages of germination at 15°C, but its activity began to rise at 7 days and peaked at 15 days. This enzyme activity was purified to homogeneity and had an  $M_r$  of 34 000 and enzymatic properties similar those of an  $M_r$  34 000 xylanase secreted by GA-induced isolated aleurone layers (Benjavongkulchai and Spencer, 1986).

Several lines of evidence suggest that this  $M_r$  34 000 endoxylanase is derived from the  $M_r$  41 000 endoxylanase purified by Slade et al. (1989), which in turn is derived from a larger precursor. All the determined peptide sequences of the purified  $M_r$  34 000 enzyme can be identified within the deduced amino-acid sequence of the  $M_r$  41 000 endoxylanase (Banik et al., 1996). Sequence analysis of a full-length barley endoxylanase cDNA clone (1951 bp), XYN-1 and the corresponding genomic clone Hv:XYN-1 isolated in this study, revealed the primary structure of the precursor of the  $M_r$  34 000. The gene encodes an  $M_r$  61 500 polypeptide, whose amino-acid sequence includes those of the  $M_r$  41 000, deduced from a homologous 1630 bp cDNA pMX1[1.6 A] (Banik et al., 1996) and the Mr 34 000 endoxylanases. As pMX1[1.6 A] cDNA is a partial cDNA, the full-length ORF and 5' intron were not recognized in the previously described endoxylanase genomic clone (Banik et al., 1996, Banik et al., 1997).

Northern analysis of germinating grain showed that Hn:XYN-1 is transcribed at 4 days germination and onwards. Antibodies were raised against both the purified  $M_{\rm r}$  34 000 endoxylanase, and a peptide corresponding to the N-terminus of the  $M_r$  41 000 endoxylanase. The polypeptides immunodetected by anti- $M_r$  34 000 in 4 days germinated grain were between  $M_r$  50 000 and 60 000, consistent in size with the XYN-1 encoded polypeptide. Additional polypeptides of circa  $M_r$  40 000 were immunodetected after 8 days germination, while the  $M_r$  34 000 enzyme was not detected until 10 days germination. The sequential appearance of these immunologically related polypeptides during grain germination supports the hypothesis that barley endoxylanase is expressed as a precursor which undergoes post-translational processing. The antibody to the  $M_r$  41 000 N-terminal peptide recognized similar polypeptides of  $M_r$  40 000–60 000 in germinated grain, but did not detect the mature  $M_r$  34 000 enzyme which lacks this peptide epitope. As the  $M_r$  41 000 endoxylanase was purified from grain germinated for a shorter period, 5 days at 26°C (Slade et al., 1989), we predict that it is a stable precursor of the  $M_r$  34 000 enzyme. In isolated aleurone layers induced with GA<sub>3</sub>, the first immunodetectable polypeptides had an  $M_r$  of circa 60 000, while a series of lower  $M_r$  forms appeared on further incubation. The  $M_r$  34 000 enzyme was first detected in the layers after 3 days incubation, followed by its release into the medium, from where it has previously been purified (Benjavongkulchai and Spencer, 1986).

These data provide the first evidence that the major endo- $\beta$ -1,4-xylanase in germinating barley grain is synthesized as an  $M_r$  61 500 precursor polypeptide and that the mature enzyme of  $M_r$  34 000 is the result of a series of

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processing events. Based on the amino-acid sequences of the N- and C-terminus of the  $M_r$  34 000 polypeptide, the mature protein sequence is flanked by N- and C-terminal propeptides of 213 and 55 residues, respectively. Although the *XYN-1* gene was expressed at 4 days germination, when endoxylanase precursors were first immunodetectable, endoxylanase activity was minimal. The appearance of endoxylanase intermediates of circa  $M_r$  40 000 at 8 days germination coincided with a rise in activity, suggesting that processing is required for activation of the enzyme.

