Ideas and Perspectives:

Climate-Relevant Marine Biologically-Driven Mechanisms in Earth System Models

Inga Hense[1], Irene Stemmler[2], and Sebastian Sonntag[2]

[1]IHF, Center for Earth System Research and Sustainability, University of Hamburg, Germany

[2]Max Planck Institute for Meteorology, Bundesstrasse 53, 20146 Hamburg, Germany

Correspondence to: Inga Hense (inga.hense@uni-hamburg.de)

Abstract. We argue that biologically-driven climate-relevant mechanisms should be represented in current Earth system models (ESMs) in more diversity than it is currently done. These mechanisms fall into three general categories: (1) "biogeochemical pumps" which affect the carbon cycling, (2) "biological gas and particle shuttles" which affect the atmospheric composition and (3) "biogeophysical mechanisms" which affect the thermal, optical, and mechanical properties of the ocean. To resolve mechanisms from all three classes, we find it sufficient to include five functional groups: bulk phyto- and zooplankton, calcifiers as well as coastal gas and surface mat producers. Considering a wider range of biologically-driven mechanisms establishes the necessary links to other Earth system components and enables a larger number of relevant feedbacks to take place.

1 Introduction

The description of the marine ecosystem in Earth system models (ESMs) used for climate projections has been significantly refined in recent years. Plankton has been split into functional groups and physiological details such as light or nutrient acclimation have been added (e.g. Vichi et al., 2011; Aumont and Bopp, 2006; Aumont et al., 2015). Most of these modifications are motivated by the interest in studying the impact of climate change on marine ecosystems or to improve the representation of biogeochemical cycles, specifically the carbon cycle. However, little attention has been paid to biologically mediated climate-relevant mechanisms – the combination of processes that lead to climate feedbacks. Here, we will present a framework to classify these mechanisms and the functional groups that are necessary to describe them.

Many of the current marine biogeochemical models used in ESMs for climate projections include several phyto- and zooplankton functional groups; a few of them even allow variations in element or chlorophyll content of organic matter (see Laufkötter et al., 2015, for an overview). To consider more biological vari-

ables in models is clearly the right way forward if one is interested in the response of the marine ecosystem to climate change (see Le Quéré, 2006, for a discussion). However, such a strategy may not be best to improve the quality of climate projections, as it "only" refines the model representation of the marine carbon cycle. While being an integral part of the climate-carbon cycle feedback, it is just involved in *one* climate feedback loop.

For climate research, however, we think it is more important to capture additional links between marine biota and different Earth system components and thereby to increase the number of climate-relevant mechanisms in ESMs. Because such mechanisms trigger climate feedbacks, they are influencing the response of the climate system to external forcing in general and to anthropogenic perturbations in particular. Thus, instead of adding more details to better represent just one mechanism, we should account for a "mechanism diversity". This way, the consequences of an altered functioning of the marine ecosystem with climate change will feed back on the climate system.

We define biologically-driven mechanisms to be *climate-relevant* on timescales of contemporary climate change if they lead to a change in global energy (heat) content and distribution. These are, with decreasing levels of directness: (a) mechanisms with an immediate impact on the planetary albedo and/or sea surface temperature, (b) mechanisms which change the content and distribution of greenhouse gases or ocean's turbulent viscosity, and (c) mechanisms which change for instance the ocean's nutrient inventory with potential consequences for the marine carbon cycle and thus atmospheric greenhouse gas concentrations. Because the climate relevance of mechanisms on the third level are difficult to evaluate, we will exclusively consider those of the first and second impact level. We are aware of the fact that quantitative estimates about their impact on the global energy content are not available in all cases. Often, however, useful semi-quantitative evaluations of their impact, for example on ocean circulation patterns, exist.

We will present a general framework that illustrates the links between the marine biota, the mechanisms and the larger feedback loops in the climate system in a systematic way. Individual processes as part of the mechanisms will be described only briefly, and only, if they are indispensable for a basic understanding. Our list of processes may thus not be complete but we find it more important to present all mechanisms at the same level of abstraction. We believe that it will prove a useful basis for classification, even if additional biological climate-relevant mechanisms are discovered.

2   What is needed

We adopt the idea to split the marine biota into different groups, but in contrast to previous approaches, we classify them according to their functional role in the *climate system*. The functions these organism groups carry are drivers of climate-relevant mechanisms.

This leads us to three classes of mechanisms (M1-M3) that generate climate feedbacks (see Fig. 1) and five functional groups (Table 1). For each class we briefly explain the main mechanisms, present the key organisms involved and highlight the climate relevance. Finally, we specifically describe the functional groups that are needed in ESMs to represent this mechanism.

M1 - biogeochemical pumps

The first class of mechanisms comprise the marine part of the carbon cycle, the *organic carbon pump*, *the microbial carbon pump* and the *alkalinity pump*.

The *organic carbon pump* includes the processes related to the uptake of carbon dioxide in the upper ocean and the sinking of organically bound carbon to deeper waters. Mainly three organism groups are involved – phyto-, zooplankton, and bacteria. Phytoplankton drives the carbon cycle, because inorganic is transferred to organic carbon via photosynthesis and zooplankton decisively contributes to carbon export to the deeper ocean via fecal pellet production. Bacteria decompose the organic matter while sinking down and thereby determine the efficiency of the organic carbon pump. The climate relevance of the organic carbon pump has been evaluated by quantifying the air-sea fluxes of CO_2 without this mechanism. Rough estimates suggest that atmospheric CO_2 levels would rise by approximately 200 ppmv after a complete shutdown of the organic carbon pump (Volk and Hoffert, 1985; Broecker and Peng, 1986). As part of the climate-carbon cycle feedback (Friedlingstein et al., 2006), this mechanism is well known and regarded as the most important marine biologically-driven mechanism. To capture the organic carbon pump in ESMs, two functional groups are in principle sufficient – a bulk phytoplankton and a bulk zooplankton group to describe the transformation process from inorganic to organic matter and sinking of the latter. However, all additional functional groups that are needed for other mechanisms will also contribute (see Table 1). As bacterial decomposition can be assumed to be roughly proportional to the available organic matter, bacteria do not need to be explicitly included as a key group to adequately represent the organic carbon pump.

The *microbial carbon pump* describes the pathway from more easily degradable to refractory organic carbon by microbes (e.g. Jiao et al., 2010). These organisms transform dissolved or particulate organic carbon into compounds that are resistant towards degradation and are therefore stored for thousands of years. The refractory organic carbon pool is large and comparable to the atmospheric CO_2 reservoir (Hansell et al., 2009), but it will have little impact on the climate system on time scales of several hundreds of years, unless an imbalance between sources and sinks evolves. Although it has been speculated that such changes may occur under ocean acidification and eutrophication (Jiao et al., 2014), there is insufficient knowledge to account for this mechanism and the corresponding functional groups in ESMs. In addition, no evaluation of the relevance of this pump with respect to contemporary climate change exists, yet.

