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How important is biological ice nucleation in clouds on a global scale?

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Abstract

The high ice nucleating ability of some biological particles has led to speculations about living and dead organisms being involved in cloud ice and precipitation formation, exerting a possibly significant influence on weather and climate. In the present study, the role of primary biological aerosol particles (PBAPs) as heterogeneous ice nuclei is investigated with a global model. Emission parametrizations for bacteria, fungal spores and pollen based on recent literature are introduced, as well as an immersion freezing parametrization based on classical nucleation theory and laboratory measurements. The simulated contribution of PBAPs to the global average ice nucleation rate is only $10^{-5}\%$, with an uppermost estimate of 0.6%. At the same time, observed PBAP concentrations in air and biological ice nucleus concentrations in snow are reasonably well captured by the model. This implies that ‘bioprecipitation’ processes (snow and rain initiated by PBAPs) are of minor importance on the global scale.

Keywords: ice nucleation, biological aerosol, aerosol–cloud interactions

1. Introduction

Ice formation in mixed-phase clouds (at temperatures between 0 and -38°C) is initiated by so-called ice nuclei (INs), which are a small subset of the aerosol population. Without INs, the droplets would remain liquid (in a metastable state) throughout this temperature range. Once the first ice crystals have formed in a mixed-phase cloud, they can rapidly grow (Wegener–Bergeron–Findeisen process), stimulating precipitation formation. Various insoluble particles like mineral dust, metallic particles, soot, and primary biological particles can act as INs. Some bacteria (especially *Pseudomonas syringae*) and fungal spores have been found to be among the most efficient INs, initiating freezing at temperatures as high as -2°C (Yankofsky *et al* 1981).

After the discovery of ice nucleating biological particles in the 1970s, it was suggested that the biosphere plays an active role in cloud glaciation and precipitation initiation (Sands *et al* 1982, Morris *et al* 2004). For a long time, observational evidence in support of the ‘bioprecipitation hypothesis’ was limited and only indirect (Möhler *et al* 2007). Recent

measurements seem to provide new indications of the possible atmospheric relevance of biogenic particles for ice formation: Christner *et al* (2008) observed that ice nucleation active bacteria are ubiquitous in precipitation on different continents; Pratt *et al* (2009) identified 33% of the ice crystal residual particles sampled in a wave cloud over Wyoming as biogenic; and Prenni *et al* (2009) found that chamber-measured INs in the Amazon basin were composed to a significant fraction of biological carbonaceous particles. However, it is unclear how representative these results are for global climatological conditions.

Sensitivity studies with small-scale models have demonstrated the potential impact of bioaerosols on cloud microphysics (e.g. Levin *et al* 1987, Diehl *et al* 2006, Grützun *et al* 2008, Ariya *et al* 2009, Phillips *et al* 2009), but extrapolation to their broader atmospheric relevance is hampered by the fact that the prescribed bioaerosol concentrations were often not realistic or not clearly specified.

The purpose of the present study is to simulate realistic biological particle concentrations and to constrain their

Table 1. Simulation description.

Simulation	Ice nucleation properties of bacteria and fungal spores
PBAP	1% <i>Pseudomonas syringae</i> -like, with a maximum allowed IN fraction of 0.1%, and 99% inactive.
PBAP-intermediate	1% <i>Pseudomonas syringae</i> -like, with a maximum allowed IN fraction of 0.1%, and 99% intermediate INA (same nucleation parameters as for mineral dust).
PBAP-MAX	100% <i>Pseudomonas syringae</i> -like, no upper limit on IN fraction. Higher bacterial emission fluxes (see table 2).

contribution to atmospheric ice nucleation for the first time in a global model. Recently published emission parametrizations for bacteria, fungal spores and pollen are implemented in the CAM-Oslo model, and the simulated concentrations are compared to observations. Heterogeneous ice nucleation via immersion freezing in mixed-phase clouds is parametrized following classical nucleation theory, with aerosol-specific parameters derived from laboratory experiments. The relative importance of biological INs compared to mineral dust and soot INs is assessed.