#### The $M_r$ 61 500 endo- $\beta$ -1,4-xylanase is a cytoplasmic proenzyme whose N- and C-terminal propeptide regions facilitate correct folding and activation of the precursor

Transient expression of the Hv:XYN-1 encoded endoxylanase in GA<sub>3</sub>-induced aleurone protoplasts revealed that the  $M_r$  61 500 precursor accumulates within the cell. This is in marked contrast to the majority of other hydrolases secreted by aleurone cells during germination (Fincher, 1992). Partial processing of the  $M_r$  61 500 precursor was also observed in protoplasts, but the mature endoxylanase appeared in the protoplast medium only after prolonged incubation. The intracellular localization of the  $M_r$  61 500 precursor, expressed as a GFP fusion protein in transfected protoplasts, was compared with that of  $\alpha\text{-amylase-GFP}$ fusion proteins using confocal microscopy. While  $\alpha$ amylase-GFP fluorescence was typical of ER localization, endoxylanase-GFP was limited to the cytoplasm. The first 50 amino-acid residues of the  $M_r$  61 500 precursor were submitted for signal peptide analysis at http://www. cbs.dtu.dk/services/SignalP. The absence of a signal peptide, characteristic of secreted proteins, supports our conclusion that the  $M_r$  61 500 endoxylanase does not enter the secretory pathway.

The rise in endoxylanase activity in germinating grain, isolated aleurone layers or protoplasts was concomitant with the processing of the  $M_r$  61 500 endoxylanase rather than its synthesis. This suggests that  $M_r$  61 500 endoxylanase initially accumulates in the aleurone as an inactive zymogen. Partial processing is sufficient to activate the endoxylanase, as the  $M_r$  41 000 processing intermediate was isolated as an active enzyme (Slade et al., 1989). The function of the propeptide domains of the  $M_r$  61 500 precursor was investigated by expressing N- or C-terminal truncated forms in aleurone protoplasts. After 2 days incubation, synthesis and activation of the wild-type enzyme was clearly detectable. Although the truncated polypeptides were also expressed and partially processed, they were largely inactive. A C-terminal truncation of just five amino acids was sufficient to halve endoxylanase activity. In contrast to the full-length endoxylanase, a significant proportion of the truncated forms expressed in protoplasts could be pelleted by low-speed centrifugation, indicative of insoluble misfolded proteins. These data suggest that the propeptide domains of the  $M_r$  61 500 precursor may both facilitate protein folding and maintain the pro-enzyme in an inactive state. The vacuolar carboxypeptidase Y from *Saccharomyces cerevisiae* is one of the best-studied examples of a zymogen, where the pro-region facilitates *in vivo* folding of the native state and prevents enzymatic activity (Winther and Sørensen, 1991). The 91-amino-acid residue pro-region of CPY appears to lower the energy barriers for folding and unfolding in a similar manner to a molecular chaperone. Site-directed mutagenesis of putative processing sites may provide further insight into the function of the endoxylanase propeptide domains.

## Maturation and release of barley endo- $\beta$ -1,4-xylanase coincides with aleurone PCD

As our studies showed that barley  $M_r$  61 500 endoxylanase does not enter the secretory pathway, alternative mechanisms leading to its release from the aleurone at a late stage of germination were considered. Recent studies have revealed that aleurone cells enter a developmental pathway in response to GA, culminating in PCD characterized by the metamorphosis of the PSVs and DNA degradation (Bethke et al., 1999; Fath et al., 1999; Wang et al., 1996, Wang et al., 1998). Acidification of the PSVs, leading to the activation of resident cysteine endoproteases and nucleases, a-amylase secretion and the onset of PSV fusion, are early events of this developmental pathway (Bethke et al., 1998). Cell death, observed in highly vacuolated aleurone protoplasts, results from the abrupt loss of plasma membrane integrity and protoplast collapse (Bethke et al., 1999).

