Characterization of the Protein-Synthesis Dependent Adaptive Acid Tolerance Response in Lactobacillus acidophilus

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Abstract

Exposure of L. acidophilus CRL 639 cells to sublethal adaptive acid conditions (pH 5.0 for 60 min) was found to confer protection against subsequent exposure to lethal pH (pH 3.0). Adaptation, which only occurred in complex media, was dependent on de novo protein synthesis and was inhibited by amino acid analogues. There was no modification in the protein synthesis rate during adaptation, but the protein degradation rate decreased. Synthesis of acid stress proteins may increase the stability of pre-existing proteins. By 2D-PAGE, induction of nine acid stress proteins and repression of several housekeeping proteins was observed. Putative heat shock proteins DnaK, DnaJ, GrpE, GroES and GroEL (70, 43, 24, 10 and 55 kDa, respectively) were among the proteins whose synthesis was induced in response to acid adaptation.

Introduction

Lactic acid bacteria (LAB) are used worldwide for the manufacture of cheese, yogurt, and fermented milk products. However, knowledge of physiological adaptations of LAB to dairy processing conditions remains limited. A better understanding of this adaptive response is important since dairy manufacturing processes often expose LAB to adverse environmental conditions such as shifts in pH and temperature.

Survival of Escherichia coli under acid stress conditions is often linked to the expression of an adaptive stress response characterized by the transient induction of specific proteins and physiological changes which frequently enhance their ability to withstand harsh environmental conditions (Bearson et al., 1997). Three complex medium-dependent acid resistance (AR) systems have been described for E. coli (Lin et al., 1995); two of them are fermentative AR systems which involve the inducible amino acid decarboxylases, arginine decarboxylase and glutamate decarboxylase. These are also present in Shigella (Lin et al., 1995) but not in Salmonella typhimurium. In summary, the enteric group of microorganisms have been shown to be diverse in the ways that they handle acid stress. Relatively little is known about stress responses in dairy starter cultures although heat shock has been studied (Hartke et al., 1997).

Molecular chaperones, which include many well-studied heat shock proteins (HSP), are essential for maintenance of bacterial growth and viability (Hartl et al., 1992). The most abundant and physiologically important chaperones in E. coli include DnaK, DnaJ, GroEL, and GroES (Georgopoulos et al., 1994), the synthesis of which is under positive control of a minor σ factor (σ32) encoded by the rpoH gene. In the gram-positive bacterium Bacillus subtilis, chaperones belong to the Class I stress genes that constitute the CIRCE regulon and are negatively controlled by HrcA (Hecker et al., 1996). Several lines of evidence have indicated that the two major chaperone teams, DnaK-DnaJ-GrpE and GroEL-GroES, play distinct but cooperative roles in protein folding, stability, and assembly of individual proteins (Georgopoulos et al., 1994). Heat shock induction of stress proteins has been observed in numerous Gram positive species, including Bacillus subtilis, Enterococcus faecalis, Lactococcus lactis subsp. lactis, Lactic acidophilus acidophilus and L. sakei demonstrating the universality of this response (Kim and Batt, 1993; Broadbent et al., 1997). Among LAB, the possible involvement of molecular chaperones in acid stress has only been addressed in Lactococcus lactis (Hartke et al., 1997).

In a previous report we observed that stationary-phase cells of L. acidophilus CRL 639 are acid sensitive during growth at pH 6.0 but naturally acid resistant when the pH of the culture gradually decreases during free fermentation runs (Lorca and Font de Valdez, 2001). Two acid tolerance responses (ATR) are induced in exponentially growing cells upon exposure to sublethal pH (3.8–6.0) (Lorca et al., 1998): (i) a homeostatic response related to an increase in ATPase activity (independent of de novo protein synthesis) induced by adaptation at pH 4.2 for 15 min (Lorca and Font de Valdez, 2001), and (ii) a protein-synthesis dependent ATR induced at pH 5.0 for 60 min. The purpose of this study is to characterize the protein-dependent ATR of L. acidophilus CRL 639 and to

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identify putative HSP's induced in response to acid adaptation.

