**Metabolism of 5-Methyltetrahydrofolate by *Lactobacillus casei***

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The metabolism of 5-[Me-14C]methyltetrahydrofolate in *Lactobacillus casei* proceeded oxidatively with incorporation of label into purine and thymidylate derivatives. No labelled methionine was formed. (l)-5-Methyltetrahydrofolate, the natural isomer, was not a substrate for the *L. casei* folylpoly-γ-glutamate synthetase although the unnatural (d)-isomer was slowly metabolized to the diglutamate form.

**INTRODUCTION**

We have previously shown that pteroylpolyglutamates, once transported, are better growth promoters of *Lactobacillus casei* than pteroylmonoglutamates (Shane & Stokstad, 1976). The rate-limiting step in the utilization of pteroylpolyglutamates by this organism is transport into the cell, while intracellular metabolism, and not transport, is rate-limiting with pteroylmonoglutamates. *In vitro* studies have also shown that pteroylpolyglutamates are often better substrates than the corresponding monoglutamates for folate-requiring enzymes (Burton & Metzenberg, 1975; Cheng, Shane & Stokstad, 1975; Coward et al., 1974, 1975; Curthoys & Rabinowitz, 1972; Kisliuk, Gaumont & Baugh, 1974; Powers & Snell, 1976; Salem, Pattison & Foster, 1972; Whitfield, Steers & Weissbach, 1970).

To investigate which step in pteroylmonoglutamate metabolism might be rate-limiting, the metabolism of 5-[Me-14C]methyl-H₄PteGlu and 5-methyl-H₄[3H]PteGlu (for nomenclature, see Methods) were compared in order to assess the turnover of intracellular folate via various metabolic pathways. Although two mechanisms have been described for 5-methyl-H₄PteGlu formation in bacteria involving the reduction of 5,10-methylene-H₄PteGlu or the direct transfer of a methyl group from trimethylsulphonium to H₄PteGlu (Wagner et al., 1967), the only known route for the metabolism of methyltetrahydrofolates is via methionine synthesis (Taylor & Weissbach, 1973) but attempts to detect methionine synthetase activity in *L. casei* have proved unsuccessful (Galivan, 1971; Kisliuk, 1971).

**METHODS**

**Nomenclature.** The abbreviations used are: PteGlu, pteroylglutamic acid, folic acid; PteGluₙ, pteroylpolymo- to pteroyloligo-γ-L-glutamic acid, n indicating the number of glutamic acid residues; H₄PteGluₙ, 5,6,7,8-tetrahydropteroylmono- to 5,6,7,8-tetrahydropteroylolo-γ-L-glutamic acid. The symbols (l) and (d) are used to denote the natural and unnatural diastereoisomers of H₄PteGluₙ, respectively, due to the asymmetric centre at the C-6 position, and do not indicate optical activity.

**Materials.** (l)-5-[Me-14C]Methyl-H₄PteGluₙ (n = 1, 3, 5 and 7) (specific activity 47 mCi mmol⁻¹), (d)-5- methyl-H₄[3H]PteGlu (sp. act., 500 mCi mmol⁻¹), and folic acid 7-polyglutamates PteGluₙ₋₇, [3H]PteGluₙ₋₇ (sp. act., 4 mCi mmol⁻¹), and PteGluₙ₋₇[14C]Glu-Glu (n = 0, 1, 2 and 3) (sp. act., 100 to 500 μCi mmol⁻¹) were synthesized and purified as described previously (Shane & Stokstad, 1976). (d)-5-[Me-14C]Methyl- H₄PteGlu (sp. act., 54 mCi mmol⁻¹), 1-[Me-14C]methionine (sp. act., 56 mCi mmol⁻¹) and S-adenosyl-L-[Me-14C]methionine (sp. act., 55 mCi mmol⁻¹) were obtained from Amersham/Searle (Arlington Heights, Illinois, U.S.A.); [8-3H]adenine (sp. act., 14 Ci mmol⁻¹), [8-3H]guanine (sp. act., 5.5 Ci mmol⁻¹), [6-3H]uracil
Unlabelled purine and pyrimidine derivatives were obtained from Sigma, DNAase (bovine pancreas; 1500 units mg\(^{-1}\)) from Worthington, and RNAase (bovine pancreas; 64 units mg\(^{-1}\)) and RNAase-CB (predominantly \(T_1\), remainder \(T_2\); 21 units mg\(^{-1}\)) from Calbiochem.

Organism and growth conditions. *Lactobacillus casei* (ATCC7469) was cultured as described previously (Tamura et al., 1972) with PteGlu (2·3 mg) added to the media.