We have followed the GA-induced events of extracellular acidification by aleurone protoplasts (Heimovaara-Dijkstra *et al.*, 1994), their vacuolization and ultimate death in relation to the fate of endogenously expressed barley endoxylanase. To monitor the final step of protoplast death, namely protoplast disintegration, we followed the loss of the ER-localized, soluble protein calreticulin. While the accumulation of the  $M_r$  61 500 precursor was detected inside GA<sub>3</sub>-induced protoplasts, the processing and release of the  $M_r$  34 000 mature enzyme were observed only in highly vacuolated protoplasts in association with disintegration of their membranes.

The close timing of the maturation and release events suggests that loss of cell membrane integrity accompanying PCD releases aleurone vacuolar proteases capable of processing the  $M_r$  61 500 precursor. The  $M_r$  61 500 precursor, present in GA<sub>3</sub>-induced aleurone layers, was processed following homogenization and incubation of the tissue, which supports this conclusion. This *in vitro* maturation of the  $M_r$  61 500 precursor, which was

enhanced at pH 4.2 and by 4 mM DTT, was particularly sensitive to inhibitors of cysteine proteases. The cysteine endoproteases detected in isolated vacuoles from barley aleurone (Bethke *et al.*, 1996) are thus good candidates to process barley endoxylanase.

## The role of barley endo- $\beta$ -1,4-xylanase in germinating barley grain

We have demonstrated that the major barley endoxylanase synthesized in germinating barley grain is released from the aleurone at a stage of germination when  $\alpha$ amylase secretion is declining. This suggests that endoxylanase is not involved in the degradation of regions of the outer aleurone cell wall which are proposed to facilitate hydrolase secretion by this tissue (Gubler *et al.*, 1987). Furthermore, a delay in endoxylanase release from the aleurone until after the cessation of hydrolase secretion may be required to maintain the structural integrity of the inner aleurone cell wall, which remains intact until the cessation of secretion (Fincher, 1992). Differences in composition and molecular organization, which underlie the differential degradation of the inner and outer layers of the aleurone cell wall, have yet to be determined.

The hydrolysis of cell-wall polymers following the release of endoxylanase may provide the growing embryo with additional carbohydrate nutrients late in the germination process, which may be advantageous under poor germination conditions. This suggests a novel role for barley aleurone PCD in regulating the release of intracellular hydrolases involved in reserve carbohydrate mobilization. Barley limit dextrinase, which is also expressed in germinating aleurone, has recently been shown to have a presequence typical of a plastid transit peptide (Burton *et al.*, 1999). If limit dextrinase is indeed intracellularly targeted, only its release following aleurone PCD would allow this starch-debranching enzyme to contribute to the hydrolysis of limit dextrins *in vivo*.

#### **Experimental procedures**

## Assay of endo- $\beta$ -1,4-xylanase and $\alpha$ -amylase in germinating barley and GA-induced aleurone layers

For whole-grain analyses, *Hordeum vulgare* L. cv. Triumph grains were sterilized with AgNO<sub>3</sub> and germinated at 15°C, as described by Slade *et al.* (1989), in the dark. Samples (five grains minus roots and shoots) were homogenized in 2 ml ice-cold buffer A (50 mM Na-malate, 50 mM NaCl, 2 mM CaCl<sub>2</sub>, 3 mM NaN<sub>3</sub> pH 5.2) using an ultra-Turrax and cell debris were removed by centrifugation (14 000 g for 10 min).