Results

ATR in Complex and Minimal Media

In L. acidophilus CRL 639 acid tolerance is induced by shifting cells to pH 5.0 (during 60 min). There is no cell growth during this adaption. The adapted cells are then challenged at pH 3.0 (Lorca et al., 1998). A synthetic medium (SM) was used to know whether acid survival of L. acidophilus in minimal versus complex medium utilizes similar mechanisms, or if distinct systems are involved. To this end, cells were grown in MRS until exponential phase, washed and resuspended in SM adjusted at pH 5.0.

Figure 1 shows that cells adapted in synthetic media (SM) were completely sensitive to acid stress while cells preincubated in complex media (MRS or a modified MRS broth, Mm) developed ATR and displayed an acid tolerant phenotype. Subsequent attempts to determine if the nitrogen component(s) of MRS were responsible for survival at pH 3.0 were made by adding an amino acid pool as peptides (80% casein hydrolysate; SM-C) or as free amino acids (80% casamino acids; SM-Ca) to SM broth. Neither amino acids nor peptides induced the ATR in SM (Figure 1), indicating that a complex pattern of induction is needed.

Rate of Protein Synthesis and Degradation During Adaptation

The induction of protein synthesis during adaptation of the cells in MRS, Mm and SM was determined by incorporation of [3H]leucine. The 3H uptake was higher (3000 c.p.m. after 60 min) in SM compared to MRS and Mm (90 c.p.m. after 60 min). However, this low rate of incorporation was completely inhibited by the addition of 50 μg ml⁻¹ of chloramphenicol, indicating a specific incorporation of leucine to the proteins. The 3H uptake was further analyzed in MRS since, as described previously, the cells adapted in SM display an acid sensitive phenotype. In MRS, adapted (pH 5.0) and non-adapted (pH 6.0) cells showed the same rate of protein synthesis (data not shown).

Amino acid analogues were added to pH 5.0-adapted cells to elucidate the role of active induced stress proteins (Figure 2). Three analogues, DL-7-azatryptophan (a tryptophan analog), S-2-aminoethyl-L-cysteine (a lysine analog), and p-fluoro-DL-phenylalanine (a phenylalanine analog) were tested. When added individually at 50 μg/ml, each of these analogues affected the ATR differently. 7-azatryptophan, like chloramphenicol, abolished the ATR response. S-2-aminoethyl-L-cysteine and p-fluoro-DL-phenylalanine reduced the ATR by 90% (Figure 2). This deleterious effect may be related to a decrease in the rate of protein synthesis and/or the synthesis of faulty proteins. To evaluate these hypotheses, the incorporation of [3H]leucine in the presence of the amino acid analogues (Figure 3A), and the activity of intracellular enzymes were determined using β-gal and PepN as physiological markers (Figure 3B). Although the rate of protein synthesis did not decrease in the presence of amino acid analogues (Figure 3A) a reduction of 96 to 98% in the specific activity of PepN and β-gal was observed (Figure 3B) compared to adapted cells without incorporation of [3H]leucine.
analogues. In addition, the protein degradation rate in adapted cells was lower (3.0%/h) than non-adapted cells (4.7%/h) that were kept at pH 6.0. In the presence of chloramphenicol, the adapted cells displayed the same degradation rate as the non-adapted ones, indicating that the synthesis of acid-induced specific proteins (ASP) during adaptation might be involved in protein stability.

Pattern of Protein Synthesis During Adaptation

The synthesis of proteins by *L. acidophilus* CRL 639 labeled with $^{35}$S-methionine during acid adaptation in MRS$_5$ was examined by SDS-PAGE. In one dimensional SDS-PAGE, overexpression of 30 proteins with apparent molecular weights ranging from 11.9 to 117.0 kDa were visualized (Table 1). Comparing the protein pattern of MRS$_5$- and Mm-adapted cells, a higher (1.6 to 3.8 fold) induction and the specific expression of 14 proteins (12.3, 13.3, 20.1, 23.0, 25.4, 27.5, 28.3, 38.8, 47.7, 59.9, 85.5, 93.0, 96.4 and 117.0 kDa) was observed in the former medium. These proteins might be involved in the higher ATR developed by the cells adapted in MRS$_5$.