2. Model description

2.1. CAM-Oslo

The aerosol–climate model CAM-Oslo with a detailed aerosol module (Seland *et al* 2008) and a prognostic double-moment cloud microphysics scheme (Storelvmo *et al* 2008, Hoose *et al* 2009) has been modified by a new treatment of ice nucleation by mineral dust, soot, bacteria, fungal spores and pollen (Hoose *et al* 2010). These primary biological aerosol particles (PBAPs) are included with emission parametrizations listed below. PBAP dry and wet deposition are treated as described for other aerosol species in Seland *et al* (2008). For wet deposition, the same in-cloud and below-cloud scavenging coefficients are assumed as for coarse mode sea salt particles, implying that the bioaerosols are easily wettable (supported by measurements reviewed in Ariya *et al* (2009)). In the absence of sufficient size-resolved measurements, the PBAPs are assumed to be monodisperse (diameters given below), spherical, and with a density of 1 g cm^{-3} .

Three simulations (see table 1) are presented, each of them integrated for five years after a four-month spin-up period: one with our best estimates on PBAP emissions and ice nucleation properties (simulation ‘PBAP’), and two sensitivity studies (‘PBAP-intermediate’ and ‘PBAP-MAX’). ‘PBAP-intermediate’ attempts to include bacteria and fungal spores with intermediate ice nucleation activity. In ‘PBAP-MAX’, extreme assumptions on bacterial emissions as well as on bacteria and fungal spore ice nucleation efficiencies are made in order to calculate an upper estimate. For pollen, the freezing efficiency assumptions are already upper estimates in the ‘PBAP’ simulation. The resolution of CAM-Oslo is $2.8125^\circ \times 2.8125^\circ$ (T42), with 26 vertical levels and a timestep for the model physics of 40 min.

Table 2. Bacterial emission fluxes (best-fit and 95th percentiles of emission estimates by Burrows *et al* (2009a)), and ecosystem area in the CLM land model (Bonan *et al* 2002). Emissions from coastal areas are not considered with a separate emission flux in the present study, because they cannot be unambiguously attributed to a plant functional type.

Ecosystem	Area (10^6 km^2)	F_i ($\text{m}^{-2} \text{ s}^{-1}$) in simulations PBAP and PBAP-intermediate	F_i ($\text{m}^{-2} \text{ s}^{-1}$) in simulation PBAP-MAX
Coastal	0	900	4 996
Crops	22.7	704	1 578
Deserts	19.1	0	52
Forests	30.3	0	187
Grasslands	32.9	648	1 811
Land-ice	15.5	7.7	16
Seas	362.6	0	226
Shrubs	20.3	502	619
Tundra	7.0	0	579
Wetlands	4.2	196	14 543

2.2. PBAP emissions

Burrows *et al* (2009a) have derived bacterial emission fluxes in different ecosystems from observation-based best estimates of near-surface number concentrations. The best-fit number fluxes F_i (see table 2) are used here, weighted by the area fraction of the respective ecosystems in the gridbox (f_i).

$$F_{\text{bacteria}} = \sum_{i=1}^{10} f_i F_i. \quad (1)$$

Here the index i runs over the up to ten ecosystems with nonzero bacterial emissions. The fractions of the different ecosystems are obtained from the corresponding plant functional type area fractions of the land model CLM (Bonan *et al* 2002) used in CAM-Oslo, and are not necessarily equal to the ones used in the Burrows *et al* (2009a) study. In simulation PBAP-MAX, the 95th percentiles of the emission estimates by Burrows *et al* (2009a) are used. The bacterial diameter is set to $1 \mu\text{m}$, assuming single cells. Bacteria can also be aggregated in clumps or rafted on plant/soil debris (Tong and Lighthart 2000). The size assumption influences the particle deposition rate. A sensitivity study by Burrows *et al* (2009a) showed that an increase of the bacterial diameter from 1 to $3 \mu\text{m}$ results in a decrease of the atmospheric residence time by up to about 20%.