The *alkalinity pump* is another essential part of the marine carbon cycle, because this mechanism alters the carbonate chemistry in the ocean. Organisms that affect the carbonate equilibrium are calcifying species, forming calcite or aragonite shells. They occur in the open ocean (e.g. coccolithophores) as well as in shallow regions (e.g. corals) where they "consume" alkalinity and release CO_2 during the calcification process, causing a decrease in alkalinity. Since alkalinity is the capacity of the ocean to buffer acids and sets the limit how much CO_2 can be stored, changes in alkalinity have consequences for the CO_2-storage. While the quantitative impact of the alkalinity pump on climate is currently unclear, its role via the "calcification feedback" on atmospheric CO_2-concentrations is assumed to be large (Zhang and Cao, 2016). Among the calcifiers, coccolithophores are the most important group (see e.g. Rost and Riebesell, 2004) and mainly responsible for the vertical gradient in alkalinity, because when coccolithophores die, they sink down to the

deeper part of the ocean, where the calcareous shells dissolve and the alkalinity increases. Other calcifying organism groups have been shown to be regionally important (see e.g. Baumann et al., 2004; Kleypas et al., 2006) or are assumed to be relevant for aragonite (Gangstø et al., 2008) but presumably only marginally for climate dynamics. To represent this mechanism in ESMs, calcifiers need to be included to generate the vertical alkalinity gradient and to adequately resolve the carbonate chemistry. From a climate perspective, the gain from representing calcifiers by more than one key group might be relatively small unless regional ESMs are applied. With one additional key group, the calcifiers, represented by coccolithophores, the basic features of the alkalinity pump will be captured.

M2 - biological gas and particle shuttles

The second class of mechanisms, the "*biological gas and particle shuttles*" addresses the impact of the marine biosphere on the atmosphere due to emission of gases and particles. These substances belong to the group of "short-lived climate-relevant air contaminants" (SCC), a subset of short-lived health- and climate-relevant air contaminants (SHCC), sensu Pöschl and Shiraiwa (2015). They may act as aerosols, being involved in cloud formation; they may affect the atmospheric chemistry or influence the thermodynamics as greenhouse gases.

Particulate SCCs of marine biogenic origin with direct effects on cloud formation are so-called "marine biogenic primary aerosols". These include entire organisms, like phytoplankton cells or organisms' remnants, or "exudates", which are substances secreted by organisms (e.g. Knopf et al., 2011; Burrows et al., 2013; Wilson et al., 2015). Although the research area of marine biogenic aerosols is relatively new, recent studies suggest that at least on a regional scale, ocean biota strongly influences the concentrations of cloud droplets with significant consequences for the reflected shortwave radiation (McCoy et al., 2015). Thus, ocean biota as a source for primary aerosols can directly contribute to the cloud-albedo feedback. As a first approximation, no additional functional group needs to be added in ESMs; a fraction of those organisms in the surface layer that are implemented in ESMs anyway may serve as a source for primary aerosols.

Gaseous SCCs may be involved in aerosol formation or participate in ozone reactions. The most important ones produced by marine organisms are dimethyl sulfide (DMS) and short-lived halocarbons. For both it is meaningful to distinguish open and coastal ocean sources since the efficiency in gas release is highly dissimilar and different organism groups are involved. DMS (or its precursor) is produced by "open ocean" (coccolithophores) and "coastal" phytoplankton (*Phaeocystis*) groups (e.g. Barnard et al., 1984; Malin et al., 1993). Zooplankton and bacteria are involved (Reisch et al., 2011) and similar to the organic carbon pump, especially bacteria determine the efficiency of the DMS shuttle to a large extent. Short-lived bromine halocarbons are associated with "open ocean" phytoplankton and "coastal" macroalgae (e.g. Moore et al., 1996; Nightingale et al., 1995; Carpenter and Liss, 2000).

Dimethyl sulfide (DMS) is a precursor of sulfate aerosols and involved in the cloud-albedo feedback (e.g. Charlson et al., 1987; Ayers and Cainey, 2008), the climate relevance of which is still under discussion (e.g. Quinn and Bates, 2011). Local effects on shortwave radiation of DMS emission by a phytoplankton bloom can induce cooling up to 15 W m^{-2} at the top of the atmosphere; such a high value is usually associated

with heavily air-polluted regions (Meskhidze and Nenes, 2006). The global direct radiative effect of DMS has been estimated to be -0.23 W m^{-2}, the indirect as -0.76 W m^{-2}. The contribution of primary producers via DMS production to sources of natural aerosols is therefore larger than for example those from sea salt or volcanoes (Rap et al., 2013).

Short-lived halocarbons, particularly brominated substances are important SCCs, because they destroy ozone and thereby significantly change the radiative forcing (Sturges et al., 2000; Saiz-Lopez et al., 2012; Laube et al., 2008). The radiative effect is estimated to be about -0.2 W m^{-2} and thus larger than the one by the widely known anthropogenically produced long-lived halocarbons such as CFCs (Hossaini et al., 2015).

For both DMS and short-lived halocarbons, it is crucial to correctly represent the spatial patterns of marine primary production and corresponding SCCs (e.g. Stemmler et al., 2015, for halocarbons). To capture the gradient between coastal and open ocean, an additional model compartment, the "coastal gas producers", has to be included in ESMs. A relatively easy way to describe them in the model is by allowing the sediment or deepest model layer being an additional nutrient pool and by taking into account relatively high emissions per unit biomass. Even if different types of organisms are involved in the coastal production of DMS and shortlived halocarbons, one functional group is sufficient, because coastal patterns of the two SCCs do not differ clearly. The group of open ocean organisms can be represented either by coccolithophores in case of DMS, or a "bulk phytoplankton" group in case of halocarbons (although parametrizations are necessary, because not the entire bulk phytoplankton produces halocarbons). Similar to the organic carbon pump, bacteria do not need to be explicitly considered for the DMS shuttle; zooplankton is included anyway, because of its role in the organic carbon pump.

Last but not least, there are a number of greenhouse gases of marine biogenic origin, notably CO_2. This gas is respired by all organisms and is more or less automatically captured in ESMs through the loss rate of all functional groups. Another important long-lived greenhouse gas is N_2O with a global warming potential for a 100 year time horizon that is approximately 300 times higher compared to CO_2 (Ramaswamy et al., 2001). About 20% of the global production of N_2O is of marine origin (Denman et al., 2007), mediated by microbes. N_2O is released mainly during denitrification, the oxidation of ammonium to nitrate under oxic, and to a lower extent during denitrification, the reduction from nitrate to dinitrogen gas under anoxic conditions (Freing et al., 2012). Two organism groups, bacteria and archea, are involved in these transformation processes. So far, our knowledge about spatial variations in the occurrence of the organisms involved and the respective rates is too fragmentary to explicitly describe them in models. Instead, these bacterial transformation processes can be implicitly considered in the same way as done for other mechanisms (by choosing turnover rates that are proportional to the available resources); thus no further model compartment is necessary.

Marine sources of other biogenic greenhouse gases like CH_4 are mainly related to marine microorganisms (e.g. Valentine, 2011). To the best of our knowledge, the effect of these greenhouse gases such as CH_4 on the climate system may be considered negligible, because the marine sources are small compared to the terrestrial or anthropogenic ones. Thus it is currently not justifiable to add more model compartments.

M3 - biogeophysical mechanisms

The third class includes all the *biogeophysical mechanisms*. These mechanisms comprise changes of thermal, optical and mechanical properties of the ocean, predominantly caused by phytoplankton species. Among them, positively buoyant cyanobacteria are particularly important, because they can produce surface mats of up to several millions of square kilometers (e.g. Capone et al., 1998). Such surface mats significantly change light absorption with consequences on the surface mixed layer heat balance (e.g. Sathyendranath et al., 1991; Kahru et al., 1993). In addition, they increase the albedo (e.g. Kahru et al., 1993), alter the turbulent viscosity and reduce the vertical mixing (e.g. Jöhnk et al., 2008). Surface mats may also reduce the air-sea gas exchange, if we assume similar effects as for surface microlayers (e.g. Liss and Duce, 2005).