$^{35}$S-labeled proteins of *L. acidophilus* CRL 639 adapted in MRS$_5$ were examined by 2D-PAGE (Figure 4) which gave a better estimation of the characteristics of the proteins synthesized (based on the isoelectric point, pI). If it is assumed that a linear pH gradient from pH 4.0 to 7.0 is formed over the entire range of the gel (as claimed by the manufacturer), a crude estimate of the pI value for a polypeptide can be obtained. It was only observed proteins with a pI between 4.4 and 5.6 (Table 2) since all proteins with neutral or basic characteristics were repressed. The expression of proteins of 10.1, 15.2, 25.4, 27.5, 28.3, and 68.1 kDa were specifically induced under acid adaptation, while proteins of 12.3, 20.1 and 59.9 kDa were overexpressed. All proteins obtained by 2D-SDS-PAGE were also detected by 1D SDS-PAGE but at a higher induction rate (Table 1).

The rate of protein formed in MRS$_5$-adapted cells was determined by: (I) pulse labeling at the beginning of the adaptation period and sampling after 15, 30, 45 and 60 min (Figure 5A) and (II) pulse labeling after 15, 30, and 45 min of adaptation and sampling at the end of the incubation period (60 min) (Figure 5B). In the first case, the protein synthesis reached its maximum after 45 min and remained unchanged for 60 min (Figure 5A). In the second case, the synthesis of almost all proteins from 10.1 to 117.0 kDa took place when the pulse labeling with $^{35}$S-methionine was applied after 15 min; the synthesis rate decreased after 30 min and no labeled proteins were detected thereafter (Figure 5B).

Identification of Heat Shock Proteins

To identify known heat shock proteins (HSP) among the polypeptides expressed under acid adaptation, Western blotting was performed using antibodies against *E. coli* HSP:s (DnaK, DnaJ, GrpE, GroEL and GroES).

All the HSP homologues were only detected in acid-adapted cultures of *L. acidophilus* CRL 639 (Figure 6). Two proteins of 43 and 50 kDa cross-reacted with rabbit anti-DnaJ (Figure 6, lines 7 and 8), the smaller one being in accordance with other DnaJ proteins already described (Van Asseldonk *et al.*, 1993). Proteins of 24 and 70 kDa cross-reacted with rabbit anti-GroE (lines 5 and 6); the first one could be related to the GroE protein while the 70 kDa-immunoreactive molecule would be either an impurity of the proteins used for antibodies production or related to

A

![Figure 3. Effect of amino acid analogues on the rate of protein synthesis (A) or in β-gal and PepN activities (B). The analogues, DL-7-azatryptophan (▲), S-2-aminoethyl-L-cysteine (▼), and p-fluoro-DL-phenylalanine (●), were included during the adaption in MRS$_5$ at pH 5.0 (●). Cells adapted at pH 5.0 without analogs (C), non adapted cells (NA).](image-url)
Specific proteins play a role in the ATR of *L. acidophilus* CRL 639 to further survive acid stress conditions. Two theories have been postulated in relation to stress tolerance and protein synthesis. According to Mandelstam (1958), the protein synthesis would be a stabilizing factor which prevents ribosomal RNA degradation under environmental stress conditions (e.g., starvation) while Reeve et al. (1987) consider the role that specific proteins play in stress resistance. To choose between these alternatives, amino acid analogues were added to cells subjected to acid adaption (Figure 2). These conditions allow continued protein synthesis but the peptide formed might be defective (Fowden et al., 1967). The presence of amino acid analogues markedly decreased acid tolerance, probably due to the synthesis of faulty proteins rather than their effect in decreasing the rate of protein synthesis. To our knowledge, we are presenting the first evidence that LAB require active proteins for survival under acid stress. Similar results have been demonstrated in *E. coli* for long term survival of carbon-starved cells (Reeve et al., 1984). The decrease in protein degradation rate (from 4.7%/h to 3.0%/h) of bulk proteins in *L. acidophilus* CRL 639 during acid adaptation at pH 5.0 was dependent on protein synthesis indicating that specific proteins (e.g., chaperones) would be necessary for stabilizing some of the preexisting proteins.