Uptake and metabolism of folates, purine and pyrimidine bases, and methionine. Bacteria were harvested by centrifuging from growth media in late exponential phase (20 to 24 h at 37 \(^{\circ}\)C) and were washed with, and resuspended in 0·05 mm-K\(_2\)HPO\(_4\)/100 mm-sodium acetate, adjusted to pH 6 with H\(_2\)PO\(_4\), and containing 1% (w/v) glucose and 5 mm-mercaptoethanol. Transport of labelled bases and methionine was measured as described previously for folates (Shane & Stokstad, 1975, 1976). Bacterial dry weight was estimated by \(E_{660}^{\text{mg}}\).

For metabolism studies, *L. casei* suspensions (0·2 mg dry wt ml\(^{-1}\)) in acetate/phosphate buffer pH 6 (containing glucose and mercaptoethanol), were preincubated for 15 min at 37 \(^{\circ}\)C with labelled methylenetetrahydrofolates or methionine, then filtered (HA filters, Millipore Corp., 0·45 \(\mu\)m pore size), washed with buffer, resuspended in fresh buffer (0·4 mg dry wt ml\(^{-1}\)) and incubated at 37 \(^{\circ}\)C with shaking. Samples (5 ml) were removed at 0, 1, 2, 5 and 24 h and filtered, and the bacteria (plus filter) were resuspended in 0·1 M-potassium phosphate buffer pH 7, containing 0·2 m-mercaptoethanol. Intracellular labelled compounds were extracted by boiling for 5 min, and insoluble material was removed by centrifuging and resuspended in water (5 ml). Mercaptoethanol was added to the cell-free medium.

The metabolism of labelled purine and pyrimidine bases was studied in a similar manner except that the bacteria were preincubated with the \(^{3}\)H-labelled bases (5 \(\mu Ci\) ml\(^{-1}\)) for 2 h before incubating with \((\beta\)-5-\([\text{Me}^{14}\text{C}]\text{methyl-H}\text{PteGlu (0·5 \(\mu m\)}\) for 15 min. After resuspension and incubation in fresh buffer for 2 h, the bacteria were filtered, washed, and extracted with boiling 0·1 M-potassium phosphate buffer pH 7, containing 0·2 m-mercaptoethanol (2 ml). Insoluble material, collected by centrifuging, was washed 10 times with H\(_2\)O (5 ml), resuspended in 20 mm-acetate buffer pH 4·5 (1 ml), containing RNAase (50 units) and RNAase-T\(_2\) (15 units), and incubated at 37 \(^{\circ}\)C for 12 h. The mixtures were heated at 100 \(^{\circ}\)C for 5 min, cooled, centrifuged and the supernatants (termed the RNAase extracts) were collected. Extracellular extracts, after addition of mercaptoethanol (0·2 m), were adjusted to pH 4 with acetic acid. Active charcoal (50 mg ml\(^{-1}\)) was added and the mixtures were stirred for 15 min. The charcoal was then collected by centrifuging, washed twice with H\(_2\)O, and extracted with 60% (v/v) ethanol containing 0·1 M-NH\(_2\)OH (50 ml g\(^{-1}\)). Charcoal was removed by filtration and the ethanol extract was evaporated to dryness under reduced pressure at 40 \(^{\circ}\)C. The residue was dissolved in 0·1 M-potassium phosphate buffer pH 7, containing 0·2 m-mercaptoethanol (2 ml).

Portions of the various fractions were added to vials together with a Triton X-100/toluene (1:2, v/v) scintillation mixture (Goldmark & Linn, 1970). Counting efficiencies, determined by external standardization or by a channels ratio method, were about 80% for \(^{14}\)C and 25% for \(^{3}\)H. In dual labelling experiments, the \(^{14}\)C efficiency was about 35%.

Identification of labelled compounds. Extracts were chromatographed on Sephadex G-25 and DEAE-cellulose (DE52, Whatman) before and after folyl-\(\gamma\)-glutamyl carboxypeptidase (conjugase) treatment as previously described (Buehring, Tamura & Stokstad, 1974; Shane & Stokstad, 1975; Tamura et al., 1972). Individual labelled peaks were rechromatographed together with appropriate standards. The chromatographic behaviour of folates on Sephadex G-25 and DEAE-cellulose has been described in detail (Buehring et al., 1974; Shin, Buehring & Stokstad, 1972a; Shin, Williams & Stokstad, 1972b).

Identification of 3'-ribonucleotides. 3'-Ribonucleotide standards were added to the RNAase extracts and portions were lyophilized to dryness, resuspended in H\(_2\)O (20 \(\mu l\)) and applied to cellulose thin-layer plates (Eastman 13255). Ribonucleotides were separated by two-dimensional chromatography using isobutyric acid/0·5 M-NH\(_2\)OH (5:3, v/v) and 2-propanol/6 M-HCl (7:3, v/v) as solvents (Delk & Rabinowitz, 1975; Nishimura, 1972). Standard compounds were detected by ultraviolet absorption (254 nm) and labelled compounds by scintillation autography (Contractor & Shane, 1969; Klagsbrun, 1973).