For GA-induced aleurone layer analyses, *H. vulgare* cv. Triumph grains were de-embryonated, halved, sterilized (1 min in 70% EtOH, 30 min in 50% H<sub>2</sub>SO<sub>4</sub>; each followed by four washes in H<sub>2</sub>O) and imbibed in H<sub>2</sub>O containing 50  $\mu$ g ml<sup>-1</sup> ampicillin, 5  $\mu$ g ml<sup>-1</sup> nystatin at 25°C for 3.5 days. The starchy endosperm was then

removed and aleurone layers from five grains were cultured in 2 ml buffer B (20 mM Na-succinate, 20 mM CaCl<sub>2</sub>, 50  $\mu$ g ml<sup>-1</sup> ampicillin, 5  $\mu$ g ml<sup>-1</sup> nystatin, 10  $\mu$ M GA<sub>3</sub> pH 4.2) at 25°C. Samples of culture medium and aleurone layers were harvested and analysed separately. Aleurone layers were washed and homogenized in buffer B and the extracts clarified by centrifugation (14 000 g for 10 min).

Aliquots (50 µl) of the grain or aleurone extracts were mixed with 50 µl buffer A containing 0.2% BSA and incubated with 3 mg birchwood AZCL-xylan (Megazyme, Bray, Co. Wicklow, Ireland) at 40°C for 2–16 h. Reactions were stopped with 0.9 ml 1% alkaline Tris, clarified (200 g for 15 min) and measured spectrophotometrically [ $\Delta A_{595}$  (1 cm cuvette) = 2.04 ×  $\Delta A_{620}$  (200 µl per titertek well)]. Endoxylanase activity is expressed as  $\Delta A_{595} \min^{-1}$  per grain or per aleurone layer in a 1 ml (stopped) reaction.

Grain and aleurone layer extracts were diluted in buffer A containing 0.02% BSA and assayed for  $\alpha$ -amylase activity using the ceralpha: $\alpha$ -amylase assay kit (Megazyme) as described by Soor and Hinke (1990), where 1 mU is defined as the  $\alpha$ -amylase activity required to release 1 µmole *p*-nitrophenol min<sup>-1</sup> from *p*-nitrophenyl maltoheptaoside in the presence of excess  $\alpha$ -glucosidase and glucoamylase, as described by the supplier.

#### Purification of barley endo- $\beta$ -1,4-xylanase

Grain of cv. Triumph (approximately 500 g), germinated for 14 days (as above), were homogenized in 2 vol ice-cold buffer C (50 mM NaAc, 5 mM NaN<sub>3</sub>, 10 mM EDTA, 3 mM  $\beta$ -mercaptoethanol, 3 mM PMSF pH 5.0) for 3 min in a Waring blender. After 30 min incubation at 0°C, the extract was clarified by centrifugation and precipitated with ammonium sulfate, taking the 20-40% cut. The precipitate was resuspended in buffer C, desalted (Sephadex G25 coarse, Amersham Pharmacia Biotech, Little Chalfont, Bucks, UK), concentrated by ultrafiltration (YM-10, Amicon, Millipore [UK], Walford, Herts, UK), and endoxylanase was then purified by two successive FPLC (Amersham Pharmacia Biotech) separations: MonoQ column (Pharmacia HR5/5), eluted with a 0-0.35 M NaCl gradient, pooling the 80-120 mM NaCl fractions containing the single activity peak, and a Merck Fractogel HW 50-superfine gel-filtration column (Pharmacia HR10/30) equilibrated and eluted in 20 mM Bis-Tris/HCl, 0.1 M NaCl pH 6.2. Fractions containing the single activity peak were pooled and concentrated on a MonoQ column (as above).

During purification, endoxylanase activity was assayed as described above. The amino-acid sequence of the N-terminus and tryptic- and cyanogen bromide-cleavage peptides of the purified enzyme were determined by Edman degradation (by Eurosequence B.V., Groningen, The Netherlands) and by Dr lb Svendsen (Department of Chemistry, Carlsberg Laboratory, Denmark).

