Using stable and radioisotope tracers, and computer simulation of resulting isotopic tracer data, the pathway of synthesis of 3-dimethylsulfoniopropionate (DMSP) was found to proceed via a hitherto unidentified route from methionine. The intermediates are: 4-methylthio-2-oxobutyrate (MTOB), 4-methylthio-2-hydroxybutyrate (MTHB) and 4-dimethylsulfonio-2-hydroxybutyrate (DMSHB). All algae tested (including Enteromorpha intestinalis, Tetraselmis sp., Melosira nummuloides and Emiliania huxleyi) metabolized supplied $^{33}$S-methionine to $^{35}$S-MTOB, $^{33}$S-MTHB, $^{35}$S-DMSHB and $^{35}$S-DMSP, and metabolized supplied $^{35}$S-DMSHB to $^{35}$S-DMSP. Enzymes catalyzing the first three enzymes of the pathway were characterized. These include a methionine:2-oxoglutarate-dependent aminotransferase with a high affinity for methionine, an NADPH-dependent reductase, and an S-methyltransferase. In certain phytoplankton, synthesis of the first intermediate may be augmented by a methioninerpyruvate-dependent aminotransferase and methionine oxidase. DMSP (a sulfur-containing osmolyte) and glycine betaine (a nitrogen-containing osmolyte) are reciprocally regulated by nitrogen supply in Tetraselmis. Accumulation of DMSP under nitrogen-limitation may in part involve derepression of methionine aminotransferase and methionine oxidase. No evidence for the involvement of S-methylmethionine or DMSP-aldehyde as pathway intermediates was found in marine algae. The pathway of DMSP synthesis in marine algae is therefore different from that found in higher plants.
To disseminate methods for computer simulation of isotopic tracer data, a computer modeling www site (acknowledging ONR grant support) has been established:

http://www.hort.purdue.edu/cfpesp/models/models.htm

This site includes interactive Java applets and downloadable Visual Basic programs that simulate the flux of $^{35}$S-Met to $^{35}$S-DMSP in Enteromorpha intestinalis, and $^{35}$S-S-methylmethionine to $^{35}$S-DMSP in the higher plant, Spartina alterniflora.

CONCLUSIONS: The key intermediates in the DMSP synthesis pathway from methionine (MTOB, MTHB and DMSHB) are the same in four diverse groups of marine algae tested, although species differ with respect to the relative contributions of 2-oxoglutarate- and pyruvate-dependent Met aminotransferases and Met oxidase in MTOB synthesis. The pathway of synthesis of DMSP in marine algae is completely different from that in higher plants, where S-methylmethionine and DMSP-aldehyde are key intermediates. The occurrence of a high affinity methionine aminotransferase that is depressed by N starvation may begin to explain why DMSP accumulation is stimulated by N-deficiency in marine algae.

SIGNIFICANCE: The work has established a novel pathway of synthesis of DMSP in marine algae. DMSP produced in oceans by marine algae is recognized to be a precursor of atmospheric dimethylsulfide (DMS) that plays an important role in the global sulfur cycle. The identification of DMSHB as an intermediate in the algal pathway raises the possibility that this compound may also contribute to DMS emissions from marine algae. Methods for computer simulation of isotopic tracer data were developed and have been made available to the scientific community.

PUBLICATIONS AND ABSTRACTS (for total period of grant):


FINAL REPORT

GRANT #: N00014-96-1-0366

PRINCIPAL INVESTIGATOR: Dr. David Rhodes

INSTITUTION: Purdue University

GRANT TITLE: Biosynthesis of 3-Dimethylsulfonipropionate in Marine Algae

AWARD PERIOD: 1 Jan 1996 - May 30 1999 (36 months plus 6 month no cost extension = 42 months total)

OBJECTIVE: To participate in a 4-investigator collaboration (Hanson, Gage, Leustek, Rhodes) to elucidate the pathway of 3-dimethylsulfonipropionate (DMSP) in marine algae, including identification of intermediates and enzymes of the pathway in the macroalga Enteromorpha intestinalis, and three diverse marine phytoplankton species; Tetraselmis sp., Melosira nummuloides and Emiliania huxleyi. Develop quantitative models describing flux of through the pathway and its competing branches, and investigate regulation of the pathway.

APPROACH: In vivo stable and radioactive isotope tracer experiments in combination with various chromatographic (ion exchange, TLC, TLE) and mass spectrometric methods, were employed to identify and quantify the intermediates and elucidate precursor-product relationships in the DMSP synthesis pathway. Computer simulation was employed to quantify metabolic fluxes. Enzyme assays, using radiotrace labeled substrates, were used to identify enzymes mediating the reactions.

ACCOMPLISHMENTS: In collaboration with Hanson, Gage and Leustek, the pathway of synthesis of DMSP in Enteromorpha intestinalis, Tetraselmis sp., Melosira nummuloides, and Emiliania huxleyi was shown to proceed via the following common steps: methionine (Met) → 4-methylthio-2-oxobutyrate (MTOB) → 4-methylthio-2-hydroxybutyrate (MTHB) → 4-dimethylsulfonio-2-hydroxybutyrate (DMSHB) → 3-35S-dimethylsulfoniopropionate (DMSP). All algae tested synthesized 35S-MTOB, 35S-MTHB, 35S-DMSHB and 35S-DMSP from supplied 35S-Met, and metabolized supplied 35S-DMSHB to 35S-DMSP.

Computer modeling showed that the 35S labeling kinetics of MTHB and DMSHB are quantitatively consistent with these compounds being intermediates in the metabolism of 35S-Met to 35S-DMSP in E. intestinalis, but may be compartmentalized between metabolically active and inactive (storage) pools. Modeling also showed that the first step must compete effectively with protein synthesis in vivo, suggesting that this step must have a high affinity for Met. Enzymes catalyzing the first three steps in the pathway were identified in E. intestinalis; a 2-oxoglutarate-dependent Met aminotransferase with a high affinity for Met (30 μM), an NADPH-dependent MTOB reductase, and an S-adenosylmethionine-dependent MTHB S-methyltransferase. Consistent with a 2-oxoglutarate-dependent aminotransferase at the head of the pathway in E. intestinalis, 15N-methionine was metabolized predominantly to 15N-glutamate in this species. In vivo 18O-labeling data indicate
that the final step (DMSHB \(\rightarrow\) DMSP) is catalyzed by an oxygenase in Enteromorpha, but the enzyme catalyzing this reaction was not characterized.

Certain of the marine phytoplankton were found to possess chromatographically distinct aminotransferase isoforms. Two separate 2-oxoglutarate-dependent Met aminotransferases were characterized in Tetraselmis, whereas only a single form of this enzyme was found in Emiliania and Melosira. However, distinct pyruvate and 2-oxoglutarate-dependent aminotransferases were found in Emiliania, with the former being induced in late stationary phase. A methionine oxidase that catalyzes MTOB synthesis from Met [Met \(\rightarrow\) MTOB + H\(_2\)O + O\(_2\) \(\rightarrow\) MTOB + H\(_2\)O\(_2\) + NH\(_3\)] was also detected in Melosira and Tetraselmis. In vivo \(^{15}\)N-Met and \(^{15}\)NH\(_3\) labeling experiments (with and without the inhibitors of transamination and ammonia assimilation, aminooxyacetate and methionine sulfoximine, respectively) showed that Met is largely (67%) reversibly transaminated to glutamate in Tetraselmis, with the remainder (33%) either deaminated to NH\(_3\) via the catalytic action of methionine oxidase (~26%) or methioninase (~7%) [Met \(\rightarrow\) 2-ketobutyrate + NH\(_3\) + CH\(_3\)-SH]. The 2-ketobutyrate derived from the action of methioninase is rapidly converted to isoleucine. NH\(_3\) generated in the methionine oxidase and methioninase reactions is reassimilated predominantly via the glutamine synthetase-glutamate synthase cycle (>95%), and in part via glutamate dehydrogenase (<5%).

A double-labeling procedure (using methyl-CD\(_3\), \(^{14}\)N-Met supplied to Tetraselmis cells pregrown on \(^{15}\)N-nitrate for several generations to fully label all N moieties with \(^{15}\)N) was developed for simultaneously determining aminotransferase, Met oxidase, methioninase and activated methyl cycle [CD\(_3\)-Met \(\rightarrow\) CD\(_3\)-S-adenosylmethionine \(\rightarrow\) S-adenosylhomocysteine \(\rightarrow\) homocysteine (+ CH\(_3\)-THF) \(\rightarrow\) CH\(_3\)-Met (+ THF)] fluxes in vivo. Computer modeling of the time-courses of changes in abundance of CD\(_3\), \(^{14}\)N-Met, CH\(_3\), \(^{14}\)N-Met, CD\(_3\), \(^{15}\)N-Met and CH\(_3\), \(^{15}\)N-Met species showed that the activated methyl cycle flux is approximately twice the Met aminotransferase flux in Tetraselmis.

Evidence was obtained that endogenous accumulation of Met inhibits flux to DMSP in Tetraselmis; this inhibition must occur at a step later than transamination/oxidation in the pathway, but earlier than the DMSHB \(\rightarrow\) DMSP step because DMSHB does not accumulate when the free Met pool is elevated. The precise mechanism of this inhibition has not been elucidated, but may involve inhibition of the MTHB S-methyltransferase by Met, or a product of Met metabolism (e.g. S-adenosylhomocysteine). Fluxes to DMSP and the nitrogenous osmolyte, glycine betaine, are reciprocally regulated by N supply in Tetraselmis. Stimulation of DMSP accumulation by N limitation may in part involve derepression of Met aminotransferases and Met oxidase, depletion of the cellular glutamate pool [favoring a shift in the equilibrium of the 2-oxoglutarate + Met \(\leftrightarrow\) Glu + MTOB aminotransferase reaction towards MTOB synthesis], and alleviation of the MTHB:S-methyltransferase from inhibition by Met (or a metabolite derived therefrom).

No evidence was found for the involvement of S-methylmethionine (SMM) or DMSP-aldehyde in DMSP synthesis in any of the marine algae tested. This contrasts to higher plants where DMSP synthesis proceeds via the following route: Met \(\rightarrow\) SMM \(\rightarrow\) DMSP-aldehyde \(\rightarrow\) DMSP.
A new route for synthesis of dimethylsulphoniopropionate in marine algae

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The 3-dimethylsulphoniopropionate (DMSP) produced by marine algae is the main biogenic precursor of atmospheric dimethylsulphide (DMS)\(^2\). This biogenic DMS, formed by bacterial and algal degradation of DMSP\(^4,5\), contributes about \(1.5 \times 10^{13}\) g of sulphur to the atmosphere annually\(^1\), and plays a major part in the global sulphur cycle, in cloud formation and potentially in climate regulation\(^1,3\). Although DMSP biosynthesis has been partially elucidated in a higher plant\(^6,7\), nothing is known about how algae make DMSP except that the whole molecule is derived from methionine\(^8,12\). Here we use in vivo isotope labelling to demonstrate that DMSP synthesis in the green macroalga Enteromorpha intestinalis proceeds by a route entirely distinct from that in higher plants. From methionine, the steps are transamination, reduction and S-methylation to give the novel sulphonium compound 4-dimethylsulphonio-2-hydroxybutyrate (DMSHB), which is oxidatively decarboxylated to DMSP. The key...
intermediate DMSPHB was also identified in three diverse phytoplankton species, indicating that the same pathway operates in other algal classes that are important sources of DMS. The fact that a transamination initiates this pathway could help explain how algal DMSP (and thereby DMS) production is enhanced by nitrogen deficiency.

Many marine phytoplankton species and intertidal macroalgae accumulate DMSP as an osmolyte and cryoprotectant, particularly when salinity is high and nitrogen is limiting. We investigated DMSP synthesis first in the green macroalgae Enteromorpha intestinalis, which is rich in DMSP (~20u.m.c.lg~ fresh weight) when grown in normal sea water. To identify biosynthetic intermediates between methionine (Met) and DMSP, we followed the metabolism of a small dose of [35S]Met. The main fates of [35S]Met were conversion to DMSP and incorporation into protein (Fig. 1a). Two stable compounds acquired [35S] rapidly and lost it as the [35S]Met dose was depleted, as expected for DMSP pathway intermediates; these were 4-methylthio-2-hydroxybutyrate (MTHB) and its S-methylated derivative DMSPHB, a new natural product (Fig. 1b).

The most plausible route from Met to these compounds is via the unstable 2-oxo acid, 4-methylthio-2-oxobutyrate (MTOB). We therefore tested for [35S] incorporation into MTOB by using a gentle extraction method (Table 1, method A) or by converting it to a stable derivative (Table 1, method B). Both approaches confirmed that MTOB acquired and lost [35S] in parallel with MTHB.

Computer modelling confirmed that the labelling kinetics of MTOB, MTHB and DMSPHB were quantitatively consistent with roles as intermediates.

None of the other compounds monitored had labelling kinetics expected of intermediates in DMSP synthesis. S-Methylmethionine (SMM) and 3-dimethylsulphonio propane-aldehyde, both known to be DMSP synthesis intermediates in higher plants, acquired little or no [35S] (Fig. 1b). 3-Methylthiopropylamine, which has been proposed to be an intermediate in algae, labelled as would be expected for a minor end product (Fig. 1b). Labelling of another hypothetical intermediate, 3-methylthiopropionate, varied from undetectable to comparable to that of MTOB in experiments with different lots of E. intestinalis. This can be attributed to a catalytic route involving oxidative decarboxylation of MTOB, which occurs in algae and other plants that do not contain DMSP, as well as in animals, and whose activity can vary with nutritional status.

These data support the pathway $\text{Met} \rightarrow \text{MTOB} \rightarrow \text{MTHB} \rightarrow \text{DMSPHB} \rightarrow \text{DMSP}$, but are not consistent with a route involving SMM. To test this, [35S]-labelled SMM, MTHB and DMSPHB were supplied (Table 2). SMM was scarcely metabolized, providing additional evidence that it is not an intermediate. MTHB was mainly converted to methionine, which in turn was incorporated into protein—a fate of MTHB well known in other plants and in animals. Some [35S] from MTHB also entered DMSP, consistent with MTHB being an intermediate; however, an indirect route via DMSPHB was identified in three phytoplankton species, indicating that the same pathway operates in other algal classes that are important sources of DMS. The fact that a transamination initiates this pathway could help explain how algal DMSP (and thereby DMS) production is enhanced by nitrogen deficiency.

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methionine cannot be excluded. As would be expected for a late intermediate in the pathway, DMSHB was metabolized efficiently to DMSP and to little else.

