DMSP synthesis and exudation in phytoplankton: a modeling approach

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ABSTRACT: In the marine environment, phytoplankton are the fundamental producers of dimethylsulfiniopropionate (DMSP), the precursor of the climatically active gas dimethylsulfide (DMS). DMSP is released by exudation, cell autolysis, and zooplankton grazing during phytoplankton blooms. In this study, we developed a model of phytoplankton DMSP and DMS production allowing quantification of the exudation rates of these compounds during different growth phases. The model was tested on published data from axenic cultures of Prorocentrum minimum and Phaeocystis sp.; DMSP exudation rates vary considerably between the 2 species. Model results show that P. minimum exudes around 1% d⁻¹ of its DMSP quota during the latent, exponential and senescent phases. This is comparable to the average exudation rate estimated from previous laboratory experiments. However, Phaeocystis sp. exudes from 3 to 11% d⁻¹ of its DMSP quota. For this species, DMSP exudation rates apparently show an inverse relationship with the population growth rate. The maximum DMSP exudation rate in Phaeocystis sp. is 10 times higher than previously reported DMSP or DMS exudation rates. Our results suggest that exudation may be as important as cell autolysis in the release of DMSP during Phaeocystis sp. blooms. We conclude that exudation should be incorporated in models of DMS cycling in the marine environment. Moreover, our results for Phaeocystis sp. suggest that a low and constant exudation rate, as sometimes used in models, is not suitable for all conditions.

KEY WORDS: DMS - DMSP - Exudation - Synthesis - Phaeocystis - Model

INTRODUCTION

Over oceanic regions, the release of marine dimethylsulfide (DMS) to the atmosphere is thought to play an important climatic role by increasing the scattering of solar radiation and by providing cloud condensation nuclei. Dimethylsulfiniopropionate (DMSP), the DMS precursor, is synthesized by many macroalgae and phytoplankton. It has been suggested that DMSP acts as an osmolyte (Vairavamurthy et al. 1985, Dickson & Kirst 1987), a cryoprotectant (Kirst et al. 1991) and a methyl donor (Ishida 1968). Cell quotas of DMSP are highly variable among species (Keller et al. 1989). Prymnesiophytes and dinoflagellates have a high intracellular DMSP concentration compared to diatoms. DMSP quotas vary also through the algal growth cycle (Stefels & van Boekel 1993, Matrai & Keller 1994) and may be influenced by nitrate (Turner et al. 1988, Groene & Kirst 1992, Keller & Korjef-Bellows 1996) and phosphate limitation (Stefels & van Boekel 1993). DMSP is released into seawater mainly during senescence or the latter phase of blooms (Matrai & Keller 1993), most likely via cell autolysis (Nguyen et al. 1988, Kwint & Kramer 1995) and zooplankton grazing (Dacey & Wakeham 1986, Cantin et al. 1996). Phytoplankton may also exude DMSP, but DMSP
liberation by phytoplankton is usually attributed to cell autolysis. Exudation is rarely considered as a DMSP liberation mechanism. In seawater, DMSP may be either demethylated by bacteria without any production of DMS or enzymatically cleaved to DMS by phytoplankton (Stefels & van Boekel 1993, Wolfe & Steinke 1996) or bacterial (Kiene & Bates 1990, Kiene 1992) DMSP-lyase. The 3 main sinks of DMS are: consumption by bacteria, photo-oxidation into dimethylsulphoxide (DMSO; Brimblecombe & Shooter 1986, Kieber et al. 1996) and ventilation to the atmosphere.

The multitude of interacting mechanisms makes modeling appropriate to study DMS dynamics and to evaluate the DMS flux to the atmosphere. Gabri et al. (1993) modified a nitrogen-based model by adding DMS-related processes to reproduce the evolution of DMS concentrations in seawater during a phytoplankton bloom. Lawrence (1993) modeled DMS dynamics both in the ocean and in the atmosphere. In his model, the food web was oversimplified, and Lawrence pointed out the lack of knowledge about DMS processes in the marine environment. Van den Berg et al. (1996b) modified a coupled physical-phytoplankton model, the FYFY model (van den Berg et al. 1996a), developed for the southern North Sea, by adding DMS-related processes. The FYFY model simulates 6 phytoplankton classes, 1 grazer size and bacteria. Their results showed, among other things, the importance of Phaeocystis DMSP-lyase on DMS flux to the atmosphere. These models improved our understanding of DMS dynamics, mainly by synthesizing present information and pointing towards areas where better understanding is needed. An ultimate goal of modeling DMS dynamics is to evaluate the impact of an anticipated climatic warming on DMS production and the possible feedback strength of the cooling effect induced by DMS emission. However, uncertainties in DMS production, DMS production, and DMS sinks limit our capability to evaluate such feedback mechanisms.

This modeling study focuses on DMS synthesis and DMSP release by phytoplankton during the growth cycle. In a minireview, Malin & Kirst (1997) stressed the lack of DMS releasing rates by organisms and particularly by phytoplankton. Only 3 rates of DMS production by phytoplankton can be extracted from different laboratory studies and uncertainties remain about them. Dacey & Wakeham (1986) and Vairavamurthy et al. (1985) estimated that the daily percentage of the DMSP quota exuded as DMS into seawater was 0.3 and 1.4% for the dinoflagellates Gymnodinium nelsoni and Hymenomonas carterae, respectively. The rate given for G. nelsoni is probably underestimated due to bacterial DMS consumption. The third rate present in the literature is from Vetter & Sharp (1993), who grew an axenic culture of the centric diatom Skeletonema costatum and estimated a DMS production rate of 10 to 40 fg S(DMS) cell\(^{-1}\) d\(^{-1}\). In these 3 studies, the reported release product by the different phytoplankton species is DMS. However, it has not been investigated whether or not these species synthesize DMSP-lyase. The presence of DMS in these cultures may have resulted from phytoplankton DMSP-lyase production or from the activity of possible bacterial contaminants. Bacteria may have consumed DMS and therefore caused DMS exudation rates to be underestimated.