The climate impact of the light absorption mechanism has been only assessed for *neutrally buoyant* phytoplankton so far. Even their impact is significant with pronounced effects on oceanic and atmospheric temperature, circulation patterns, cloudiness, humidity, precipitation and evaporation, as well as sea ice cover (Patara et al., 2012); also ENSO dynamics is shown to be influenced through light absorption (e.g. Jochum et al., 2010). The strong response triggered by this mechanism results from multiple feedback loops that involve different Earth system components.

A rough estimate indicates that changes of albedo through phytoplankton, specifically coccolithophores can result in a cooling by roughly 0.2 W m^{-2} globally (Tyrrell et al., 1999). A more sophisticated evaluation, however, points towards a negligible impact on the albedo, at least on the basin-scale (Gondwe et al., 2001). In any case there is a direct link to the albedo-temperature feedback (Watson and Lovelock, 1983).

Unfortunately, the climate effect through biotic induced changes of ocean's turbulent viscosity has not been addressed, yet. However, idealized model studies (Sonntag, 2013) suggest that biologically induced increase or decrease of turbulent viscosity by surface mats can affect ocean circulation patterns on a basin-scale.

To account for biogeophysical aspects in ESMs one additional key group, the "surface mat producers" is needed. Cyanobacteria are a good candidate to represent this group. They possess the trait "positive buoyancy" which they do not share with other phytoplankton and should therefore be considered separately. Clearly, all other groups of marine primary producers that are explicitly described in ESMs have an impact on light absorption, too, but by distinguishing neutrally or negatively from positively buoyant phytoplankton a more realistic representation of the light absorption feedback will be achieved.

To summarize, including the above mentioned 5 functional groups (Table 1) will meet the requirements for an adequate representation of biologically-driven mechanisms in ESMs.

3   What are the future impacts

The marine biota itself as well as the strength of the individual mechanisms may evolve under climate change. Most obvious are immediate consequences due to the three climate stressors – temperature, pH
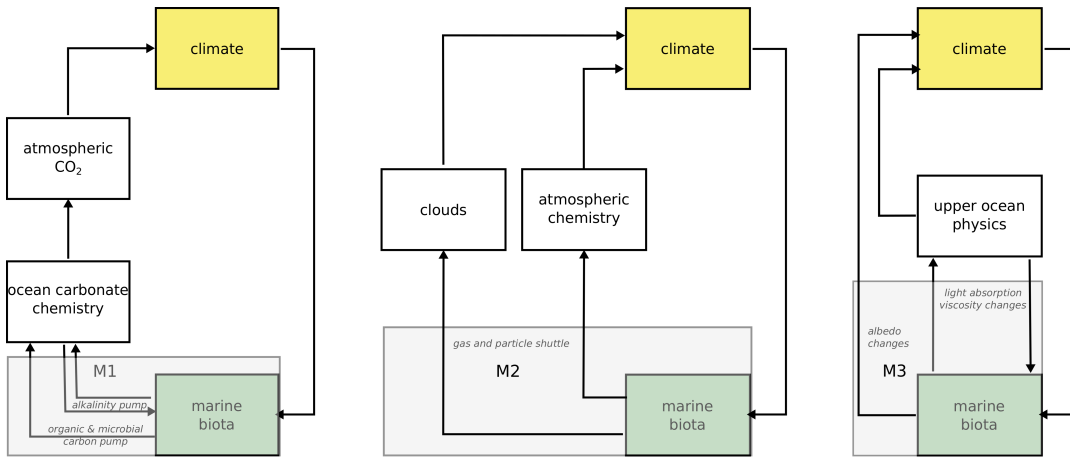
Figure 1. Major globally acting climate feedback loops, based on the three classes of mechanisms (light grey-shaded boxes), driven by marine biota (green-shaded boxes). Only links originating from the marine biota are shown; additional inter- and cross-links between the different boxes are omitted for a clarity. a) the three mechanisms (the organic and the microbial carbon pump, and the alkalinity pump) affect the CO_2 inventory in the ocean, which in turn leads to changes in atmospheric CO_2 and thus in climate. An altered global climate influences the marine biota (through e.g. changes in SST, near surface stratification and circulation patterns), closing the marine part of the climate-carbon cycle feedback loop which also includes the CO_2-calcification feedback. b) the gas and particle shuttle alter cloud formation rates and distribution as well as atmospheric chemistry. There is a complex interplay between different atmospheric components that ultimately lead to climate change, again with consequences for the marine biota. A number of atmospheric feedbacks (e.g. the cloud-albedo feedback, the longwave radiation feedback, the chemistry feedbacks) are involved in this loop. Note that the influence of marine biota on *local* cloud cover is not illustrated here. c) two biogeophysical mechanisms (based on light absorption and turbulent viscosity changes) directly affect the upper ocean physics such as heat distribution and circulation and hence the biota. The third one (albedo changes) has a direct effect on the planetary radiation budget which influences in turn the marine biota.

organism groups	M1	M2	M3
bulk phytoplankton	✓	✓	✓
bulk zooplankton	✓	(✓)	-
calcifier	✓	✓	✓
coastal gas producer	✓	✓	✓
surface mat producer	✓	✓	✓

Table 1. Organism groups that drive climate mechanisms 1: biogeochemical pumps; 2: gas and particle shuttle and 3: biogeophysical mechanisms. Note that zooplankton is partly involved in the production of DMS due to grazing and thus checked in parenthesis.

and oxygen. As a rule of thumb, higher temperatures increase the metabolic rates of organisms. Lower pH may increase growth of non-calcifiers and decrease that of calcifiers (e.g. Raven, 2011). Low oxygen concentrations will particularly impact higher trophic levels and microbial processes. In principle, however, the response will be species-specific.

Among the phytoplankton, cyanobacteria are assumed to strongly benefit from climate change and thus they are expected to become more abundant in future (e.g. O'Neil et al., 2012; Hense et al., 2013). In particular, a moderate rise of sea surface temperature (Fu et al., 2014) as well as a decrease in pH will favor their growth conditions (Hutchins et al., 2007). More cyanobacteria will intensify the biogeophysical feedback mechanisms and possibly also the particle shuttle. The response of other phytoplankton to pH is not well understood. While ocean acidification may significantly affect calcifiers and the calcification rate, the response is not uniform (see e.g. Kleypas et al., 2006) and genetic adaptation (Lohbeck et al., 2012) might outweigh the negative consequences of a decreasing pH. Ocean acidification (but also temperature) may directly affect DMS-producing organisms and thus outgassing of DMS. Under ocean acifidification DMS production is either enhanced (Kim et al., 2010) or reduced (Archer et al., 2013); the higher production has been attributed to grazing. A strong response of the climate system to reduced DMS-production on the radiative forcing has been proposed (Six et al., 2013).

