Purification and characterization of an endopeptidase from Lactococcus lactis subsp. cremoris SK11

Graham G. Pritchard,1 Andrea D. Freebairn1 and Tim Coolbear2

An endopeptidase has been purified from Lactococcus lactis subsp. cremoris SK11. The enzyme is a 70 kDa monomer, strongly inhibited by the metalloproteinase inhibitors 1,10-phenanthroline and phosphoramidon but relatively insensitive to EDTA. It is not significantly inhibited by the thiol enzyme inhibitor p-chloromercuribenzoate nor by the serine protease inhibitor phenylmethylsulphonyl fluoride. The action of the endopeptidase in catalysing the hydrolysis of several peptide hormones has been studied and the hydrolysis products identified by sequence analysis. The enzyme catalyses hydrolysis of peptide bonds in which a hydrophobic amino acid (most commonly a Phe or Leu) residue occupies the position immediately C-terminal to the hydrolysed bond. It thus has a specificity very similar to that of thermolysin. Two of the oligopeptides produced during the early stages of \( \beta \)-casein digestion by the lactococcal cell-wall proteinases were hydrolysed by the endopeptidase, the others were resistant to hydrolysis. Cell fractionation studies have shown that the distribution of endopeptidase activity between the different cell fractions is the same as that of the intracellular marker enzyme fructose bisphosphate aldolase, and thus indicate a cytoplasmic location for the enzyme. These observations argue against a role for this enzyme in the early stages of casein breakdown by the lactococcal proteolytic system.

Keywords: Lactococcus lactis subsp. cremoris, endopeptidase, proteases, dairy microbiology

INTRODUCTION

The hydrolysis of milk proteins by dairy starter lactic acid bacteria involves the action of a cell-envelope-associated proteinase, various peptidases and transport systems for peptides and amino acids (Kok, 1990; Smid et al., 1991; Pritchard & Coolbear, 1993; Tan et al., 1993). The cell-envelope-associated proteinase catalyses the partial hydrolysis of one or more of the casein components of bovine milk to a series of oligopeptide products, the nature of which has been well characterized (Monnet et al., 1989, 1992; Visser et al., 1988, 1991; Reid et al., 1991a, b). The subsequent degradation of these oligopeptides to provide the free amino acids required for starter growth is less clearly defined. Several peptidases have now been isolated from lactococci (Kok, 1990; Smid et al., 1991; Tan et al., 1993). Most of these are aminopeptidases which could potentially degrade the large casein oligopeptides by systematic cleavage of amino acids or dipeptides from the N-terminus. This would require some of the aminopeptidases to be located external to the cell membrane since large oligopeptides are probably not readily transported across the membrane (Law, 1978; Rice et al., 1978). However, current evidence on the cellular location of the aminopeptidases indicates that they are mostly located intracellularly (Tan et al., 1992; Exterkate et al., 1992; Nardi et al., 1991; Booth et al., 1990).

Compared to the well-defined characterization and classification of the aminopeptidase enzymes from lactococci and other lactic acid bacteria (Kok, 1990; Tan et al., 1993), the relationship of the various enzymes with endopeptidase activity which have been reported from lactic acid bacteria, under a variety of names and designations, is less clearly understood. Two different endopeptidases, designated LEP-I and LEP-II, were isolated from Lactococcus lactis subsp. cremoris H61 (Yan et al., 1987a, b). LEP-I was shown to be a 98 kDa monomer, unable to...
hydrolyse \( \alpha_{s1} \), \( \beta \)- or \( \kappa \)-caseins or insulin B-chain but catalysing hydrolysis of smaller peptides such as bradykinin, angiotensin, neurotensin and the N-terminal 23-residue fragment from \( \alpha_{s1} \)-casein. LEP-II was reported to be a dimer of two identical 40 kDa subunits catalysing hydrolysis of a wider range of oligopeptides including insulin B-chain, glucagon and two \( \alpha_{s1} \)-casein oligopeptides, although as with LEP-I, whole \( \alpha_{s1} \), \( \beta \)-, and \( \kappa \)-caseins were not hydrolysed. More recently an endopeptidase was isolated from \textit{L. lactis} subsp. cremoris Wg2 (Tan \textit{et al.}, 1991) which, like LEP-II, could catalyse hydrolysis of insulin B-chain and glucagon although the particular bonds hydrolysed were not identified. However, it differed from LEP-II in its molecular mass (70 kDa for both the native and subunit molecular mass). This enzyme was shown, by immunoreactivity to a polyclonal antibody raised to the purified enzyme, to be present in several strains of lactococci (Tan \textit{et al.}, 1992). An apparently similar enzyme, designated a neutral oligo-endopeptidase (NOP), has been described from \textit{L. lactis} subsp. cremoris C13 (Baankreis, 1992). The nucleotide sequence of the gene (designated \textit{pepO}) encoding an endopeptidase in \textit{L. lactis} subsp. cremoris P8-2-47 has been determined (Mierau \textit{et al.}, 1993) and shown to have sequence homology to mammalian enkephalinase.