The goal of the present study was to model DMSP synthesis and DMSP exudation by marine phytoplankton. To study these processes it is essential to use axenic phytoplankton cultures to eliminate DMSP and DMS losses due to bacterial consumption. The data from 2 published axenic culture studies were used to constrain the model. These 2 studies dealt with 2 important DMSP producers (Keller et al. 1989), the dinoflagellate Proorocentrum minimum and the pyrnesiophyte Phaeocystis sp. P. minimum has a wide distribution, forming large blooms in temperate and subtropical waters bordering the North Pacific (Russia, China, Japan, Canada), the east and south coasts of the USA, the NE Atlantic, the North Sea and the Mediterranean Sea (Grzebyk & Berland 1996). Phaeocystis sp. is known to produce DMSP-lyase (Stefels & van Boekel 1993) and is an important player in the DMS cycle. Phaeocystis forms large blooms in the North Sea (Veldhuis & Admiraal 1987, van Boekel et al. 1992, Turner et al. 1996), the Arctic (Wassmann et al. 1990, Matrai & Vernet 1997) and the Antarctic (Gibson et al. 1988, Crocker et al. 1995), where it has been associated with the highest DMS concentrations ever measured in the oceans (Gibson et al. 1988, Crocker et al. 1995).

**EXPERIMENTAL DATA AND MODELING APPROACH**

We used data from Matrai & Keller (1994) and Stefels & van Boekel (1993), who grew axenic cultures of Proorocentrum minimum and Phaeocystis sp., respectively. Both species were grown in 1 l flasks. P. minimum was grown in K-medium (Keller et al. 1987) at 18°C with a light intensity of 166.1 μE m\(^{-2}\) s\(^{-1}\) in a 14 h light:10 h dark cycle. Phaeocystis sp. was grown in a medium described by Veldhuis & Admiraal (1987), with the exception that nitrate was the only nitrogen source. The culture was maintained at 10°C with a light intensity of 85 μE m\(^{-2}\) s\(^{-1}\) in a 14 h light:10 h dark cycle. Changes in nutrient concentrations were not measured in either study, but nitrogen limitation was expected for P. minimum and phosphorus limitation for Phaeocystis sp. More details on the materials and methods are available in the respective papers.
Variations in algal cell numbers. The temporal change in algal cell numbers was simulated with a logistic equation. Since nutrient depletion was not followed and since the light was saturating in the batch cultures, we could not model the nutrient or light dependence of the phytoplankton population growth. The growth of the phytoplanktonic population is determined by:

$$\frac{d\text{CELL}}{dt} = \frac{R \cdot \text{CELL} \cdot (K - \text{CELL})}{K}$$

(1)

where CELL is cell numbers (cells 1-'), $t$ is time (d), $R$ is the maximum specific growth rate (d$^{-1}$), and $K$ is the carrying capacity of the cultures (cells 1$^{-1}$). To simulate the decrease in cell numbers during the senescent phase, we added a mortality term to the equation of the temporal changes in cell numbers through time:

$$\frac{d\text{CELL}}{dt} = \frac{R \cdot \text{CELL} \cdot (K - \text{CELL})}{K} - m \cdot \text{CELL}$$

(2)

where $m$ (d$^{-1}$) is the specific mortality rate.

In our modeling work, the ratio $g/g_{max}$ is used as an index of growth limitation, where $g$ (cells 1$^{-1}$ d$^{-1}$) represents the realized population growth rate, described by Eq. (1), and $g_{max}$ (cells 1$^{-1}$ d$^{-1}$) is the maximal population growth rate. Prior to reaching the inflection point of the growth curve (where the derivative of Eq. 1 is zero, Day 10 and 12 for *Prorocentrum minimum* and *Phaeocystis* sp., respectively), the microalgae are assumed to grow at maximal rates, unlimited by either light or nutrients. The ratio $g/g_{max}$ is set at 1 for this part of the culture cycle. After the inflection point, growth limitation is assumed to occur, and $g/g_{max}$ is computed for each time step by dividing the growth rate calculated from Eq. (1) (normalized by cell numbers) by the maximum rate attained at the inflection point.

**DMSP synthesis.** To model DMSP synthesis, we assigned a DMSP synthesis rate to each phytoplankton cell. This is represented by the following equation:

$$\frac{d\text{DMSP}}{dt} = \rho_{syn} \cdot \text{CELL}$$

(3a)

where DMSP$*$ is the total amount of DMSP synthesized (µmol DMSP 1$^{-1}$) in the culture, $\rho_{syn}$ is the cellular synthesis rate (µmol DMSP$*$ cell$^{-1}$ d$^{-1}$) and CELL (cells 1$^{-1}$) is calculated by Eq. (2). To model the DMSP, we used a parameterization simulating maximal DMSP synthesis, when cells are growing fast and duplicating, and minimal DMSP synthesis, when cell growth becomes limited. Thus, we set the DMSP synthesis rate dependent on the relative growth rate:

$$\rho_{syn} = \max \left[ S_{MIN}, S_{MAX} \left( \frac{g}{g_{max}} \right)^A \right]$$

(3b)
The expression $\text{max}[S_{\text{MIN}}, S_{\text{MAX}} \cdot (g/g_{\text{MAX}})^A]$ means that $p_{\text{syn}}$ is set as the maximal value between $S_{\text{MIN}}$ and $S_{\text{MAX}} \cdot (g/g_{\text{MAX}})^A$. $S_{\text{MIN}}$ [Åumol DMSP/Åumol cell⁻¹ d⁻¹] and $S_{\text{MAX}}$ [Åumol DMSP/Åumol cell⁻¹ d⁻¹] are constants representing respectively the minimum and maximum DMSP synthesis rate per cell, and $A$ (dimensionless) is a species-specific coefficient for DMSP synthesis. The constant $A$ represents the sensitivity of DMSP synthesis to variations in the population growth rate. A high $A$ value indicates a strong response of the DMSP synthesis rate to a change in algal growth rate.