Sensitivity to climate stressors has been also described for many microbial organisms; one example are nitrifiers. For lower pH, nitrification and therefore N_2O production is strongly reduced (Beman et al., 2011). Nevertheless, it is expected that an expansion of oxygen minimum zones will increase the production of N_2O (Naqvi et al., 2010), because the highest production rates occur at the anoxic-oxic boundary layer. Another group of bacteria that seems to benefit from climate change are those involved in aerobic decomposition of organic matter. A rise in temperature and a drop in pH stimulates bacterial turnover rates (Pomeroy and Deibel, 1986; Piontek et al., 2010). With enhanced remineralization, the efficiency of the organic carbon pump will be reduced, altering the ocean's carbon uptake capacity (Segschneider and Bendtsen, 2013). On the other hand, bacterial decomposition rates may be affected through a decrease in oxygen concentrations with an expansion of oxygen minimum zones (Stramma et al., 2008). It is still unclear, however, whether low oxygen concentrations will really impair bacterial degradation of organic matter or not (see, e.g. Kristensen et al., 1995; Devol and Hartnett, 2001).

Besides the immediate effect of climate stressors on ocean biota, we expect significant alterations in the environment with potentially large long-term consequences on the organisms and biologically-driven mechanisms. For example, the organic carbon pump will likely to be altered by changes in stratification (Steinacher et al., 2009), the ocean's molecular viscosity (Taucher et al., 2014) and plankton community composition (see, e.g. Laufkötter et al., 2016); the alkalinity pump may be affected by changes in freshwater input or evaporation (see e.g. Steinacher et al., 2009; Jiang et al., 2014). Overall, it is quite certain that the relative abundance of some phytoplankton organisms will change, as a result of their response to climate stressors and altered environmental conditions. Such a shift in community composition will affect

the strength of all three classes of mechanisms and with that their relative importance within the climate system.

4 What has been done

Today's ESMs represent the marine biogeochemical part related to the carbon cycle reasonably well (Table 2). Most of these models explicitly consider phyto- and zooplankton. Both organism groups are described in such a way that the model results give reasonable values for export production (see e.g. Ilyina et al., 2013; Palmer and Totterdell, 2001). Also, the carbonate chemistry is relatively well represented, even though calcifiers are not explicitly included but parametrized by assuming that they constitute a certain proportion of bulk phytoplankton.

The second class of mechanisms, which affect the atmospheric composition, has received less attention. Some of the ESMs do consider DMS/N_2O (Table 2) and the results support the earlier hypothesis about the importance of this SCC (Six et al., 2013). Other marine biologically produced SCCs (except CO_2) and aerosols are usually not included; but there is a number of recent model activities in which the pertinent processes have been implemented, and the climate impact of these substances has been evaluated at least partly (e.g. Kirkevåg et al., 2013; Stemmler et al., 2014, 2015; Hossaini et al., 2015). The largest deficiency of ESMs in this respect is that primary production is still not sufficiently well represented, in particular in coastal regions (e.g. Schneider et al., 2008; Anav et al., 2013). Even though the respective ESMs as well as global marine biogeochemical models have become more and more complex in recent years (see e.g. Aumont et al., 2003; Le Quéré et al., 2005; Dunne et al., 2013; Buitenhuis et al., 2013), the situation has only marginally improved. Not surprisingly, models generally fail to simulate SCC concentrations and air-sea fluxes on the shelf (see e.g. Halloran et al., 2010; Stemmler et al., 2015); much could be gained if coastal primary production is captured more realistically.

Finally, marine biogeophysical aspects are hardly addressed in today's ESMs; so far, only half of them include the light absorption mechanism with feedback on temperature (Table 2). Recent studies with neutrally or negatively buoyant phytoplankton indicate that consequences for the upper ocean heat balance and the climate system are substantial (e.g. Patara et al., 2012; Lengaigne et al., 2009). Thus, the effects might be even stronger if positively buoyant organisms are added; whether organisms stay at the surface or whether they are homogeneously distributed in the surface mixed layer makes a big difference for the upper ocean heat budget (e.g. Sonntag and Hense, 2011). None of today's ESMs or coupled global biogeochemical ocean circulation models account for other biogeophysical effects, i.e. changes in albedo and turbulent viscosity.

ESMs	MBMs	mechanisms 1	2	3	functional groups P	Z	C	cG	S	B
BCC_CSM1.1	OCMIP	✓ bcp	–	–	–	–	–	–	–	–
CanESM1	CMOC	✓	–	–	✓[1]	✓[1]	–	–	–	–
CESM1	BEC	✓	–	✓ LA−nbp	✓[3]	✓[1]	(✓)	–	–	–
ESM2M/ESM2G	TOPAZ2	✓	–	✓ LA−nbp	✓[3]	(✓)	(✓)	–	–	–
HadGEM2-ES	Diat-HadOCC	✓	✓ DMS	–	✓[2]	✓[1]	(✓)	–	–	–
CMCC-CESM	PELAGOS	✓ bcp	–	✓ LA−nbp	✓[3]	✓[3]	–	–	–	✓[1]
IPSL-CM5A	PISCES	✓	(✓ DMS,N$_2$O)	✓ LA−nbp	✓[2]	✓[2]	(✓)	–	–	–
MIROC-ESM	NPZD	✓ bcp	–	–	✓[1]	✓[1]	–	–	–	–
MPI-ESM	HAMOCC	✓	✓ DMS	–	✓[1]	✓[1]	(✓)	–	–	–

Table 2. Different marine biosphere modules (MBMs) in Earth System Models (ESMs) that participated in CMIP5 (Arora et al., 2013; Laufkötter et al., 2015): OCMIP: Wu et al. (2013); CMOC: Christian et al. (2010); BEC: Moore et al. (2013); TOPAZ2: Dunne et al. (2010, 2013); Diat-HadOCC: Palmer and Totterdell (2001); Martin et al. (2011), PELAGOS: Vichi et al. (2007, 2011); PISCES: Aumont and Bopp (2006); Lengaigne et al. (2009); Aumont et al. (2015), NPZD: Watanabe et al. (2011); Kawamiya et al. (2000); HAMOCC: Maier-Reimer et al. (2005); Ilyina et al. (2013). We only use the most recent peer-reviewed reference of each MBM. MBMs are only listed once, even though some of them are used in more than one ESM. The Roman numerals refer to the biologically-driven mechanisms while P, Z, C, cG, S, B denote the organism groups phytoplankton, zooplankton, calcifiers, coastal gas producers, surface mat producers and bacteria. Organism groups that are not explicitly described but parametrized are in parenthesis. Checkmarks with additions refer to the biogeochemical carbon pump (bcp), DMS or N$_2$O (specific SCCs), light absorption by neutrally/negatively buoyant phytoplankton (LA-nbp) or to the numbers of explicitly described functional groups. In PISCES, the SCCs are not included by default but available through additional modules.

5 What needs to be done

Marine biological modules of Earth system models include a relatively high number of biological variables but are generally characterized by a low mechanism diversity. In fact, most of the models include more functional groups than we think are necessary to capture all three classes of mechanisms. Hence, it should not be impossible to increase the mechanism diversity and thus establish links between the marine biota and other Earth system components, which is crucial for climate projections.

Given our process understanding, the first class of mechanisms with the biological and alkalinity carbon pump should be included in all biological modules of ESMs. Within the second class of mechanisms, at least one gas shuttle should be considered and pilot studies with biogenic primary aerosols should be conducted. Biogeophysical mechanisms (the 3rd class) should be taken into account. The mechanism that is easiest to implement is light absorption but again sensitivity experiments with the other two mechanisms should be performed, too.