Given this data, we wondered if *L. acidophilus* CRL 639 triggered similar mechanisms for survival in minimal and complex media. The ATR was only developed in complex media (MRS or Mm), and even then at different rates, while the cells in SM remained acid sensitive. It is not known which of the components present in MRS$_5$ are required for the full induction of the ATR system. In enteric bacteria, many genes require co-induction by low pH or specific molecules that presumably serve as substrates for the gene product (Pearson et al., 1997). Examples are mannose for *aniG* (Foster, 1993), lysine for *cadBA* (Auger et al., 1989), and formate for *hyd* (Birkman and Böck, 1989). Melnykovych and Snell (1958) reported that the addition of arginine, methionine, tyrosine, asparagine, glutamate, and iron to minimal media would allow full induction of arginine decarboxylase in *E. coli* which is involved in the cell homeostasis. This evidence reflects the strikingly different acid survival strategies within the bacteria kingdom according to their ecological niches.

The L-$[^{35}S]$methionine incorporation during acid adaptation of *L. acidophilus* CRL 639 made it possible to link the stress response to the induction of particular proteins. A good relationship between the 1D- and 2D-SDS PAGE:s was observed in the autoradiograms. The lower number of proteins (nine in total) separated in the latter case could be due the concentration of proteins used for loading in 2D-PAGE compared to 1D-PAGE. The protein profiles obtained for other microorganisms subjected to acid stress are quite different. In *Streptococcus thermophilus*, only ten proteins were expressed after acid shock (González-Marques et al. 1997) while *Leuconostoc oenos* only overexpressed one protein of 42 kDa which has been related to an acid tolerant phenotype (Guzzo et al., 1994). In contrast, *Lac. lactis* displays about 30 independent mutations which confer acid stress resistance (Rallu et al., 1996).

It has been proposed that the DnaK-DnaJ-GrpE chaperon team maintains nascent or other preexisting proteins in un-folded states, while the GroEL-GroES chaperone complex can interact with partially folded polypeptides and assist in additional folding (Hartl, 1992). Environmental stresses that induce some or all HSP:s are heat, ethanol, certain heavy metals,
puromycin, nalidixic acid, hydrogen peroxide as well as alkaline and acidic conditions (Van Bogelen et al., 1987). However, chaperone induction has only been described in lactobacilli in response to heat (Broadbent et al., 1997). In this study we have identified proteins of 10, 24, and 43 kDa that were immunologically reactive to the co-chaperons: GroES, GrpE, and DnaJ, respectively. Two faint bands of 70 and 55 kDa cross-reacted with GrpE and GroES antibodies, respectively, which could be linked to the proteins DnaK and GroEL. Hendrick and Hartl (1993) found significant similarity between the sequences of Cpn10 and Cpn60 (GroES and GroEL homologues). These observations could explain the cross reactivity of polyclonal antisera against GrpE (to DnaK) and GroES (to GroEL) found in \textit{L. acidophilus} CRL 639.

Interestingly, HSP's were only detected after adaptation at pH 5.0. Since DnaJ, GrpE and DnaK