**Particulate and dissolved DMSP pools.** In an axenic culture, the temporal changes in the DMSPₚ pool result from the balance between DMSP synthesis, exudation and cellular autolysis, as given by the following equation:

$$\frac{d(DMSP_p)}{dt} = p_{\text{syn}} \cdot CELL - p_{\text{exo}} \cdot CELL \cdot QUOTA - m \cdot CELL \cdot QUOTA \quad (4)$$

The first term on the right-hand side of Eq. (4) is DMSP synthesis as defined by Eq. (3a). The second term represents the loss by exudation, where $p_{\text{exo}}$ (d⁻¹) is the specific exudation rate and QUOTA (Åumol DMSP cell⁻¹) is the instantaneous ratio of DMSPₚ to cell number. The third term represents the amount of DMSP released in seawater via mortality (autolysis).

The accumulation of DMSPₚ is the sum of DMSP released by exudation and by autolysis:

$$\frac{d(DMSP_p)}{dt} = p_{\text{exo}} \cdot CELL \cdot QUOTA + m \cdot CELL \cdot QUOTA \quad (5)$$

Parameters are the same as in Eq. (4).

The model was applied to the experimental data. The parameters were obtained through manual iterations to minimize differences between experimental and modeled results as expressed by Eq. (6) (below). A mathematical tool was used to evaluate the model misfit of the experimental results. The misfit was expressed as the average percentage of model error:

$$\text{% model error} = \frac{\sum_{t=0}^{n} \left( \frac{\text{DMSP}_{\text{exp}}(t) - \text{DMSP}_{\text{mod}}(t)}{\text{DMSP}_{\text{exp}}(t)} + \frac{\text{DMSP}_{\text{d}(t)} - \text{DMSP}_{\text{d}(t)}}{\text{DMSP}_{\text{d}(t)}} \right)}{2n} \times 100 \quad (6)$$

where DMSP_{exp}(t) and DMSP_{mod}(t) are the experimental and modeled values of DMSPₚ at time $t$, DMSP_{d}(t) and DMSP_{d}(t) are the experimental and modeled values of DMSPₚ at time $t$ and $n$ is the number of observations. A percentage-based index was selected as a way to give similar weights to small and large experimental values. This prevents errors on large values from determining total error. A percentage of 0 from Eq. (6) represents a perfect fit while a value of 100% signifies that the model simulates the experimental results with an average error of 100%. The model is coded with the software Matlab (The Mathworks Inc., Natick, MA, USA) and is solved by finite differences with time steps of 14 min, determined by trial and error to be the optimal interval to get accurate numerical solutions.

**MODEL RESULTS**

**Algal cell numbers**

The adjustment of the model parameters, related to temporal changes in algal cell numbers (Eq. 2), to the experimental data resulted in the values presented in Table 1 for $K, R$ and $\text{CELL}(0)$ (i.e. cell number at $t = 0$). We fixed $m$ at 0 until maximum cell number was reached (Day 16 for both species), then a null growth rate and a constant mortality rate (Table 1) were imposed in order to reproduce the temporal changes of cell numbers (Fig. 1) throughout the cultures.

**DMSP synthesis**

Adjusting the model DMSP synthesis parameters (Eqs. 3a & 3b), $S_{\text{MIN}}, S_{\text{MAX}}$ and $A$, to minimize differences between experimental and modeled results led to the values presented in Table 1. The sum of the experimental values of DMSPₚ, DMSPₚ and DMS represented the total DMSP (DMSPₚ) synthesized in the cultures (circles in Fig. 2). The accurate reproduction of experimental DMSP, concentrations by the model provided the basis to model further transfers from the intracellular DMSP to the dissolved DMSP.

**Particulate and dissolved DMSP pools**

Different formulations for the parameters of Eqs. (4) & (5) were tested (Figs. 3 & 4) to reproduce the measured DMSPₚ and DMSPₚ pools (DMSP for *Phaeocystis* sp.). The simplest assumption is that cell mortality (autolysis) is the only source of DMSPₚ. This was tested by setting $p_{\text{exo}}$ at 0 d⁻¹ (see Eqs. 4 & 5). Figs. 3A & 4A show that such a parameterization overestimated the particulate fraction and underestimated the dissolved fraction. This parameterization yielded a model error of 34% and 58% for *Prorocentrum minimum* and *Phaeocystis* sp., respectively. Therefore, exudation had to be included to accurately reproduce experimental results. A constant exudation rate of 1% of the DMSP quota per day was then used in the model ($p_{\text{exo}} = 0.01$ d⁻¹). Such an exudation rate is the only one suggested in the literature (Dacey & Wakeham 1986). Gabric et al. (1993)
used this value to simulate DMSP exudation by phytoplankton. This parameterization reproduced experimental DMSP and DMS results for *P. minimum* in exponential phase and gave a slight misfit in late senescent phase (Fig. 3B). This simulation led to a model error of 15%. Other parameterizations were attempted to decrease the model error for *P. minimum* results, but the improvement was small (model error of 12%) relative to the complexity induced in the equations by these changes. Thus, we consider a constant exudation rate of 1% of the DMSP quota per day to be appropriate to reproduce exudation by *P. minimum*.

In contrast to *Prorocentrum minimum*, the utilization of a constant exudation rate of 1% d\(^{-1}\) of the DMSP quota was not appropriate to simulate exudation by *Phaeocystis* sp. (Fig. 4B). Model results using such an exudation rate led to considerable overestimation of experimental DMSP\(_d\) and considerable underestimation of DMS. The model error for this simulation was 44%.