Most ESMs already include several functional groups, but their inclusion is associated with their role in the organic carbon or alkalinity pump (see Laufkötter et al., 2015). A more diverse suite of mechanisms, however, is important if we want more climate feedbacks to take place. The community composition is already changing and will likely continue to do so in future (e.g. Hallegraeff, 2010; Hinder et al., 2012). Since the key groups respond differently to climate change, the strength of biologically driven mechanisms will

also be altered. We thus suggest to allow that shifts in the "mechanisms driver community" and changes in the strength of mechanisms can occur in climate projections. To do so, calcifiers and coastal gas and surface mat producers should be explicitly taken into account. Parametrizing calcification may work out for today's ocean but might become problematic if climate projections are conducted. Under future acidified conditions, the composition of calcifying and non-calcifying species of the phytoplankton as well as the growth behavior of calcifiers may significantly change due to competing selection pressures. To allow for such shifts in community composition, calcifiers should be explicitly implemented as a separate state variable. Surface mat producers, represented by cyanobacteria, are included in a few ESMs (e.g. Dunne et al., 2013), because of their role as nitrogen fixers in the nitrogen cycle. They are not included, because of their role in biogeophysical mechanisms and we suggest to account for that by adding the trait "surface buoyancy".

Including functional dependencies of pH-dependent growth of the marine biota seems to be too early, because the uncertainties are large. The same is true for our knowledge about genetic adaptation towards climate stressors. Perhaps, already in the near future, however, it may be reasonable to account for these aspects in climate projections. The most important feedbacks loops, involving marine biota are covered if all mechanisms are represented. With increasing model resolution and with improved process knowledge, however, more mechanisms may have to be added while others may turn out to be unimportant and can be omitted. Nevertheless during the process of model development, mechanism diversity should be generally increased.

6 Summary and Conclusions

We distinguish three main classes of marine biota driven climate-relevant mechanisms. We have argued that progress will be achieved if we include all of them in ESMs for climate projections. To resolve them, five functional groups are needed, including bulk phyto- and zooplankton, calcifiers as well as coastal gas and surface mat producers. Our suggested marine biosphere module for ESMs is less complex than those modules currently used for climate projections. But in contrast to these state-of-the-art concepts, we consider a wider range of important links between the marine biosphere and other Earth system components and allow for more important feedback loops to take place. We believe that our framework is better suited to account for possible changes in the strength of various feedbacks. Such changes can be expected, because with global warming and ocean acidification the marine ecosystem and consequently links to other Earth system components will be altered. For instance, if surface buoyant cyanobacteria will increase in future (Hense et al., 2013), they will intensify the biogeophysical mechanisms. The feedback loops associated with these mechanisms will change accordingly. Thus, to evaluate the response of the climate system, the mechanism diversity should be increased.

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References

Anav, A., Friedlingstein, P., Kidston, M., Bopp, L., Ciais, P., Cox, P., Jones, C., Jung, M., Myneni, R., and Zhu, Z.: Evaluating the land and ocean components of the global carbon cycle in the CMIP5 Earth System Models, Journal of Climate, 26, 6801–6843, 2013.

Archer, S. D., Kimmance, S. A., Stephens, J. A., Hopkins, F. E., Bellerby, R., Schulz, K. G., Piontek, J., and Engel, A.: Contrasting responses of DMS and DMSP to ocean acidification in Arctic waters, Biogeosciences, 10, 1893–1908, 2013.

Arora, V., Boer, G., Friedlingstein, P., Eby, M., Jones, C., Christian, J., Bonan, G., Bopp, L., Brovkin, V., Cadule, P., et al.: Carbon–concentration and carbon–climate feedbacks in CMIP5 Earth system models, Journal of Climate, 26, 5289–5314, 2013.

Aumont, O. and Bopp, L.: Globalizing results from ocean in situ iron fertilization studies, Global Biogeochemical Cycles, 20, GB2017, 2006.

Aumont, O., Maier-Reimer, E., Blain, S., and Monfray, P.: An ecosystem model of the global ocean including Fe, Si, P colimitations, Global Biogeochemical Cycles, 17, 1060, doi:10.1029/2001GB001745, 2003.

Aumont, O., Ethé, C., Tagliabue, A., Bopp, L., and Gehlen, M.: PISCES-v2: an ocean biogeochemical model for carbon and ecosystem studies, Geoscientific Model Development, 8, 2465–2513, http://www.geosci-model-dev.net/8/2465/2015/gmd-8-2465-2015.pdf, 2015.

Ayers, G. and Cainey, J.: The CLAW hypothesis: a review of the major developments, Environmental Chemistry, 4, 366–374, 2008.

Barnard, W., Andreae, M., and Iverson, R.: Dimethylsulfide and *Phaeocystis poucheti* in the southeastern Bering Sea, Continental Shelf Research, 32, 103–113, 1984.

Baumann, K.-H., Böckel, B., and Frenz, M.: Coccolith contribution to South Atlantic carbonate sedimentation, in: Coccolithophores: from molecular processes to global impact, edited by Thierstein, R. and Young, J. R., pp. 367–402, Springer, 2004.

Beman, J. M., Chow, C.-E., King, A. L., Feng, Y., Fuhrman, J. A., Andersson, A., Bates, N. R., Popp, B. N., and Hutchins, D. A.: Global declines in oceanic nitrification rates as a consequence of ocean acidification, Proceedings of the National Academy of Sciences, 108, 208–213, 2011.

Broecker, W. and Peng, T.: Carbon cycle: 1985 Glacial to interglacial changes in the operation of the global carbon cycle, Radiocarbon, 28, 309–327, 1986.

Buitenhuis, E., Hashioka, T., and Le Quéré, C.: Combined constraints on global ocean primary production using observations and models, Global Biogeochemical Cycles, 27, 847–858, 2013.

Burrows, S., Hoose, C., Pöschl, U., and Lawrence, M.: Ice nuclei in marine air: biogenic particles or dust?, Atmospheric Chemistry and Physics, 13, 245–267, 2013.

Capone, D., Subramaniam, A., Montoya, J., Voss, M., Humborg, C., Johansen, A., Siefert, R., and Carpenter, E.: An extensive bloom of the N_2-fixing cyanobacterium *Trichodesmium erythraeum* in the central Arabian Sea, Marine Ecology Progress Series, 172, 281–292, 1998.

Carpenter, L. and Liss, P. S.: On temperate sources of bromoform and other reactive organic bromine gases, Journal of Geophysical Research - Oceans, 105, 20 539–20 547, 2000.

Charlson, R. J., Lovelock, J. E., Andrae, M. O., and Warren, S. G.: Oceanic phytoplankton, atmospheric sulfur, cloud albedo and climate, Nature, 326, 655–661, 1987.

Christian, J. R., Arora, V. K., Boer, G. J., Curry, C. L., Zahariev, K., Denman, K. L., Flato, G. M., Lee, W. G., Merryfield, W. J., Roulet, N. T., and Scinocca, J. F.: The global carbon cycle in the Canadian Earth system model (CanESM1): Preindustrial control simulation, Journal of Geophysical Research: Biogeosciences, 115, http://dx.doi.org/10.1029/2008JG000920, g03014, 2010.