Treatment of kinetic data. \(K_m\) and \(V_{\text{max}}\) values were calculated by an unweighted non-linear regression method (Wilkinson, 1961) with six cycles of reiteration (Cleland, 1967). Where appropriate, \(V_{\text{max}}\) values are expressed as micromolar increase in intracellular concentration per minute, assuming an intracellular water volume of 4 ml (g dry wt bacteria\(^{-1}\)) (Kepes & Cohen, 1962).
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**RESULTS**

**General characteristics of 5-methyl-\(\text{H}_4\)PteGlu metabolism**

After bacteria had been preincubated with labelled 5-methyl-\(\text{H}_4\)PteGlu for 15 min, more than 95% of the intracellular label chromatographed on Sephadex G-25 at the position of 5-methyl-\(\text{H}_4\)PteGlu. The initial exit rates of radioactive label after resuspending the bacteria in fresh buffer were 0.01 to 0.02 min\(^{-1}\).

The Sephadex G-25 elution profiles obtained with extracts from bacteria incubated with \((l)-5-[\text{Me}^{14}\text{C}]\text{methyl-\(\text{H}_4\)PteGlu showed that within 1 h about 90% of the \(\text{^14C}\)-label had been transferred to four major metabolites (peaks I, III, IV and V, Fig. 1) together with some high molecular weight material eluting at the void volume. About 20% of the label at 1 h was not extracted from bacteria by boiling buffer. By 2 h, practically no \(\text{^14C}\)-label in the bacteria or medium eluted at the 5-methyl-\(\text{H}_4\)PteGlu position (peak VII, Fig. 1). Treatment of the intracellular extracts with conjugase did not affect the Sephadex G-25 elution profiles of \(\text{^14C}\)-labelled metabolites, indicating that none of the labelled compounds was a folylpolyglutamate. Also, no labelled metabolites comparable to compounds I to VI were found when bacteria were incubated with 5-methyl-\(\text{H}_4\)[\(\text{PH}\)]PteGlu (Fig. 3), indicating that they were non-folate in nature. This was confirmed by their chromatographic properties on DEAE-cellulose (not shown). With the exception of unmetabolized 5-methyl-\(\text{H}_4\)PteGlu, none of the labelled compounds chromatographed at the position of

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**Fig. 1.** Metabolism of \((l)-5-[\text{Me}^{14}\text{C}]\text{methyl-\(\text{H}_4\)PteGlu by Lactobacillus casei. Bacteria were pre-}

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incubated for 15 min with \((l)-5-[\text{Me}^{14}\text{C}]\text{methyl-\(\text{H}_4\)PteGlu (0.45 \text{mM; sp. act., 47 mCi mmol}^{-1}) to an intracellular \(\text{^14C}\)-labelled vitamin concentration of 99 \text{mM, then filtered, washed, and resuspended in fresh buffer and reincubated with shaking, as described in Methods. At 1 (--), 2 (---), 5 (-----) and 24 h (---), portions were removed, filtered and extracted with boiling buffer, and intracellular extract (equivalent to 0.8 mg dry wt bacteria) and cell-free medium (2 ml) were applied to Sephadex G-25 columns (200x0.7 cm). The columns were eluted with 0.1 M-phosphate buffer pH 7, containing 0.2 M-mercaptoethanol, and fractions (1-7 ml) were collected from the void volume (\(V_0\) as indicated by the elution position of Blue Dextran 2000. The columns were pre-calibrated with standards whose approximate elution positions were as follows: PteGlu (fraction 9), 5-methyl-H\(_4\)PteGlu (14), PteGlu (16), PteGlu (20), PteGlu (26), 10-formyl-H\(_4\)PteGlu (33), 10-formyl-PteGlu (35), PteGlu (35), 5-methyl-H\(_4\)PteGlu (49), PteGlu (55), dTTP (16), dTMP (23), ATP (23), methionine (23), formaldehyde (24), formate (24), d'T (27), \(\text{^3H}_2\)O (27), p-aminobenzoylglutamate (28), S-adenosylmethionine (31), AMP (37), adenosine (51), adenine (64).**
Fig. 2. Metabolism of \((dl)-5-[Me-^{14}C]methyl-H_4PteGlu\) by \textit{Lactobacillus casei}. Experimental conditions were as described in Fig. 1, except that bacteria were preincubated for 15 min with \((dl)-5-\left[{Me-^{14}C}\right]methyl-H_4PteGlu (0.66 \mu\text{M}; \text{sp. act.,} 54 \text{mCi mmol}^{-1})\) to an intracellular \(^{14}C\)-labelled vitamin concentration of 167 \(\mu\text{M}\). The chromatographic patterns of metabolites at 5 (-----) and 24 h (-----) are shown.