Stable isotope labelling was used to confirm and extend the radiotracer findings. We first verified the presence of the novel intermediate DMSHB and tested whether its conversion to DMSP involves an oxygenase reaction, perhaps analogous to that mediated by lactate oxidase. To do this, *E. intestinalis* was given \([U-^{13}\text{C}]\text{Met}\) in an atmosphere containing \(^{16}\text{O}_2\) or \(^{18}\text{O}_2\). Gas chromatography–mass spectrometry (GC-MS) with selected ion monitoring (SIM) revealed a small pool of DMSHB that became labelled with \(^{13}\text{C}\) in five or six positions, but not with \(^{18}\text{O}\) (Fig. 2). Fast atom bombardment (FAB)-MS showed that most of the newly synthesized DMSHP had four or five \(^{13}\text{C}\) atoms and that 30–40% of this DMSHB became labelled with \(^{18}\text{O}\) (Fig. 2b). Note that recycling of the \([^{13}\text{C}]\)homocysteine moiety formed in methylation reactions would yield Met (and hence DMSHB and DMSP) with an unlabelled methyl group. The presence of such Met was confirmed by GC-MS, and modelling showed the observed proportions of \([^{13}\text{C}]\) and \([^{13}\text{C}]\)DMSP conformed to expectations for recycling of the \([^{13}\text{C}]\)homocysteine moiety generated by the methylation step in DMSHP synthesis. Also, photosynthetically generated \(^{13}\text{C}\) atoms and that 30–40% of this DMSHB became labelled with \(^{18}\text{O}\) (Fig. 2b). Note that recycling of the \([^{13}\text{C}]\)homocysteine moiety formed in methylation reactions would yield Met (and hence DMSHB and DMSP) with an unlabelled methyl group. The presence of such Met was confirmed by GC-MS, and modelling showed the observed proportions of \([^{13}\text{C}]\) and \([^{13}\text{C}]\)DMSP conformed to expectations for recycling of the \([^{13}\text{C}]\)homocysteine moiety generated by the methylation step in DMSHP synthesis. Also, photosynthetically generated \(^{13}\text{O}\) lowers the intracellular abundance of \(^{18}\text{O}\). The \(^{13}\text{C}\) and \(^{18}\text{O}\) data are thus fully consistent with a pathway in which the last step is an oxygenase-mediated oxidative decarboxylation of DMSHB.

We also used stable isotope labelling to investigate the conversion of methionine to MTOB. *E. intestinalis* was given \([^{35}\text{S}]\text{Met}\) (5 \(\mu\text{mol per 100 mg}\)) and GC-MS was used to follow the labelling of amino acids. Glutamate acquired \(^{15}\text{N}\) readily (7.0% abundance at 2 h), as did asparagine and alanine, but the amide group of glutamine did not (<1% abundance at 2 h). This is consistent with transamination of methionine, but not with oxidative deamination: the \(^{15}\text{NH}_2\) lost from a deamination reaction would have led to labelling of glutamine amide via the action of glutamine synthetase. The operation of glutamine synthetase in *E. intestinalis* was confirmed by supplying \(^{15}\text{NH}_4^+\) (1 \(\mu\text{mol per 100 mg}\)) and showing that glutamine amide nitrogen was rapidly labelled (42% \(^{15}\text{N}\) abundance at 2 h). The conversion of MTHB to Met (Table 2) indicates that the Met → MTOB step is reversible, which is consistent with transamination.

Collectively, the data for the chlorophyll macroalgae *E. intestinalis* indicate that the pathway for synthesis of DMSP is that shown in Fig. 3. We tested for this pathway in marine planktonic species as these are major producers of DMSP and DMS. For this, we chose a prymnesiophyte (*Emiliania huxleyi*), a diatom (*Melosira nummuloidea*) and a prasinophyte (*Tetraselmis loides*). These algae all contained small pools of the key intermediate DMSHB which acquired label from \([^{35}\text{S}]\)Met and lost it as the \([^{35}\text{S}]\)Met was consumed (Fig. 4). All of them metabolized supplied \([^{35}\text{S}]\)DMSP to \([^{35}\text{S}]\)DMSHB (Fig. 4, inset). It is therefore likely that they have the same pathway as *E. intestinalis*.

### Table 1 Metabolism of \([^{35}\text{S}]\)Met by *E. intestinalis*

<table>
<thead>
<tr>
<th>Extraction method</th>
<th>Incubation time (h)</th>
<th>(^{35}\text{S}) incorporation (nCi per 100 mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td><strong>MTOB</strong></td>
</tr>
<tr>
<td>A</td>
<td>0.5</td>
<td>17.3</td>
</tr>
<tr>
<td></td>
<td>4.0</td>
<td>6.2</td>
</tr>
<tr>
<td>B</td>
<td>0.5</td>
<td>18.9</td>
</tr>
<tr>
<td></td>
<td>4.0</td>
<td>&lt;2.0</td>
</tr>
</tbody>
</table>

Fronds (50 or 100 mg) were labelled and analysed as for Fig. 1, apart from the extraction (see Methods). The fronds extracted by methods A and B came from separate samples of algae.

### Table 2 Uptake and metabolism of \([^{35}\text{S}]\)-precursors by *E. intestinalis*

<table>
<thead>
<tr>
<th>Precursor</th>
<th>(^{35}\text{S}) uptake (nCi)</th>
<th>(^{35}\text{S}) incorporation (% of uptake)</th>
</tr>
</thead>
<tbody>
<tr>
<td>([^{35}\text{S}]\text{Met})</td>
<td>454</td>
<td>6.2</td>
</tr>
<tr>
<td>([^{35}\text{S}]\text{MTHB})</td>
<td>461</td>
<td>&lt;0.2</td>
</tr>
<tr>
<td>([^{35}\text{S}]\text{DMSHB})</td>
<td>196</td>
<td>2.7</td>
</tr>
<tr>
<td>([^{35}\text{S}]\text{DMSP})</td>
<td>442</td>
<td>15.5</td>
</tr>
</tbody>
</table>

Data for Met are included for comparison. Fronds (100 mg) were incubated for 4 h with 500 nCi (1.1–1.4 nmol) of each compound. L-lomers were supplied for all compounds, although these could have been racemized/n.

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**Figure 3** Proposed pathway of DMSHP synthesis in *E. intestinalis* and other algae. The second step is shown as reversible because MTHB can be converted to Met (Table 2).

**Figure 4** Evidence that DMSHB participates in DMSHP synthesis in *Emiliania huxleyi* (EH), *Melosira nummuloidea* (MN) and *Tetraselmis* sp. (TS). The main figure shows conversion of \([^{35}\text{S}]\)Met to DMSHP and DMSHB. Data are for \(10^7\) (EH and TS) or \(10^6\) cells (MN). Cultures were incubated with \([^{35}\text{S}]\)Met (5–10 \(\mu\text{Ci}\); about 0.5 nmoI) for a short time \((t_1)\) to label heavily the pools of free Met and intermediates, and for a long time \((t_2)\) to allow \([^{35}\text{S}]\) to chase from these pools. Times \(t_1\) and \(t_2\) (h), culture volumes (ml) and cell numbers were: EH, 1.5, 23.2, 5 \(\times\) \(10^7\); MN, 2.6, 23, 12, 5 \(\times\) \(10^7\); TS, 0.2, 25, 16, 25, 4.4 \(\times\) \(10^7\). The inset shows synthesis of \([^{35}\text{S}]\)DMSP (nCi per \(10^7\) cells) from \([^{35}\text{S}]\)DMSHB (2-3 \(\mu\text{Ci}\), 0.2–0.3 nmoI). Incubation was for 17–23 h. Culture volumes (ml) and cell numbers were: BH, 10, 5 \(\times\) \(10^7\); MN, 12, 5 \(\times\) \(10^7\); TS, 10, 1.4 \(\times\) \(10^7\).
Our data establish a pathway for DMSP biosynthesis in marine algae. This pathway has no steps in common with that in higher plants, which proceeds via SMM and 3-dimethylsulphonio-propionaldehyde. DMSP biosynthesis must therefore have evolved independently at least twice. Our results have two other implications. The first stems from the finding that a transaminase reaction stands at the head of the DMSP pathway; this may help explain why nitrogen deficiency enhances DMSP production. Depletion of cellular amino acids would favour the transamination reaction, thereby promoting DMSP synthesis when nitrogen is limiting. Second, our results suggest that DMSP may not be the only precursor of the DMS produced by living algae: DMSHB is another potential precursor in vivo. In support of this possibility, we have obtained preliminary evidence for extensive catabolism of supplied DMSHB to DMS in Tetraselmis sp. and E. huxleyi.

Methods

Algae. E. intestinalis was collected in Florida and kept in aerated sea water at 18°C in continuous fluorescent light (photosynthetic photon flux density, 50 μmol m−2 s−1). M. munaloides (CCMP 482) and Tetraselmis sp. were cultured axenically at 25°C in the above light regime in modified Goody’s medium33 with 1 mM NaNO3. For M. munaloides, 0.1 mM Na2SO3 was added and Tris omitted. E. huxleyi (CCMP 373) was grown in f/2 medium33 in daylight at 22°C.

Radiochemicals. L-[35S]methionine was synthesized enzymatically from L-[35S]methionine or by treating L-[35S]methionine with 250 mM methanol in 6 M HCl at 110°C for 4 h (ref. 27), and converted to L-[35S]DMSH with HNO3 (ref. 28). [35S]MTOB was made from L-[35S]methionine using L-amino acid oxidase, and converted to L-[35S]MTHB using 3-tactic dehydrogenase and NADH. [35S]Methylthiosulfonate was obtained as a byproduct. Compounds were purified by ion exchange and TLC.

Labelling conditions. E. intestinalis fronds (50 or 100 mg) were incubated in 0.3–2.5 ml sterile sea water; 35S labelling was carried out in 50-ml flasks. For phytoplankton species, labelled compounds were added to growing cultures. Incubation was at 18–21°C for E. intestinalis and E. huxleyi and 25°C for Tetraselmis and M. munaloides, under fluorescent light and with gentle agitation. Uptake of 35S was estimated from its disappearance from the medium.

Metabolite analysis. Most metabolites were isolated by methanol–chloroform–water extraction, ion exchange, TLC and TLC5. As MTOB broke down in these procedures, forming MTP, these compounds were isolated using 0.1 M HCl followed by ether extraction5 (method A) or by using paired samples extracted in 0.3 ml 66 mM NaBH4 (to reduce MTOB to MTHB) or in pre-neutralized NaBH4 (to give the endogenous MTHB level) (method B). MTOB was estimated by difference. Method B was also used to isolate 3-dimethylsulphonio-propionaldehyde as its hydroxy derivative. Metabolites were identified by their respective mobility and stability in cold 2 M NaOH. 35S data were corrected for recovery, determined using labelled standards, and for products formed during extraction. Protein synthesis was estimated from 35S labelling of the insoluble residue; the 35S was shown to be in protein-bound Met by proteolysis and TLC.

Mass spectrometry. DMSP was analysed without derivatization by FAB-MS5. DMSHB was derivatized as its t-butylmethylsilyl ester/ether and analysed by GC-MS with SIM after on-column nucleophile-assisted S-demethylation9. Authentic DMSHB was used to calibrate the SIM parameters. The diagnostic fragment ion cluster at m/z 321 (loss of a t-butyl radical) was monitored at the appropriate retention time. N-amino acids were analysed as described2,3, except that amide-14N abundance was determined using N-ethoxycarbonyl isobutyl esters by electron impact GC-MS2.
Identification and Stereospecificity of the First Three Enzymes of 3-Dimethylsulfoniopropionate Biosynthesis in a Chlorophyte Alga

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Many marine algae produce 3-dimethylsulfoniopropionate (DMSP), a potent osmoregulatory compound whose degradation product dimethylsulfide plays a central role in the biogeochemical S cycle. Algae are known to synthesize DMSP via the four-step pathway, \( \text{L-Met} \rightarrow 4\text{-methylthio-2-oxobutyrate} \rightarrow 4\text{-methylthio-2-hydroxybutyrate} \rightarrow 4\text{-dimethylsulfonio-2-hydroxybutyrate (DMSP)}. \) Substrate-specific enzymes catalyzing the first three steps in this pathway were detected and partially characterized in cell-free extracts of the chlorophyte alga \( \text{Enteromorpha intestinalis}. \)

The tertiary sulfonium compound DMSP is synthesized biogenically from the amino acid L-methionine (Met) in higher plant and marine algae (Blunden et al., 1986). DMSP is environmentally significant because it is biodegraded to DMS, an atmospheric gas with major roles in the global S cycle, in cloud formation, and possibly in climate regulation (Charlson et al., 1987; Malin, 1996). The DMS produced by marine algae is the main biogeochemical precursor of oceanic DMS, which contributes about \( 1.5 \times 10^{13} \) g of S to the atmosphere annually (Groene, 1995; Malin, 1996).

Like betaines, of which it is a S analog, DMSP acts as a cytoplasmic compatible solute or osmoregulatory compound and so has a key physiological function in adaptation to osmotic stress (Hanson and Gage, 1996). It is also an effective cryoprotectant and contributes to the acclimation of polar algae to freezing temperatures (Karsten et al., 1996). Because DMSP has protectant properties comparable to those of betaines and does not contain N, the DMSP biosynthetic pathway is a rational target for metabolic engineering of stress resistance in N-poor, S-rich environments (Hanson and Burnet, 1994; Le Rudulier et al., 1996).

The prospect of engineering this pathway led us to investigate the steps involved in DMSP synthesis from Met in the higher plant \( \text{Wollastonia biflora} \) and in marine algae. The higher plant pathway proceeds via the intermediates S-methylmethionine and dimethylsulfoniopropionaldehyde (Hanson et al., 1994; James et al., 1995). The route in the marine macroalga \( \text{Enteromorpha intestinalis} \) and in three phytoplankton species is completely different (Gage et al., 1997) (Fig. 1). The first step in this pathway is loss of the amino group, giving the 2-oxo acid MTOB; \( ^{15}\text{N}-\text{labeling} \) evidence strongly implies that the amino group is removed via transamination rather than deamination (Gage et al., 1997). The subsequent steps are reduction to MTHB, S-methylation to yield DMSHB, and oxidative decarboxylation to yield DMS.

We report here the detection and partial characterization of enzymes catalyzing the first three steps of the DMSP synthesis pathway in a chlorophyte alga.