Other lactococcal enzymes with endopeptidase activity (apart from the cell-envelope-associated protease) include enzymes designated as intracellular proteasins (Desmazeaud & Zevaco, 1976; Muset \textit{et al.}, 1989; Zevaco & Desmazeaud, 1980). These enzymes differ from the endopeptidases described above in their ability to hydrolyse \( \beta \)-casein.

The present study describes the purification and properties of an endopeptidase from \textit{L. lactis} subsp. cremoris SK11. A comparison of the specificity and other properties of this enzyme with those of previously studied lactococcal endopeptidases and ‘proteasines’ suggests that many of these enzymes have a very similar specificity of action in hydrolysing peptides and may therefore be related enzymes.

**METHODS**

**Bacterial strain, growth conditions and harvest.** \textit{Lactococcus lactis} subsp. cremoris SK11 was obtained from the culture collection of the New Zealand Dairy Research Institute, Palmerston North, New Zealand (isolate number 5221). Bacterial cultures for enzyme purification were grown in a 40 litre fermenter in a lactose/peptone/yeast extract medium following the procedure described by Lloyd & Pritchard (1991). Bacterial cells were harvested by centrifugation at the end of the exponential phase (approximately 6 h after inoculation), washed twice with cold 50 mM phosphate buffer (pH 6.4), and the washed pellets were stored frozen at \(-15^\circ\text{C} \) until required.

**Enzyme assays.** Endopeptidase activity was determined using the peptide hormone bradykinin as substrate. The rate of hydrolysis was followed by measuring the decrease in bradykinin concentration after separating substrate and products by reverse-phase HPLC. The standard assay mixture contained 80 \( \mu \)l bradykinin (0.5 mg ml\(^{-1}\) in deionized water) and 20 \( \mu \)l appropriately diluted enzyme solution in either 20 mM phosphate buffer (pH 6.4) or 20 mM-Bis-tris propane (BTP) buffer (pH 6.4). The reaction mixture was incubated at room temperature and, at appropriate times, 50 \( \mu \)l samples were removed and added to 25 \( \mu \)l 3% (v/v) trifluoroacetic acid (TFA) to stop further reaction. The samples were centrifuged at 10000 \( g \) in a microcentrifuge (MSE, MicroCentaur) and then 50 \( \mu \)l of supernatant was injected onto a Vydac 218 TP C18 reverse-phase column (250 mm \( \times \) 4.6 mm; Alltech Associates) linked to a Philips PU4100 HPLC system. Residual bradykinin was separated from the peptide products using the following elution conditions. Solution A contained 0.1% TFA in glass-distilled deionized water; solution B contained 0.08% TFA in acetonitrile. Elution was by a linear gradient of 5–40% B at 1 ml min\(^{-1}\) over 15 min. Peptides were detected by their absorbance at 220 nm. The system was calibrated using known concentrations of bradykinin. One unit of endopeptidase activity is defined as that amount of enzyme catalysing the hydrolysis of 1 \( \mu \)mol bradykinin min\(^{-1}\).

Lysine aminopeptidase activity was measured using lysyl p-nitroanilide as substrate and following the rate of appearance of p-nitroanilide spectrophotometrically at 405 nm. The reaction mixture contained: 780 \( \mu \)l 100 mM MES buffer (pH 6.8); 200 \( \mu \)l lysine p-nitroanilide (5 mM) and 20 \( \mu \)l appropriately diluted enzyme. One unit of enzyme is defined as that amount catalysing the formation of 1 \( \mu \)mol p-nitroaniline min\(^{-1}\).

Fructose-1,6-bisphosphate aldolase activity was measured essentially according to the procedure of Crow & Thomas (1982).