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**Figure 4.** Autoradiograms of 2D-PAGE analysis of extracts of \textit{L. acidophilus} labeled with $[^{35}\text{S}]$methionine during acid adaption in MRS$_2$ at pH 5.0 (A) and MRS$_2$ at pH 6.0 (B) (control). The first dimension is the isoelectric separation in a range of pH 4.0 to pH 7.0. The second dimension is a SDS-PAGE with a linear polyacrylamide gradient from 10 to 15%. Arrows numbers indicate the spot number in Table 2.
act in concert, the genes for these proteins are often grouped on an operon that forms part of the heat regulon (HR). Genetic studies performed in *Lac. lactis* demonstrated that the structural gene encoding DnaK is situated in the *hrcA-grpE-dnaK* operon (Eaton et al., 1993) while GroEL is encoded in the *groES-groEL* operon (Kim and Batt, 1993). The *dnaJ* is not included in the *grpE-dnaK* operon of this bacteria, but both operons are still included in the HR (Eaton et al., 1993). Our preliminary data indicate that the *dnaJ* gene is encoded in the same operon as *dnaK* in *L. acidophilus* CRL 639 (unpublished results). This finding would explain why *dnaK* and *dnaJ* are induced together under acid adaptation (Figure 6) while in other lactobacilli *dnaJ* has been found to be constitutively induced (Broadbent et al., 1997).

It appears that low pH serves as an important signal for the induction of mechanisms that protect *L. acidophilus* against several environmental stresses. The molecular regulation of HSP in *L. acidophilus* CRL 639 during acid adaptation is under study.

### Experimental Procedures

#### Bacterial Strain and Growth Conditions

The strain *L. acidophilus* CRL 639, isolated from fermented dairy products, was obtained from the Culture Collection of CERELA. Cultures were routinely carried out at 37°C in MRS broth (De Man, 1960) containing 0.5% (w/v) glucose (MRS₅) at an initial pH of 6.5 under CO₂ (5%). Incorporation of labelled (³H and ³⁵S) amino acids were performed in the following media: MRS₅, Mm (modified MRS₅) broth in which meat peptone and meat extract were replaced by 0.5% (w/v) casein hydrolysate and a synthetic medium, SM (Hebert et al., 2000). When necessary, 0.5% casein hydrolysate (Sigma) and 0.5% (w/v) casamino acids (Sigma) were added.

#### Acid Adaption

A 16h-old culture of *L. acidophilus* CRL 639 in MRS₅ was used to inoculate the same media at an A₆₅₀ of 0.1 in MRS₅ broth, unless otherwise stated. The cells were grown to an A₆₅₀=0.25 (early exponential phase), harvested by centrifugation at 5000 g and resuspended at 37°C for 60 min in the different media (SM, Mm and MRS₅) adjusted to pH 5.0 with concentrated lactic acid. Non-adapted

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**Table 2. Properties of the induced proteins at pH 5.0 separated by 2D-PAGE.**

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*pl, estimated isoelectric point.

†AU, maximal absorbance.

V, volume (AU x mm²); A, spot volume of acid adapted cells at pH 5.0 during 60 min; NA, spot volume of non-adapted cells (pH 6.0); as subscripts.

§SI, specific induction during acid adaptation.

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**Figure 5. Autoradiograms of 1D-SDS-PAGE of adapted cells pulse labeled at pH 5.0 with [³⁵S]methionine during 15, 30, 45, or 60 min (A) or after 15, 30, or 45 min (B).**

**Figure 6. Western blot analysis of extracts separated by 1D-SDS-PAGE from *L. acidophilus* CRL 639 with polyclonal rabbit antibodies raised against recombinant DnaJ (lanes 7 and 8), GrpE (lanes 5 and 6) and GroES (lanes 1 and 2) of *Escherichia coli* and mouse monoclonal antibodies raised against GroEL (lanes 3 and 4) and DnaK (lanes 9 and 10) of *E. coli*. Non-adapted cells (lanes 1, 3, 5, 7 and 9); cells adapted at pH 5.0 during 60 min (lanes 2, 4, 6, 8 and 10) in MRS₅.**
cells resuspended at pH 6.0 were used as control (Lorca et al., 1998). Chloramphenicol and the amino acid analogues β-7-saturotryptophan, p-fluoro-ty, phenylalanine, and S-2-aminoethyl-cysteine (CN) were added (50 μg/ml each) at the beginning of acid adaptation.