**Abbreviations:** AdoMet, S-adenosyl-L-Met; ammediol, 2-amino-2-methyl-1,3-propanediol; DMS, dimethylsulfide; DMSHB, 4-dimethylsulfonio-2-hydroxybutyrate; DMSP, 3-dimethylsulfoniopropionate; LDH, lactate dehydrogenase; MDH, malate dehydrogenase; MTHB, 4-methylthio-2-hydroxybutyrate; MTOB, 4-methylthio-2-oxobutyrate; MTP, 3-methylthioisopropionate; TLE, thin-layer electrophoresis.

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Figure 1. The biosynthesis of DMSP from Met in marine algae. In vivo isotope tracer data indicate that the first two steps are reversible (Cage et al., 1997).

The following algal species were collected from the intertidal zone or from water ≤2 m deep at the sites and times specified: Enteromorpha intestinalis (L.) Link from Marineland in Florida year-round; Caulerpa ashenaeii Harvey and Udotea conglutinata (Ellis et Solander) Lamouroux from Crystal River, FL, July, 1996; Ulva fasciata Delile, Ulva reticulata Forsskal, Enteromorpha flexuosa (Wulfen) J. Agardh, and Halimeda discoida Decaisne from Oahu, HI, January, 1996. E. intestinalis for in vivo radiolabeling was used after culturing for up to 1 week, as described previously (Cage et al., 1997). For enzyme extraction, algae were frozen in liquid N₂ or dry ice within a few hours of collection. For enzyme extraction, algae were frozen in liquid N₂ or dry ice within a few hours of collection. DMSP levels were estimated by a GC method (Paquet et al., 1994).

Chemicals

[^35]S]Met (43.5 TBq mmol⁻¹) and [methyll-¹⁴]C]AdoMet (2.15 GBq mmol⁻¹) were purchased from NEN-DuPont and were mixed with unlabeled compounds to give the desired specific radioactivities. AdoMet was obtained from Boehringer Mannheim and was used without further purification. DL-MTHB (Ca²⁺ salt) was obtained from Sigma; the Sigma product was recrystallized from aqueous ethanol. DMSP was purchased from Research Plus, Inc. (Bayonne, NJ). MTP was purchased from TCI (Tokyo, Japan) and neutralized with KOH. Ion-exchange resins were purchased from Bio-Rad.

Synthesis of [³⁵S]MTHB, [³⁵S]MTP, and [³⁵S]MTOB

DL- and L-[³⁵S]MTHB were prepared by incubating (24 h, 37°C) 15 MBq of [³⁵S]Met [37 kBq nmol⁻¹], treated with AG-1 (formate) to remove anionic impurities in a 750-μL reaction mixture containing 25 μmol K₂PO₄, pH 7.4, 3.4 μmol GSH, 20,000 units of catalase, 2 units of L-amino acid oxidase (Sigma A-9378), 1 μmol of NADH, and 40 units of either Staphylococcus epidermidis D-LDH (Sigma L-9636) or rabbit muscle L-LDH (Sigma L-2500). [³⁵S]MTP was a byproduct of these reactions. For the synthesis of [³⁵S]MTOB, the NADH and LDH were omitted and the incubation time was cut to 10 h. Products were isolated by acidifying reaction mixtures with 0.1 volume of 12 N HCl and extracting with 3 x 3 mL of ether. The combined ether extracts were back-extracted into 200 μL of 10 mM NaOH, which was concentrated in vacuo and fractionated by TLC as described below. Products were located by autoradiography, eluted with 0.5 mM β-mercaptoethanol, and stored at −80°C; their radiochemical purity was ≥95%, as determined by TLC and TLC. The optical purity of [³⁵S]MTHB enantiomers was ≥95%, as determined by susceptibility to oxidation by D- and L-LDH, as described below.

Synthesis of [³⁵S]DMSHB

DL- and L-[³⁵S]DMSHB were prepared by treating 0.93 MBq of DL- or L-[³⁵S]MTHB (37 kBq nmol⁻¹) with 50 μmol methanol in 0.4 mL of 6 N HCl for 4 h at 110°C (Lavine et al., 1995). [³⁵S]DMSHB was isolated by ion exchange (James et al., 1995) and TLC as described below; radiochemical purity was ≥99% as determined by TLC and TLC.

Synthesis of MTHB and DMSHB Enantiomers

Unlabeled D- and L-MTHB were synthesized from D- and L-Met by reaction with HNO₃ (Kleemann et al., 1979). Met (5 mmol) was dissolved in 4.25 mL of 0.9 M H₂SO₄ and cooled to 0°C; 1 mL of ice-cold 6.2 μM NaNO₂ was added dropwise, and the reaction mixture was then incubated for 2 h at 22°C. The MTHB product was extracted into 4 x 3 mL of ether, dried in a stream of N₂, and dissolved in 1 mL of water. MTHB was then purified by passage onto a 1.25-mL AG-1 (OH⁻) column, from which it was eluted with 6 mL of 2.5 N HCl, extracted again with ether, and lyophilized. Purity was about 98%, as determined by TLC and TLC. D- and L-DMSHB were prepared from 0.12 mmol of the corresponding form of MTHB by heating at 110°C for 2 h with 0.25 mmol of methanol in 0.5 mL of 6 N HCl. After removing the HCl in vacuo, DMSHB was isolated by ion exchange (James et al., 1995). The product was lyophilized and freed of a small amount (10%) of putative dimer by hydrolysis with 0.1 N HCl at 100°C for 2 h. The optical purity of the D and L forms of MTHB and DMSHB was estimated as ≥92% by circular dichroism measurements. DL-DMSHB was synthesized from DL-MTHB by the method of Toennies and Kolb (1943).

TLE and TLC

TLE separations were on glass-backed 0.1-mm cellulose plates (Merck, Darmstadt, Germany) at 1.8 kV for 20 min at 4°C. The buffers were pyridine:glacial acetic acid:water (1:1.38, v/v/v) for thioethers, and 1.5 N formic acid for sulfoxonium compounds. TLC of thioethers and amino acids was carried out on cellulose plates developed with n-butanol:glacial acetic acid:water (60:20:20, v/v/v); sulfoxonium compounds were separated on plastic-backed 0.25-mm silica gel G plates (Machery-Nagel, Düren, Ger-
many) developed with methanol:acetone:concentrated HCl (90:10:4, v/v/v). Compounds were visualized using the spray reagents described previously (James et al., 1995).

**Enzyme Extraction**

Tissue was pulverized in liquid N$_2$ and extracted with 3.5 volumes of buffer A (50 mM Bis-Tris [bis(2-hydroxyethyl)iminotris(hydroxymethyl)methane]-HCl, pH 8.0, 5 mM DTT, 2 mM K$_2$EDTA, and 1 mg mL$^{-1}$ BSA); for MTHB S-methyltransferase in *E. intestinalis*, the pH was 7.0 and BSA was omitted. Subsequent steps were performed at 4°C. The brei was centrifuged at 10,000g for 10 min, and the supernatant was desalted on Sephadex G-25 equilibrated in buffer A. For Met aminotransferase and MTOB reductase assays the supernatant was then concentrated 10-fold with a Centricon-30 (Amicon). For all three DMSP synthesis enzymes, the desalted supernatants contained $\approx$70% of the activity present in the brei. Centrifugation at 100,000g for 1 h did not pellet activity of any of the enzymes. Desalted supernatants were in some cases flash-frozen in liquid N$_2$ and stored at $-80^\circ$C; this did not affect enzyme activity. Enzyme assays were carried out under conditions in which enzyme concentration.

**Enzyme Assays**

**MDH, Asp Aminotransferase, and Ala Aminotransferase**

MDH assays contained 0.1 mM Tris-acetate, pH 8.0, 0.2 mM NADH, and 2.5 mM oxaloacetate; oxaloacetate-dependent oxidation of NADH was followed by the fall in $A_280$. Asp aminotransferase assays contained 0.1 mM potassium phosphate buffer, pH 7.5, 25 mM L-Asp, 5 mM 2-oxoglutarate, 0.2 mM NADH, and 60 units mL$^{-1}$ of porcine heart MDH (Sigma M-2634); 2-oxoglutarate-dependent NADH oxidation was monitored. Ala aminotransferase was assayed in the same way except that 100 mM L-Ala replaced Asp, and 120 units mL$^{-1}$ rabbit muscle LDH (Sigma L-2500) was used in the coupling reaction.

**Met Aminotransferase and Met Oxidase**

Standard aminotransferase assays (60 mL final volume) contained 0.1 mM ammediol-HCl, pH 9.1, 100 mM L-Met (7–22 kBq, treated with AG-1 [formate]) and 1 mM 2-oxoglutarate. Met oxidase assays were the same except that 2-oxo acid was excluded. After 1 h at 25°C, reactions were stopped on ice and acidified with 10 mL of 2.5 N HCl after adding carrier Met and MTOB (0.2 mM). The $^{[35]}$SMTOB formed was extracted into 0.8 mL of ether, then back-extracted into 100 mL of 10 mM NaOH, of which 80 mL was taken for scintillation counting. Aminotransferase activity with other 2-oxo acids was assayed using a $^{[35]}$SMet concentration of 25 mM. Aminotransferase activity was assayed in the Met-synthesis direction in 30-$\mu$L reaction mixtures containing 0.1 mM ammediol-HCl, pH 9.1, 3.1 mM $^{[35]}$SMTOB (0.63 kBq), and 10 mM amino acid. Incubation and carriers were as above. The $^{[35]}$Met product was isolated by passage onto 1-mL AG-50 (H$^+$) columns, washing with 25 mL of water, and eluting with 5 mL of 2.5 N HCl. The product was shown to be $^{[35]}$Met by TLC. Data were corrected for Met recovery and for $^{35}$S found in the AG-50 eluate of blank assays lacking amino acid.

**MTOB Reductase**

Standard assays (final volume 30 mL) contained 0.1 mM ammediol-HCl, pH 8.0, 150 mM NADPH, and 30 mM $^{[35]}$SMTOB (7.4 kBq). After incubation for 1 h at 25°C, 50 nmol MTOB and 100 nmol MTHB carriers were added, followed at once by 50 mL of 10 mM 2,4-dinitrophenylhydrazine in 2.5 N HCl. The samples were then incubated for 1 h at 22°C and extracted with 0.5 mL of ether. The ether phase was back-extracted with 50 mL of 10 mM NaOH containing 3 mL of 1 mM acetic acid, which was concentrated in vacuo and subjected to TLC. $^{[35]}$SMTOB zones were located with iodoplatinate reagent and quantified by scintillation counting. Data were corrected for MTOB recovery and for $^{35}$S in the MTHB zone in assays without NADPH. Assays of MTHB oxidation (final volume 50 mL) contained 0.1 mM ammediol-HCl, pH 8.0, 30 mM $^{[35]}$SMTOB (46 kBq), and 1 mM NADP. Incubation was for 2 h at 25°C. Oxidation products were measured as described below for determination of $^{[35]}$SMTOB configuration.

**d-MTHB S-Methyltransferase**

Standard assays (final volume 50 mL) contained 50 mM Bis-Tris-HCl, pH 7.0, 1 mM AdoMet, and 25 mM d-$^{[35]}$SMTOB (1.9–3.7 kBq). After incubation at 22°C for 1 h, 1 mL of 0.2 mM DMSHB carrier was added and the mixture was immediately applied to a 1-mL mixed-resin column (AG-1 [OH$^-$/BioRex 70 [H$^+$], 2:1, v/v, firmly packed). The $^{[35]}$SMTOB product was eluted with 5 mL of water and quantified by scintillation counting. In some cases the enzyme was assayed using unlabeled MTHB and 100 mM [methyl-$^{14}$C]AdoMet (3.7 kBq). These reactions were stopped after 1 h by adding 25 mL of 10% (w/v) TCA, 2 mL of 100 mM DMSHB, and 215 mL of an activated charcoal suspension (38 mg mL$^{-1}$) in 0.1 N acetic acid to bind AdoMet (Cook and Wagner, 1984). After centrifuging for 5 min at 14,000g, [14C]DMSHB in the supernatant was quantified by scintillation counting. Values were corrected for DMSHB recovery and for blanks lacking the unlabeled substrate. The identities of the $^{35}$S- and $^{14}$C-labeled DMSHB reaction products were confirmed by TLE and TLC.

**Configuration of MTHB**

$^{[35]}$SMTOB was prepared from $^{[35]}$SMTOB by scaling up the standard MTOB reductase assay, and then purified by TLE. Samples (2.6 kBq, 110 pmol) were incubated for 20 h in darkness at 30°C in 30-$\mu$L reaction mixtures containing 50 mM ammediol-HCl, pH 9.0, 5 mM NAD$^+$, either 6 units...
of S. epidermidis d-LDH (Sigma L-9636) or 3 units of rabbit muscle l-LDH (Sigma L-1254), and 0.3 unit of Photobacterium fischeri NAD(P)H:FMN oxidoreductase. Controls of authentic d- and l-[35S]MTHB were treated the same way. The reactions were stopped with 70 μL of 0.54 N HCl, mixed with carrier MTHB, MTOB, and MTP (100 nmol each), and extracted with 3 × 0.8 mL of ether. The combined ether fraction was back-extracted into 70 μL of 10 mM NaOH, which was concentrated in vacuo and subjected to TLE. [35S]MTHB, [35S]MTOB, and [35S]MTP (a breakdown product of [35S]MTOB) were located by autoradiography and by I2 staining, and quantified by scintillation counting. Control reactions without LDH showed no [35S]MTHB oxidation.

In Vivo Radiotracer Experiments

Samples (100 mg fresh weight) of tissue cut from the basal 1- to 2-cm region of E. intestinalis fronds were incubated in 0.5 mL of 0.2-μm filtered seawater containing 37 or 74 kBq (1 or 2 nmol) of [35S]MTHB or [35S]DMSHB. For experiments with [35S]MTHB, the pH was lowered to an initial value of 5.7 by adding Mes-KOH (final concentration 100 mM) to the seawater. Incubation was at 22°C in the light, as described previously (Gage et al., 1997); label uptake was monitored by sampling the medium. After incubation, the tissue was rinsed for 5 min in seawater, blotted dry, and extracted using a methanol-chloroform-water procedure (Hanson et al., 1994; James et al., 1995). Water-soluble metabolites were fractionated by ion-exchange chromatography and analyzed by TLC and TLE. Incorporation of 35S into the insoluble fraction was estimated by scintillation counting after suspending samples in Ready Gel (Beckman) containing 50% (v/v) water; the counting efficiency of this system was determined to be 65%.

