CORRECTION

Tetrahydrofolate and tetrahydromethanopterin compared: functionally distinct carriers in C_1 metabolism

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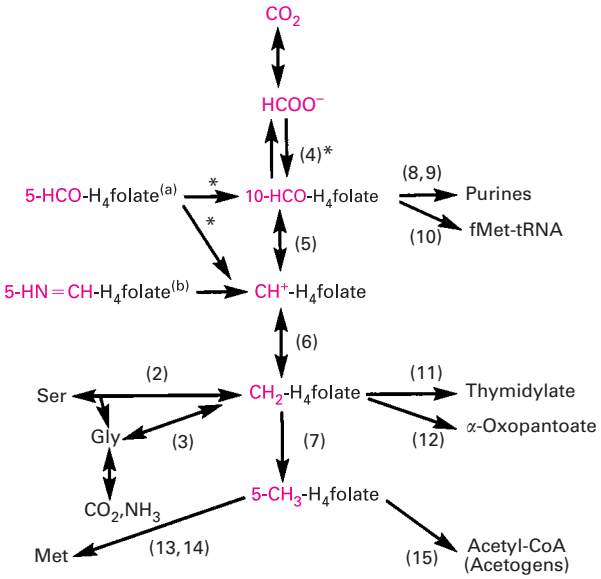
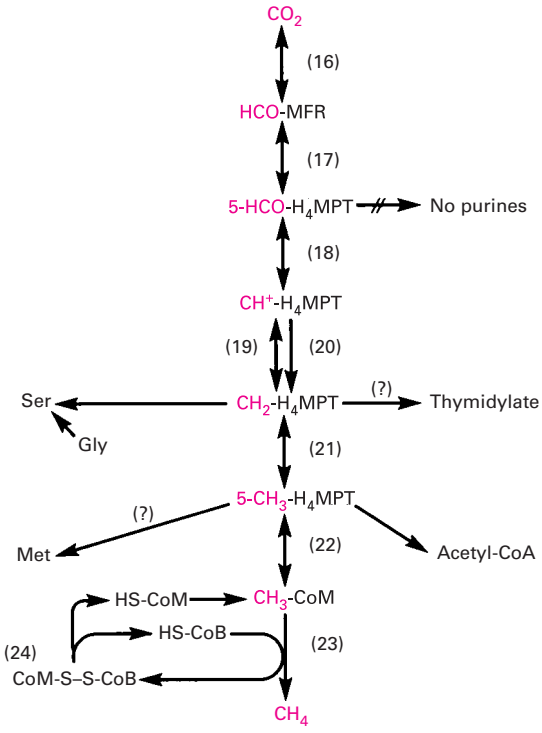
Owing to a printer's error in the above paper, Scheme 1 (on page 612), Scheme 2 (on page 615) and Figure 2 (on page 618) were reproduced incorrectly in that areas of the Schemes and Figure which should have been printed in red were omitted. The correct Schemes and Figure are reproduced below with their appropriate legends:



Scheme 1 Map of C_1 flux through H_4folate

Single-headed arrows denote reactions that are normally unidirectional. Double-headed arrows denote reactions that flow in either direction, in different organisms or under different metabolic conditions. Numbers indicate the correspondingly numbered reactions in Table 2, in which redox and other cofactors and names of enzymes are given. (Reaction 1 of Table 2 is not included in the Figure.) Asterisks denote reactions in which ATP is consumed (liberating ADP and P_i). Reaction (4) consumes ATP, but the reverse reaction is most commonly catalysed by a separate hydrolase. However, reaction (4) as listed in Table 2 may run in reverse in purine fermenters [39]. Notes: [a] 5-HCO-H_4folate is metabolically derivable from formylglutamate [34] and is a minor source of H_4folate in human nutrition [183]; [b] 5-formimino-H_4folate is metabolically derived from formiminoglutamate (from histidine degradation in mammals [35]) or formiminoglycine (from purine degradation in some bacteria ([39] and references cited therein). The C_1 group of 5-formimino-H_4folate is sufficiently activated to be convertible into CH^+-H_4folate by a cyclodeaminase without hydrolysis of ATP [184], whereas enzymic conversion of 5-HCO-H_4folate into CH^+-H_4folate or 10-HCO-H_4folate involves consumption of ATP ([36]; see the text).