## Preparation of barley endoxylanase antibodies and immunodetection

A synthetic peptide, having the sequence of the first 30 amino-acid residues of the  $M_r$  41 000 endoxylanase (Slade *et al.*, 1989), was prepared by solid-phase synthesis using Fmoc-protected amino acids in an automated Milligan 9050 Continuous Flow Synthesizer (Millipore Co., Milford, MA, USA). The peptide was purified, essentially as described by Zegers *et al.* (1991), and the amino-acid composition determined as described by Janssen *et al.* (1986). To enhance the antigenicity of the peptide, it was conjugated to keyhole limpet hemocyanin, using *m*-maleimidobenzoyl-*N*-

hydroxysuccinimide as a coupling agent reactive for the terminal cysteine residue added to the peptide (Boersma *et al.*, 1992).

New Zealand white rabbits were subcutaneously immunized with either the peptide conjugate (250  $\mu$ g) or the purified  $M_r$ 34 000 endoxylanase (100 µg) emulsified (1 : 1, v/v) with Freund's adjuvant followed by three booster immunizations. Immunodetection assays were performed on samples separated on 10% SDS-PAGE (Laemmli, 1970), transferred to nitrocellulose by semidry blotting. Blots were soaked in phosphate-buffered saline with 0.05% Tween 20 containing successively 1% BSA, antibody and alkaline phosphatase-conjugate or horse radish peroxidaseconjugate (Promega, Madison, WI, USA) and stained with nitroblue tetrazolium/5-bromo-4-chloro-3-indolyl-phosphate (Promega, USA) or Enhanced Chemi-Luminescence (Amersham Pharmacia Biotech, UK). Polyclonal antibodies raised against N-terminal peptide of  $M_r$  41 000 barley endoxylanase (N-Xyl), barley endoxylanase (Xyl), barley  $\alpha$ -amylase (Juge *et al.*, 1993) and tobacco calreticulin (anti-RPL60; Denecke et al., 1995) were used at 1:500, 1:2000, 1:10 000 and 1:10 000 dilutions, respectively.

#### Isolation and analysis of RNA, cDNA and genomic clones

Total RNA, isolated according to Hensgens and Van Os-Ruygrok (1989), was separated on a denaturing glyoxal/DMSO 1.2% agarose gel (15 µg per lane), blotted to nylon membrane and hybridized to random-primed cDNA probes after standard protocols (Ausubel et al., 1997). Partial barley endoxylanase cDNA clones (pFL0083, pFL400) were identified among ESTs in a cDNA library from 24 h GA<sub>3</sub>-induced aleurone layers of cv. Himalaya (Leah et al., 1991). The barley genomic clone (Hv:XYN-1) was screened from a Lambda FIX II, cv. Igri library (Stratagene, La Jolla, CA, USA) according to the manufacturer's instructions. A 5' region of the endoxylanase cDNA was obtained from total RNA of germinated cv. Himalaya grain by RT-PCR using the One-Step RT-PCR kit (Qiagen, Hilden, Germany) with forward 5'-CCACTCGCGTAAGAT-3' and reverse 5'-ACGCGGTAAGTGAGA-3' primers based on the Hv:XYN-1 gene sequence. DNA sequences were determined by dideoxy chain termination using the Ampli Cycle Sequencing Kit (PE Biochemicals, Foster City, CA, USA) and sequencer (model 373A, Applied Biosystems, Foster City, CA, USA) and analysed by GCG (Devereaux et al., 1984).