For fungal spores (including spores of lichen fungi), we follow the approach by Heald and Spracklen (2009), which is based on observations compiled by Elbert *et al* (2007). Heald and Spracklen (2009) assume that the fungal spore emissions are linear functions of the LAI (leaf area index) and of the specific humidity q at the surface. As in Elbert *et al* (2007), we assume a spore diameter of $5 \mu\text{m}$. To approximately match the Heald and Spracklen (2009) emissions, we apply the following formulation for the number emission flux:

$$F_{\text{fungal spores}} = 500 \text{ m}^{-2} \text{ s}^{-1} \times \frac{\text{LAI}}{5} \times \frac{q}{1.5 \times 10^{-2} \text{ kg kg}^{-1}}. \quad (2)$$

The grid cell mean LAI is given by the land model CLM and undergoes month-to-month variations.

Jacobson and Streets (2009) provided the first pollen emission parametrization for a global model. We apply it here in a simplified form, neglecting dependence on time of the day, relative humidity and turbulent kinetic energy.

$$F_{\text{pollen}} = 0.5 \text{ m}^{-2} \text{ s}^{-1} \times \text{LAI} \times R_{\text{month}} \quad (3)$$

R_{month} is a factor accounting for seasonal variations (in the Northern Hemisphere 0.5 for October to March, 2.0 for April to June, and 1.0 for July to September; in the Southern Hemisphere shifted by six months). As in Jacobson and Streets (2009), we assume a pollen diameter of 30 μm .

While the representation of PBAPs in CAM-Oslo is not complete (lacking e.g. viruses and plant debris), the considered groups are assumed to cover the most relevant airborne biological INs known today.

2.3. Ice nucleation parametrization

Immersion freezing is parametrized based on classical nucleation theory as described in Chen *et al* (2008). The aerosol-specific parameters are derived from fits to laboratory measurements, and listed in Hoose *et al* (2010). The nucleation rates per aerosol particle and second, J_{imm} , are displayed as a function of temperature in figure 1. As temperature decreases, nucleation increases sharply around the freezing onset temperature, and flattens off or slightly decreases again at lower temperatures. The onset temperatures are about -5°C for *Pseudomonas syringae* bacteria, -8°C for pollen, -13°C for montmorillonite dust and -24°C for soot (see the discussion in Hoose *et al* (2010)). According to cloud model calculations, condensation/immersion freezing accounts for the major part of heterogeneous ice nucleation in mixed-phase clouds (Meyers *et al* 1992, Phillips *et al* 2007). As calculated in CAM-Oslo, more than 85% of the heterogeneous ice nucleation events are via immersion freezing (Hoose *et al* 2010). In particular, it is the most likely freezing pathway for the large and hydrophilic biological particles. The roles of deposition and contact nucleation are a matter of discussion in current literature. These processes require the presence of interstitial, unactivated particles, such that black carbon and mineral dust particles are likely to be favoured and the inclusion of these processes would reduce the contribution from biological particles.

In the absence of better information, we assume only one value of the freezing parameters per aerosol species. Classical theory predicts a constant freezing rate, while observations indicate a superposition of stochastic and singular behaviour of ice nucleation (Vali 2008). In order to avoid excessive ice nucleation due to the assumption of a stochastic freezing process, upper limits of 1% (soot) and 0.1% (bacteria and fungal spores) are set for the fraction of particles nucleating ice. For each species, the freezing rate as shown in figure 1 is applied until the limit is reached. After this, no further ice nucleation by this particle class is allowed, assuming that the remaining particles are inefficient INs. Mineral dust and pollen particles can theoretically be 100% activated to ice crystals (no upper limit applied; see the discussion in Hoose *et al* (2010)). The limit is removed for bacteria and fungal spores in simulation PBAP-MAX.