**Enzyme purification.** All steps, except where specified otherwise, were carried out at a temperature of 0–4 \( ^\circ\text{C} \). Approximately 100 g frozen cells (collected from about 7.5 l of culture) were thawed and resuspended in 170 ml 20 mM phosphate buffer (pH 6.4). Bacterial cells were disrupted by a single passage through a French pressure cell operated at 55 MPa. The resulting homogenate was centrifuged at 27000 \( g \) for 15 min and the supernatant collected. The supernatant was loaded onto a column (3.5 cm \( \times \) 17 cm) of DEAE-cellulose (Whatman DE23) equilibrated with 10 mM sodium phosphate buffer (pH 6.4). The column was washed with 100 ml 10 mM sodium phosphate buffer (pH 6.4) containing 0.1 M NaCl and then bound protein was eluted with a linear 0–0.6 M NaCl gradient using a total elution volume of 500 ml and a flow rate of 1.2 ml min\(^{-1}\). Fractions containing high endopeptidase (bradykinin-hydrolysing) activity (eluting between 0.4 and 0.6 M NaCl) were pooled and concentrated to a volume of 5–10 ml by ultrafiltration through a PM 30 Diaflo membrane (Amicon). The concentrated sample was loaded onto a column (2.6 cm \( \times \) 90 cm) of Sephacryl S300 equilibrated with 20 mM BTP buffer (pH 6.4) containing 0.1 M NaCl and eluted with the same buffer at a flow rate of 0.2 ml min\(^{-1}\). Fractions with high endopeptidase activity (eluting at 280–330 ml) were pooled and concentrated to less than 10 ml by ultrafiltration. The concentrated fractions were then loaded onto a Mono Q HR 10/10 FPLC column (Pharmacia) equilibrated with 20 mM BTP buffer (pH 6.5) and operated at room temperature. The column was washed with approximately 10 ml equilibration buffer and bound protein was then eluted with a linear 0–1 M NaCl gradient over 40 min at a flow rate of 2 ml min\(^{-1}\). Fractions containing high endopeptidase activity were pooled and dialysed for 3 h against 20 mM-BTP buffer (pH 6.5) containing 3 M NaCl. The dialysed solution was loaded onto a 0.7 cm \( \times \) 6.5 cm column of phenyl-Sepharose equilibrated with the 20 mM BTP (pH 6.5) containing 3 M NaCl, the column was washed with approximately 50 ml of equilibration buffer and enzyme eluted with a linear 3–0 M NaCl gradient using a total elution volume of 240 ml and a flow rate of 0.5 ml min\(^{-1}\). Contaminating proteins were eluted in the wash buffer, while the endopeptidase activity bound to the phenyl-Sepharose
and was eluted as a homogeneous protein between 1.75 and 1 M NaCl. Active fractions were pooled and concentrated by ultrafiltration using a Centricon 10 (Amicon) micro-concentrator.

**Protein determination.** Protein concentration was measured using the bicinchoninic acid method of Smith et al. (1985) with bovine serum albumin as the standard.

**Polyacrylamide gel electrophoresis (PAGE).** Samples for analysis by SDS-PAGE were prepared by boiling with an equal volume of 0.125 M Tris/HCl (pH 6.8) containing 4% (w/v) SDS, 20% (v/v) glycerol and 10% (v/v) β-mercaptoethanol. SDS-PAGE was carried out according to the procedure of Laemmli (1970).

**Determination of molecular mass.** The molecular mass of the denatured monomer was determined using SDS-PAGE with the following proteins as standards: myosin (205 kDa), β-galactosidase (116 kDa), phosphorylase b (97.4 kDa), bovine serum albumin (66 kDa), egg albumin (45 kDa) and carbonic anhydrase (29 kDa). The molecular mass of the native purified protein was determined from its elution volume from a Superose 12 gel permeation column (Pharmacia) eluted with 20 mM BTP (pH 6.5) containing 0.15 M NaCl at a flow rate of 0.5 ml min−1. The following proteins were used as standards: β-amylose (200 kDa); alcohol dehydrogenase (150 kDa); bovine serum albumin (66 kDa), carbonic anhydrase (29 kDa), cytochrome c (12.4 kDa).

**N-terminal sequence analysis.** The N-terminal amino acid sequence of the purified enzyme was determined by the automated Edman method using a gas-phase protein sequencer (Applied Biosystems 470A, with a 120A PTH analyser).

**Isolation and identification of peptide products of hydrolysis.** The products of peptide hydrolysis by the purified endopeptidase were separated by HPLC using the apparatus and procedure described above for bradykinin (see Enzyme assays). Peptide peaks were collected and dried under vacuum. Peptides were identified by sequence analysis.