Fig. 3. Metabolism of \((dl)-5\text{-methyl-}H_4[^{3}H]PteGlu\) by \textit{Lactobacillus casei}. Experimental conditions were as described in Fig. 1, except that bacteria were preincubated for 15 min with \((dl)-5\text{-methyl-H}_4[^{3}H]PteGlu (0.44 \mu\text{M}; \text{sp. act.,} 500 \text{mCi mmol}^{-1})\) to an intracellular \(^{14}C\)-labelled vitamin concentration of 156 \(\mu\text{M}\). The chromatographic patterns of metabolites at 2 (-----), 5 (-----) and 24 h (-----) are shown. The numbers 1-6 indicate the elution positions of \(\text{5-methyl-}H_4\text{PteGlu}_{1-4}\) (---) respectively.

known folate standards. Also, no labelled dTMP, methionine or \(S\)-adenosylmethionine or its major labelled breakdown product, thiomethyladenosine, was detected.

The metabolism of \((dl)-5-\left[{Me-^{14}C}\right]methyl-H_4PteGlu\) was similar to that observed with \((l)-5\text{-}[Me-^{14}C]\text{methyl-}H_4\text{PteGlu}\) except that at 5 h, the bacteria and medium still contained a large amount of \(5\text{-}[Me-^{14}C]\text{methyl-}H_4\text{PteGlu}\) which presumably represented the \((d)\)-isomer of the vitamin (Fig. 2). This unnatural diastereoisomer is transported at approximately the same rate as the natural \((l)\)-isomer (Shane & Stokstad, 1976). In addition, at 5 h the bacteria contained a labelled metabolite (A, Fig. 2) not detected in bacteria preincubated with \((l)-5\text{-methyl-}H_4\text{PteGlu}\) and by 24 h most of the \((d)\)-5-methyl-\(H_4\text{PteGlu}\) had disappeared and another labelled metabolite (B, Fig. 2) had appeared in the bacteria and medium. The elution position of compound B was unaffected by conjugase treatment and it was probably a breakdown product of \((d)-5\text{-methyl-}H_4\text{PteGlu}\). After conjugase treatment, compound A, which eluted at the position of a pteroyldiglutamate, had identical chromatographic properties to authentic \((d)-5\text{-methyl-}H_4\text{PteGlu}\) both on Sephadex G-25 and DEAE-cellulose. Compound A was thus identified as \((d)-5-\left[{Me-^{14}C}\right]methyl-H_4\text{PteGlu}_5\).

The Sephadex G-25 elution profiles obtained with bacteria preincubated with \((dl)-5\text{-methyl-H}_4[^{3}H]PteGlu\) showed that by 2 h there was a variety of \(^{3}H\)-labelled metabolites (Fig. 3). None of these was similar to metabolites I to VI obtained with \((l)-5\text{-}[Me-^{14}C]\text{methyl-}H_4\text{PteGlu}\) (Fig. 1) and no \(^{3}H\)-labelled material eluted at the void volume. The large 5-methyl-\(H_4\text{PteGlu}\) peak (Fig. 3) presumably represented the \((d)\)-isomer. After conjugase treatment of the intracellular extract, practically all the \(^{3}H\)-label eluted from DEAE-
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Cellulose at the position of 5-methyl-H₄PteGlu and H₄PteGlu. After 2 h the bacteria contained folates with glutamate chain lengths of up to six, the tetraglutamate (l-isomer) and monoglutamate (d-isomer) predominating. By 5 h, further elongation up to pteroylhexaglutamate had occurred (Fig. 3) and over 80% of the intracellular ³H-labelled vitamin was identified (after conjugase treatment) as 5-methyl-H₄PteGlu and H₄PteGlu. Compound A, observed with bacteria incubated with (dl)-5-[Me-¹⁴C]methyl-H₄PteGlu (Fig. 2), was also a labelled metabolite of (dl)-5-methyl-H₄[³H]PteGlu (Fig. 3) and again its chromatographic properties on Sephadex G-25 and DEAE-cellulose, before and after conjugase treatment, indicated that it was (d)-5-methyl-H₄PteGlu₂. By 24 h, most of the intracellular folate had been released into the medium. Intracellular folates had glutamate chain lengths of up to eight and (d)-5-methyl-H₄[³H]PteGlu₁,₂ had disappeared. The chromatographic properties of the two major compounds found in the medium at 2, 5 and 24 h (Fig. 3) were unaffected by conjugase treatment and represented breakdown products, probably ³H-labelled _p_-aminobenzoylglutamate and ³H₂O. The material eluted in the higher polyglutamate region (fractions 5 to 16, Fig. 3), however, was hydrolysed by conjugase to monoglutamate derivatives. Possibly the presence of these polyglutamates in the medium at 24 h reflected losses in cell viability under the conditions of the experiment, rather than release by the bacteria.