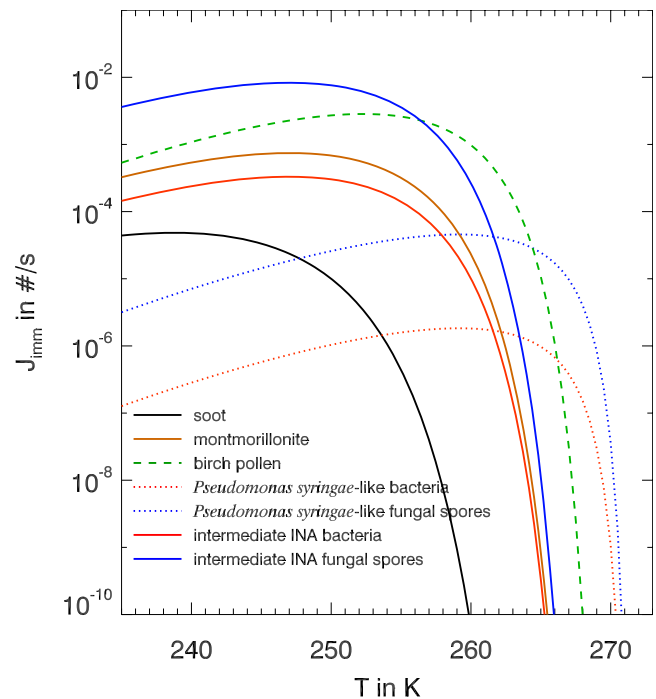


Figure 1. Parameterized immersion freezing rates J_{imm} . For soot, montmorillonite dust, birch pollen, *Pseudomonas syringae*-like bacteria and fungal spores, see the parametrization description in Hoose *et al* (2010). For intermediate INA bacteria and fungal spores, the same contact angle and activation energy as for montmorillonite are assumed. The rates are material and size dependent and are shown here for particle radii of 40 nm (soot), 750 nm (dust), 12.5 μm (pollen), 500 nm (bacteria) and 2.5 μm (fungal spores).

2.4. Fraction of ice nucleation active (INA) PBAPs

Only a small subset of all primary biological particles belongs to highly ice nucleation active (INA) species, which can nucleate ice at very warm subzero temperatures ($\approx -5^\circ\text{C}$). In simulation PBAP, we assume that, on global average, 1% of all atmospheric bacteria belong to highly INA species, represented by *Pseudomonas syringae* (table 1). This assumption follows Phillips *et al* (2009), based on episodic observations of bacteria INA fractions in air and precipitation ranging from 0 to 15% (e.g. Maki and Willoughby 1978, Lindemann *et al* 1982, Constantinidou *et al* 1990). For fungal spores, data are rarer. We assume 1% of the airborne fungal spores (including spores of lichen fungi) to nucleate ice with the same characteristics as *Pseudomonas syringae* (Pouleur *et al* 1992), which is probably an upper estimate. The assumed bacteria and fungal spore INA fraction is uncertain and requires further atmospheric measurements to be better constrained. Note that calling a species ‘ice nucleation active’ only means that a small fraction of cells, not all cells, of this species carries the necessary gene(s) and/or expresses the phenotype, i.e. is able to nucleate ice at high temperatures (Hirano and Upper 1995).

In simulation PBAP-intermediate, the remaining 99% of bacteria and fungal spores are allowed to act as ice nuclei, too, but at lower temperatures. In addition to well characterized INA bacteria like *Pseudomonas syringae*, other, more common bacterial species have been observed to show

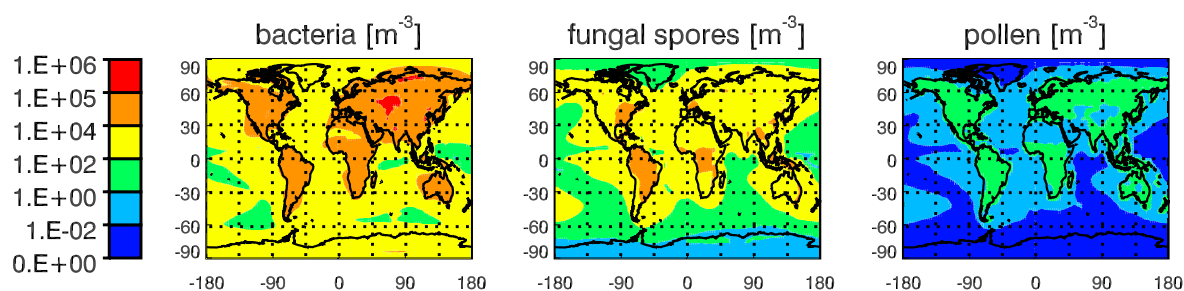


Figure 2. Simulated annual average near-surface bioaerosol concentrations.