As previously explained, DMS was measured in the *Phaeocystis* sp. culture since this species produces DMSP-lyase. To improve our reproduction of *Phaeocystis* sp. experimental results, an optimization of \(\rho_{exu}\) was carried out to minimize the model error index. It was found that a \(\rho_{exu}\) of 0.036 d\(^{-1}\) (Fig. 4C) satisfactorily modeled the experimental DMSP\(_d\) and DMS values during latent and exponential phases. However, the model still overestimated experimental results for DMSP\(_d\) and underestimated experimental results for DMS production during the senescent phase. This simulation reduced the model error to 21%. The model error cannot be decreased further using the equations presented here.

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**Table 1. Model variables and parameters used to simulate DMSP and DMS production by *Prorocentrum minimum* and *Phaeocystis* sp.**

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Units</th>
<th><em>P. minimum</em></th>
<th><em>Phaeocystis</em> sp.</th>
</tr>
</thead>
<tbody>
<tr>
<td>(t)</td>
<td>Time</td>
<td>d(^{-1})</td>
<td>200 \times 10(^6)</td>
<td>300 \times 10(^6)</td>
</tr>
<tr>
<td>CELL</td>
<td>Cell numbers</td>
<td>cells l(^{-1})</td>
<td>0.45</td>
<td>0.48</td>
</tr>
<tr>
<td>(g)</td>
<td>Realized growth rate</td>
<td>cells l(^{-1}) d(^{-1})</td>
<td>2.8 \times 10(^6)</td>
<td>1.5 \times 10(^6)</td>
</tr>
<tr>
<td>DMSP(_t)</td>
<td>Concentration of DMSP(_t)</td>
<td>(\mu)M</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>DMSP(_p)</td>
<td>Concentration of DMSP(_p)</td>
<td>(\mu)M</td>
<td>22.4 \times 10(^6)</td>
<td>35.4 \times 10(^6)</td>
</tr>
<tr>
<td>(\rho_{syn})</td>
<td>DMSP synthesis rate</td>
<td>(\mu)mol DMSP cell(^{-1}) d(^{-1})</td>
<td>8.4 \times 10(^{-9})</td>
<td>0.67 \times 10(^{-9})</td>
</tr>
<tr>
<td>DMSP(_d)</td>
<td>Concentration of DMSP(_d)</td>
<td>(\mu)M</td>
<td>53.8 \times 10(^{-9})</td>
<td>4.8 \times 10(^{-9})</td>
</tr>
<tr>
<td>DMS</td>
<td>Concentration of DMS</td>
<td>(\mu)M</td>
<td>10</td>
<td>1.6</td>
</tr>
<tr>
<td>(\rho_{exu})</td>
<td>DMSP exudation rate</td>
<td>d(^{-1})</td>
<td>46.9 \times 10(^{-9})</td>
<td>10.0 \times 10(^{-9})</td>
</tr>
<tr>
<td>(K)</td>
<td>Carrying capacity</td>
<td>cells l(^{-1})</td>
<td>0.01</td>
<td>0.03</td>
</tr>
<tr>
<td>(R)</td>
<td>Maximal potential growth</td>
<td>d(^{-1})</td>
<td>0.018</td>
<td>0.18</td>
</tr>
<tr>
<td>CELL(0)</td>
<td>Initial cell number</td>
<td>cells l(^{-1})</td>
<td>0.018</td>
<td>0.18</td>
</tr>
<tr>
<td>(m_{expo})</td>
<td>Mort. rate in expo. phase</td>
<td>d(^{-1})</td>
<td>0.18</td>
<td>0.11</td>
</tr>
<tr>
<td>(m_{sen})</td>
<td>Mort. rate in senes. phase</td>
<td>d(^{-1})</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>(S_{MIN})</td>
<td>Min. synthesizing rate</td>
<td>(\mu)mol DMSP(_p) cell(^{-1}) d(^{-1})</td>
<td>1.6</td>
<td></td>
</tr>
<tr>
<td>(S_{MAX})</td>
<td>Max. synthesizing rate</td>
<td>(\mu)mol DMSP(_p) cell(^{-1}) d(^{-1})</td>
<td>0.03</td>
<td></td>
</tr>
<tr>
<td>(A)</td>
<td>Specific coef. of synthesis</td>
<td>Dimensionless</td>
<td>10</td>
<td>1.6</td>
</tr>
<tr>
<td>QUOTA(0)</td>
<td>Initial DMSP quota</td>
<td>(\mu)mol DMSP(_p) cell(^{-1})</td>
<td>0.11</td>
<td></td>
</tr>
<tr>
<td>(E_{MIN})</td>
<td>Min. exudation constant</td>
<td>d(^{-1})</td>
<td>46.9 \times 10(^{-9})</td>
<td>10.0 \times 10(^{-9})</td>
</tr>
<tr>
<td>(E_{MAX})</td>
<td>Max. exudation constant</td>
<td>d(^{-1})</td>
<td>1.6</td>
<td></td>
</tr>
</tbody>
</table>

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**Fig. 1. Temporal variations of the abundance of 2 axenic cultures of *Prorocentrum minimum* and *Phaeocystis* sp., grown by Matrai & Keller (1994) and Stefels & van Boekel (1993), respectively. (a, — — —) Experimental and modeled values, respectively, for *Phaeocystis* sp.; (•, — — —) Experimental and modeled values, respectively, for *P. minimum*.**
These results suggest that exudation rates are higher during the senescent phase than during the exponential growth phase. Such a concept has already been used in modeling carbon flux in a pelagic environment. Baretta et al. (1988) simulated a continuous base excretion rate plus additional excretion when the phytoplankton growth rate was decreasing due to nutrient limitation. Some field and laboratory studies support this possibility. Matrai & Keller (1993) reported very high DMSP_d values in the older parts of a coccolithophore bloom. Other studies (Nguyen et al. 1988, Stefels & van Boekel 1993, Kwint & Kramer 1995) reported higher DMS production in the senescent phase of blooms than during the initial phase, but they did not investigate whether this higher DMS production was due to autolysis or exudation.