*Methionine metabolism by *L. casei*

Although no labelled methionine was detected in bacteria metabolizing 5-[Me-¹⁴C]methyl-H₄PteGlu, methionine is probably rapidly converted to other compounds. To investigate this possibility further, transport and metabolism studies were carried out with L-[Me-¹⁴C]methionine in an analogous manner to those previously described for (l)-5-methyl-H₄PteGlu.

The kinetics of methionine uptake by *L. casei* under these conditions (acetate/phosphate buffer pH 6, containing glucose and mercaptoethanol; see Methods) were best described by two uptake systems with _K_m values of 0.14 μM and 150 μM and _V_max values of 4.0 and 120 μM min⁻¹, respectively. No attempt was made to optimize the conditions for uptake or to ascertain if mercaptoethanol in the buffer had any effect on transport.

If *L. casei* metabolizes 5-methyl-H₄PteGlu by transfer of the methyl group to homocysteine, then a similar pattern of ¹⁴C-labelled metabolites would be expected with [Me-¹⁴C]methionine, as 90% of the (l)-5-[Me-¹⁴C]methyl-H₄PteGlu in preincubated cells was metabolized within 1 h (Fig. 1). However, when bacteria were preincubated with [Me-¹⁴C]methionine to about the same intracellular levels and reincubated in fresh buffer, over 80% of the intracellular label was not extracted with boiling buffer, compared with about 20% when bacteria were incubated with ¹⁴C-labelled folate.

The Sephadex G-25 elution profiles obtained with extracts from bacteria incubated with L-[Me-¹⁴C]methionine (Fig. 4) were very different from the profiles obtained with bacteria metabolizing (l)-5-[Me-¹⁴C]methyl-H₄PteGlu (Fig. 1).

*Properties of labelled bacterial metabolites not solubilized by buffer extraction*

Various treatments were tried to solubilize the ¹⁴C-labelled metabolites that were not extracted by boiling buffer from *L. casei* metabolizing (l)-5-[Me-¹⁴C]methyl-H₄PteGlu. About 60% of the label was solubilized after treatment with pancreatic RNAase, about 11% by DNAase, and the remainder by heating with 1 M-perchloric acid. None of these treatments effectively solubilized ¹⁴C-labelled metabolites derived from L-[Me-¹⁴C]methionine, suggesting that the metabolism of 5-methyl-H₄PteGlu proceeded via its oxidation with the incorporation of its one-carbon moiety into purines and pyrimidines rather than via methionine synthesis. To examine this conclusion further, *L. casei* was incubated with labelled purines and pyrimidines, and the metabolites derived from these bases were compared with those derived from 5-methyl-H₄PteGlu.
Fig. 4. Metabolism of L-[Me-14C]methionine by Lactobacillus casei. Experimental conditions were as described in Fig. 1, except that bacteria were preincubated for 15 min with L-[Me-14C]methionine (7 μM) to an intracellular concentration of 138 μM. The chromatographic patterns of 14C-labelled metabolites in the intracellular and extracellular extracts at 1 (---), 2 (-----) and 5 h (----) are shown. Standards used to calibrate the column were methionine (A) and 3H2O (B).

Fig. 5. Sephadex G-25 chromatography of labelled metabolites solubilized by RNAase T2 treatment of insoluble material derived after extraction of Lactobacillus casei with boiling buffer. Experimental conditions were as described in Methods. Labelled metabolites solubilized by RNAase treatment of cell debris derived from 10 mg dry wt bacteria were chromatographed on Sephadex G-25 as described in Fig. 1. (a) Patterns of 14C-labelled metabolites derived from (l)-5-[Me-14C]-methyl-H4PteGlu after incubating bacteria in the presence (----) and absence (-----) of unlabelled adenosine (0.1 mM). (b) Patterns of 3H-labelled metabolites of [3H]adenine (-----) and [3H]uracil (-----). Standards used to calibrate the columns were 3'-UMP (A), 3H2O (B), 3'-AMP (C), 3'-GMP (C) and adenine (D).

Table 1. Distribution of labelled metabolites in Lactobacillus casei extracts after incubation with (l)-5-[Me-14C]methyl-H4PteGlu and 3H-labelled bases

<table>
<thead>
<tr>
<th>Extract</th>
<th>5-Methyl-H4PteGlu*</th>
<th>Adenine</th>
<th>Guanine</th>
<th>Uracil</th>
<th>Cytosine</th>
<th>Thymine</th>
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<tr>
<td>Intracellular</td>
<td>250</td>
<td>65</td>
<td>531</td>
<td>66</td>
<td>1</td>
<td>107</td>
</tr>
<tr>
<td>Insoluble material</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(i) RNAase T2 extract</td>
<td>25</td>
<td>74</td>
<td>747</td>
<td>72</td>
<td>1</td>
<td>7</td>
</tr>
<tr>
<td>(ii) Residue</td>
<td>250</td>
<td>25</td>
<td>282</td>
<td>29</td>
<td>5</td>
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<td>1660</td>
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<td>544</td>
<td>176</td>
<td>1660</td>
<td>184</td>
<td>8</td>
<td>596</td>
</tr>
</tbody>
</table>