Table 3. Bioaerosol emissions and burdens in simulation PBAP. For the total PBAP (primary biological aerosol particle) emissions and burdens, the simulated contributions from bacteria, fungal spores and pollen are summed up.

Aerosol	CAM-Oslo global emissions (Tg yr ⁻¹)	Literature values for global emissions (Tg yr ⁻¹)	CAM-Oslo global burden (Gg)	Literature values for global burdens (Gg)
Bacteria	0.75	0.74 (0.4–1.8) ^a , 28.1 ^b	4.3	8.7 ^a
Fungal spores	31	28 ^c , 50 ^d , 186 ^b	94	180 ^c
Pollen	47	84.5 ^b	22	
Total PBAPs	78	<10 ^e , 186 ^f , 296 ^b	121	

Literature values are from ^a Burrows *et al* (2009a), ^b Jacobson and Streets (2009), ^c Heald and Spracklen (2009),

^d Elbert *et al* (2007), ^e Winiwarter *et al* (2009) and ^f Mahowald *et al* (2008).

intermediate ice nucleation activity at temperatures around $\approx -15^\circ\text{C}$ (Mortazavi *et al* 2008). While insufficient data are available to derive the nucleation parameters with Chen *et al* (2008)'s method, we include the intermediate INA bacteria in simulation PBAP-intermediate by assigning them the same nucleation parameters as for mineral dust (montmorillonite, see figure 1). This is justified by noting that Mortazavi *et al* (2008) found similar median freezing temperatures for montmorillonite suspensions and a large number of bacterial samples isolated from snow. However, the ratio of ice nucleating cells to the total cell number was not determined, and our assumption that 99% of all bacteria and fungal spores can nucleate ice with an efficiency comparable to mineral dust is probably a high estimate.

In simulation PBAP-MAX, the fraction of *Pseudomonas syringae*-like bacteria and fungal spores is raised to a value of 100%, which is unrealistically high.

A wide variety of pollen species have been found to nucleate ice (Diehl *et al* 2002, Chen *et al* 2008). von Blohn *et al* (2005) concluded that ice nucleating ability seems to be a general property of pollen. Therefore we assume that 100% of pollens have ice nucleation properties similar to birch pollen (Diehl *et al* 2002).

3. Results

3.1. Bioaerosol emissions and concentrations

Table 3 summarizes the simulated bioaerosol emission strengths and atmospheric burdens as compared to previous studies. Bacterial emissions and concentrations are highest in number (figure 2), but smallest in mass. Fungal spore and pollen mass emissions are comparable, but fungal spores are more numerous and reside longer in the atmosphere due to their

smaller size. The global PBAP emissions are estimated to be 78 Tg yr^{-1} .

The simulated bacterial, fungal spore, and total PBAP number concentrations are compared to observations at various locations in figures 3(a)–(c). As the global model data are monthly mean values for the $2.8^\circ \times 2.8^\circ$ gridbox, their comparability to point measurements is limited. This can also be seen in similar comparisons for better quantified aerosol species (e.g. Stier *et al* 2005, Seland *et al* 2008). Taking into account the uncertainties in measurement methods and the possibly limited representativeness of short-term, locally influenced observations for a larger region and longer time span, the agreement between measurements and observations is satisfactory overall. Note that, while the bacterial concentrations shown here have entered the formulation of the emission parametrization (Burrows *et al* 2009a), the fungal spore and total PBAP data are independent. The good match in fungal spore number concentrations confirms that a monodisperse size distribution with a particle diameter of $5\text{ }\mu\text{m}$ is a reasonable first assumption. Regional and seasonal variations are less well represented than average concentrations, and therefore the correlation between model and measurements is low.

Although the simulated bacteria and fungal spore concentrations are of the correct order of magnitude, the model tends to underestimate total PBAPs (figure 3(c)). This probably indicates that either pollen or other (possibly submicron) PBAPs that are not considered here contribute significantly to the total PBAP number at the measurement locations. A larger database of long-term observations with world-wide coverage would be desirable for a more precise model evaluation.