**Cell fractionation.** Bacteria were grown in reconstituted skim milk and harvested following the procedures described by Coolbear et al. (1992a). The harvested cells were separated into "cell-wall lysate", "cytoplasmic" and "particulate" fractions using lysozyme plus mutanolysin to solubilize cell wall material and sucrose as osmostatitizer following the procedures described by Crow et al. (1993).

**Materials.** Bradykinin, neurotensin, insulin B-chain, metenkephalin and other small peptides were obtained from Sigma, as were other enzyme assay substrates. Oligopeptides produced by digestion of β-casein by purified cell-envelope-associated proteases from *L. lactis* subsp. cremoris strains H2 and SK11 were isolated and identified as described by Reid et al. (1991b). Glycerol-3-phosphate dehydrogenase/triosephosphate isomerase was from Boehringer. Angiotensin was synthesised by Dr D. Engelbreten of the Massey University Separation Science Unit. DEAE-cellulose DE23 was from Whatman Biochemicals, and all other column matrices and pre-packed columns were from Pharmacia. Acetonitrile and 2-propanol were HPLC-grade solvents from either BDH or Mallinckrodt. Yeast extract was from Gibco and Trypticase peptone from BBL.

### RESULTS AND DISCUSSION

**Purification**

A typical purification is summarized in Table 1. The use of hydrophobic interaction chromatography on phenyl-Sepharose was particularly effective in removing protein contaminants at the final stage, yielding a virtually homogeneous protein as determined by SDS-PAGE (Fig. 1).

**Molecular mass**

The subunit molecular mass, estimated from three separate SDS-polyacrylamide gels, was 69.5 ± 1.2 kDa. This is in agreement with the value of 70 kDa reported by Tan et al. (1991) for the molecular mass of the endopeptidase from *L. lactis* subsp. cremoris Wg2 and with the value of 71.5 kDa calculated from the gene sequence for the endopeptidase from *L. lactis* subsp. *cremoris* P8-2-47 (Mierau et al., 1993). The native molecular mass determined by gel permeation was 93 kDa (two separate determinations agreeing within ±2 kDa). Thus this method results in an overestimation of the molecular mass. This is of interest since the mass of the intracellular proteinase purified from *L. lactis* subsp. *cremoris* NCDO 763 (Muset et al., 1989) was also found to be 93 kDa by gel permeation. A value of 80 kDa (also determined by gel permeation) was reported for the LEP-II endopeptidase from *L. lactis* subsp. *cremoris* H61 by Yan et al. (1987a) although the subunit molecular mass of this enzyme, determined by SDS-PAGE, was only 40 kDa, indicating a dimeric native enzyme.

**N-terminal sequence**

The sequence of the first 20 amino acid residues of the purified endopeptidase was determined (Table 2) except for the initial N-terminal residue which could not be unambiguously identified. This N-terminal sequence is identical to that predicted from the nucleotide sequence for the endopeptidase from *L. lactis* subsp. *cremoris* P8-2-47 (Mierau et al., 1993). However, it shows almost no homology with the N-terminal sequence determined for LEP-II from *L. lactis* subsp. *cremoris* H61 by Yan et al. (1987a) except for the three residues which are the same in both sequences (see Table 2).

**pH dependence**

The pH dependence of the endopeptidase using the peptide metenkephalin as substrate (as used in the work of Tan et al., 1991) showed a simple pH profile with an optimum value of around 6.0. This is in agreement with values reported for other lactococcal endopeptidases (Desmazeaud & Zevaco, 1976; Yan et al., 1987a; Tan et al., 1991). However, when the pH dependence was studied using bradykinin as the peptide substrate, high enzyme activity was maintained over the range from pH 6.0 to 9.5. No difference in the bradykinin hydrolysis products was observed over this pH range. The reason for this difference in pH profiles using the two different substrates is unknown.

**Effect of proteinase inhibitors**

The sensitivity of the endopeptidase purified in the present study to various proteinase inhibitors (Table 3) was similar in most respects to previously reported findings on
Table 1. Purification of an endopeptidase from *L. lactis* subsp. *cremoris* SK11

The results presented are for a purification from 75 g wet wt of cells.