Bacterial Osmoprotection Experiments

The Escherichia coli strains used were K-10 and FF4169, an otsA (trehalose-deficient) mutant of K-12 (Giaever et al., 1988). Experiments with K-10 were as described by Hanson et al. (1991), except that the medium was that of Neidhardt et al. (1974) and cultures were inoculated with cells growing exponentially in the presence of NaCl. FF4169 was grown at 37°C to stationary phase in M63 medium (Miller, 1972), pH 7.0, containing 0.2% (w/v) Glc. This culture was used to inoculate experimental M63 media (25 mL) containing NaCl and various supplements (final concentration 1 mM). Supplement solutions were adjusted to pH 7.0 and filter-sterilized before addition; care was taken to avoid alkaline pH while neutralizing the DMSP solution. Experimental cultures were incubated at 37°C, and growth was monitored by the change in A₆₀₀.

RESULTS

Estimation of the Rate of DMSP Synthesis in Vivo

To provide a benchmark for the activities of DMSP pathway enzymes in E. intestinalis, we first estimated the in vivo flux of Met to DMSP by computer modeling of published [35S]Met-tracer kinetic data for this alga (Gage et al., 1997). The computer model used was that described by Mayer et al. (1990). The starting free pool size of free Met was taken to be up to 10 nmol g⁻¹ fresh weight, based on published values for the chlorophyte alga Chlorella sorokiniana (Giovanelli et al., 1980). The flux values from Met to DMSP that gave satisfactory fits to the published labeling patterns of MTHB, DMSHB, and DMSP ranged from 1.2 to 4.2 nmol h⁻¹ g⁻¹ fresh weight.

Met Aminotransferase Activity

Met aminotransferase activity was readily detected in assays containing MTOB or 2-oxoglutarate as the amino acceptor for [35S]Met, but the activities found with other 2-oxo acids were far lower (Table I). 2-Oxoglutarate was therefore used to further characterize the activity. Activity was not inhibited by a 5-fold excess of unlabeled d-Met, indicating that it was not due to the tandem action of a racemase and a d-Met aminotransferase. The pH profile showed an optimum at 9.1, and 40 to 60% of optimal activity in the physiological range of 7.5 to 8.0. The affinity for Met was high, as shown by velocity versus Met concentration curves (Fig. 2A). Double-reciprocal plots indicated that half-maximal velocity was reached at 30 μM Met, although they also suggested the presence of a minor activity with much lower affinity (not shown). The 2-oxoglutarate concentration giving half-maximal velocity was 400 μM at 100 μM [Met].

Table I. Substrate preference of Met aminotransferase activity

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Relative Activity</th>
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<tr>
<td>2-Oxo acids</td>
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<td>MTOB</td>
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</tr>
<tr>
<td>2-Oxoglutarate</td>
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</tr>
<tr>
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<tr>
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<tr>
<td>Asn</td>
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</tr>
</tbody>
</table>
Met Oxidase Activity

E. intestinalis extracts showed NADPH- and NADH-dependent MTOB reductase activities of similar magnitude at saturating NAD(P)H levels, but half-maximal rates were attained at 30 μM NADPH versus 650 μM NADH (Fig. 3). The two activities were not additive, consistent with their being due to the same enzyme(s) (Fig. 3B). Because NAD(P)H levels in plant cytoplasm are typically not more than 50 to 150 μM (Heber and Santarius, 1965; Hampp et al., 1984), the NADPH-linked activity appeared likely to be the dominant one in vivo. This activity was therefore characterized further. It was highest at pH 8.0, and about 70% as high at pH 7.0. Velocity versus MTOB concentration plots showed clearly that affinity for MTOB was high (Fig. 2B). Since double-reciprocal plots were nonlinear (showing apparent negative cooperativity), the MTOB concentration giving half-maximal velocity could not be determined precisely, but appeared to be approximately 40 μM. LDH and acetoxyhydroxy acid isomeroreductase can both catalyze the reduction of various 2-oxo acids, and LDH is specifically known to attack MTHB (Meister, 1957; Umbarger, 1996). However, MTOB reductase activity was not attributable to either of these enzymes since [35S]MTOB reduction was scarcely inhibited (≤30%) by a 200-fold excess of unlabeled pyruvate or 2-oxoisovalerate (data not shown).

The configuration of the [35S]MTHB produced by the E. intestinalis MTOB reductase was determined by testing it as a substrate for purified D- and L-LDH; authentic D- and L-[35S]MTHB were included as controls (Table III). The controls behaved as predicted, and the reductase product was strongly suppressed when unlabeled amino acids that are good substrates for other L-amino acid oxidases (Meister, 1965) were present (Table II). Figure 2A shows that oxidase activity was only 8% of aminotransferase activity even at a Met concentration of 200 μM. Since cytoplasmic levels of Met in algae and other plants are most probably ≤200 μM (Giovanelli et al., 1980), the oxidase seemed unlikely to mediate much MTOB synthesis in vivo and was not investigated further.

MTOB Reductase Activity

Consistent with the strong preference for 2-oxoglutarate as the amino acceptor, assays in the reverse (Met synthesis) direction using [35S]MTOB showed that L-Glu was by far the best amino donor after Met itself (Table I). All other amino acids tested were ≥10-fold less effective, including Gin and Asn. Met aminotransferase activity was not increased by including pyridoxal-5'-phosphate (0.1 mM) in extraction and assay buffers. This is not unusual, since the pyridoxal-5'-phosphate of plant aminotransferases is typically tightly bound and few are activated by its addition (Ireland and Joy, 1985).

Met Oxidase Activity

E. intestinalis extracts catalyzed the slow conversion of [35S]Met to [35S]MTOB in the absence of 2-oxo acid (Fig. 2A). This activity was ascribed to a nonspecific L-amino acid oxidase because it was decreased by lowering the O2 concentration and increased by raising it, and because it was strongly suppressed when unlabeled amino acids that are good substrates for other L-amino acid oxidases (Meister, 1965) were present (Table II).
AdoMet-dependent S-methylation of d-MTHB but not L-MTHB. This was demonstrated in two types of assays based on enzymatically synthesized d- and L-[35S]MTHB or on chemically synthesized, unlabeled d- and L-MTHB as substrates (Table IV). There was no detectable activity with MTP as substrate (Table IV), which is in accord with the in vivo radiotracer evidence against a role for this compound in DMSP synthesis in *E. intestinalis* (Gage *et al.*, 1997). Nor did the enzyme attack other naturally occurring thiocarboxylates (3-methylthiopropylamine, d- or L-Met, L-S-methylcysteine), as judged from their complete failure to inhibit d-[35S]MTHB methylation when present in unlabeled form in 40-fold excess (data not shown). The d-MTHB methyltransferase activity had a broad pH optimum in the region of 6.5 to 8.0. Plots of velocity versus [d-MTHB] showed that activity was half-maximal at 8 μM d-MTHB (Fig. 2C); the AdoMet concentration giving half-maximal velocity was 30 μM at 25 μM [d-MTHB].

**Comparative Biochemistry of DMSP-Accumulating and Nonaccumulating Algae**

Evidence that the Met aminotransferase, MTOB reductase, and d-MTHB methyltransferase activities found in *E. intestinalis* are specific to DMSP synthesis was sought by assaying these enzymes in extracts of six other marine chlorophyte algae, three with DMSP and three without (Table V). The activities of three housekeeping enzymes (Asp and Ala aminotransferases and MDH) were also measured as a check on the quality of the extracts. All six algae had housekeeping enzyme activities comparable to those of *E. intestinalis* (Table V). Those that accumulated DMSP all showed Met aminotransferase, MTOB reductase, and d-MTHB methyltransferase activities at least as high as those of *E. intestinalis*. In contrast, the algae lacking DMSP had about 30-fold less Met aminotransferase activity than *E. intestinalis*, ≥20-fold less MTOB reductase, and no detectable methyltransferase. All six algae had very low levels of Met oxidase (0.5–2.3 pkat g⁻¹ fresh weight; not shown), providing further evidence that this activity is not importantly related to DMSP synthesis.

**Table IV. Enantiomer and substrate specificity of S-methyltransferase activity**

Desalted extract equivalent to 3.8 mg fresh weight was incubated with 25 μM [35S]MTHB or [35S]MTP and 1 mM AdoMet, or with 25 μM unlabeled MTHB and 0.1 mM [methyl-14C]Ado-Met. Incorporation of label into methylated product (DMSP or DMSP) was measured. The L-[35S]MTHB and L-MTHB could have contained small amounts of the d forms (see “Materials and Methods”), which may account for the slight activity observed with the L enantiomers.

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Enantiomer</th>
<th>Methyltransferase Activity pkat g⁻¹ fresh wt</th>
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<tbody>
<tr>
<td>[35S]MTHB</td>
<td>d</td>
<td>2.42</td>
</tr>
<tr>
<td></td>
<td>l</td>
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<td></td>
<td>l</td>
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<tr>
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</table>

**Table III. Evidence that the product of MTOB reductase is the d-enantiomer of MTHB**

[35S]MTHB synthesized from [35S]MTOB using desalted *E. intestinalis* extract equivalent to 8.6 mg fresh weight, 30 μM [35S]MTOB, and various concentrations of NADPH or NADH. Data points are means ± se (*n* = 3). Where error bars are not shown they were smaller than the symbols. The open symbol in B shows the activity given by 1 mM NADH plus 100 μM NADPH.

**Figure 3. NADPH-dependent (A) and NADH-dependent (B) MTOB reductase activity.** Reaction mixtures contained desalted *E. intestinalis* extract equivalent to 8.6 mg fresh weight, 30 μM [35S]MTOB, and various concentrations of NADPH or NADH. Data points are means ± se (*n* = 3). Where error bars are not shown they were smaller than the symbols. The open symbol in B shows the activity given by 1 mM NADH plus 100 μM NADPH.

was attacked only by d-LDH. The in vitro product of *E. intestinalis* MTOB reductase is therefore d-MTHB; it is also very probable that the d-enantiomer predominates in vivo, as shown below. Knowing that reductase produces d-MTHB, it was of interest to seek the reverse reaction, i.e. NADP-dependent d-[35S]MTHB oxidation. This was readily detectable; in the presence of 35 μM d-[35S]MTHB and 1 mM NADP at pH 8.0, the reaction rate was 0.4% of the forward rate in comparable conditions. Adding NADH (P)H:FMN oxidoreductase plus FMN (to remove NADPH) did not accelerate the reverse reaction.

**MTHB S-Methyltransferase Activity**

Consistent with the product of MTOB reductase being the d form of MTHB, *E. intestinalis* extracts catalyzed Consistent with the product of MTOB reductase being the d form of MTHB, *E. intestinalis* extracts catalyzed

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Specificity of LDH Used</th>
<th>[35S]MTHB Oxidation %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reductase product</td>
<td>d</td>
<td>15.5</td>
</tr>
<tr>
<td>d-[35S]MTHB</td>
<td>l</td>
<td>&lt;0.5</td>
</tr>
<tr>
<td>L-[35S]MTHB</td>
<td>d</td>
<td>16.0</td>
</tr>
<tr>
<td>L-[35S]MTHB</td>
<td>l</td>
<td>&lt;0.5</td>
</tr>
</tbody>
</table>

**Table V. Comparative enzyme activities of marine algae**

Comparative activity of several enzymes in extracts of six chlorophyte algae, three with DMSP and three without, is shown. The activities of three housekeeping enzymes (Asp and Ala aminotransferases and MDH) were also measured as a check on the quality of the extracts. All six algae had housekeeping enzyme activities comparable to those of *E. intestinalis*. Those that accumulated DMSP all showed Met aminotransferase, MTOB reductase, and d-MTHB methyltransferase activities at least as high as those of *E. intestinalis*. In contrast, the algae lacking DMSP had about 30-fold less Met aminotransferase activity than *E. intestinalis*, ≥20-fold less MTOB reductase, and no detectable methyltransferase. All six algae had very low levels of Met oxidase (0.5–2.3 pkat g⁻¹ fresh weight; not shown), providing further evidence that this activity is not importantly related to DMSP synthesis.
Table V. Activities of putative enzymes of DMSP synthesis in various marine chlorophyte algae

Activities were measured in E. intestinalis, in three other algal species that accumulate DMSP, and in three that do not. Desalted extracts were prepared as described under "Materials and Methods" for E. intestinalis. Asp and Ala aminotransferases (Asp-AT and Ala-AT) and MDH were assayed spectrophotometrically, and Met aminotransferase (Met-AT), MTOB reductase (MTOB-R), and D-MTHB methyltransferase (MTHB-MT) were assayed radiochemically, as described in "Materials and Methods."

<table>
<thead>
<tr>
<th>Species</th>
<th>DMSP Content</th>
<th>DMSHB Pathway Enzyme Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>MDH</td>
</tr>
<tr>
<td></td>
<td>µmol g⁻¹ fresh wt</td>
<td>nkat g⁻¹ fresh wt</td>
</tr>
<tr>
<td>E. intestinalis</td>
<td>19.4</td>
<td>30</td>
</tr>
<tr>
<td>E. flexuosa</td>
<td>17.5</td>
<td>155</td>
</tr>
<tr>
<td>U. reticulata</td>
<td>18.5</td>
<td>138</td>
</tr>
<tr>
<td>U. fasciata</td>
<td>12.5</td>
<td>185</td>
</tr>
<tr>
<td>H. discoidea</td>
<td>&lt;0.03</td>
<td>71</td>
</tr>
<tr>
<td>C. ashmeadii</td>
<td>&lt;0.03</td>
<td>116</td>
</tr>
<tr>
<td>U. conglutinata</td>
<td>&lt;0.03</td>
<td>22</td>
</tr>
</tbody>
</table>

Confirmation of d-Enantiomer Preferences in Vivo

E. intestinalis fronds converted d-[35S]MTHB to DMSP very efficiently (Table VI). As reported by Gage et al. (1997), the l form was also converted to DMSP, but 5-fold less efficiently than the d form. These data confirm the preference of DMSP synthesis for d-MTHB in vivo. Much of the l-MTHB was metabolized to protein-bound Met, and more label from the l form remained in the intermediate DMSPH (Table VI), presumably because the [35S] flux was small in relation to the pool size of DMSPH. The conversion of l-MTHB to Met indicates that it can be oxidized to MTOB and then transaminated to yield Met, as occurs in other organisms (Livesey, 1984; Miyazaki and Yang, 1987). MTOB formed in this way could also be converted to d-MTHB, which would explain the small [35S] flux from l-MTHB to DMSHB and DMSP.

Since the MTHB methyltransferase produces d-DMSHB, the enzyme(s) converting DMSHB to DMSP might be expected to prefer d-DMSHB. Supplying d- and l-[35S]DMSHB confirmed this expectation; the d form was converted to DMSP 9-fold more efficiently than the l form (Table VI).