In order to simulate a greater DMS exudation in the senescent phase, the exudation rate \( \rho_{\text{exu}} \) was taken to vary with the population growth rate, as suggested by Baretta et al. (1988), following the equation:

\[
\rho_{\text{exu}} = \max \left( E_{\text{MIN}}, E_{\text{MAX}} \left( \frac{g_{\text{max}} - g}{g_{\text{max}}} \right) \right)
\]

where \( E_{\text{MIN}} \) (d\(^{-1}\)) and \( E_{\text{MAX}} \) (d\(^{-1}\)) are constants representing the minimum and maximum exudation rates, respectively. As previously mentioned, \( \rho_{\text{exu}} \) was set to \( E_{\text{MIN}} \) during the latent phase and early exponential phase. Adjustment of \( E_{\text{MIN}} \) and \( E_{\text{MAX}} \) to minimize the model error for Phaeocystis sp. resulted in values of 3% and 11%, respectively (Fig. 4D). These model results represented a better simulation of the releasing mechanisms in the latent, exponential and senescent phases. The model error was 13%. However, there was still a discordance between experimental and modeled results in the early senescent phase, as reflected in the DMSP_p and DMS values on Day 16 (Fig. 4D). Since this deviation was found for both DMSP_p and DMS, and the time of appearance of the DMSP_p peak was not reproduced by the model, we considered this disparity worthy of investigation. Further structural changes to the model were made by simulating a burst of exudation in the early senescent phase. Such parameterization improved the fit between experimental and modeled results (not shown) and
Latent and exponential phase

Senescent phase

A) Autolysis only
Model error: 58%

B) Autolysis + constant exudation of 1% d^{-1} of DMSP quota
Model error: 44%

C) Autolysis + constant exudation of 3.6% d^{-1} of DMSP quota
Model error: 21%

D) Autolysis + exudation ranging from 3 to 11% d^{-1} of DMSP quota
Model error: 13%

Fig. 4. Model simulations representing different possibilities of DMS release by Phaeocystis sp. Symbols represent experimental results and lines modeled results (● DMSP_p; △ DMS). Model error represents the relative difference between experimental and modeled results for DMSP_p and DMS.

decreased the model error to 8%. However, such changes led to greater complexity and to a much more species-specific model. These 2 disadvantages and the absence of a theoretical explanation for such phenomena do not justify the small improvement in the data fit. Considering the available data, the optimal method to simulate the DMSP exudation by Phaeocystis sp. is to use a growth-rate-dependent equation to simulate low exudation in healthy growing conditions and higher exudation in limiting growth conditions.

INTERPRETATION OF MODEL RESULTS

Comparison between the two species

Our results show that the main difference between the 2 species is the high exudation rate by Phaeocystis sp. compared with the low rate by Prorocentrum minimum. Since P. minimum is about 10 times larger than Phaeocystis sp. (1437 µm³ cell⁻¹ compared to 113 µm³ cell⁻¹, respectively), simulated DMSP quotas, synthesis and exudation rates are presented on a cell volume basis in Table 2. DMSP quotas and synthesis rates were very similar for the 2 species. However, the DMSP exudation rate in Phaeocystis sp. was 1 order of magnitude higher than the one for P. minimum. Our results, showing a high exudation rate for Phaeocystis sp., and this species’ known capability to cleave DMSP into DMS (Stefels & van Boekel 1993) reinforce its key role in the DMS cycling in seawater. Keller & Korjuff-Bellows (1996) noted that prymnesiophytes, in general, have high levels of DMSP_d in the culture medium.

DMSP synthesis

The usual method utilized to model DMSP is to associate a constant DMSP quota to phytoplankton biomass (Gabric et al. 1993, van den Berg et al. 1996b). This method was not used for 3 reasons: firstly, the DMSP quota varies through time in the phytoplankton cultures used for this work; secondly, DMSP quotas are known to vary under nutrient limitation (Turner et al. 1988, Groene & Kirst 1992, Keller & Korjuff-Bellows 1996); and thirdly, the DMSP measured in the cultures continued to increase after the maximum cell number was reached (Fig. 2). Such features cannot be reproduced with a constant DMSP quota. We cannot really study the transfer mechanisms between the DMSP pools without first reproducing the total DMSP synthesized in the cultures.

According to the results of our model, the DMSP synthesis rate varied by 1 order of magnitude through the growth cycle. As shown in Fig. 2, the simulated DMSP synthesis rates were maximal from the latent to mid-exponential growth phases, decreased sharply during the second half of exponential phase and remained low thereafter. One interesting feature is that to simulate the experimental data, the decrease in the modeled DMSP synthesis rate had to occur a few days before the maximum of algal cell numbers was reached. This decrease in DMSP synthesis began soon after the decrease in the population growth rate. These model results suggest that the decrease of DMSP synthesis is associated with physiological stress situations, such as
Table 2. DMSP quotas and characteristics per cellular volume for *Prorocentrum minimum* and *Phaeocystis* sp.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Units</th>
<th><em>P. minimum</em></th>
<th><em>Phaeocystis</em> sp.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DMSP quota</td>
<td>fmol (S) µm⁻³</td>
<td>0.03 – 0.15</td>
<td>0.08 – 0.14</td>
</tr>
<tr>
<td>DMSP synthesis</td>
<td>fmol (S) µm⁻³ d⁻¹</td>
<td>0.006 – 0.037</td>
<td>0.006 – 0.042</td>
</tr>
<tr>
<td>DMSP exudation</td>
<td>fmol (S) µm⁻³ d⁻¹</td>
<td>0.0003 – 0.0015</td>
<td>0.003 – 0.015</td>
</tr>
</tbody>
</table>

Table 3. Percentage of the algal DMSP quota exuded per day determined during laboratory studies or utilized in modeling studies