Challenge Conditions and Viability Determinations

For challenge assays, cells were harvested by centrifugation (5000 g for 10 min) and resuspended in fresh MRSb at pH 3.0 (adjusted with lactic acid) for 60 min at 37°C. Serial dilutions of each sample were plated in mass in MRS agar (MRS broth with 1.5% agar) by the plate dilution method, and plates were incubated at 37°C for 2 h. Results were expressed as colony-forming units (cfu) as a function of time and No is the c.f.u./ml at zero time (without acid shift).

Enzyme Activities

The β-galactosidase (β-gal) activity was determined according to Noh and Gilliland (1993) with o-nitrophenyl-β-D-galactopyranoside (Sigma Chemical Co.) as substrate. One unit (UE) of β-gal activity was defined as the amount of enzyme that released 1 μmol of o-nitrophenol per min. Specific activity was expressed as UE per milligram of protein (UE/mg).

Leucyl-aminopeptidase (PepN) activity was determined at 40°C using L-leucine-[14C] (Amersham Pharmacia Biotech) as substrate. One unit (UE) of PepN activity was defined as the amount of enzyme that released 1 μmol of L-leucine per minute at pH 7.0 (adjusted with NaOH). The reaction was stopped by the addition of 0.5 ml of 80% acetic acid. The samples were centrifuged and the resulting supernatant was analyzed for radioactivity.

Western Blot Assays

Protein extracts from L. acidophilus CRL 639 were separated by SDS-PAGE. Following Western Blot, proteins were blotted onto nitrocellulose paper, blocked in 5% nonfat dry milk, and probed with the primary antibody. Secondary antibody was conjugated with horseradish peroxidase (HRP) at a dilution of 1:2000, and antibodies were detected by reaction in 50 mM sodium acetate (pH 5.2), containing 2% (v/v) Tween 20, 0.25% of milk and 2% (v/v) Pharmalyte range 4–7 as recommended by the manufacturer (Amersham Pharmacia Biotech) and the sample (50 μg) was included during this period. Protein bands were considered as significantly overexpressed when the integrated intensity ratios were greater than 2.0.

Acid Tolerance Response in Lactobacillus acidophilus

Preparation of Cell Extracts and 1D SDS-PAGE

Harvested cells were washed twice with 0.1 M potassium phosphate buffer (pH 7.0) and disrupted by grinding with glass beads. Protein concentration was determined according to Bradford (1976). The cell extract was used for protein analysis by sodium dodecyl sulfate-polyacrylamide gels electrophoresis (SDS-PAGE) (30 μg proteins per line) according to Laemmli (1970), modified by using a 10–15% acrylamide gel gradient (BioRad) and molecular weight markers in a range of 14 to 94 kDa (BioRad). Polyacrylamide gels were silver stained for total protein detection (Oakley et al., 1980). Quantitative measurements were based on peak areas of the densitograms obtained by using an Ultrascan XL densitometer with the Gel Scan XL 2.1 software (Pharmacia LKB, Uppsala, Sweden). The protein bands were considered as significantly overexpressed when the integrated intensity ratios were greater than 2.0.

2D-PAGE

The first isoelectric focusing was performed using the Multiphor II horizontal electrophoresis apparatus (Amersham Pharmacia Biotech). Immobiline DryStrip linear immobilised pH gradient (IPG) gel strips (11 cm) with a pH range of 4–7 were rehydrated in 250 μl sample buffer (SB) containing 8 M urea, 2% (v/v) Nonidet P-40, 10 mM DTT (Sigma) and 2% (v/v) Pharmalyte range 4–7 as recommended by the manufacturer (Amersham Pharmacia Biotech) and the sample (50 μg) was included during this period. The gel was cast overnight at room temperature in a reswelling cassette with strips covered with silicone oil to avoid evaporation. The proteins were focused overnight at 15°C under a protective layer of silicone oil using 300 V for 1 h, a linear ramp from 300 to 3500 V during 1.5 h and 3500 V for 3.5 h. After focusing, the IPG gel strips were immediately subjected to a second dimension electrophoresis. The gel and separation conditions were as described above. Immediately before SDS-PAGE, the IPG strips were gently shaken in 10 ml of 50 mM Tris-HCl (pH 6.8), 2% (v/v) SDS, 26% (v/v) glycerol and bromophenol blue for 2 x 15 min. DTT (100 mg) was added to the first equilibration solution, and iodoacetamide (250 mg) to the second. The IPG strips were quickly loaded on top of the gel, and the separation was performed at 15°C at 500 V until the bromophenol blue dye front reached the bottom of the gel. After SDS-electrophoresis the proteins were transferred to immobilized PVDF membranes (0.45 μm, Micron Separations Inc) using a semi-dry electroblotter (Ancos) for 1.5 h at a constant current of 0.8 mA/cm². Molecular weight standards (BioRad) including proteins ranging from 14.3 to 97.4 kDa were treated identically. After transfer- ring, the membranes were dried and exposed to X-ray films (Hyperfilm p-max, Amersham) for 21 days and films were developed with Kodak D19. The spots were quantified by densitometry as described above.