Denman, K. L., Brasseur, G., Chidthaisong, A., Ciais, P., Cox, P., Dickinson, R., Hauglustaine, D., Heinze, C., Holland, E., Jacob, D., Lohmann, U., Ramachandran, S., da Silva Dias, P., Wofsy, S., and Zhang, X.: Couplings Between Changes in the Climate System and Biogeochemistry., in: Climate Change 2007: The Physical Science Basis. Contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change, edited by Solomon, S., Qin, D., Manning, M., Chen, Z., Marquis, M., Averyt, K., M.Tignor, and Miller, H., pp. 498–587, Cambridge University Press, 2007.

Devol, A. H. and Hartnett, H. E.: Role of the oxygen-deficient zone in transfer of organic carbon to the deep ocean, Limnology and Oceanography, 46, 1684–1690, 2001.

Dunne, J., Gnanadesikan, A., Sarmiento, J., and Slater, R.: Technical description of the prototype version (v0) of tracers of phytoplankton with allometric zooplankton (TOPAZ) ocean biogeochemical model as used in the Princeton IFMIP model, Biogeosciences, 7, 3593, http://www.biogeosciences.net/7/3593/2010/bg-7-3593-2010-supplement.pdf, 2010.

Dunne, J., John, J., Shevliakova, E., Stouffer, R., Krasting, J., Malyshev, S., Milly, P., Sentman, L., Adcroft, A., Cooke, W., and Dunne, K.: GFDL's ESM2 Global Coupled Climate–Carbon Earth System Models. Part II: Carbon System Formulation and Baseline Simulation Characteristics, Journal of Climate, 26, 2247–2267, 2013.

Freing, A., Wallace, D. W. R., and Bange, H. W.: Global oceanic production of nitrous oxide, Philosophical Transactions of the Royal Society B: Biological Sciences, 367, 1245–1255, 2012.

Friedlingstein, P., Cox, P., Betts, R., Bopp, L., Von Bloh, W., Brovkin, V., Cadule, P., Doney, S., Eby, M., and Fung, I.: Climate-carbon cycle feedback analysis: Results from the C4MIP model intercomparison, Journal of Climate, 19, 3337–3353, 2006.

Fu, F.-X., Yu, E., Garcia, N. S., Gale, J., Luo, Y., Webb, E. A., and Hutchins, D. A.: Differing responses of marine N_2 fixers to warming and consequences for future diazotroph community structure, Aquatic Microbial Ecology, 72, 33–46, 2014.

Gangstø, R., Gehlen, M., Schneider, B., Bopp, L., Aumont, O., and Joos, F.: Modeling the marine aragonite cycle: changes under rising carbon dioxide and its role in shallow water $CaCO_3$ dissolution, Biogeosciences, 5, 1057–1072, 2008.

Gondwe, M., Klaassen, W., Gieskes, W., and Baar, H.: Negligible direct radiative forcing of basin-scale climate by coccolithophore blooms, Geophysical Research Letters, 28, 3911–3914, 2001.

Hallegraeff, G. M.: Ocean climate change, phytoplankton community responses, and harmful algal blooms: a formidable predictive challenge, Journal of Phycology, 46, 220–235, 2010.

Halloran, P., Bell, T., and Totterdell, I.: Can we trust empirical marine DMS parameterisations within projections of future climate?, Biogeosciences, 7, 1645–1656, http://www.biogeosciences.net/7/1645/2010/bg-7-1645-2010.pdf, 2010.

Hansell, D. A., Carlson, C. A., Repeta, D. J., and Schlitzer, R.: Dissolved organic matter in the ocean: A controversy stimulates new insights, Oceanography, 22, 202–211, 2009.

Hense, I., Meier, H., and Sonntag, S.: Projected climate change impact on Baltic Sea cyanobacteria, Climate Dynamics, 119, 391–406, 2013.

Hinder, S. L., Hays, G. C., Edwards, M., Roberts, E. C., Walne, A. W., and Gravenor, M. B.: Changes in marine dinoflagellate and diatom abundance under climate change, Nature Climate Change, 2, 271–275, 2012.

Hossaini, R., Chipperfield, M., Montzka, S., Rap, A., Dhomse, S., and Feng, W.: Efficiency of short-lived halogens at influencing climate through depletion of stratospheric ozone, Nature Geoscience, 8, 186–190, 2015.

Hutchins, D. A., Fu, F.-X., Zhang, Y., Warner, M. E., Feng, Y., Portune, K., Bernhardt, P. W., and Mulholland, M. R.: CO_2 control of *Trichodesmium* N_2 fixation, photosynthesis, growth rates, and elemental ratios: Implications for past, present, and future ocean biogeochemistry, Limnology and Oceanography, pp. 1293–1304, 2007.

Ilyina, T., Six, K., Segschneider, J., Maier-Reimer, E., Li, H., and nez Riboni, I. N.: Global ocean biogeochemistry model HAMOCC: Model architecture and performance as component of the MPI-Earth system model in different CMIP5 experimental realizations, Journal of Advances in Modeling Earth Systems, 5, 287–315, http://onlinelibrary.wiley.com/doi/10.1029/2012MS000178/pdf, 2013.

Jiang, Z.-P., Tyrrell, T., Hydes, D. J., Dai, M., and Hartman, S. E.: Variability of alkalinity and the alkalinity-salinity relationship in the tropical and subtropical surface ocean, Global Biogeochemical Cycles, 28, 729–742, 2014.

Jiao, N., Herndl, G. J., Hansell, D. A., Benner, R., Kattner, G., Wilhelm, S. W., Kirchman, D. L., Weinbauer, M. G., Luo, T., Chen, F., et al.: Microbial production of recalcitrant dissolved organic matter: long-term carbon storage in the global ocean, Nature Reviews Microbiology, 8, 593–599, 2010.

Jiao, N., Robinson, C., Azam, F., Thomas, H., Baltar, F., Dang, H., Hardman-Mountford, N. J., Johnson, M., Kirchman, D. L., Koch, B. P., et al.: Mechanisms of microbial carbon sequestration in the ocean–future research directions, Biogeosciences, 11, 5285–5306, 2014.

Jochum, M., Yeager, S., Lindsay, K., Moore, K., and Murtugudde, R.: Quantification of the feedback between phytoplankton and ENSO in the Community Climate System Model, Journal of Climate, 23, 2916–2925, 2010.

Jöhnk, K., Huisman, D., Sharples, J., Sommeijer, B., Visser, P., and Stroom, J.: Summer heatwaves promote blooms of harmful cyanobacteria, Global Change Biology, 14, 495–512, 2008.

Kahru, M., Leppaenen, J.-M., and Rud, O.: Cyanobacterial blooms cause heating of the sea surface, Marine Ecology Progress Series, 101, 1–7, 1993.

Kawamiya, M., Kishi, M., and Suginohara, N.: An ecosystem model for the North Pacific embedded in a general circulation model: Part I: Model description and characteristics of spatial distributions of biological variables, Journal of Marine Systems, 25, 129–157, 2000.

Kim, J.-M., Lee, K., Yang, E. J., Shin, K., Noh, J. H., Park, K., Hyun, B., Jeong, H.-J., Kim, J.-H., Kim, K. Y., et al.: Enhanced production of oceanic dimethylsulfide resulting from CO_2-induced grazing activity in a high CO_2 world, Environmental Science and Technology, 44, 8140–8143, 2010.