<table>
<thead>
<tr>
<th>Phytoplankton</th>
<th>% of DMSP quota exuded (d⁻¹)</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Gymnodinium nelsoni</em></td>
<td>0.2</td>
<td>Dacey &amp; Wakeham (1986)</td>
</tr>
<tr>
<td><em>Hymenomonas carterae</em></td>
<td>1.4</td>
<td>Vairavamurthy et al. (1985)</td>
</tr>
<tr>
<td><em>Prorocentrum minimum</em></td>
<td>1</td>
<td>Present study</td>
</tr>
<tr>
<td><em>Phaeocystis</em> sp.</td>
<td>3–11</td>
<td>Present study</td>
</tr>
</tbody>
</table>

**Magnitude of DMSP exudation**

The results of the model show that DMSP exudation rates vary significantly between species and may be approximately 10 times higher than previously reported (Table 3). The exudation rate for *Prorocentrum minimum* found in this study (1% d⁻¹ of the DMSP quota) is comparable to the other exudation rates reported in the literature. However, the exudation rate for *Phaeocystis* sp. ranged from 3 to 11% d⁻¹ of the DMSP quota. Dacey & Wakeham (1986) calculated that 0.3% d⁻¹ of the DMSP quota of *Gymnodinium nelsoni* was released as DMS in seawater (Table 3). Vairavamurthy et al. (1985) reported that 1.4% of the DMSP quota was exuded daily as DMS in the culture of the prymnesiophyte *Hymenomonas carterae*. The presence of DMS in these cultures suggests that either *G. nelsoni* and *H. carterae* produce DMSP-lyase or that the cultures were contaminated by bacteria after a few days. The presence of bacteria would have lowered the measurements of the exudation rates, but this possible underestimation cannot be quantified. In our modeling approach, it was assumed that no DMSP or DMS sinks occurred in the cultures. If such sinks occurred, the concentrations of DMSP and DMS measured would be underestimated. Under this circumstances the exudation rates obtained in this study would be underestimated as well.

Current DMS models neglect or underestimate phytoplankton exudation (Table 3). Gabric et al. (1993) modeled a 9 species phytoplankton community including *Phaeocystis* sp. They used a constant DMSP exudation rate of 1% d⁻¹ of the DMSP quota. They also attributed a DMS exudation rate of 0.85% d⁻¹ of the DMSP quota to all species of the community. Thus every species released both DMSP and DMS, for a total exudation equaling 1.85% of the DMSP quota. Lawrence (1993) and van den Berg et al. (1996b) ignored exudation in their model. DMSP and DMS releases were attributed exclusively to cell autolysis and grazing. These releasing mechanisms may represent, under certain circumstances, the major factors of DMSP release in seawater. However, neglecting algal exudation could frequently lead to large underestimations of DMSP release into seawater.

The physiological reason for phytoplankton release of DMSP is unknown. That phytoplankton release dissolved organic matter has been demonstrated. Based on a literature review, Baines & Pace (1991) obtained an average percent of extracellular release of 13% of total carbon fixation. DMSP may represent more than 10% of the organic carbon present in certain species of phytoplankton (Matrai & Keller 1994). DMSP could belong to the metabolites exuded. In the case of *Phaeocystis*, the exudation of DMSP and its conversion to DMS and acrylic acid, through DMSP-lyase, may allow this species to benefit from the antibiotic properties of acrylic acid (Davidson & Marchant 1987), although the effectiveness of the properties is still under debate. Ledyard et al. (1993) reported that bacteria may grow on the acrylic acid concentrations found in natural environments. However, new evidence reported by Noordkamp et al. (1998) suggests that acrylic acid may reach very high concentrations (a few mM) inside the mucus holding *Phaeocystis* colonies together. This
could have an antibiotic effect in protecting the polysaccharide mucus. In such circumstances the exuded DMS could simply be a by-product.

**Robustness of the results: a numerical experiment**

The way the model is structured may overemphasize the importance of exudation. It is possible that the simulation of the same experimental data with a different approach, for example simulating the phytoplankton abundance with an approximation of the carbon biomass instead of the cell numbers, could have led to different exudation rates. The structure of the base model we used may have underestimated cell mortality (autolysis) during the exponential and senescent phases. Mortality was not included in the simulations of the exponential phase (Table 1), assuming that culture conditions were optimal for phytoplankton growth during this period. However, mortality may have occurred during this period since cell counts in the culture represented net growth (growth minus mortality). In our base model, the mortality rate during senescence was set to reproduce the decrease in cell numbers measured in both cultures. This rate may have been underestimated since the population may have still been growing, at a reduced rate, during senescence. Since the cultures were axenic, no regeneration of organic matter occurred. However, the phytoplankton may have grown on amino nitrogen (Wheeler et al. 1977) and on organic phosphorus compounds (Nalewajko & Lean 1980) released by algal autolysis. Duplicating cells in the senescent phase could thus theoretically explain the increase of DMSP, observed during this period (Fig. 2), even in the absence of continued DMSP synthesis.

The model was modified to investigate the impact of higher phytoplankton mortality during the exponential and senescent phases. This investigation was done for both *Prorocentrum minimum* and *Phaeocystis* sp., but only the data from the *Phaeocystis* sp. culture are presented. In the *Phaeocystis* sp. culture, the maximal DMSP release during the exponential phase was 3% d$^{-1}$ of the DMSP. Assuming that this release was entirely from autolysis, the autolysis rate was set at 3% d$^{-1}$ and the exudation rate at 0% d$^{-1}$ (Table 4). This increase of the autolysis rate required slight modifications of the carrying capacity ($K$), the initial cell number [CELL(0)], the initial DMSP quota [QUOTA(0)] and the maximal synthesis rate ($S_{\text{MAX}}$) to correctly simulate experimental cell numbers and DMSP$_{\text{t}}$ (Fig. 5A).