<table>
<thead>
<tr>
<th>Purification step</th>
<th>Protein concn (mg ml⁻¹)</th>
<th>Total protein (mg)</th>
<th>Activity (units ml⁻¹)</th>
<th>Total activity (units)</th>
<th>Specific activity (units mg⁻¹)</th>
<th>Purification (-fold)</th>
<th>Yield (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crude extract</td>
<td>37.5</td>
<td>3700</td>
<td>3.4</td>
<td>256.7</td>
<td>0.085</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>DEAE-cellulose</td>
<td>50.6</td>
<td>359</td>
<td>14.5</td>
<td>97.3</td>
<td>0.271</td>
<td>3.1</td>
<td>37</td>
</tr>
<tr>
<td>Sephacryl S300</td>
<td>12.2</td>
<td>73</td>
<td>2.4</td>
<td>27.1</td>
<td>0.371</td>
<td>4.3</td>
<td>10</td>
</tr>
<tr>
<td>MonoQ</td>
<td>6.8</td>
<td>98</td>
<td>4.9</td>
<td>13.0</td>
<td>1.32</td>
<td>16.0</td>
<td>5</td>
</tr>
<tr>
<td>Phenyl-Sepharose</td>
<td>0.52</td>
<td>0.2</td>
<td>6.1</td>
<td>2.5</td>
<td>12.5</td>
<td>147</td>
<td>1</td>
</tr>
</tbody>
</table>

![Fig. 1. SDS-PAGE showing purification of an endopeptidase from *L. lactis* subsp. *cremoris* SK11.](image)

Table 3. Effect of protease inhibitors on activity of an endopeptidase from *L. lactis* subsp. *cremoris* SK11

The enzyme was preincubated for 30 min in the presence of inhibitor at the concentration shown and then the reaction was started by addition of substrate. Final inhibitor concentrations after addition of substrate were 60% of the concentrations shown.

<table>
<thead>
<tr>
<th>Inhibitor</th>
<th>Activity (percentage of uninhibited control)</th>
</tr>
</thead>
<tbody>
<tr>
<td>EDTA (10 mM)</td>
<td>62</td>
</tr>
<tr>
<td>0-Phenanthroline (1 mM)</td>
<td>0</td>
</tr>
<tr>
<td>Phosphoramidon (0.1 mM)</td>
<td>0</td>
</tr>
<tr>
<td>pCMB (1 mM)</td>
<td>89</td>
</tr>
<tr>
<td>PMSF (1 mM)</td>
<td>83</td>
</tr>
</tbody>
</table>

The inhibition of lactococcal endopeptidases. However, a significant difference was the inability of EDTA (even at 10 mM) to inhibit the enzyme to less than 60% of the control activity, although activity was completely inhibited by two other metalloproteinase inhibitors, phosphoramidon (0.1 mM) and 1,10-phenanthroline (1 mM). Previous studies on lactococcal endopeptidases

(Table 3. Effect of protease inhibitors on activity of an endopeptidase from *L. lactis* subsp. *cremoris* SK11)

![Table 2. N-terminal amino acid sequences of lactococcal endopeptidases](image)

<table>
<thead>
<tr>
<th>Endopeptidase*</th>
<th>N-terminal sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>(a)</td>
<td>?-Arg-Ile-Gln-Asp-Leu-Phe-Ala-Thr-Val-Asn-Ala-Glu-Trp-Leu-Ala-Glu-Ile...</td>
</tr>
<tr>
<td>(b)</td>
<td>Thr-Arg-Ile-Gln-Asp-Leu-Phe-Ala-Thr-Val-Asn-Ala-Glu-Trp-Leu-Ala-Glu-Ile...</td>
</tr>
<tr>
<td>(c)</td>
<td>?-Phe-Thr-Leu-Leu-Val-Leu-Glu-Pro-Pro-Tyr-Ala-Pro-Asn-Asn-Leu-Glu-Phe-Phe-Cys-Met...</td>
</tr>
</tbody>
</table>

* (a) Endopeptidase purified from *L. lactis* subsp. *cremoris* SK11 in the present study; (b) endopeptidase PepO from *L. lactis* subsp. *cremoris* P8-2-47 (Mierau et al., 1993); (c) endopeptidase LEP II from *L. lactis* subsp. *cremoris* H61 (Yan et al., 1987a).
Table 4. Peptide bonds hydrolysed in hormone peptides by the endopeptidase from
*Lactococcus lactis* subsp. cremoris SK11