* Values for the labelled metabolites of (l)-5-[Me-14C]methyl-H4PteGlu represent the mean of five experiments.
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Metabolism of purine and pyrimidine bases

Tritium-labelled bases, with the exception of cytosine, were rapidly taken up by L. casei. Initial uptake rates under the conditions described for methionine transport were 10.1 μM min⁻¹ for adenine (initial concentration in medium 0.27 μM), 86.8 μM min⁻¹ for guanine (10 μM), 13.8 μM min⁻¹ for uracil (0.19 μM), 0.08 μM min⁻¹ for cytosine (0.18 μM), and 10.4 μM min⁻¹ for thymine (0.5 μM). The poor uptake of cytosine was not investigated further but may have been a result of ³H exchange at the 5-position due to metabolism.

*Lactobacillus casei* was preincubated for 2 h with the ³H-labelled bases and for 15 min with (l)-5-[Me-¹⁴C]methyl-H₄PteGlu, and was then resuspended in fresh buffer and incubated for 2 h. The distribution of radioactive label in the bacteria and medium at this time is shown in Table I. Approximately 60% of the non-extractable bacterial ¹⁴C-label (insoluble material, Table I) and over 80% of the adenine, guanine, and uracil metabolites were solubilized by RNAase T₂, while less than 2% of the thymine metabolites were solubilized by this treatment. When the above experiment was repeated with unlabelled nucleosides (0.1 mM) in the preincubation and resuspension buffers, ¹⁴C-label in the RNAase extract was reduced in the presence of adenosine while label in the fraction not solubilized by RNAase was reduced in the presence of thymidine. Uridine had no effect. The insoluble material thus appeared to contain denatured RNA and DNA. This was confirmed by Sephadex G-25 chromatography as ¹³C-labelled metabolites solubilized by RNAase treatment co-eluted with standard 3'-AMP and 3'-GMP (Fig. 5a) and at the same position as the labelled adenine derivative solubilized by this treatment (Fig. 5b). The early-eluting labelled adenine metabolite (Fig. 5b, fraction 29) was ³H₂O. Two-dimensional thin-layer chromatography demonstrated that the ¹³C-label was incorporated into the purine ring. All the ¹⁴C-label chromatographed at the positions of 3'-AMP and 3'-GMP and no methylated purine derivatives or 3'-TMP were detected.

The Sephadex G-25 chromatographic profiles obtained with bacterial and extracellular extracts (Table I) are shown in Fig. 6. The ¹⁴C-labelled peak I derived from (l)-5-[Me-¹⁴C]-methyl-H₄PteGlu coincided with a labelled metabolite derived from uracil (Fig. 6c, fraction 18) and thymine (Fig. 6d, fraction 18) and eluted just prior to an adenine derivative (Fig. 6a, fraction 19). Material in peak I was a thymidylate derivative as a variety of uracil derivatives were detected which were not labelled with ¹⁴C (Fig. 6c, fractions 10, 14) and its synthesis was decreased when bacteria were preincubated with unlabelled thymidine (0.1 mM) but was unaffected by preincubation with unlabelled uridine (0.1 mM). Peak I co-eluted from Sephadex G-25 with UTP, CTP and dTTP. However, the ¹⁴C-labelled compound and [³H]thymine metabolite in this peak (Fig. 6d) eluted from DEAE-cellulose at the position of dTMP (Fig. 7a, fraction 15). No [¹⁴C]- or [³H]dTTP was detected. With bacteria incubated with [³H]uracil, about 90% of the ³H-label in peak I (Fig. 6c) eluted from DEAE-cellulose at the position of dTMP and about 10% at the position of UTP. Peak I therefore contained a thymidylate derivative. It also contained a more electronegative ¹³C-labelled compound (Fig. 7a, fraction 40) which co-eluted with a [³H]purine derivative (Fig. 6a, fraction 19).

The remaining ¹⁴C-labelled peaks, with the exception of unmetabolized (l)-5-[Me-¹⁴C]-methyl-H₄PteGlu, corresponded almost entirely to purine derivatives (Fig. 6a, b). The major intracellular peak derived from [³H]adenine was contaminated with ³H₂O (Fig. 6a, fraction 29). This was not observed in the extracellular extract (Fig. 6b) as the medium was concentrated and desalted before chromatography by absorption and elution from active charcoal. ¹⁴C-Labelled material not absorbed by charcoal from the medium eluted at the position of formaldehyde (Fig. 6b, fraction 28) and condensed with dimedone.