Kirkevåg, A., Iversen, T., Seland, O., Hoose, C., Kristjánsson, J., Struthers, H., Ekman, A., Ghan, S., Griesfeller, J., Nilsson, E., and Schulz, M.: Aerosol–climate interactions in the Norwegian Earth System Model–NorESM1-M, Geoscientific Model Development, 6, 207–244, http://www.geosci-model-dev.net/6/207/2013/gmd-6-207-2013.pdf, 2013.

Kleypas, J. A .and Feely, R. A., Fabry, V. J., Langdon, C., and Sabine, C. L .and Robbins, L. L.: Impacts of ocean acidification on coral reefs and other marine calcifiers: a guide for future research, in: Report of a workshop held 18–20 April 2005, St. Petersburg, vol. 18, p. 88, 2006.

Knopf, D., Alpert, P., Wang, B., and Aller, J.: Stimulation of ice nucleation by marine diatoms, Nature Geoscience, 4, 88–90, 2011.

Kristensen, E., Ahmed, S. I., and Devol, A. H.: Aerobic and anaerobic decomposition of organic matter in marine sediment: Which is fastest?, Limnology and Oceanography, 40, 1430–1437, 1995.

Laube, J., Engel, A., Bönisch, H., Möbius, T., Worton, D., Sturges, W., Grunow, K., and Schmidt, U.: Contribution of very short-lived organic substances to stratospheric chlorine and bromine in the tropics–a case study, Atmospheric Chemistry and Physics, 8, 7325–7334, http://www.atmos-chem-phys.net/8/7325/2008/acp-8-7325-2008.pdf, 2008.

Laufkötter, C., Vogt, M., Gruber, N., Aita-Noguchi, M., Aumont, O., Bopp, L., Buitenhuis, E., Doney, S., Dunne, J., Hashioka, T., et al.: Drivers and uncertainties of future global marine primary production in marine ecosystem models, Biogeosciences, 12, 6955–6984, 2015.

Laufkötter, C., Vogt, M., Gruber, N., Aumont, O., Bopp, L., Doney, S. C., Dunne, J. P., Hauck, J., John, J. G., Lima, I. D., Seferian, R., and Völker, C.: Projected decreases in future marine export production: the role of the carbon flux through the upper ocean ecosystem, Biogeosciences, 13, 4023–4047, 2016.

Le Quéré, C.: Reply to Horizons Article 'Plankton functional type modelling: running before we can walk' Anderson (2005): I. Abrupt changes in marine ecosystems?, Journal of Plankton Research, 28, 871–872, 2006.

Le Quéré, C., Harrison, S. P., Prentice, I. C., Buitenhuis, E. T., Aumont, O., Bopp, L., Claustre, H., da Cunha, L. C., Geider, R., Giraud, X., Klaas, C., Kohfeld, K. E., Legendre, L., Manizza, M., Platt, T., Rivkin, R. B., Sathyendranath, S., Uitz, J., Watson, A. J., and Wolf-Gladrow, D.: Ecosystem dynamics based on plankton functional types for global ocean biogeochemistry models, Global Change Biology, 11, 1–25, doi:10.1111/j.1365-2486.2005.1004.x, 2005.

Lengaigne, M., Madec, G., Bopp, L., Menkes, C., Aumont, O., and Cadule, P.: Bio-physical feedbacks in the Arctic Ocean using an Earth system model, Bio-physical feedbacks in the Arctic Ocean using an Earth system model, 36, L21 602, http://onlinelibrary.wiley.com/doi/10.1029/2009GL040145/full, 2009.

Liss, P. and Duce, R.: The sea surface and global change, Cambridge University Press, 2005.

Lohbeck, K., Riebesell, U., and Reusch, T. B. H.: Adaptive evolution of a key phytoplankton species to ocean acidification, Nature Geoscience, 5, 346–351, 2012.

Maier-Reimer, E., Kriest, I., Segschneider, J., and Wetzel, P.: The Hamburg oceanic carbon cycle circulation model HAMOCC5.1–Technical Description Release 1.1, in: Tech. Rep. 14, Reports on Earth System Science, Max Planck Institute for Meteorology, Hamburg, Germany, 2005.

Malin, G., Turner, S., Liss, P., Holligan, P., and Harbour, D.: Dimethylsulphide and dimethylsulphoniopropionate in the Northeast Atlantic during the summer coccolithophore bloom, Deep Sea Research Part I: Oceanographic Research Papers, 40, 1487–1508, 1993.

Martin, G., Bellouin, N., Collins, W., Culverwell, I., Halloran, P., Hardiman, S., Hinton, T., Jones, C., McDonald, R., McLaren, A., and O'Connor, F.: The HadGEM2 family of MET Office unified model climate configurations, Geoscientific Model Development, 4, 723–757, http://www.geosci-model-dev.net/4/723/2011/gmd-4-723-2011.pdf, 2011.

McCoy, D., Burrows, S., Wood, R., Grosvenor, D., Elliott, S., Ma, P., Rasch, P., and Hartmann, D.: Natural aerosols explain seasonal and spatial patterns of Southern Ocean cloud albedo, Science advances, 1, e1500 157, 2015.

Meskhidze, N. and Nenes, A.: Phytoplankton and cloudiness in the Southern Ocean, Science, 314, 1419–1423, 2006.

Moore, J., Lindsay, K., Doney, S., Long, M., and Misumi, K.: Marine ecosystem dynamics and biogeochemical cycling in the Community Earth System Model [CESM1 (BGC)]: Comparison of the 1990s with the 2090s under the RCP4. 5 and RCP8. 5 scenarios, Journal of Climate, 26, 9291–9312, http://escholarship.org/uc/item/19g4j6p7, 2013.

Moore, R. M., Webb, M., Tokarczyk, R., and Wever, R.: Bromoperoxidase and iodoperoxidase enzymes and production of halogenated methanes in marine diatom cultures, Journal of Geophysical Research - Oceans, 101, 20 899–20 908, 1996.

Naqvi, S. W. A., Bange, H. W., Farias, L., Monteiro, P. M. S., Scranton, M. I., and Zhang, J.: Marine hypoxia/anoxia as a source of CH_4 and N_2O, Biogeosciences, 7, 2159–2190, 2010.

Nightingale, P., Malin, G., and Liss, P.: Production of chloroform and other low-molecular-weight halocarbons by some species of macroalgae, Limnology and Oceanography, 40, 680–689, 1995.

O'Neil, J. M., Davis, T. W., Burford, M. A., and Gobler, C. J.: Harmful Algae, 14, 313–334, 2012.

Palmer, J. and Totterdell, I.: Production and export in a global ocean ecosystem model, Deep Sea Research Part I: Oceanographic Research Papers, 48, 1169–1198, iPCC-model, 2001.

Patara, L., Vichi, M., Masina, S., Fogli, P., and Manzini, E.: Global response to solar radiation absorbed by phytoplankton in a coupled climate model, Climate dynamics, 39, 1951–1968, 2012.

Piontek, J., Lunau, M., Handel, N., Borchard, C., Wurst, M., and Engel, A.: Acidification increases microbial polysaccharide degradation in the ocean, Biogeosciences, 7, 1615–1624, 2010.

Pomeroy, L. R. and Deibel, D.: Temperature regulation of bacterial activity during the spring bloom in Newfoundland coastal waters, Science, 233, 359–361, 1986.

Pöschl, U. and Shiraiwa, M.: Multiphase Chemistry at the Atmosphere–Biosphere Interface Influencing Climate and Public Health in the Anthropocene, Chemical Reviews, 115, 4440–4475, 2015.