<table>
<thead>
<tr>
<th>Peptide</th>
<th>Sequence and peptide bond(s) hydrolysed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Metenkephalin</td>
<td>Tyr-Gly-Gly - Phe-Met</td>
</tr>
<tr>
<td>Bradykinin</td>
<td>Arg-Pro-Pro-Gly - Phe-Ser-Pro - Phe-Arg</td>
</tr>
<tr>
<td>Angiotensin</td>
<td>Asp-Arg-Val-Tyr-Ile-His-Pro - Phe-His-Leu</td>
</tr>
<tr>
<td>Neurotensin</td>
<td>pGlu-Leu - Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-Tyr-Ile-Leu</td>
</tr>
</tbody>
</table>

Peptides (150–160 µg) were incubated with purified endopeptidase (1–4 µg protein in 20 mM BTP buffer, pH 6.0) from *Lactococcus lactis* subsp. cremoris SK11 for periods up to 4 h. For insulin B-chain, 240 µg peptide was incubated with 9 µg endopeptidase for up to 1 h. Hydrolysis products were separated by HPLC and identified by amino acid sequence determination as described in Methods. Hydrolysed bonds are indicated by ▼. For comparison the bonds cleaved by the endopeptidase LEP-II from *Lactococcus lactis* subsp. cremoris H61 (Yan et al., 1987a) are shown by △.

Substrate specificity

The bonds hydrolysed in various hormone peptides are shown in Table 4, which also indicates the sites of hydrolysis found by Yan et al. (1987a) for LEP-II from *Lactococcus lactis* subsp. cremoris SK11. It is evident that the specificity of action of endopeptidase from *Lactococcus lactis* subsp. cremoris SK11 in cleaving these five peptides is almost identical to that found for LEP-II (except for an additional three sites found only in the present study). Most of the bonds identified as cleavage sites in insulin B-chain in the present study were also found for the intracellular protease from *Lactococcus lactis* subsp. lactis NCDO 763 by Muset et al. (1989) and for an endopeptidase from *Lactococcus lactis* subsp. lactis bv. *diacetylactis* by Desmazeaud & Zevaco (1976), although these two studies also reported a few additional cleavage sites. However, the cleavage patterns found in the present study are very different from those found for the endopeptidase LEP-I from the H61 strain (Yan et al., 1987b), which does not hydrolyse insulin B-chain and which hydrolyses neurotensin and bradykinin in a different manner.

Hydrolysis of casein oligopeptides

As found for other lactococcal endopeptidases (Yan et al., 1987a, b; Tan et al., 1991), the endopeptidase from *Lactococcus lactis* subsp. cremoris SK11 was not able to hydrolyse intact α-, β- or κ-caseins. However, it did catalyse hydrolysis of...
Table 5. Peptide bonds hydrolysed in casein oligopeptides by the endopeptidase from L. lactis subsp. cremoris SK11

<table>
<thead>
<tr>
<th>Peptide Sequence and peptide bond(s) hydrolysed</th>
</tr>
</thead>
<tbody>
<tr>
<td>k-Casein (161–169) Thr-Val-Gln-Val-Thr-Ser-Thr-Ala-Val</td>
</tr>
<tr>
<td>(\beta)-Casein (1–209; total sequence) Not hydrolysed</td>
</tr>
<tr>
<td>(47–52) Asp-Lys-Ile-His-Pro-Phe; not hydrolysed</td>
</tr>
<tr>
<td>(166–175) Ser-Gln-Ser-Lys-Val-Leu-Pro-Val-Pro-Gln; not hydrolysed</td>
</tr>
<tr>
<td>(176–182) Lys-Ala-Val-Pro-Tyr-Pro-Gln; not hydrolysed</td>
</tr>
<tr>
<td>(183–193) Arg-Asp-Met-Pro-Ile-Gln-Ala-Phe-Leu-Leu-Tyr ▼</td>
</tr>
<tr>
<td>(194–209) Gln-Glu-Pro-Val-Leu-Gly-Pro-Val-Arg-Gly-Pro-Phe-Pro-Ile-Ile-Val</td>
</tr>
</tbody>
</table>