The modest conversion of the l form to DMSP is in accord with our previous data (Gage et al., 1997).

Osmoprotection of E. coli by DMSHB

E. intestinalis does not accumulate high levels of the intermediate DMSHB (Gage et al., 1997). However, from its structure this compound is predicted to be an effective osmoprotectant, whereas its precursor, MTHB, is not (Yancey, 1994). This prediction was tested using standard osmoprotection bioassays with two E. coli strains; DMSHB and MTHB were compared with DMSP and Gly betaine as benchmarks. Figure 4 shows data for the osmosensitive strain FF4169; results with strain K-10 were similar except for a higher growth rate in the absence of osmoprotectants. Although less effective than Gly betaine and DMSP, dl-

Table VI. Metabolism of enantiomers of MTHB and DMSHB by E. intestinalis

Algal fronds (0.1 g fresh weight) were incubated with 74 kBq (2 nmol) of [35S]MTHB or 37 kBq (1 nmol) of [35S]DMSHB in 0.5 mL of seawater for 6 h in the light. For [35S]MTHB, the initial pH of the seawater was adjusted to 5.7 with Mes-KOH. Precursor uptake was estimated from disappearance from the medium. Radiolabel incorporated into the insoluble fraction was shown to be in protein-bound Met by protease digestion and acid hydrolysis (Gage et al., 1997). The data are representative of three separate experiments.

<table>
<thead>
<tr>
<th>35S-Precursor</th>
<th>Precursor Uptake</th>
<th>Insoluble</th>
<th>DMSHB</th>
<th>DMSP</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>kBq</td>
<td>% of uptake</td>
<td></td>
<td></td>
</tr>
<tr>
<td>d-MTHB</td>
<td>9.1</td>
<td>5.1</td>
<td>&lt;0.1</td>
<td>77.2</td>
</tr>
<tr>
<td>l-MTHB</td>
<td>16.4</td>
<td>16.4</td>
<td>27.4</td>
<td>16.1</td>
</tr>
<tr>
<td>d-DMSHB</td>
<td>29.3</td>
<td>6.9</td>
<td>23.7</td>
<td>69.5</td>
</tr>
<tr>
<td>l-DMSHB</td>
<td>34.8</td>
<td>3.6</td>
<td>71.7</td>
<td>8.1</td>
</tr>
</tbody>
</table>

Figure 4. Osmoprotection by DMSHB. The osmosensitive (trehalose-deficient) E. coli strain FF4169 was grown aerobically at 37°C in M63-Glc medium containing 0.45 M (A) or 0.65 M (B) NaCl alone (control) and with 1 mM DL-DMSHB, DL-MTHB, DMSP, or Gly betaine (Gly Bet). Growth was monitored by A600.
DMSHB was much more potent than DLMTHB, which protected the cells slightly or not at all. Tested separately, the D and L forms of DMSHB and MTHB behaved like the racemic mixtures. The osmoprotective effect of DMSHB involved its intracellular accumulation, but not any metabolism. Thus, when 1 mM D- or L-[^35]S]DMSHB was included in media containing 0.5 mM NaCl, all of the label taken up by K-10 cells was shown by TLE to be in DMSHB; the intracellular concentration of[^35]S]DMSHB was estimated to be 0.5 to 0.7 µM by assuming cell volume to be 0.4 fl (Hanson et al., 1991).

**DISCUSSION**

In the marine alga *E. intestinalis*, the first three steps of the DMSP biosynthesis pathway are Met → MTOB → MTHB → DMSHB (Fig. 1). We report here enzyme activities that catalyze these steps, and show that the d-enantiomers of the chiral intermediates MTHB and DMSHB are very strongly preferred. As summarized in Table VII, all three enzymes show high affinities for their substrates and have extractable activities 4- to 25-fold above our highest estimate of the in vivo rate of DMSP synthesis (4.2 nmol h⁻¹ g⁻¹ fresh weight). Moreover, much of the activity was probably not extracted because our extracts contained about 0.5 mg protein g⁻¹ fresh weight, whereas the total protein content (Kjeldahl × 6.25) of *E. intestinalis* fronds was found to be 5.9 mg g⁻¹ fresh weight, in accord with published values (2-10 mg g⁻¹ fresh weight; Edwards et al., 1988).

The conversion of MTOB to Met via transamination is the last step in the Met salvage pathway whereby the methylthio moiety of 5'-methylthioadenosine is recycled to Met (Cooper, 1996). Since this pathway is ubiquitous, all algae would be expected to show some Met aminotransferase activity, and indeed this was the case (Table V). However, the activity was 30- to 100-fold higher in the DMSP-accumulating algae, indicating that DMSP synthesis involves either overexpression of a housekeeping Met aminotransferase or expression of a novel enzyme. A novel enzyme appears more likely for two reasons.

First, the strong preference for Glu as an amino donor distinguishes the *E. intestinalis* activity from the aminotransferases known to be involved in Met salvage in plants, animals, and bacteria, which appear to prefer Gln and Asn (Cooper, 1996). Second, the estimated apparent *Kₘ* for Met is exceptionally low (30 µM); aminotransferases typically have *Kₘ* values for amino acids in the mM range (Jenkins and Fonda, 1985), and Gln and Asn aminotransferases are no exception (Cooper and Meister, 1985). The *E. intestinalis* enzyme is also clearly distinct from a Met-glyoxylate aminotransferase involved in glucosinolate synthesis in crucifers, which shows little activity with 2-oxoglutarate as amino acceptor (Chappie et al., 1990), and from a nonspecific, low-affinity Met aminotransferase in pea (Kutacek, 1985). Because DMSP represents about 90% of the reduced S in *E. intestinalis*, a high-affinity aminotransferase may be needed to sustain a high Met flux to DMSP in the face of competition for Met from AdoMet and methionyl-tRNA synthetases, which can have high affinities for Met (Burbach and Schimmel, 1992; Schröder et al., 1997).

As with Met transamination, a small capacity to convert MTOB to MTHB may be widespread, because MTHB (of undetermined configuration) has been detected as a metabolite of radiotracer Met or MTOB in diverse higher and lower plants, including algae that lack DMSP (Pokorny et al., 1970; Kushad et al., 1983; Miyazaki and Yang, 1987). However, MTHB formation in these cases may be just a reversible side reaction of the Met salvage pathway (Miyazaki and Yang, 1987), which would be expected to carry very little flux compared with DMSP synthesis. Consistent with this interpretation, DMSP-free algae had no more than 5% of the MTOB reductase activity found in DMSP accumulators.

Unlike the Met → MTOB → MTHB reaction sequence, the conversion of MTHB to DMSHB is known only in association with DMSP synthesis, for which it may be the committing step (Gage et al., 1997). The d-MTHB S-methyltransferase catalyzing this step would thus appear to be a novel enzyme of potential regulatory importance. Our finding that its product is an osmoprotectant has both evolutionary and metabolic engineering implications. Supposing that, like many extant plants, ancient algae had some capacity to form MTHB, evolution of an MTHB methyltransferase could have enabled some DMSHB synthesis to occur and so conferred a selective advantage. DMSHB might thus have served as an ancestral sulfonium osmoprotectant from which synthesis of the more potent protectant DMSP later evolved. In this connection it is noteworthy that two other algal sulfonium compounds, gonyauline (cis-2-[dimethylsulfonio]cyclopropanecarboxylate) (Nakamura et al., 1992) and 4-dimethylsulfonio-2-methoxybutyrate (Blunden and Gordon, 1986), are structurally related to DMSHB and that both could hypothetically be derived from it by single-step reactions.

With respect to metabolic engineering of the DMSP pathway in crops or other organisms, it may be necessary to get only as far as DMSHB to achieve a useful degree of osmotic stress resistance. Whereas genes for Met aminotransferase, MTOB reductase, and MTHB methyltransferase might all be required for this, some crucifers have high Met-glyoxylate aminotransferase activities (4-50 pkat g⁻¹ fresh weight).

<table>
<thead>
<tr>
<th>Table VII. Estimated activities and affinities of DMSP-synthesis enzymes</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Enzyme</strong></td>
</tr>
<tr>
<td>Met aminotransferase</td>
</tr>
<tr>
<td>MTOB reductase</td>
</tr>
<tr>
<td>D-MTHB methyltransferase</td>
</tr>
</tbody>
</table>

* Approximate value only (see text).
ACKNOWLEDGMENTS

We thank D.A. Gage for carrying out circular dichroism analyses of MTHB and DMSHB, and J.S. Davis for help in obtaining and identifying algal material from Florida.

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Paquet L, Rathinasabapathi B, Saini H, Zamir L, Gage DA, Huang Z-H, Hanson AD (1994) Accumulation of the compatible solute 3-dimethylsulfiniopropionate in sugarcane and its rela-


CHAPTER 10

SALINITY, OSMOLYTES AND COMPATIBLE SOLUTES

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West Lafayette, IN 47907, USA

Abstract

In order to maintain low cytosolic Na$^+$, and cytosolic K$^+$ concentrations within narrow limits (100 - 150 mM) across a broad range of external and vacuolar concentrations of NaCl, it is essential that other solutes be accumulated in the cytoplasm to keep this compartment in osmotic balance with the external medium and vacuole. Such solutes should be osmolytes that are non-toxic and "compatible" with cytoplasmic enzymes over wide concentration ranges. A number of such solutes have been identified, their pathways of synthesis elucidated, and progress has been in isolating genes encoding key enzymes of their biosynthetic pathways.

10.1. Introduction

In general, the enzymes of salt-tolerant plants are no more tolerant of deleterious inorganic ions, such as Na$^+$, than are the enzymes of salt-sensitive plants (Flowers et al., 1977). Plant adaptation to saline environments therefore requires the maintenance of low levels of Na$^+$ in the cytoplasm, achieved in part by accumulation of Na$^+$ in the vacuole (Flowers et al., 1977). Eukaryotic cells are remarkably uniform in maintaining a fairly constant cytoplasmic K$^+$ concentration of between 100 and 150 mM (Wyn Jones et al., 1977). In contrast to Na$^+$, K$^+$ is essential for many processes in plants, including protein synthesis, membrane transport processes, generation of turgor, charge balance, and activation of certain enzymes (Leigh and Wyn Jones, 1984; Matoh et al., 1988). The primary role of K$^+$ in the cytoplasm is for protein synthesis to maintain the association between tRNA and ribosomes during translation (Leigh and Wyn Jones,
1984). However, concentrations of $K^+$ exceeding 180 mM are inhibitory to protein synthesis because such concentrations promote dissociation of polysomes and conformational changes in monosomes (Brady et al., 1984). In general, $K^+$ is less inhibitory than $Na^+$ to enzyme function, but nevertheless both ions can be regarded as "strongly perturbing" to macromolecular structure and function at concentrations above 200 mM (Hochachka and Somero, 1984; Yancey, 1994). The sensitivity of protein synthesis to inorganic ions may set the boundaries for cell ionic strength (Leigh and Wyn Jones, 1984; Yancey, 1994).

Given the need to maintain low cytosolic $Na^+$, and cytosolic $K^+$ concentrations within narrow limits (100 - 150 mM) across a broad range of external and vacuolar concentrations of NaCl, it is essential that other solutes be accumulated in the cytoplasm to keep this compartment in osmotic balance with the external medium and vacuole. Ideally, such solutes should be osmolytes that are non-toxic and "compatible" with cytoplasmic enzymes over wide concentration ranges (Wyn Jones et al., 1977).

### 10.2. Compatible and non-compatible solutes

Figure 1 shows the Hofmeister series, representing a ranking of anions and cations in the order in which they influence macromolecular systems (Hochachka and Somero, 1984; Yancey, 1994). Ions to the left generally stabilize and enhance catalysis of macromolecular systems, while those to the right destabilize them. Those to the left promote "salting-out", while those to the right promote "salting-in" of proteins. Salting-out and salting-in refer to the capacities of these ions to either decrease, or increase, respectively, the solubilities of proteins (Hochachka and Somero, 1984; Yancey, 1994). Note that $Na^+$ and $K^+$ rank in the middle of the series, but that $K^+$ is less destabilizing than $Na^+$. Effects of the anions and cations are algebraically additive, leading to counteraction if opposing ion types in the series are paired (Yancey, 1994).

<table>
<thead>
<tr>
<th>Anions</th>
<th>Destabilizing (Salting-Out)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$F^-$</td>
<td></td>
</tr>
<tr>
<td>$PO_4^{3-}$</td>
<td></td>
</tr>
<tr>
<td>$SO_4^{2-}$</td>
<td></td>
</tr>
<tr>
<td>$CH_3COO^-$</td>
<td></td>
</tr>
<tr>
<td>$Cl^-$</td>
<td></td>
</tr>
<tr>
<td>$Br^-$</td>
<td></td>
</tr>
<tr>
<td>$I^-$</td>
<td></td>
</tr>
<tr>
<td>$SCN^-$</td>
<td></td>
</tr>
<tr>
<td>Cations</td>
<td>Stabilizing (Salting-Out)</td>
</tr>
<tr>
<td>$N^+{(CH_3)_4}$</td>
<td></td>
</tr>
<tr>
<td>$N^+{(CH_3)_2H_2}$</td>
<td></td>
</tr>
<tr>
<td>$N^+H_4$</td>
<td></td>
</tr>
<tr>
<td>$K^+$</td>
<td></td>
</tr>
<tr>
<td>$Na^+$</td>
<td></td>
</tr>
<tr>
<td>$Ca^{2+}$</td>
<td></td>
</tr>
<tr>
<td>$Mg^{2+}$</td>
<td></td>
</tr>
<tr>
<td>$Li^+$</td>
<td></td>
</tr>
<tr>
<td>$Ba^{2+}$</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 1.** The Hofmeister (lyotropic) series of inorganic ions. Anions and cations are ranked in the order (from left to right) of their increasing destabilizing effects on proteins. The ions that are the most stabilizing tend to promote "salting-out" of proteins (Hochachka and Somero, 1984; Yancey, 1994).

The perturbing ions to the right of Figure 1 are destabilizing to proteins because they readily enter the hydration sphere of proteins and bind to non-specific sites (e.g. charged
protein groups), shifting the protein conformational equilibrium toward the unfolded state (Low, 1985; Yancey, 1994). The non-perturbing or "compatible" ions to the left of Figure 1 are stabilizing because they are preferentially excluded from the protein hydration domain shell. This preferential exclusion causes proteins to fold more compactly by aggregation, or precipitation (salting-out) (Low, 1985; Yancey, 1994).