The mortality rate during the senescent phase was increased from 18 to 22%. A population growth rate equivalent to 15% of the maximal realized growth rate ($g_{\text{max}}$) was required in the senescent phase to compensate for increased mortality. Such simulations of population growth in the senescent phase represent cell duplication in the culture. These cell duplications are assumed to produce the DMSP, increase observed during the senescent phase of cultures (Fig. 5A). A constant DMSP quota, equal to that on Day 15, was attributed to each newly replicated cell. A null DMSP synthesizing rate was then attributed to cells carried over from the exponential phase, now assumed to be inactive (no growth). This new way to simulate the DMSP, increase during the senescent phase necessitated a population growth rate as high as 15% of the maximal population growth rate.

The same model modification for *Prorocentrum minimum* necessitated a growth rate, for the senescent phase, equivalent to 70% of $g_{\text{max}}$ (not shown). Such a high growth rate is unlikely to occur in *P. minimum* cultures during the senescent phase, but a growth rate equivalent to 15% of $g_{\text{max}}$ may be possible in the case of *Phaeocystis* sp. Therefore, we cannot preclude the possibility that a fraction of the DMSP, increase occurring during the senescent phase (Fig. 2) resulted from continuous cell duplication, balanced by higher mortality. However, it is unlikely that such high growth rates occurred in the senescent phase of axenic cultures with no nutrient regeneration.

The utilization of a higher mortality rate (Table 4) in the model leads to more DMSP$_{\text{a}}$ liberated by autolysis. A lower exudation rate may then reproduce the DMSP$_{\text{a}}$ and DMS concentrations observed in the cultures. Fig. 5B

---

Table 4. Model parameters used to simulate DMSP and DMS production by *Phaeocystis* sp. in the base model, and in the models with continuous cell duplication (Fig. 5) and applied to the mesocosm data (Fig. 6). Symbols are the same as in Table 1.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Units</th>
<th>Base</th>
<th>Continuous duplication</th>
<th>Mesocosm</th>
</tr>
</thead>
<tbody>
<tr>
<td>$K$</td>
<td>cells l$^{-1}$</td>
<td>$300 \times 10^6$</td>
<td>$335 \times 10^6$</td>
<td>$110 \times 10^6$</td>
</tr>
<tr>
<td>$R$</td>
<td>d$^{-1}$</td>
<td>0.48</td>
<td>0.48</td>
<td>0.46</td>
</tr>
<tr>
<td>CELL(0)</td>
<td>cells l$^{-1}$</td>
<td>$1.5 \times 10^6$</td>
<td>$1.7 \times 10^6$</td>
<td>$1.6 \times 10^6$</td>
</tr>
<tr>
<td>$m_{\text{ex}}$</td>
<td>d$^{-1}$</td>
<td>0</td>
<td>0.03</td>
<td>0</td>
</tr>
<tr>
<td>$m_{\text{aut}}$</td>
<td>d$^{-1}$</td>
<td>0.18</td>
<td>0.22</td>
<td>0.15</td>
</tr>
<tr>
<td>$g_{\text{max}}$</td>
<td>cells l$^{-1}$ d$^{-1}$</td>
<td>$33.4 \times 10^6$</td>
<td>$39.5 \times 10^6$</td>
<td>$12.5 \times 10^6$</td>
</tr>
<tr>
<td>$S_{\text{MIN}}$</td>
<td>$\mu$mol DMSP$_{\text{a}}$ cell$^{-1}$ d$^{-1}$</td>
<td>$0.67 \times 10^{-9}$</td>
<td>0</td>
<td>$0.67 \times 10^{-9}$</td>
</tr>
<tr>
<td>$S_{\text{MAX}}$</td>
<td>$\mu$mol DMSP$_{\text{a}}$ cell$^{-1}$ d$^{-1}$</td>
<td>$4.8 \times 10^{-9}$</td>
<td>$4.4 \times 10^{-9}$</td>
<td>$4.8 \times 10^{-9}$</td>
</tr>
<tr>
<td>$A$</td>
<td>Dimensionless</td>
<td>1.6</td>
<td>1.6</td>
<td>1.6</td>
</tr>
<tr>
<td>QUOTA(0)</td>
<td>$\mu$mol DMSP$_{\text{a}}$ cell$^{-1}$</td>
<td>$10.0 \times 10^{-9}$</td>
<td>$9.0 \times 10^{-9}$</td>
<td>$10.0 \times 10^{-9}$</td>
</tr>
<tr>
<td>$E_{\text{MIN}}$</td>
<td>d$^{-1}$</td>
<td>0.03</td>
<td>0.00</td>
<td>0.03</td>
</tr>
<tr>
<td>$E_{\text{MAX}}$</td>
<td>d$^{-1}$</td>
<td>0.11</td>
<td>0.10</td>
<td>0.11</td>
</tr>
</tbody>
</table>
The results presented in Fig. 4 show that the utilization of an exudation rate of 1% d⁻¹ of the DMSP quota, such as presented in the literature, may underestimate the DMSP release (autolysis and exudation) by *Phaeocystis* sp. by as much as 44% on average. Our modeling strategy simulated the experimental data with a mean error of 13% (Fig. 4D). To achieve this we used (1) a higher DMSP exudation rate for *Phaeocystis* sp. and (2) a higher exudation rate for the senescent phase than for the exponential phase. Higher DMS production in the senescent phase of blooms than during the initial phase has previously been reported (Nguyen et al. 1988, Matrai & Keller 1993, Stefels & van Boekel 1993, Kwint & Kramer 1995). This has usually been attributed to cell autolysis (Nguyen et al. 1988, Kwint & Kramer 1995). Autolysis certainly plays an important role, but this mechanism was not sufficient in our model results to explain the accumulation of dissolved DMSP and DMS in the cultures. Exudation must also be taken into account.