Fig. 2. Time course of hydrolysis by the endopeptidase of two oligopeptides derived from \(\beta\)-casein by action of the cell envelope proteinase from L. lactis subsp. cremoris H2. 1. The peptide Arg-Asp-Met-Pro-Ile-Gln-Ala-Phe-Leu-Leu-Tyr (Arg\textsubscript{183}-Tyr\textsubscript{193} in \(\beta\)-casein). 1a–1c, Hydrolysis products of peptide 1: 1a, Phe\textsubscript{190}-Tyr\textsubscript{193}; 1b, Arg\textsubscript{183}-Ala\textsubscript{186}; 1c, the tetrapeptide Arg\textsubscript{183}-Pro\textsubscript{186} plus the dipeptide Leu\textsubscript{192}-Tyr\textsubscript{193} (these two peptides have the same retention time in the HPLC system used). 2. The peptide Gln-Glu-Pro-Val-Leu-Gly-Pro-Val-Arg-Gly-Pro-Ile-Ile-Val (Gln\textsubscript{194}-Val\textsubscript{209} in \(\beta\)-casein). 2a, Hydrolysis product of peptide 2: Gln\textsubscript{194}-Pro\textsubscript{206}. |

some oligopeptides derived from these caseins (Table 5). The peptides shown in Table 5 were isolated from digests obtained by incubating the intact \(\beta\)- and \(\kappa\)-caseins with purified cell-envelope-associated proteinases from either L. lactis subsp. cremoris SK11 (a \(\Pi\)\textsubscript{II}-type proteinase-producing strain) or L. lactis subsp. cremoris H2 (a \(\Pi\)\textsubscript{I}-type proteinase-producing strain). The \(\kappa\)-casein (161–169) peptide, a major product of \(\kappa\)-casein digestion by the \(\Pi\)\textsubscript{II}-type proteinase at the earliest digestion times (J. R. Reid, T. Coolbear & G. G. Pritchard, unpublished), is readily hydrolysed by the endopeptidase at the Gin\textsubscript{166}-Val\textsubscript{169} bond. Of the four major peptides generated during the initial stage of hydrolysis of \(\beta\)-casein by the \(\Pi\)\textsubscript{I}-type lactococcal cell envelope-associated proteinase (Reid et al., 1991b), the peptides Arg\textsubscript{183}-Tyr\textsubscript{193} and Gln\textsubscript{194}-Val\textsubscript{209} were hydrolysed by the endopeptidase at one or more of the peptide bonds with hydrophobic residues in the P1' position (Table 5). There was, however, a significant difference in the rate of hydrolysis of these two peptides. At identical enzyme concentrations, the peptide Arg\textsubscript{183}-Tyr\textsubscript{193} was almost completely degraded after 1 h whereas the C-terminal \(\beta\)-casein peptide Gln\textsubscript{194}-Val\textsubscript{209} was more slowly hydrolysed over a period of 6 h (Fig. 2). Hydrolysis of the former peptide (Arg\textsubscript{183}-Tyr\textsubscript{193}) occurred initially at the Ala\textsubscript{186}-Phe\textsubscript{190} bond, leading to the transient accumulation of the heptapeptide Arg-Asp-Met-Pro-Ile-Gln-Ala and the tetrapeptide Phe-Leu-Leu-Tyr (Fig. 2). Both of these initial peptide products were subsequently degraded to smaller peptides at the bonds indicated in Table 5. The C-terminal \(\beta\)-casein peptide (Gln\textsubscript{194}-Val\textsubscript{209}) was hydrolysed only at the Pro\textsubscript{206}-Ile\textsubscript{207} bond. The large N-terminal product of this hydrolysis (Gln\textsubscript{194}-Pro\textsubscript{206}) accumulated and was still present as a major product after 24 h digestion. The relative resistance of this peptide to hydrolysis is surprising in view of the presence of hydrophobic residues in the sequence which
Table 6. Subcellular distribution of endopeptidase activity in L. lactis subsp. cremoris SK11

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Cell wall lysate (%)</th>
<th>Cytoplasmic fraction (%)</th>
<th>Particulate fraction (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lysine aminopeptidase</td>
<td>0·2</td>
<td>99·1</td>
<td>0·7</td>
</tr>
<tr>
<td>Fructose 1,6-bisphosphate aldolase</td>
<td>0·3</td>
<td>99·0</td>
<td>0·7</td>
</tr>
<tr>
<td>Endopeptidase</td>
<td>1·4</td>
<td>98·0</td>
<td>0·6</td>
</tr>
</tbody>
</table>

could indicate likely cleavage sites, suggesting that conformational factors as well as the primary sequence determine the susceptibility to hydrolysis. The peptides from this region of β-casein have been shown to be extremely bitter (Shinoda et al., 1985) and have implicated as contributing to the bitter flavour defect of cheese (Visset et al., 1983). Other early products of P11-type cell-envelope associated proteinase action on β-casein, namely the peptides Lys176-Gln182, a series of three overlapping, not easily separated, peptides from the sequence Ser166-Gln175 and also the hexapeptide Asp17-Phe33, an early product of P11-type proteinase action (Reid et al., 1991b), were not hydrolysed by the endopeptidase even after 24 h incubation.