Scheme 2 Map of C_1 flux through H_4MPT

Conventions for arrows are as in Scheme 1. Numbers indicate the correspondingly numbered reactions in Table 3, in which the redox and other co-reactants and names of enzymes are given. The crossed arrow indicates that this pathway is thought not to occur, and the queries denote uncertainties concerning aspects of the indicated reactions; see under the section entitled 'Biosynthetic roles for H_4MPT?'.

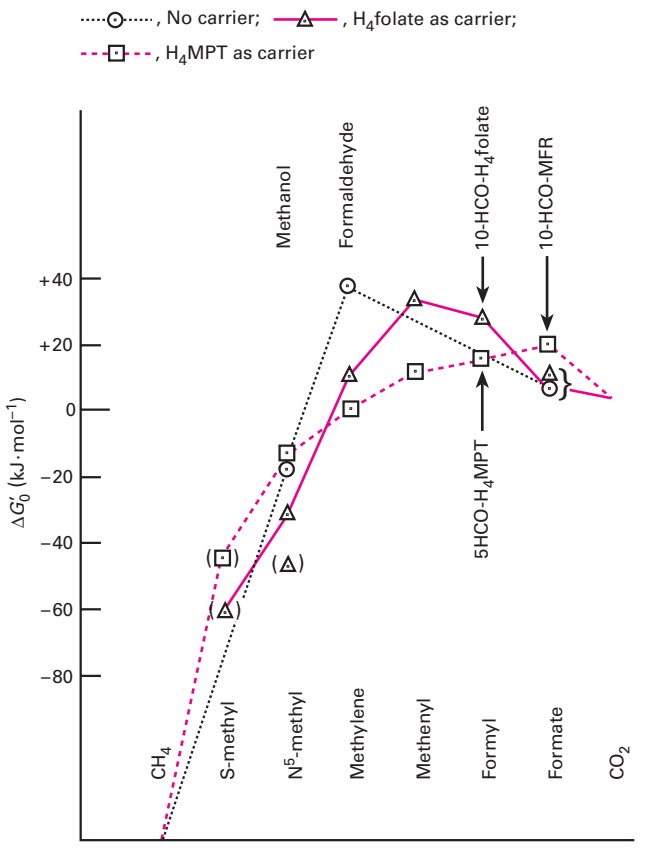


Figure 2 Free-energy profiles of C_1 reduction pathways, based on 'best available' thermodynamic values as discussed in the text

Reduction is from right to left. The data are those in Tables 4(a)–(c) for hydrogen under standard conditions as reductant, and without ATP for reaction (4) (i.e. reaction 4a in Table 4b). These values allow direct comparability between the pathways; see the text. The relationships between compounds in the different pathways are defined in the text and in Tables 1–3. (For example, in the H_4folate pathway CO_2 is first reduced to formate, whereas in the H_4MPT pathway CO_2 is first reducted to HCO-MFR.) At the methyl-oxidation level the triangle below the continuous line is derived from the early value for the MTHFR reaction (reaction 7) [41], whereas the triangle on the line is from the recent value [72] (see the text and Table 4b). $\Delta G'_0$ values for the methyl-transfer reactions (13) and (22) have been reported. In a detailed study of reaction (22), a $\Delta G'_0$ of -10 kJ·mol^{-1} was found for methyl transfer from H_4MPT to cobamide, and -20 kJ·mol^{-1} from cobamide to CH_3-S-CoM, i.e. -30 kJ overall [108]. The only study on the equilibrium of reaction (13) [189] gave a value for K_{eq} of 7×10^{-6} in the direction of homocysteine and CH_3-H_4folate formation, which converts to -29 kJ·mol^{-1} in the direction of methionine synthesis. The potential of the S-methyl group in methionine and CH_3-S-CoM might be expected to be fairly similar, but not necessarily identical, because CoM also contains a strongly negative sulphate group [10] which might conceivably influence the overall reactivity of the compound. Given that the equilibrium points of the S-methyltransferase reactions (13) and (22) are far to the right in the directions written, the reported free-energy values may be viewed as being somewhat approximate.

There was an error in the legend to Table 1 in this paper. On page 611, legend to Table 1, line 4, reference [78] has been cited incorrectly in place of reference [77]. The correct text should read: '…derivatives of H_4MPT [77]…'.

In addition, there was an error in the legend to Table 3 in this paper. On page 614, legend to Table 3, line 1, the text incorrectly refers to Figure 3 in place of Scheme 2. The correct text should read: '…Reactions are numbered as in Scheme 2 and the text…'.