#### DNA constructs

The nucleotide sequences and protein translation products of all genes described in this article are deposited at EMBL with the following designated names and EMBL accession numbers. Barley endoxylanase DNA sequences: partial cDNA clones pFL400 (EMBL: AF287723) and pFL0083 (EMBL: AF287722); fulllength cDNA pXYN-1 (EMBL: AF287731); and genomic clone Hv:XYN-1 (EMBL: AF287726). Wild-type and mutant barley endoxylanase expression constructs fused to nt -737/-1 of the α-amylase promoter, AMY6-4 (Rogers, 1985; ), [expressed aminoacid residues are shown in brackets]: pAMY6-4/XYN [1-556] (EMBL: AF287724), pAMY6-4/XYN [1-551] (EMBL: AF287725), pAMY6-4/XYN [1-546] (EMBL: AF287721), pAMY6-4/XYN [1-536], pAMY6-4/XYN [1-501] (EMBL: AF287728), pAMY6-4/XYN [130-556] (EMBL: AF370887), pAMY6-4/XYN [209-501] (EMBL: AF370888). Thermostable 1,3–1,4- $\beta$ -glucanase [H(A12-M) $\Delta$ Y13] expression construct, fused to the promoter and signal peptide  $[\alpha]$  coding sequence of the high-pl  $\alpha$ -amylase gene (Jensen *et al.*, 1996), is referred to as pAMY/[ $\alpha$ H(A12-M) $\Delta$ Y13]GC-NOS and without signal peptide as pAMY/[H(A12-M) $\Delta$ Y13]GC-NOS. GFPfusion protein expression constructs fused to the *Hv:XYN-1* (nt – 1000/–1) or AMY6-4 (nt –737/–1) promoters: pXYN/[XYN1-556/L/ GFP], pAMY6-4/[AMY/L/GFP], pXYN/[XYN1-213/GFP/XYN502-556] (EMBL: AF287730), pAMY6-4/[AMY1-29/GFP/AMY419-423] (EMBL: AF287729), where GFP is a fluorescence-enhanced variant encoded by the synthetic gene hGFP-C3 (Nielsen *et al.*, 1999) and L is the linker peptide from *Erwinia carotovora* CeIN cellulase. The DNA constructs were assembled from PCR-amplified cDNA and genomic sequences according to standard molecular cloning protocols described by Ausubel *et al.* (1997), and their nucleotide sequences were verified by double-strand sequencing.

#### Preparation and analysis of transfected aleurone protoplasts

Hordeum vulgare L. cv. Himalaya grain (1988 harvest, Department of Agronomy, Washington State University, Pullman WA, USA) were de-embryonated, halved, sterilized (1 min 70% EtOH, 30 min 0.2% NaOCI, 10 min 10 mM HCI; each step followed by four washes in H<sub>2</sub>O) and imbibed in H<sub>2</sub>O containing 50 µg ml<sup>-1</sup> ampicillin, 5 µg ml<sup>-1</sup> nystatin at 25°C for 3.5 days prior to removal of the starchy endosperm. Harvested layers from 200 grains were rinsed in H<sub>2</sub>O.

Protoplasts were prepared from isolated cv. Himalaya aleurone layers by cellulase treatment according to Jacobsen et al. (1985) and Skriver et al. (1991), modified by adjusting the isolation buffers to 800 mOsm with mannitol. Aliquots (1 ml) of protoplast  $(2.5-10.10^5 \text{ ml}^{-1})$  were transfected at 0°C with 100-200 µg plasmid DNA or mock-transfected with 100-200 µg sheared salmon sperm DNA using PEG-mediated DNA uptake (Lee et al., 1997). Transfected protoplasts were resuspended in 1 ml APM buffer (10 mM MES, 0.385% (w/v) Gamborg B5, 0.1 M glucose, 10 mM Larginine, 20 mM CaCl<sub>2</sub>, 0.67 M mannitol, 50 µg ml<sup>-1</sup> ampicillin, 5  $\mu$ g ml<sup>-1</sup> nystatin, pH 5.4, 1080 mOsm) with 10  $\mu$ M GA<sub>3</sub> and cultured in 96-well microtitre plates (100 µl per well), at 25°C in the dark. The culture medium was harvested from the wells after mixing and pelleting the protoplasts (10 g, 1 min). Protoplasts were washed, pelleted, and lysed (5 sec sonication) in APM buffer.