Determination of Protein Degradation

An overnight culture of L. acidophilus CRL 639 was inoculated in MRSb at an A650 = 0.1. The culture was grown for one generation, at which time 1 g (8.25 mM) of L-[14C]-[5-Th]leucine/ml was added. The culture was grown for another generation in the presence of the radioactive label and then harvested, washed twice with 0.1 M Tris-HCl buffer (pH 7.0) and calibrated to cell dry weight (0.06 g/l) in MRSb broth previously adjusted at pH 7.0 and calibrated to cell dry weight (0.06 g/l) in MRSb broth previously adjusted at pH 7.0, and resuspended in the adaption media Mm (CRL 639 was grown exponentially at 37°C in MRSb medium to an A650 = 0.2. Cells were harvested, washed twice with 0.1 M Tris-HCl buffer (pH 7.0), and resuspended in the adaption media Mm and MRSb, which were adjusted at pH 5.0 or 6.0. At various time points, 150 μl of culture were transferred to an Eppendorf tube containing 15 μCi (355 kBq) of [35S]methionine. After 10 min, unlabelled methio nine was added at a final concentration of 0.8 mg/ml to complete synthesis of labelled proteins (Klisstrup et al., 1997). After 2 min of incubation, 10 μl of chloramphenicol (20 mg/ml) was added, and the cells were pelleted by centrifugation, washed twice with 0.1 M Tris-HCl buffer (pH 7.0) and disrupted by grinding with glass beads.

Determination of Protein Synthesis

An overnight culture of L. acidophilus CRL 639 was inoculated in MRSb at an A650 = 0.1. Cultures were grown to an A650 = 0.25. The cells were harvested, washed twice with 0.1 M Tris-HCl buffer (pH 7.0) and resuspended to 0.06 g/l in MRSb broth previously adjusted at pH 5.0 or 6.0 with lactate (Sigma). At zero time of adaptation, 5 μCi (9.25 mMq) of L-[14C]-[5-Th]leucine/ml was added to the culture. Then, at zero time and at desired intervals thereafter, duplicate TCA precipitates were formed and counted as described above. Protein synthesis was expressed as the increase in TCA-precipitable counts with time (Reeve et al., 1984).

[35S]Methionine Labelling of Polypeptides

L. acidophilus CRL 639 was grown exponentially at 37°C in MRSb medium to an A650 = 0.25. Cells were harvested, washed twice with 0.1 M Tris-HCl buffer (pH 7.0), and resuspended in the adaption media Mm and MRSb, which were adjusted at pH 5.0 or 6.0. At various time points, 150 μl of culture were transferred to an Eppendorf tube containing 15 μCi (355 kBq) of [35S]methionine. After 10 min, unlabelled methionine was added at a final concentration of 0.8 mg/ml to complete synthesis of labelled proteins (Klisstrup et al., 1997). After 2 min of incubation, 10 μl of chloramphenicol (20 mg/ml) was added, and the cells were pelleted by centrifugation, washed twice with 0.1 M Tris-HCl buffer (pH 7.0) and disrupted by grinding with glass beads.
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