3.2. Ice nucleation rates

In the simulation with the best assumptions about PBAP ice nucleation abilities, ice nucleation is dominated by mineral

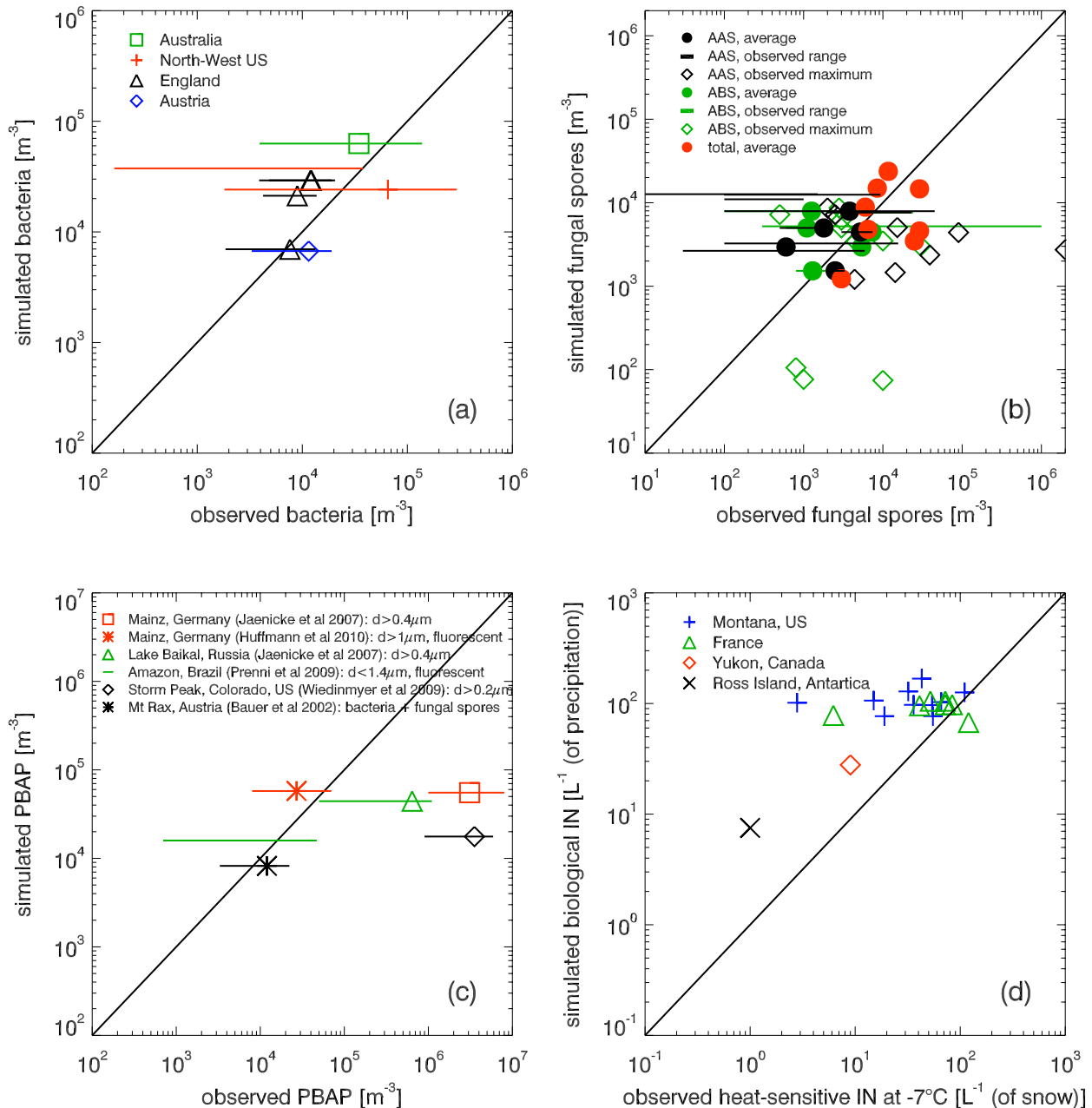


Figure 3. Simulated bioaerosol concentrations compared to observations. Observations are averages over different time periods, and the simulated data are taken for the corresponding months at the gridboxes containing the measurement location. Where available, ranges of observed concentrations are indicated by the horizontal bars. (a) Bacteria. Observations include the ‘total bacteria’ concentrations listed in Burrows *et al* (2009b) and those observations of ‘culturable bacteria’ from which Burrows *et al* (2009b) estimated total concentrations. (b) Actively wet discharged ascospores (AAS), basidiospores (ABS) and total fungal spores. In the model, AAS and ABS are assumed to contribute one-third each to total fungal spores. The observations are from the references listed in Elbert *et al* (2007) and from Bauer *et al* (2008). (c) Total PBAPs. For observations to a certain size or subset of particles, only the corresponding size range and species were taken from the model. The observations of ‘fluorescent PBAPs’ have to be seen as a lower limit to total PBAPs. (d) Biological INs $<15 \mu\text{m}$ in precipitation water compared to measurements of heat-sensitive INs $<15 \mu\text{m}$ at -7°C by (Christner *et al* 2008). The observations represent single snowfall events.

dust (88% of the global total immersion freezing), followed by soot (12%), while PBAPs only contribute to $10^{-5}\%$ (figure 4). The PBAP freezing rate splits up into 11% bacteria, 1% fungal spores, and 88% pollen. Including bacteria and fungal spores with intermediate ice nucleation activity (simulation PBAP-intermediate), the PBAP contribution to heterogeneous ice nucleation is estimated to be 0.03%. In simulation

PBAP-MAX, the PBAP contribution to total freezing is raised to 0.6% (98% bacteria and 2% fungal spores), and PBAP freezing can become a significant process in some regions in the lower troposphere, where temperatures are warm and PBAP concentrations are high. We would like to emphasize that the PBAP-MAX simulation includes extreme assumptions on the bacteria and fungal spore ice nucleation and should not