Compatible solutes are solutes which mimic the Hofmeister stabilizing ions of Figure 1 by being preferentially excluded from the protein surface and its immediate hydration sphere, and which stabilize folded protein structures, promote subunit assembly and tend to promote salting-out (Low, 1985; Yancey, 1994). Structures of several compatible solutes accumulated by plants are illustrated in Figure 2. These include amino acids, methylated onium compounds, and polyols (acyclic and cyclic polyhydric alcohols [cyclitols]). The compounds shown in Figure 2 will be the focus of this review. However, these represent only a small fraction of the known compatible solutes in the plant kingdom. A large number of other methylated onium compounds (not shown in Fig. 2) have been identified in marine algae (Blunden and Gordon, 1986). The diversity of cyclic polyols found in higher plants is also far greater than depicted in Figure 2 (Popp and Smirnoff, 1995). Because of space constraints we will not consider carbohydrates (e.g. sucrose, trehalose, raffinose, stachyose and fructans) which may play important roles as compatible molecules during desiccation and freezing.

The methylated quaternary ammonium and tertiary ammonium compounds of Figure 2 can be seen to be structural homologs of the stabilizing Hofmeister anion, N'(CH₃)₄. All of the compatible solutes shown in Figure 2 share the properties of being highly soluble in water, and are electrically neutral in the physiological pH range. Generally they are non-inhibitory to enzymes at high concentrations (Wyn Jones et al., 1977), they can block the inhibition of enzyme activity caused by perturbing solutes (Yancey, 1994), and they elevate the denaturation temperatures of proteins (Low, 1985; Yancey, 1994). Many of the compatible solutes listed in Figure 2 have been shown to stimulate the growth of salt-sensitive bacteria (e.g. *Escherichia coli* and *Salmonella typhimurium*) in highly saline media (> 0.6 M NaCl) (Strom et al., 1983; Hanson et al., 1991; 1994 a). The growth stimulation properties of these compatible solutes is often referred to as "osmoprotection" (Strom et al., 1983; Hanson et al., 1994 a). The term "osmoprotectant" is therefore commonly applied to many of these compounds (Hanson and Burnet, 1994; McNeil et al., 1999; Nuccio et al., 1999). When provided at low concentrations (<1 mM), compounds such as glycine betaine and proline are accumulated to near 1 M concentrations in the bacterial cytoplasm, facilitating Na⁺ and Cl⁻ exclusion and replacement of K⁺ and glutamate, which serve as the principal osmolytes in the absence of an exogenous supply of compatible solute (Cayley et al., 1991; 1992). This replacement of K⁺/glutamate restores cell water content and growth (Cayley et al., 1991; 1992).
Two explanations have been offered for the mechanism of compatible solute preferential exclusion from protein surfaces (Low, 1985; Yancey, 1994). First, many (but not all) of the solutes raise the surface tension of water, perhaps increasing the cohesive forces within the water structure; thus, they are proposed to be water structure-makers, enhancing water-water interactions (Low, 1985; Yancey, 1994). They either enhance the existing structure of water or perhaps reorganize the bulk water to a lesser degree at their molecular surfaces than structure-breaking solutes (Low, 1985). Second, they may be sterically excluded from the protein surface (Low, 1985; Yancey, 1994). Because compatible solutes take up more space than a water molecule, they are less able to pack next to a protein than water. Bulky solutes will increase protein activity by "crowding" proteins into a smaller space (Yancey, 1994). Osmolytes with -OH groups that could
form hydrogen bonds with proteins may have a poorer geometrical fit than water in the hydration lattice around the protein (Yancey, 1994).

In evolutionary terms the compatible solute accumulation strategy of adaptation to saline environments has key advantages over accumulation of cheaper, non-compatible, perturbing solutes, such as Na\(^+\) and Cl\(^-\), in the cytoplasm. Accumulation of perturbing solutes would require evolution of a large number of salt-tolerant enzymes, requiring substantial changes in protein amino acid composition to offset general Na\(^+\) and Cl\(^-\) destabilization phenomena (Hochachka and Somero, 1984). Accumulation of a compatible solute for cytoplasmic osmoregulation would require far fewer changes, e.g. modification of the regulatory mechanisms controlling biosynthesis or catabolism of a non-perturbing compound (Hochachka and Somero, 1984). There is therefore great interest in identifying genes encoding key enzymes of compatible solute synthesis and/or catabolism because these genes hold promise for improving crop resistance to osmotic stresses (Strem et al., 1983; Bohert and Jensen, 1996; Bohnert and Shen, 1999; Jain and Selvarej, 1997; McNeil et al., 1999; Nuccio et al., 1999). In subsequent sections we will highlight recent progress in pathway characterization, gene identification and metabolic engineering of compatible solute accumulation in higher plants.

10.3. Pathways of synthesis and catabolism of compatible solutes found in plants

10.3.1. PROLINE

The imino acid proline is accumulated in the leaves of many halophytic plants from diverse families in response to salinity stress (Stewart and Lee, 1974; Treichel, 1975; Wyn Jones et al., 1977; Briens and Larher, 1982; Stewart and Larher, 1980). Proline is derived primarily from glutamic acid in reactions catalyzed by \(\Delta^1\)-pyrroline-5-carboxylate synthetase (P5CS) and \(\Delta^1\)-pyrroline-5-carboxylate reductase (P5CR) (Fig. 3) (Verma and Zhang, 1998). P5CS is a bifunctional enzyme that phosphorylates glutamate in the 5- (\(\gamma\)-) position to form \(\gamma\)-glutamyl phosphate, and then reduces this labile intermediate to glutamic-5-semialdehyde (GSA) (Hu et al., 1992). GSA spontaneously cyclizes (with loss of water) to \(\Delta^1\)-pyrroline-5-carboxylate (P5C) (Fig. 3). P5C is subsequently reduced to proline in the reaction catalyzed by P5CR (Verma and Zhang, 1998). P5CS is strongly feedback inhibited by proline (Verma and Zhang, 1998). Both enzymes of proline biosynthesis are localized in the cytosol. This contrasts with the proline catabolism pathway (catalyzed by proline dehydrogenase (PDH) and P5C dehydrogenase (P5CDH)), which is mitochondrial (reviewed by Hare and Cress (1997)) (Fig. 3). Control of proline accumulation in response to salinity stress involves both increased synthesis and decreased proline oxidation, mediated (at least in some plant species) at the level of enhanced gene transcription of P5CS (Igarashi et al., 1997; Yoshiha et al., 1995; Strizhov et al., 1997) and P5CR (Williamson and Slocum, 1992; Verbruggen et al., 1993), and concomitant down-regulation of PDH gene expression.
Figure 3. Pathways of synthesis and oxidation of proline in plants. GSA, glutamic-5-semialdehyde; P5C, $\Delta^1$-pyrroline-5-carboxylate; P5CDH, $\Delta^1$-pyrroline-5-carboxylate dehydrogenase; P5CR, $\Delta^1$-pyrroline-5-carboxylate reductase; P5CS, $\Delta^1$-pyrroline-5-carboxylate synthetase. The dotted line denotes feedback inhibition of P5CS by proline.
Salinity, osmolytes and compatible solutes

(Kiyosue et al., 1996; Peng et al., 1996; Yoshioka et al., 1997). Whereas PDH is normally induced by proline, this induction does not occur under osmotic stress (Peng et al., 1996). It is noteworthy, however, that in tomato cell cultures adapted to salinity stress (15 g NaCl/L) a 30-fold increase in proline level occurs without any notable change in P5CS mRNA abundance (Fujita et al., 1998). Ketchum et al. (1991) conclude from inhibitor studies with suspension cells of the halophytic grass, Distichlis spicata, that mRNA translation but not transcription is necessary for salinity stress induced proline accumulation, implying a post-transcriptional control mechanism(s).

Over-expression of P5CS in tobacco leads to proline accumulation and increased resistance to salinity stress (Kishor et al., 1995). It is not clear whether the enhanced salt resistance of these transgenic plants can be ascribed solely to proline acting as a cytoplasmic compatible solute. Proline can also function as a hydroxyl radical scavenger (Smirnoff and Cumbes, 1989), and may play a role in the transport of reducing equivalents between cells and intracellular compartments (i.e. between cytoplasm and mitochondrion) (Hare and Cress, 1997).

10.3.2. GLYCINE BETAIN

Glycine betaine is widely distributed in the plant kingdom (Wyn Jones and Storey, 1981). It is accumulated to osmotically significant levels by many halophytic higher plants, including members of the Chenopodiaceae and salt-tolerant species of the Poaceae (Rhodes and Hanson, 1993). In chenopods, glycine betaine is synthesized from choline in reactions catalyzed by ferredoxin (Fd)-dependent choline monooxygenase (CMO) and betaine aldehyde dehydrogenase (BADH) (Fig. 4A). Both CMO and BADH are predominantly localized in the chloroplast stroma of chenopods (Weigel et al., 1986; 1988; Brouquisse et al., 1989). Glycine betaine is also localized in the chloroplasts of salinized spinach leaves, where it provides osmotic adjustment (Robinson and Jones, 1986), and may play a key role in protection of the photosynthetic apparatus, particularly photosystem II (Murata et al., 1992; Papageorgiou et al., 1991; Homann, 1992; Williams and Gounaris, 1992; Mohanty et al., 1993; Papageorgiou and Murata, 1995).

Both CMO (Burnet et al., 1995) and BADH (Weretilnyk and Hanson, 1989) have been purified to homogeneity from spinach. cDNAs encoding BADH have been isolated from spinach (Weretilnyk and Hanson, 1990; Rathinasabapathi et al., 1994) and sugar beet (McCue and Hanson, 1992 b). A cDNA encoding CMO has also been cloned from spinach (Rathinasabapathi et al., 1997). The cDNA sequence confirms that CMO is an Fe-S protein and that CMO has a typical chloroplast transit peptide sequence.

BADH may be a relatively non-specific aldehyde dehydrogenase, acting on other aldehyde substrates in addition to betaine aldehyde (Trossat et al., 1997). Thus, BADH will utilize 3-dimethylsulfoxiopropionaldehyde, an intermediate in 3-dimethylsulfonylopropionate (DMSP) synthesis [see 10.3.6 below] and aldehydes (3-aminopropionaldehyde and 4-aminobutyraldehyde) involved in polyamine metabolism.
Salinity stress leads to two- to three-fold increases of CMO and BADH gene expression, and concomitant increases in enzyme level in spinach, sugar beet, and amaranth.
Abscisic acid (ABA) is implicated in the induction of BADH in cereals (Ishitani et al., 1985). The signal causing induction of BADH in sugar beet does not appear to be either turgor reduction, NaCl, or ABA, but rather an unidentified biochemical signal translocated from roots to leaves in salinized plants (McCue and Hanson, 1992 b). Note that unlike proline, glycine betaine is not actively catabolized, so that control of glycine betaine concentration resides primarily at the level of synthesis rate and the rate of pool dilution with growth (Rhodes and Hanson, 1993).

In both maize and sorghum a number of naturally occurring glycine betaine-deficient inbred lines have been identified (Brunk et al., 1989; Grote et al., 1994). Glycine betaine-deficient maize lines lack the ability to accumulate glycine betaine in leaf tissue in response to either salinity stress or water deficits, due to a single recessive gene (betI) (Yang et al., 1995). Homozygous betI/betI maize lines are more salt-sensitive than near-isogenic homozygous BetI/BetI lines (Saneoka et al., 1995), and exhibit greater membrane injury and damage to photosystem II in response to heat stress (Yang et al., 1996). Glycine betaine-deficient maize lines lack the capacity to metabolize \(^1^4\)C-choline to \(^1^4\)C-glycine betaine, but are unimpaired in their ability to metabolize \(^2^H_3\)-betaine aldehyde to \(^2^H_3\)-glycine betaine, suggesting a lesion at the CMO step [or equivalent choline oxidizing activity] in the glycine betaine biosynthetic pathway (Lerma et al., 1991). Because BADH appears to be localized in peroxisomes of monocotyledonous plants (Nakamura et al., 1997), this raises the question of whether the subcellular localization [and mechanism] of choline oxidation is the same in grasses as in chenopods. Whereas chenopods derive choline destined for oxidation to glycine betaine predominantly from phosphocholine, via the action of a phosphocholine phosphatase (Hanson and Rhodes, 1981; Hanson et al., 1995), grasses obtain choline primarily from phosphatidylcholine (Hitz et al., 1981), presumably via the action of phospholipase D (Rhodes and Hanson, 1993).

In bacteria such as Escherichia coli, choline is an osmoprotectant only because it is oxidized to glycine betaine. The choline-glycine betaine pathway of E. coli consists of several genes encoding the functions of choline transport (betT), choline dehydrogenase (betA), betaine aldehyde dehydrogenase (betB), and a regulatory locus (betL) encoding a repressor protein (Lamark et al., 1991; 1996). The entire E. coli bet gene cluster has been introduced into the freshwater cyanobacterium, Synechococcus, and this confers glycine betaine accumulation (60 to 80 mM) and increased salt tolerance, due in part to stabilization of photosystems I and II (Nomura et al., 1995), and protection of ribulose 1,5-bisphosphate carboxylase/oxygenase from inactivation (Nomura et al., 1998). However, this increased salt tolerance appears to depend on the presence of an exogenous supply of choline (Nomura et al., 1995).

Because tobacco, rice and Arabidopsis are non-glycine betaine accumulators, these have been the organisms of choice for preliminary metabolic engineering experiments to test whether introduction of a capacity to synthesize glycine betaine influences higher plant salt tolerance (Hayashi and Murata, 1998; Takabe et al., 1998; Nuccio et al., 1998;
Transgenic tobacco plants expressing the *E. coli* betA gene encoding choline dehydrogenase, putatively capable of oxidizing both choline and betaine aldehyde, are reported to have increased salt tolerance (Lilius *et al.*, 1996), but because glycine betaine was not measured in these plants it is uncertain whether the salt tolerance phenotype can be attributed to glycine betaine accumulation. Transgenic rice plants expressing the *E. coli* betA gene are reported to accumulate up to 5 μmol/g fresh weight of glycine betaine associated with increased salt tolerance (Takabe *et al.*, 1998).