**Applying our model to a *Phaeocystis* sp. bloom in a mesocosm**

Synchronization between maximum DMS concentration and *Phaeocystis* sp. cell numbers was observed in mesocosm studies (Kwint et al. 1996). Results from our exudation model may reproduce some aspects of this phenomenon. Kwint et al. (1996) observed that the peak of DMS did not correspond to the senescent phase of the *Phaeocystis* sp. bloom, but
was always synchronized with maximum cell numbers. They observed that zooplankton abundance peaked before the DMS maximum and concluded that grazing had no direct relation to the accumulation of DMSP\textsubscript{d} and DMS in the mesocosms. Phytoplankton autolysis is unlikely to have produced the DMS peak, since the latter was synchronized with the maxima of cell numbers. Osinga et al. (1996) worked on the same data set and rejected the possibility that the DMS peak was caused by a mass sedimentation event followed by massive lysis at the bottom of the mesocosm.

The application of our model to this data set shows that DMSP exudation may explain a significant part of the DMS peak observed to be simultaneous with the algal biomass maximum. Our model simulates axenic monospecific cultures, while the mesocosms include the whole pelagic community. However, the blooms in the mesocosms were largely dominated by Phaeocystis sp. (Kwint et al. 1996), allowing us to apply our model to the mesocosm data.

The parameters related to the temporal changes in the algal cell numbers (Table 4; third column) were modified to approximate the rise in cell numbers up to the bloom maximum (Fig. 6A). The simulation was stopped when the maximal cell number was reached. Population growth led to a rise in DMSP\textsubscript{p} up to the bloom maximum (Fig. 6B). There were high frequency variations in the DMSP\textsubscript{p} concentrations, but we did not expect or intend to simulate perfectly these temporal changes since other phytoplankton species, grazers, and bacteria interacted in the mesocosms. The use of a low and constant DMSP exudation rate (1 \text{d}^{-1}, as suggested in the literature) resulted in the simulated DMS concentration represented by the dashed line in Fig. 6C. Subtracting bacterial DMS consumption as measured by Kwint et al. (1996) (23 nM \text{d}^{-1} averaged for the Phaeocystis sp. bloom period) led to null values (not shown). On Day 14 (DMS maximum), the simulated DMS concentration produced by the 1 \text{d}^{-1} exudation rate accounted for 18% of the DMS concentration measured in the mesocosm when no bacterial consumption was considered, and 0% when bacterial consumption of DMS was considered. Applying the model with the variable exudation rates as found in this study for Phaeocystis sp. generated the DMS concentrations represented by the solid line in Fig. 6C. On Day 14, the simulated DMS concentrations represented 76% of the DMS measured when no bacterial consumption was considered, and 35% when it was considered.

The data in the shaded area in Fig. 6 may be interpreted as a burst of exudation when the population growth became nitrogen limited. During this last day of population growth the DMSP\textsubscript{p} concentration dropped from -2400 to -600 nM, while the DMS concentration increased from -25 to -425 nM. As for the simulation of the laboratory data on Phaeocystis sp. (‘Model results: Particulate and dissolved DMSP pools’), the DMSP\textsubscript{p} and the DMS concentrations in the mesocosm would be better modeled by the introduction of a burst of exudation synchronized with growth limitation.

Fig. 6. Model results when applied to a mesocosm experiment (Kwint et al. 1996). Symbols represent experimental results while solid lines represent model results. The dashed line in (A) links measured nitrate concentrations. The dashed line in (C) represents model DMS concentrations. The modeled DMS concentrations would be lower if bacterial consumption had been taken into account (see ‘Interpretation of model results: Applying our model to a Phaeocystis sp. bloom in a mesocosm’). The shaded area represents a putative massive exudation of DMSP\textsubscript{d} (converted to DMS) by the phytoplankton.
Importance of considering exudation by *Phaeocystis* sp. in modeling *in situ* conditions

Kwint & Kramer (1996) suggested that high DMS fluxes to the atmosphere seem to occur over short periods of weeks. *Phaeocystis* sp. blooms can potentially result in important DMS releases to the atmosphere. Van den Berg et al. (1996b) showed in a modeling experiment the importance of DMSP-lyase, synthesized by *Phaeocystis* sp., on the overall DMS concentration in seawater and on the DMS flux to the atmosphere over the North Sea. Little attention has been paid to DMSP exudation. However, Wassmann et al. (1990) suggested a sequence of events during *Phaeocystis pouchetii* blooms in the Barents Sea by which nutrient depletion induced heavy exudation in the upper layer of the water column followed by massive sedimentation and autoysis out of the euphotic layer. Under such circumstances, exudation is the main DMSP-releasing mechanism in surface water since autoysis is mostly confined to the deeper layer.

The model developed by van den Berg et al. (1996b) is the most advanced in simulating annual marine DMS dynamics in the natural environment. They pointed out 2 main periods during which the model fails to reproduce the field observations. One of them is an overestimation by the model of the total DMS concentrations in April, and the other is an underestimation in May and June. The phytoplankton bloom simulated by the FYFY model is in exponential growth in April and in senescence in May. We suggest that the utilization of a variable exudation rate, simulating low exudation during the exponential phase and strong exudation during the senescent phase, as we developed in this study, would decrease the discrepancy encountered by van den Berg et al. (1996b) between modeled and measured DMS concentrations.

Conclusion

This paper emphasizes the importance of considering DMSP exudation in DMSP-releasing mechanisms. In this study, only 2 species of phytoplankton were examined with relatively small data sets. There is certainly a need for data on other species and more accurate knowledge of the physiological mechanisms underlying exudation. Our work indicated that *Phaeocystis* sp. deserves special attention in this regard. In the modeling exercise of simulating both data sets on *Phaeocystis* sp., the laboratory and the mesocosm, the utilization of a quick and large release of DMSP at the end of the exponential phase would have led to better simulation of the data. Such a large release could help to explain observations on the synchronization of maximum chlorophyll with DMS concentrations (Kwint & Kramer 1996, Kwint et al. 1996).

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