Rechromatography of labelled bacterial compounds in peaks II to V (Fig. 6a) on DEAE-cellulose (Fig. 7b, c, d, e) in this case with bacteria preincubated with guanine instead of adenine, demonstrated that nearly all the ¹⁴C-labelled compounds were purine metabolites.
Fig. 6. Metabolism of (l)-5-[Me-14C]methyl-H4PteGlu and 3H-labelled bases by Lactobacillus casei. Experimental conditions were as described in Table 1. Intracellular and extracellular extracts (equivalent to 20 mg dry wt bacteria), obtained by incubating L. casei with (l)-5-[Me-14C]methyl-H4PteGlu and 3H-labelled bases (as indicated), were chromatographed on Sephadex G-25 as described in Fig. 1: 14C-labelled compounds (-----); 3H-labelled compounds (---). Extracellular extracts (b) were concentrated by absorption and elution from active charcoal as described in Methods; the elution pattern of 14C-labelled metabolites not absorbed by charcoal is also shown (-----). The columns were precalibrated with standards whose elution positions were as follows: dTTP (fraction 15), UTP (16), CTP (17), NADP (22), ATP (26), ADP (32), FAD (34), NAD (34), AMP (41), GMP (41), adenosine (53), adenosine (64), formate (25), formaldehyde (26), 3H2O (28), 10-formyl-H4PteGlu (34) and 5-methyl-H4PteGlu (51).

Fig. 7. DEAE-cellulose chromatography of labelled metabolites of (l)-5-[Me-14C]methyl-H4PteGlu and 3H-labelled bases. Experimental conditions were as described in Fig. 6. Individual peak fractions obtained by Sephadex G-25 chromatography of intracellular extracts (Fig. 6) were diluted to 30 ml with H2O and applied to 25 x 0.9 cm DEAE-cellulose columns equilibrated with 0.01 M-phosphate buffer pH 6. Each column was eluted by an exponential phosphate gradient formed with 0.01 M-phosphate buffer (100 ml) in a closed mixing chamber attached to a reservoir containing 0.5 M-phosphate buffer pH 6. Fractions (30 ml) are numbered from the beginning of the elution; 14C-labelled compounds (-----); 3H-labelled compounds (---). (a) Elution pattern obtained with intracellular labelled material derived from (l)-5-[Me-14C]methyl-H4PteGlu and [3H]thymine that eluted at the position of peak I from Sephadex G-25 (Fig. 6d, fraction 18). (b-e) Equivalent data for peaks II-V, respectively, obtained from bacteria incubated with (l)-5-[Me-14C]methyl-H4PteGlu and [3H]guanine (equivalent to Fig. 6a, fractions 23, 27, 33 and 39, respectively). The elution positions of unlabelled standards applied with the samples are indicated on the figures. The elution positions of unlabelled standards applied with the samples are indicated on the figures. The elution positions of unlabelled standards applied with the samples are indicated on the figures. The elution positions of unlabelled standards applied with the samples are indicated on the figures. The elution positions of unlabelled standards applied with the samples are indicated on the figures.
Although differences in specific labelling due to different incubation times and differences in initial metabolic routes were observed, practically all the $^3$H- and $^{14}$C-label co-eluted.

The major purine metabolites in peaks II to IV were not further identified (Fig. 7b, c, d). Peak III contained some ATP/GTP (Fig. 7c, fraction 39) and labelled material not absorbed by the column consisted of $^3$H$_2$O and $^{14}$C-formaldehyde. Peak IV contained some ADP/GDP (Fig. 7d, fraction 31) while most of the labelled material in peak V was identified as AMP/GMP (Fig. 7e, fraction 23). The overall distribution of $^{14}$C-label in this experiment was as follows: thymidylate derivatives (15%), purine derivatives (43%), formaldehyde (11%), and 5-methyl-H$_4$PteGlu (31%). No labelled 10-formyl-H$_4$PteGlu was detected. Practically all the labelled formaldehyde was found in the medium and presumably resulted from degradation of 5,10-methylene-H$_4$PteGlu under the conditions of this experiment.