Introduction of the choline oxidase (codA) gene from *Arthrobacter* spp. into *Arabidopsis thaliana*, targeted to the chloroplast, leads to modest glycine betaine accumulation (1 μmol/g fresh weight) [approx. 50 mM if assumed to be confined solely to the chloroplast], and enhanced salt and cold tolerance associated with protection of photosystem II (Hayashi *et al.*, 1997; Hayashi and Murata, 1998). The codA gene also appears to confer increased heat and light stress tolerance in *Arabidopsis* (Alia *et al.*, 1998; 1999). The codA gene has also been expressed in either the chloroplast or cytosol of rice (Sakamoto *et al.*, 1998). Chloroplastic expression appears to confer greater tolerance to photoinhibition under salinity and low temperature stress (Sakamoto *et al.*, 1998).

However, expression of the cDNA encoding spinach CMO in the chloroplasts of tobacco leads to glycine betaine accumulation to levels of only a few percent of those found in natural glycine betaine accumulators (Nuccio *et al.*, 1998). Detailed analyses of choline metabolism in these transgenic tobacco plants suggests that the supply of choline may be limiting (Nuccio *et al.*, 1998; 1999). In tobacco, cytosolic choline is channeled almost exclusively into phosphatidylcholine via phosphocholine, making it difficult to divert choline to glycine betaine (Nuccio *et al.*, 1998). Glycine betaine accumulation places large demands on the synthesis of choline moieties, and on methyl groups required to generate choline (Hanson *et al.*, 1995). The capacity to accumulate glycine betaine may depend on special adaptations in choline and methyl group biogenesis that are not expressed in non-accumulators (Hanson *et al.*, 1995; McNeil *et al.*, 1999). In tobacco, and other non-glycine betaine accumulators, choline synthesis may be constrained at the first step in methylation of phosphoethanolamine en route to phosphocholine, catalyzed by phosphoethanolamine N-methyltransferase (Nuccio *et al.*, 1998; 1999).

### 10.3.3. CHOLINE-O-SULFATE

All members of the Plumbaginaceae accumulate choline-O-sulfate (Hanson *et al.*, 1994a). This compound is synthesized from choline by a salt stress-inducible choline sulfotransferase (Rivoal and Hanson, 1994) (Fig. 4B). Salt glands of members of the Plumbaginaceae can excrete chloride but not sulfate; conjugation of sulfate with choline may therefore be a mechanism of sulfate detoxification, converting a normally destabilizing anion to a compatible solute (Hanson *et al.*, 1994a). Consistent with this, accumulation of choline-O-sulfate is enhanced when Cl⁻ is replaced with SO₄²⁻ in the salinization medium (Hanson *et al.*, 1991). Because choline-O-sulfate synthesis competes with glycine betaine synthesis for available choline, this may have contributed
to the evolution of alternative betaine biosynthesis pathways (β-alanine betaine or proline betaine) which draw on substrates other than choline (Hanson et al., 1994 a).

10.3.4. β-ALANINE BETAINES

β-Alanine betaine is restricted to species of the Plumbaginaceae (Hanson et al., 1994 a). It is synthesized by direct N-methylation of the amino acid β-alanine, catalyzed by at least two S-adenosylmethionine (AdoMet)-dependent N-methyltransferases (Hanson et al., 1991; 1994 a) (Fig. 4C). Unlike glycine betaine, β-alanine betaine synthesis does not require O₂ (Hanson et al., 1994 a). This pathway may therefore represent an adaptation to anoxic saline environments (Hanson et al., 1994 a). The β-alanine betaine biosynthesis pathway is active in both leaves and roots of β-alanine betaine-accumulating Limonium species (Hanson et al., 1991). However, the precise origin of β-alanine in the Plumbaginaceae is not known.

10.3.5. PROLINE BETAINES AND HYDROXYPROLINE BETAINES

Proline betaine is accumulated by many higher plant species from diverse families (Wyn Jones and Storey, 1981; Hanson et al., 1994 a; Gorham, 1995; Nolte et al., 1997). The synthesis of proline betaine is thought to involve N-methylation of proline, via the intermediate N-methylproline (hygric acid) (Essery et al., 1962), presumably catalyzed by AdoMet-dependent methyltransferases (Fig. 4D) (Hanson et al., 1994 a). However, these enzymes have not yet been characterized. Hydroxyproline betaine often accumulates with proline betaine (Hanson et al., 1994 a; Nolte et al., 1997). The proline and/or N-methylproline hydroxylase(s) putatively involved in hydroxyproline betaine synthesis have not yet been identified (Hanson et al., 1994 a).

Proline betaine and hydroxyproline betaine accumulate at the expense of free proline (Hanson et al., 1994 a; Nolte et al., 1997). Because proline betaine is a more potent osmoprotectant than proline, this may confer increased osmotic stress resistance (Hanson et al., 1994 a). Synthesis of proline betaine would be expected to both alleviate P5CS from feedback regulation by proline, and restrict proline oxidation and hence compatible solute catabolism, perhaps contributing to maintenance of a greater compatible solute concentration (Samaras et al., 1995).

10.3.6. DIMETHYLSULFONIOPROPIONATE

The sulfonium analog of β-alanine betaine, 3-dimethylsulfoniopropionate (DMSP), is synthesized and accumulated to osmotically significant levels by many marine algae (see e.g. Blunden and Gordon, 1986; Dickson and Kirst, 1986), and by a few higher plant species from diverse families; Asteraceae (e.g. Wollastonia biforma), and Poaceae (some species of Spartina and Saccharum) (Paquet et al., 1994; James et al., 1995). DMSP is as effective as glycine betaine as an osmoprotectant for E. coli (Paquet et al., 1994), and
is noted to be a potent cryoprotectant (Nishiguchi and Somero, 1992; Karsten et al., 1996).

Figure 5. Pathways of synthesis of 3-dimethylsulfoniopropionate (DMSP) in higher plants (left) and marine algae (right). For the higher plant pathway Wb denotes the pathway found in Wollastonia biflora (Asteraceae), and Sa the pathway in Spartina alterniflora (Poaceae). The question mark adjacent to Wb indicates that the precise mechanism of conversion of SMM to DMSP-aldehyde in Wollastonia is not known; it may involve transamination and decarboxylation. AdoHcy, S-adenosylhomocysteine; AdoMet, £-adenosyl-methionine; DADH, DMSP-aldehyde dehydrogenase; DMSHB, 4-dimethylsulfonio-2-hydroxybutyrate; DMSP-amine, 3-dimethylsulfoniopropylamine; DMSP-aldehyde, 3-dimethylsulfonio-propionaldehyde; MAT, methionine:2-oxoglutarate aminotransferase; Met, methionine; MMT, AdoMet:methionine S-methyltransferase; MOx, methionine oxidase; MTHB, 4-methylthio-2-hydroxybutyrate; MTHBMT, AdoMet:MTHB S-methyltransferase; MTOB, 4-methylthio-2-oxobutyrate; MTOBR, MTOB reductase; SMM, S-methylmethionine.
In *Wollastonia*, DMSP is synthesized by methylation of methionine to S-methylmethionine (SMM) in the cytosol (Hanson *et al.*, 1994 b; James *et al.*, 1995 a,b), transport of SMM into the chloroplast, transamination or deamination and decarboxylation of SMM to DMSP-aldehyde (James *et al.*, 1995 b), and oxidation of the aldehyde to DMSP in the chloroplast (Trossat *et al.*, 1996; 1997) (Fig. 5). The first enzyme of the pathway, AdoMet:L-methionine S-methyltransferase (MMT) has been purified from *Wollastonia* leaves (James *et al.*, 1995 a), and its cDNA cloned (Bourgis *et al.*, 1999). The final step in the pathway is catalyzed by a chloroplast localized DMSP-aldehyde dehydrogenase (DADH), which may be identical to the BADH involved in glycine betaine synthesis (Trossat *et al.*, 1997; Vojtechová *et al.*, 1997). The enzyme(s) responsible for metabolism of SMM to DMSP-aldehyde in *Wollastonia* is not yet known. It is proposed that SMM is converted to DMSP-aldehyde via a specialized transaminase-decarboxylase (Rhodes *et al.*, 1997).

The pathway of DMSP synthesis in the salt marsh grass *Spartina alterniflora* is similar to that in *W. biflora* except with respect to the SMM $\rightarrow$ DMSP-aldehyde steps in the pathway (Fig. 5). In *Spartina*, radiolabeling experiments with $^{35}$S-methionine and $^{35}$S-SMM show that DMSP-amine behaves as an intermediate, implicating SMM decarboxylation as the first step in the conversion of SMM to DMSP-aldehyde (Kocsis *et al.*, 1998). DMSP-amine may then be metabolized to the aldehyde via an amine oxidase, but this enzyme has not been characterized.

The pathway of DMSP synthesis in higher plants is completely different from that found in marine algae (Gage *et al.*, 1997). In marine algae methionine is first converted to the 2-keto acid, 4-methylthio-2-oxobutyrate (MTOB), via the action of either methionine:2-oxoglutarate aminotransferase or methionine oxidase (Gage *et al.*, 1997; Summers *et al.*, 1998) (Fig. 5). MTOB is then reduced to 4-methylthio-2-hydroxybutyrate (MTHB) by an NADPH-dependent reductase (Summers *et al.*, 1998). MTHB is subsequently S-methylated to 4-dimethylsulfonio-2-hydroxybutyrate (DMSHB) which is then oxidatively decarboxylated to DMSP (Gage *et al.*, 1997; Summers *et al.*, 1998) (Fig. 5). The latter enzyme has not been identified.

Because DMSP does not contain N, the accumulation of DMSP as a compatible solute could represent a special adaptation to N-limiting environments. N-deficiency increases DMSP levels in *Wollastonia* (Hanson *et al.*, 1994 b) and marine algae (Gage *et al.*, 1997; Dickson and Kirst, 1986).

10.3.7. POLYOLS

Like DMSP, polyhydric alcohols (polyols) also lack N, and so could represent important compatible solutes where synthesis of nitrogenous solutes (e.g. proline and/or betaines) is limited by N availability. The acyclic polyols, sorbitol and mannitol are accumulated by many marine algae, lower plants and species from diverse higher plant families, including certain halophytes (Ahmad *et al.*, 1979; Briens and Larher, 1982; 1983; Popp...
and Smirnoff, 1995). Sorbitol is accumulated to high levels (up to 70 mM on a tissue water basis) by members of the Plantaginaceae in response to salinity stress, while mannitol can reach concentrations as high as 200 mM on a tissue water basis in leaf and stem tissues of the mangrove species Laguncularia racemosa (Popp and Smirnoff, 1995).

Figure 6 shows the pathways of synthesis of sorbitol, mannitol and the cyclic polyols (cyclitols), D-ononitol and D-pinitol. Note that sorbitol and mannitol draw directly from the glucose-6-phosphate and fructose-6-phosphate pools, and that sorbitol synthesis potentially competes with myo-inositol synthesis, and hence the synthesis of D-ononitol.
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and D-pinitol. The latter cyclic polyols are accumulated by many legumes in response to water deficits and salinity stress (Popp and Smirnoff, 1995). D-Pinitol is also accumulated by the halophytic facultative crassulacean acid metabolism plant, *Mesembryanthemum crystallinum*, in response to salinization (Bohnert *et al.*, 1995; Bohnert and Jensen, 1996).

In the Rosaceae, and Apiaceae, sorbitol and mannitol, respectively, are utilized as phloem translocated photoassimilates (Locy, 1994; Popp and Smirnoff, 1995). These polyols are actively catabolized in non-photosynthetic sink tissues by NAD⁺-dependent sorbitol and mannitol dehydrogenases (Locy, 1994; Williamson *et al.*, 1995). The mannitol dehydrogenase of celery has been cloned and has been shown to be repressed by salinity stress (Williamson *et al.*, 1995). In celery plants mannitol dehydrogenase activity and mannitol pool size are inversely correlated, suggesting that regulation of catabolism of mannitol is a major determinant of the tissue concentration of this compatible solute (Williamson *et al.*, 1995). However, little is known about the regulation of sorbitol and mannitol catabolism in members of the Plantaginaceae and mangroves that accumulate high levels of these solutes in response to salinity stress (Locy, 1994; Popp and Smirnoff, 1995). The cyclic polyols, D-ononitol and D-pinitol, appear to be less rapidly catabolized (Popp and Smirnoff, 1995), and control of tissue concentrations may therefore be primarily determined by synthesis rate.

In members of the Apiaceae (e.g. celery and celeriac), mannitol is synthesized from fructose-6-phosphate via mannose-6-phosphate via the action of mannose-6-phosphate isomerase and an NADPH-dependent mannose-6-phosphate reductase (M6PR) (Fig. 6). The gene encoding M6PR has been cloned from celery, and shows considerable sequence similarity to the sorbitol-6-phosphate dehydrogenase of apple (Everard *et al.*, 1997). M6PR is expressed in green tissues and is under tight transcriptional regulation during leaf development (Everard *et al.*, 1997).

Tobacco has served an excellent model system to explore the potential contribution of the acyclic and cyclic polyols. Wild-type tobacco lacks mannitol, sorbitol, D-ononitol and D-pinitol, but contains myo-inositol (Sheveleva *et al.*, 1997; 1998). Tobacco has been engineered to accumulate mannitol by introducing the mannitol-1-phosphate dehydrogenase gene (*mtlD*) from *Escherichia coli* (Tarczynski *et al.*, 1992; 1993). This enzyme converts fructose-6-phosphate to mannitol-1-phosphate which is then cleaved to mannitol, presumably by a constitutive, non-specific sugar alcohol-phosphate phosphatase (Fig. 6). Constitutive production of mannitol in tobacco has been achieved by expressing *mtlD* in either the cytosol (Tarczynski *et al.*, 1992; 1993) or chloroplast (Shen *et al.*, 1997 a,b); both result in increased salt tolerance. Expression of *mtlD* in the chloroplast results in accumulation of mannitol to concentrations of up to 100 mM in tobacco chloroplasts (Shen *et al.*, 1997 b). Mannitol may function not only as a compatible solute, but also as a hydroxyl radical scavenger in this compartment (Smirnoff and Cumbes, 1989; Shen *et al.*, 1997 b).
In apple, sorbitol is derived from glucose-6-phosphate via the catalytic action of an NADPH-dependent sorbitol-6-phosphate dehydrogenase (Tao et al., 1995), and sorbitol-6-phosphate phosphatase (Popp and Smirnoff, 1995) (Fig. 6). Constitutive expression of the apple sorbitol-6-phosphate dehydrogenase in tobacco, leads to necrotic lesions in proportion to the size of the sorbitol pool accumulated [up to 130 mM on a whole tissue water basis] (Sheveleva et al., 1998). Again, as with mannitol, it is presumed that sorbitol-6-phosphate is catabolized to sorbitol by a constitutive non-specific sugar alcohol-phosphate phosphatase in these transgenic tobacco plants (Sheveleva et al., 1998). The autotoxicity of sorbitol accumulation in tobacco may be the result of depletion of myo-inositol (Sheveleva et al., 1998), although toxic accumulation of sorbitol-6-phosphate cannot yet be ruled out. Because of the growth inhibition caused by overproduction of sorbitol in transgenic tobacco, it has not been possible to accurately assess the contribution of this solute to salt tolerance of tobacco (Sheveleva et al., 1998).