Aliquots (50 µl) of the incubation media and protoplast extracts were assayed for endoxylanase activity as described for germinating grain extracts. Expression of the thermostable H(A12-M) $\Delta$ Y13 β-glucanase activity was assayed in aliquots (15 µl), mixed with 15 µl assay buffer (50 mM NaAc, 5 mM CaCl<sub>2</sub>, 0.2% BSA pH 6.0) following 10 min incubation at 56°C to inactivate endogenous glucanase activity. The β-glucanase assay was performed in microtitre plates at 56°C with 30 µl Azo-barley glucan substrate (Megazyme) for 15–120 min and terminated with 180 µl stopping reagent, and 200 µl per well of the clarified reactions were measured spectrophotometrically (A<sub>620</sub>). β-Glucanase activity is expressed as mU per 10<sup>-5</sup> protoplasts (mU ml<sup>-1</sup> = ( $\Delta$ A<sub>620</sub> h<sup>-1</sup>) 42.19), where 1 U is defined as the release of 1 µmole reducing sugar equivalent min<sup>-1</sup> by a standard malt extract determined according to Megazyme's instructions.

Transient expression of GFP fusion proteins in aleurone protoplasts was visualized by confocal laser scanning microscopy as described by Nielsen *et al.* (2000), where the specimens were excited with monochromatic light ( $\lambda$  488 nm), and GFP fluorescence emission was detected at  $\lambda$  500–530 nm, thereby avoiding aleurone autofluorescence between 555 and 605 nm.

#### In vitro endoxylanase processing

Extracts containing  $M_r$  61 500 endoxylanase precursor were prepared as follows: aleurone layers were isolated from 200 imbibed cv. Himalaya grain as described above, rinsed and homogenized by ultra-Turrax in 20 ml H<sub>2</sub>O at 0°C, and the extract was clarified by centrifugation (14 000 *g* for 10 min).

The aleurone extract (9  $\mu$ l) was incubated with 9  $\mu$ l APM buffer pH 5.4 or 4.2 (adjusted with 3  $\mu$ l 200 mM Na succinate buffer pH 4.1), with or without addition of 4 mM DTT and adjusted to a final volume of 30  $\mu$ l with H<sub>2</sub>O. Aleurone extracts incubated with the following inhibitors were similarly tested: 10  $\mu$ g ml<sup>-1</sup> E-64 (Roche Diagnostics, Basel, Switzerland), 10  $\mu$ g ml<sup>-1</sup> leupeptin (Sigma, St Louis, MO, USA), 200  $\mu$ g ml<sup>-1</sup> PMSF (Sigma), 2 mM EDTA, 10  $\mu$ g ml<sup>-1</sup> pepstatin (Sigma).

#### Acknowledgements

We thank Sjef van Asten, Ton Blom, Ron van den Dool, Marijke Kottenhagen, Heleen Mocking-Bode, Maj-Britt Rask, Riek Vlooswijk and Suksawad Vongvisuttikun for technical assistance and Dr lb Svendsen for peptide sequencing. Dr Albert Doderer, Dr Robert Leah, Kees van Rijn, and Sascha Wijsman are thanked for valuable discussions. Dr David Simpson, Dr Ole Olsen and Dr Mei Wang are thanked for critically reading the manuscript. We are grateful for the gift of (1,3–1,4)- $\beta$ -glucanase [H(A12-M) $\Delta$ Y13], hGFP-C3 and CelN cellulase linker expression constructs from Dr Ole Olsen (Carlsberg Laboratory, Copenhagen, Denmark);  $\alpha$ -amylase antiserum from Dr Birthe Svensson (Carlsberg Laboratory, Copenhagen), and RPL60 antiserum from Dr Jürgen Denecke (University of Leeds, UK). This work was supported by a grant from Eureka Project No. 927-30, Adaptation of Barley for Industrial Needs (ABIN), ABIN Publication No. 160.

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EMBL accession numbers AF287721, AF287722, AF287723, AF287724, AF287725, AF287726, AF287728, AF287729, AF287730, AF287731, AF370887 and AF370888.