**DISCUSSION**

Although pteroylmono- and pteroyldiglutamates are the forms preferred for transport of folate (Shane & Stokstad, 1975, 1976), in practically every case investigated pteroylpolyglutamates are the predominant, if not the only, intracellular forms of the vitamin (Baugh, Braverman & Nair, 1974; Brown, Davidson & Scott, 1974a; Buehring et al., 1974; Houlihan & Scott, 1972; LaVoie et al., 1975; Leslie & Baugh, 1974; Shin, Buehring & Stokstad, 1974a; Shin et al., 1972b). In *L. casei*, octoglutamates predominate if the organism is grown on low levels of folate (Brown et al., 1974b; Buehring et al., 1974); if high levels of folate are supplied in the medium, shorter chain length folates are found, predominantly the tetruglutamate derivative (Baugh et al., 1974). Pteroylpolyglutamates were originally thought to be intracellular storage forms of the vitamin. However, in vitro studies have shown them to be equally or more effective than monoglutamates as enzyme substrates. One of these enzymes, a B$_12$-independent methionine synthetase, which is present in some micro-organisms (Taylor & Weissbach, 1973; Whitfield et al., 1970) but not in mammalian tissues (Cheng et al., 1975; Coward et al., 1975), either only functions with folypolyglutamate substrates or utilizes the monoglutamate derivative extremely poorly. In vivo studies have also shown that while the rate-limiting step in the utilization of pteroylpolyglutamates by *L. casei* is their transport into the cell, once taken up, they are more effectively utilized for growth than the monoglutamate derivatives (Shane & Stokstad, 1976). The rate-limiting step in the utilization of monoglutamates is some step other than transport.

*Lactobacillus casei* preincubated with (l)-5-[Me-$^{14}$C]methyl-H$_4$PteGlu metabolized this compound to a variety of labelled metabolites which were non-folate in nature. These were identified as purine and thymidylate derivatives by co-chromatography on Sephadex G-25 and DEAE-cellulose with metabolites derived from $[^3]$Hthymine and $[^3]$HPurines. Delk & Rabinowitz (1975) have shown that folate is involved in the methylation of uridine in RNA of *Streptococcus faecalis*. We did not detect any labelled 3'-TMP in *L. casei* RNA hydrolysates or any methylated purines, demonstrating that the one-carbon moiety of 5-[Me-$^{14}$C]methyl-H$_4$PteGlu was incorporated into the purine ring. This does not rule out the possibility that folate is involved in the methylation of RNA in *L. casei* as our technique was probably not sensitive enough to detect small amounts of labelled methylated bases. In respect to this, we were unable to detect labelled methylated bases in the RNA of cells incubated with $[^3]$Hadenine or $[^3]$Huracil.

No labelled methionine was detected in these experiments and completely different labelled metabolites were obtained with bacteria incubated with 1-[Me-$^{14}$C]methionine. These data indicate that the initial step in the metabolism of 5-methyl-H$_4$PteGlu by *L. casei* proceeds via its oxidation rather than through methionine synthesis. This is different from mammalian metabolism where the one-carbon moiety of 5-methyl-H$_4$PteGlu is transferred to methionine (Nixon et al., 1973) and oxidation to 5,10-methylene-H$_4$PteGlu does not occur under physiological conditions (Kutzbach & Stokstad, 1971).
Although no labelled pteroylpolyglutamates were detected in cells incubated with (l)-5-[Me-14C]methyl-H4PteGlu, (d)-5-[Me-14C]methyl-H4PteGlu was slowly metabolized to the diglutamate form, but not to higher polyglutamates. In human lymphocytes, however, labelled polyglutamates were not formed from (dl)-5-[Me-14C]methyl-H4PteGlu (LaVoie, Tripp & Hoffbrand, 1974), although in this case the (d)-isomer may not have been transported. (dl)-5-Methyl-H4[3H]PteGlu was metabolized to labelled polyglutamate forms, mainly to (l)-5-methyl-H4PteGluₙ and H₄PteGluₙ (n ≤ 8) and (d)-5-methyl-H₄PteGlu₂, suggesting that (l)-5-methyl-H₄PteGlu is not a substrate for the L. casei folyypolyglutamate synthetase, and that removal of its one-carbon moiety is necessary before folypolyglutamates can be synthesized.

Little is known of the specificity of the enzymes responsible for the formation of pteroylpolyglutamates. Sakami et al. (1973) reported the presence of two enzymes in Neurospora crassa, one specific for the formation of pteroyldiglutamate and the other for synthesis of longer chain polyglutamates and both specific for H₄PteGlu derivatives. Escherichia coli contains a 10-formyl-H₄PteGlu synthetase (Masurekar & Brown, 1975) which will also utilize a variety of other pteroylmonoglutamates but not 5-methyl-H₄PteGlu while Gawthorne & Smith (1973), in studies with mixed folate diastereoisomers, reported that 5-formyl-H₄PteGlu, 5-methyl-H₄PteGlu and H₄PteGlu were substrates for the enzyme in sheep liver. Shorter chain length polyglutamates of PteGlu in L. casei (Shin, Buhring & Stokstad, 1974b) and methotrexate (Baugh, Krumdieck & Nair, 1973; Shin et al., 1974b) in rat liver have also been reported. In a previous study (Shane & Stokstad, 1975), we showed that L. casei metabolized low levels of PteGlu to a variety of H₄PteGlu polyglutamates. All these data suggest the presence of two synthetases, with the diglutamate-forming enzyme having a specificity for a variety of pteroylmonoglutamates and the higher polyglutamate synthetase having a specificity for H₄PteGluₙ.

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