Myo-inositol is derived from glucose-6-phosphate via the action of glucose-6-phosphate cycloaldolase [myo-inositol-1-phosphate synthase] and myo-inositol-1-phosphate phosphatase (Fig. 6). D-Ononitol is then formed by O-methylation of myo-inositol, catalyzed by an AdoMet-dependent myo-inositol O-methyltransferase (Vernon and Bohnert, 1992). D-Pinitol is derived from D-ononitol via the action of an ononitol epimerase (Bohnert and Jensen, 1996) (Fig. 6). In M. crystallinum the entire pathway is salinity stress inducible (Vernon and Bohnert, 1992; Bohnert and Jensen, 1996). Myo-inositol may not only serve as a substrate for the production of compatible solutes but also as a leaf-to-root signal that promotes sodium uptake in M. crystallinum (Nelson et al., 1999). Note that wild-type tobacco has the capacity to synthesize and accumulate myo-inositol in response to salinity and drought stress, but lacks the terminal methyltransferase and epimerase of the pathway (Sheveleva et al., 1997). Sheveleva et al. (1997) have constitutively expressed the M. crystallinum gene encoding myo-inositol-O-methyltransferase in tobacco. This confers stress-induced D-ononitol accumulation [up to 35 mM on a whole tissue water basis] and increased salt tolerance (Sheveleva et al., 1997). Unlike constitutive sorbitol accumulation, stress-inducible D-ononitol accumulation does not result in necrotic lesions (Sheveleva et al., 1997).

10.4. Evidence for cytoplasmic localization of compatible solutes

Central to the compatible solute hypothesis is that these solutes are accumulated in the cytosol and/or cytoplasmic organelles such as chloroplasts. Approaches to testing this fundamental premise of this hypothesis have been to isolate intact vacuoles and chloroplasts from salinized plant tissues, demonstrating that the ratios of compatible solutes to inorganic ions in these compartments are substantially different from those of whole tissue extracts (Leigh et al., 1981; Wyn Jones et al., 1977; Robinson and Jones, 1986). However, considerable technical difficulties are associated with correcting for solute leakage from organelles during aqueous extraction (see e.g. Leigh et al., 1981; Robinson and Jones, 1986).
Using organelle isolation methods evidence for a predominantly cytoplasmic (extra-vacuolar) localization of proline has been obtained for red beet cells (Leigh et al., 1981) and Distichlis spicata cell cultures (Ketchum et al., 1991). The cytoplasmic concentration of proline in 200 mM NaCl-grown Distichlis cells has been determined to be within the range 237 - 311 mM; approximately 10-times the concentration in the cell as a whole (Ketchum et al., 1991).

Robinson and Jones (1986) have determined that the glycine betaine concentration of chloroplasts isolated from leaves of spinach plants salinized to 200 mM NaCl, can approach 300 mM, contributing at least one-third of the total osmotic potential of the chloroplast. This is consistent with other investigations of the compartmentation of glycine betaine in chenopods which have demonstrated that this solute is extra-vacuolar (Wyn Jones et al., 1977; Hall et al., 1978; Leigh et al., 1981; Matoh et al, 1987) or chloroplastic (Schröppel-Meier and Kaiser, 1988; Genard et al., 1991). It is not known whether glycine betaine is localized in chloroplasts of grasses which accumulate this solute. The intracellular localizations of choline-O-sulfate, β-alanine betaine, proline betaine and hydroxyproline betaine in the Plumbaginaceae have not been investigated. However, there is strong circumstantial evidence that these solutes have replaced the function of glycine betaine as cytoplasmic compatible solutes. Thus, the total quaternary ammonium compound levels of contrasting glycine betaine and β-alanine betaine accumulating Limonium species are both tightly correlated with total solute potential (at 100% relative water content) in leaf tissues of plants grown in nutrient solutions containing 0 - 600 mM NaCl (Hanson et al., 1991).

Consistent with the chloroplastic localization of the terminal enzymes of the DMSP synthesis pathway in Wallastonia biflora, DMSP is predominantly localized in the chloroplasts of salinized W. biflora plants, where its concentration may exceed 130 mM (Trossat et al., 1998).

Pinitol concentrations in the chloroplasts isolated from leaves of M. crystallinum plants have been estimated to be 230 mM, whereas the cytosol concentration was estimated to be 100 mM [cf. 10 mM on a tissue sap basis] (Paul and Cockburn, 1989). Pinitol was not detected in vacuoles (Paul and Cockburn, 1989). However, as discussed by Popp and Smirnoff (1995) the concentrations of certain cyclitols in the Fabaceae and mangroves can exceed 200 mM on a tissue water basis and it seems highly unlikely that these could be exclusively localized in the cytoplasm in these species. Vacuolar accumulation of polyols or other carbohydrates may provide osmotic adjustment in saline environments when Na⁺ and Cl⁻ are excluded from leaf tissues (Briens and Larher, 1982). Thus, Briens and Larher (1982) have noted an inverse correlation between leaf inorganic ion content and organic solute concentration among diverse halophytic plant species.

10.5. Concluding discussion
It has long been recognized that salt-tolerant and salt-sensitive plant species differ dramatically with respect to their accumulation of organic solutes, particularly in response to salinity stress (Wyn Jones and Storey, 1981; Blunden and Gordon, 1986; Gorham, 1995; Smirnoff and Stewart, 1985; Rhodes and Hanson, 1993; Popp and Smirnoff, 1995; Bohnert and Jensen, 1996). Because these organic solutes/osmolytes are non-toxic to enzyme systems across a wide concentration range, and there is sparse but growing evidence that these solutes are accumulated in the cytoplasm, it seems likely that these solutes play a central role in cytoplasmic osmotic adjustment by acting as "compatible cytoplasmic solutes" in plants (Wyn Jones et al. 1977), as in other organisms (Hochachka and Somero, 1984; Yancey, 1994). According to Hochachka and Somero (1984) the selection of a particular organic solute for use as an osmotic agent is subsidiary to the fundamental "design principle of establishing a microenvironment for macromolecules in which their structural and functional properties are optimized for catalysis, metabolic regulation, information transfer, and mechanical work, and in which a balance is achieved between stability and instability of structure." Because many different organic compounds can satisfy this microenvironmental design principle, we should not be surprised by the great diversity of the metabolic pathways of plant osmolyte synthesis discussed above.

Recent studies with transgenic glycophytic plants engineered for the synthesis and accumulation of certain of these compounds (including proline, glycine betaine, mannitol and D-ononitol) indicate that such accumulation may confer modest increases in salt tolerance, and in some cases, increased resistance/tolerance to other stresses (drought, cold, heat or light). In the case of mannitol accumulation it appears that the mode of action of this solute may not be solely in cytoplasmic osmotic adjustment; mannitol may play a more significant role as a hydroxyl radical scavenger in chloroplasts (Shen et al., 1997b). These advances with model glycophytes, achieved by manipulating single genes, hold substantial promise for designing and implementing engineering strategies to enhance salinity stress resistance of crop plants (Bohnert and Jensen, 1996; Bohnert and Shen, 1999; Jain and Selvarej, 1997). However, these preliminary genetic interventions have also shown that: (i) the introduction of a foreign gene conferring synthesis of a solute may substantially disturb normal metabolism and growth (Sheveleva et al., 1998; Serrano et al., 1999), and (ii) the engineered gene may often be embedded in a rigid metabolic network that resists change and restricts solute accumulation (Nuccio et al., 1998, 1999). Hare et al. (1998) suggest that disturbance of hexose sensing may be an important contributing factor to the stress-tolerance phenotypes of plants engineered for carbohydrate osmolytes, and that there is a need for re-assessment of the significance of proline and glycine betaine accumulation as mechanisms for buffering cellular redox potential. Further work is needed to identify the unique regulatory features of metabolism that permit the accumulation of substantial levels of compatible solutes found in nature (Jain and Selvarej, 1997), and to combine these traits with other equally important osmoregulatory features of halophytes discussed in this volume, including potassium/sodium discrimination, sodium exclusion, and sodium compartmentation in the vacuole.
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References


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Metabolic Networking in Plants

April 22-25, 1999

The 1st annual Plant Biochemistry and Molecular Biology Conference
Program

Thursday, April 22

2:00 - 4:00 Registration (2nd floor lobby)
2:00 - 4:00 Reception (2nd floor lobby)

Plenary Session I  Eve Syrkin Wurtele, Session Chair

4:00 - 4:10 Welcome: Dean Patricia Swan
4:10 - 4:55 Coruzzi, Amino acid signaling and sensing in Arabidopsis
4:55 - 5:40 Stitt, Coordinate regulation in central metabolic pathways
5:40 - 7:20 Dinner (Stagedoor Cafe), Jack Gallup, guitar

Friday, April 23

8:30 - 9:00 Continental Breakfast (1st floor lobby)

Plenary Session II  Martha G. James, Session Chair

9:00 - 9:45 Oliver, Glutathione synthesis in plants: Multiple controls in response to multiple stresses
9:45 - 10:30 Chappie, Secondary metabolism in Arabidopsis: biochemistry and biotechnology
10:30 - 11:00 Break with refreshments (1st floor lobby)
11:00 - 12:15 Presented Papers - Session I
12:15 - 2:00 Lunch (Stagedoor Cafe)

Plenary Session III  John P. Davies, Session Chair

2:00 - 2:45 Nikolau, Molecular biology of acetyl-CoA generation and metabolism in plants
2:45 - 3:30 Browse, Arabidopsis mutants reveal many roles for lipid metabolism in plants
3:30 - 4:30 Poster Session I and coffee
4:30 - 5:15 Bush, Resource allocation and multicellular growth: Molecular analysis of plant sugar and amino acid transporters
5:15 - 6:00 Leustek, Environmental factors that regulate sulfur assimilation in plants
6:00 - 6:15 Group photo
6:15 - 7:45 Dinner (Stagedoor Cafe), Paula Helmuth, piano
7:45 - 9:30 Dessert Party, Eve Syrkin Wurtele’s home (3425 Oakland Street)
Saturday, April 24

8:00 - 8:30 Continental breakfast (1st floor lobby)

Plenary Session IV  Martin H. Spalding, Session Chair

8:30 - 9:15 Sheen, Sugar and hormonal signaling network
9:15 - 10:00 Rhodes, Computer simulation of isotope labeling kinetics of metabolic networks: Uses in interpreting precursor-product relationships, fluxes and compartmentation of pools
10:00 - 10:30 Break with refreshments (1st floor lobby)
10:30 - 12:15 Presented Papers - Session II
12:15 - 1:45 Lunch (Stagedoor Cafe)

Plenary Session V  Basil J. Nikolau, Session Chair

1:45 - 2:30 Pichersky, Pathways that lead to the synthesis of scent and flavor compounds
2:30 - 3:00 Presented Paper - Session III: Computational Biology
3:00 - 4:45 Poster Session II with coffee
4:45 - 5:30 Shanklin, Encouraging enzymes to do what we want them to do: Rational and irrational design
5:30 - 6:15 Murata, CARVER LECTURER, Metabolic feedback in the fatty-acid desaturation of membrane lipids
6:15 - 8:00 Dinner (Stagedoor Cafe), Mary Foss, harp

Sunday, April 25

8:00 - 9:00 Continental breakfast (1st floor lobby)

Plenary Session VI  Parag R. Chitnis, Session Chair

9:00 - 9:30 Presented Papers - Session IV
9:30 - 10:15 Grotewold, Plant Myb-domain proteins and metabolic diversity: Tools for engineering secondary metabolism?
10:15 - 10:40 Break with refreshments (1st floor lobby)
10:40 - 11:25 Bohnert, Metabolic engineering of plant abiotic stress tolerance
11:35 - 12:10 Buses leave for the airport
Interactive computer models for interpreting in vivo isotopic tracer data will be described and discussed. Simplified hypothetical examples will first be employed to introduce modeling principles - the deduction of precursor-product relationships, fluxes and compartmentation of metabolite pools from carefully timed in vivo isotope labeling data and pool size measurements. These principles will be applied to analysis of the pathways of synthesis of the osmolyte 3-dimethylsulfoniopropionate (DMSP) in the marine alga, Enteromorpha intestinalis, and the higher plant, Spartina alterniflora. Both organisms synthesize DMSP from methionine, but employ different intermediates. Computer modeling of 35S tracer data demonstrates that in Enteromorpha DMSP synthesis proceeds via the steps methionine -> 4-methylthio-2-hydroxybutyrate -> 4-dimethylsulfoniopropionate -> DMSP (Gage et al., 1997), whereas in Spartina the pathway proceeds via the steps methionine -> S-methylmethionine -> 3-dimethylsulfoniopropylamine -> DMSP (Kocsis et al., 1998). In both cases computer-assisted analysis of the pathways permit estimates to be made of the fluxes to DMSP, the sizes of metabolically active and relatively inactive (storage) pools of intermediates, and the transport rates between them.

We then extend these models to consider the network of choline metabolism in tobacco leaves, with emphasis on identifying the metabolic constraints that limit the synthesis and accumulation of the osmolyte, glycine betaine, in transgenic tobacco expressing ferrodoxin-dependent choline monoxygenase (CMO) in the chloroplast (Nuccio et al., 1998). Modeling of [14C]-choline metabolism (including phosphocholine and phosphatidylcholine synthesis and catabolism) suggests that the primary constraint is a low affinity of the chloroplast choline transport system. The latter does not compete effectively with the high affinity choline kinase and tonoplast choline transport system for available cytosolic choline. The models reveal other constraints on glycine betaine synthesis that may help guide future rounds of metabolic engineering to enhance glycine betaine synthesis. Greatly elevating flux to glycine betaine is likely to occur at the expense of flux to phosphatidylcholine, with potentially growth inhibitory consequences unless the synthesis of choline moieties is also enhanced. This example illustrates how mathematical models can help build understanding of the complex interactions of metabolic networks which often confound metabolic engineering efforts to redirect fluxes (Bailey, 1998).

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Literature cited:


for additional information on computer simulation of metabolism and examples of interactive, online models see http://www.hort.purdue.edu/cfpesp/models/models.htm