Cellular location of endopeptidase activity

Harvested cells were separated into three subcellular fractions designated 'cell-wall lysate', 'cytoplasmic' and 'particulate' fractions using the procedure described by Crow et al. (1993). The cell-wall lysate fraction contains proteins, such as the cell-envelope-associated proteinase, released from the cell wall by treatment with the lytic enzymes, lysozyme and mutanolysin. The cytoplasmic fraction contains soluble (and possibly loosely membrane-bound) proteins released into the supernatant when spheroplasts are lysed and centrifuged, while the particulate fraction contains proteins and other materials tightly bound to the cell wall and membrane (Coolbear et al., 1992b; Crow et al., 1993). The distribution of endopeptidase activity between the three fractions was compared with that of the cytoplasmic marker enzyme, fructose-1,6-bisphosphate aldolase, and of the enzyme lysine aminopeptidase which, on the basis of current evidence, also has a cytoplasmic location (Tan et al., 1992; Esterkate et al., 1992). The results of the present study (Table 6) clearly indicate that endopeptidase (bradykinin-degrading) activity is located in the cytoplasm fraction. The endopeptidase isolated from L. lactis subsp. cremoris Wg2 was also shown, by immunogold labelling and antibody binding to subcellular fractions, to be located predominantly in the cytoplasm (Tan et al., 1992). In the recently determined nucleotide sequence of the endopeptidase gene, pepO, from L. lactis subsp. cremoris P8-2-47 (Mierau et al., 1993), the translation start site corresponds to the codon specifying the N-terminus of the mature protein, showing that no signal sequence characteristic of membrane-translocated proteins is present; this provides further confirmation of the intracellular location.

Concluding remarks

The endopeptidase purified in the present study is probably closely related to, or identical with, the 70 kDa enzymes from the L. lactis subsp. cremoris strain Wg2 (Tan et al., 1991), C13 (Baankreis, 1992) and P8-2-47 (Mierau et al., 1993). It also resembles the endopeptidase LEP-II from L. lactis subsp. cremoris H61 (Yan et al., 1993) in its specificity of hydrolysis of five different oligopeptides (see Table 4) but its molecular mass and N-terminal amino acid sequence clearly distinguish it from the latter enzyme. This raises the question of the relationship of the endopeptidase LEP-II from L. lactis subsp. cremoris H61 to the other recently studied lactococcal endopeptidases. It would seem rather improbable that a totally different enzyme, with identical specificity to that of the 70 kDa enzyme purified in the present study, exists in L. lactis subsp. cremoris H61, especially since Tan et al. (1991) showed, using an antibody raised to the purified endopeptidase from the Wg2 strain, that a 70 kDa endopeptidase was present in the H61 strain. The specificity properties of the endopeptidase from L. lactis subsp. cremoris SK11 (Table 4) suggest that it could potentially contribute to the degradation of β-casein oligopeptides with a high content of hydrophobic residues. The hydrophobic C-terminal peptide of β-casein (Pro96-Val207) has been shown to be very bitter (Shinoda et al., 1985). This peptide was slowly hydrolysed by the endopeptidase but only at one peptide bond, leaving a relatively large hydrophobic fragment undegraded. The endopeptidase NOP from L. lactis subsp. cremoris C13 was also found to hydrolyse this peptide (Baankreis, 1992). However, the cytoplasmic location of the endopeptidase would suggest that it plays only a very limited, if any, role in the casein degradation pathway in the intact cell, unless the recently described oligopeptide transport system (Kunji et al., 1993) is capable of transporting peptides larger than the previously suggested upper size limit (6 to 7 amino acid residues) for transport across the cell membrane (Rice et al., 1978; Law, 1978). Indeed, Mierau et al. (1993), using gene disruption to obtain a pepO mutant lacking this endopeptidase, showed that the growth and rate of acid production of this mutant were identical to the parent pepO* strain, demonstrating clearly that this endopeptidase is not essential for lactococcal growth in milk. It may, however, play a significant role in the ripening phase of cheese manufacture if it is liberated by starter lactococci into the cheese curd.

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