Quinn, P. K. and Bates, T. S.: The case against climate regulation via oceanic phytoplankton sulphur emissions, Nature, 480, 51–56, 2011.

Ramaswamy, V., Boucher, O., Haigh, J., Hauglustaine, D., Haywood, J., Myhre, G., Nakajima, T., Shi, G., Solomon, S., and Betts, R. E. e. a.: Radiative Forcing of Climate Change, in: Chapter 6 of the IPCC Third Assessment Report Climate Change 2001: The Scientific Basis, edited by Houghton, J.T., e. a., pp. 349–416, Cambridge University Pres, 2001.

Rap, A., Scott, C., Spracklen, D., Bellouin, N., Forster, P., Carslaw, K., Schmidt, A., and Mann, G.: Natural aerosol direct and indirect radiative effects, Geophysical Research Letters, 40, 3297–3301, 2013.

Raven, J. A.: Praeger Review: Effects on marine algae of changed seawater chemistry with increasing atmospheric CO_2, in: Biology and Environment: Proceedings of the Royal Irish Academy, vol. 111B, pp. 1–17, Royal Irish Academy, 2011.

Reisch, C. R., Moran, M. A., and Whitman, W. B.: Bacterial catabolism of dimethylsulfoniopropionate (DMSP), Frontiers in Microbiology, 2, 1–12, 2011.

Rost, B. and Riebesell, U.: Coccolithophores and the biological pump: responses to environmental changes, in: Coccolithophores: from molecular processes to global impact, edited by Thierstein, R. and Young, J. R., pp. 99–125, Springer, 2004.

Saiz-Lopez, A., Lamarque, J.-F., Kinnison, D., Tilmes, S., Ordinez, C., Orlando, J., Conley, A., Plane, J. M. C., Mahajan, A., Santos, G. S., Atlas, E., Blake, D., Sander, S., Schauffler, S., Thompson, A., and Brasseur, G.: Estimating the climate significance of halogen-driven ozone loss in the tropical marine troposphere, Atmospheric Chemistry and Physics, 12, 3939–3949, 2012.

Sathyendranath, S., Gouveia, A. D., Shetye, S. R., Ravindran, P., and Platt, T.: Biological control of surface temperature in the Arabian Sea, Nature, 349, 54–56, 1991.

Schneider, B., Bopp, L., Gehlen, M., Segschneider, J., Frolicher, T., Cadule, P., Friedlingstein, P., Doney, S., Behrenfeld, M., and Joos, F.: Climate-induced interannual variability of marine primary and export production in three global coupled climate carbon cycle models, Biogeosciences,, 5, 597–614, 2008.

Segschneider, J. and Bendtsen, J.: Temperature-dependent remineralization in a warming ocean increases surface pCO2 through changes in marine ecosystem composition, Global Biogeochemical Cycles, 27, 1944–9224, 2013.

Six, K. D., Kloster, S., Ilyina, T., Archer, S. D., Zhang, K., and Maier-Reimer, E.: Global warming amplified by reduced sulphur fluxes as a result of ocean acidification, Nature Climate Change, 3, 975–978, 2013.

Sonntag, S.: Modeling biological–physical feedback mechanisms in marine systems, Ph.D. thesis, Universität Hamburg, http://ediss.sub.uni-hamburg.de/volltexte/2013/6427, 2013.

Sonntag, S. and Hense, I.: Phytoplankton behavior affects ocean mixed layer dynamics through biological-physical feedback mechanisms, Geophysical Research Letters, 38, L15 610, doi:10.1029/2011GL048205, 2011.

Steinacher, M., Joos, F., Frolicher, T. L .and Plattner, G.-K., and Doney, S. C.: Imminent ocean acidification in the Arctic projected with the NCAR global coupled carbon cycle-climate model, Biogeosciences, 6, 515–533, 2009.

Stemmler, I., Hense, I., Quack, B., and Maier-Reimer, E.: Methyl iodide production in the open ocean, Biogeosciences, 11, 4459–4476, 2014.

Stemmler, I., Hense, I., and Quack, B.: Marine sources of bromoform in the global open ocean – global patterns and emissions, Biogeosciences, 12, 1967–1981, 2015.

Stramma, L., Johnson, G. C., Sprintall, J., and Mohrholz, V.: Expanding oxygen-minimum zones in the tropical oceans, Science, 320, 655–658, 2008.

Sturges, W. T., Oram, D. E., Carpenter, L. J., Penkett, S. A., and Engel, A.: Bromoform as a source of stratospheric bromine, Geophysical Research Letters, 27, 2081–2084, 2000.

Taucher, J.and Bach, L. T., Riebesell, U., and Oschlies, A.: The viscosity effect on marine particle flux: A climate relevant feedback mechanism, Global Biogeochemical Cycles, 28, 415–422, 2014.

Tyrrell, T., Holligan, P. M., and Mobley, C. D.: Optical impacts of oceanic coccolithophore blooms, Journal of Geophysical Research - Oceans, 104, 3223–3241, 1999.

Valentine, D.: Emerging topics in marine methane biogeochemistry, Annual review of marine science, 3, 147–171, 2011.

Vichi, M., Pinardi, N., and Masina, S.: A generalized model of pelagic biogeochemistry for the global ocean ecosystem. Part I: Theory, Journal of Marine Systems, 64, 110–134, 2007.

Vichi, M., Manzini, E., Fogli, P., Alessandri, A., Patara, L., Scoccimarro, E., Masina, S., and Navarra, A.: Global and regional ocean carbon uptake and climate change: sensitivity to a substantial mitigation scenario, Climate dynamics, 37, 1929–1947, 2011.

Volk, T. and Hoffert, M.: Ocean carbon pumps: Analysis of relative strengths and efficiencies in ocean-driven atmospheric CO_2 changes, The Carbon Cycle and Atmospheric CO: Natural Variations Archean to Present, pp. 99–110, 1985.

Watanabe, S., Hajima, T., Sudo, K., Nagashima, T., Takemura, T., Okajima, H., Nozawa, T., Kawase, H., Abe, M., Yokohata, T., and Ise, T.: MIROC-ESM 2010: model description and basic results of CMIP5-20c3m experiments, Geoscientific Model Development, 4, 845–872, 2011.

Watson, A. and Lovelock, J.: Biological homeostasis of the global environment: the parable of Daisyworld, Tellus B, 35B, 284–289, 1983.

Wilson, T., Ladino, L., Alpert, P., Breckels, M., Brooks, I., Browse, J., Burrows, S., Carslaw, K., Huffman, J., Judd, C., and Kilthau, W.: A marine biogenic source of atmospheric ice-nucleating particles, Nature, 525, 234–238, 2015.

Wu, T., Li, W., Ji, J., Xin, X., Li, L., Wang, Z., Zhang, Y., Li, J., Zhang, F., Wei, M., and Shi, X.: Global carbon budgets simulated by the Beijing Climate Center Climate System Model for the last century., Journal of Geophysical Research: Atmospheres, 118, 4326–4347, http://onlinelibrary.wiley.com/doi/10.1002/jgrd.50320/pdf, 2013.

Zhang, H. and Cao, L.: Simulated effect of calcification feedback on atmospheric CO_2 and ocean acidification, Scientific reports, 6, 20 284, 2016.