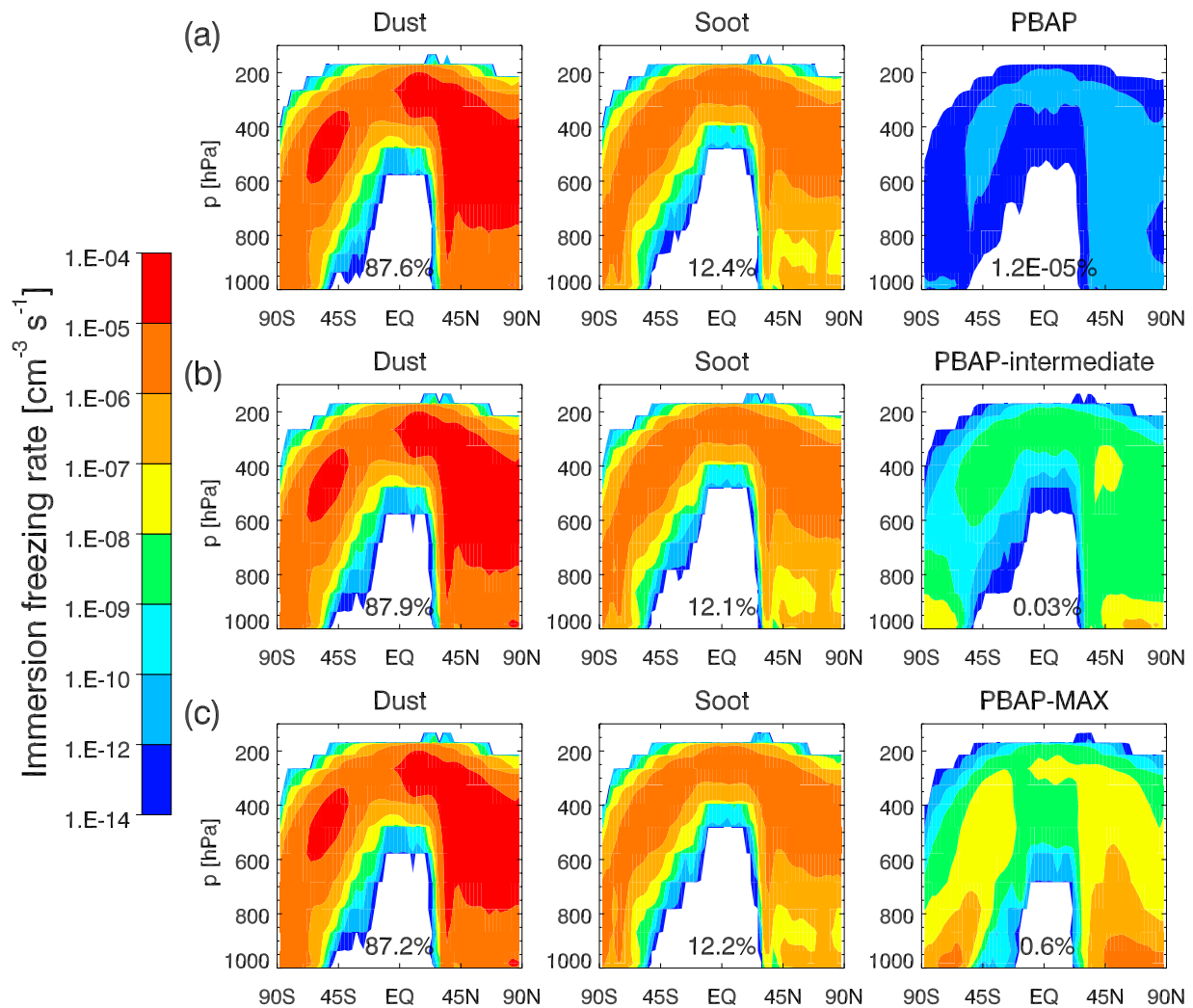


Figure 4. Zonal annual mean immersion freezing rates (a) in simulation PBAP, (b) in simulation PBAP-intermediate, and (c) in simulation PBAP-MAX. The percentage contributions to the total immersion freezing rate are indicated.

be considered a realistic scenario, but is intended to provide an uppermost estimate, taking into account today's uncertainties on biological ice nucleation.

3.3. Biological INs in snow

We now compare the measurements of biological INs in snow by Christner *et al* (2008) to the simulated bacteria and fungal spore concentrations in precipitation, scaled with the fraction of ice nucleation active species (1%) and with the maximum fraction acting as immersion nuclei (0.1%). These data are from simulation PBAP. The particle concentration in snow is a result of both nucleation scavenging and in-and below-cloud impaction scavenging. Figure 3(d) shows that, while the highest observed biological IN concentrations are captured by the model, in general the concentrations are overestimated. This means that the measured data are broadly consistent our 'best-guess' scenario, which yields a biological IN contribution to heterogeneous ice nucleation of only $10^{-5}\%$. In other words, the assumed fraction of biological INs and the simulated concentration fields in simulation PBAP are not too low, yet

their contribution to atmospheric ice formation is marginal. This implies that the observed biological INs in precipitation are not evidence for an important role of PBAPs in global cloud ice nucleation and precipitation formation.

4. Conclusions

In this exploratory study, we present global model simulations of bacterial, fungal spore and pollen concentrations and their contribution to atmospheric ice nucleation. We find that simple bioaerosol emission parametrizations can reproduce average observed concentrations, but have less ability for their regional and seasonal variability. The simulated global average PBAP contribution to heterogeneous ice nucleation in mixed-phase clouds is very small. Even with unrealistically high freezing efficiency assumptions, it is not higher than 1%. However, these results do not rule out the local, regional and seasonal importance of biological ice nuclei. If present in high enough concentrations (significantly higher than the climatological concentrations simulated in this study), PBAPs may trigger glaciation of clouds at warmer temperatures and lower altitudes

than in their absence. The observed high biological IN/ice crystal residue concentrations in specific cases and events are possibly linked to variations in PBAP concentrations and/or ice nucleation efficiencies far above the average. The observed concentrations of PBAP ice nuclei in snow can be explained with our 'best-guess' assumptions for PBAP emissions and ice nucleation efficiencies. More observations of airborne biological INs are necessary to further constrain uncertain model parameters and assumptions, in particular on pollen emissions, PBAP size distributions, attachment to other particles (e.g. dust), and ice nucleation active fractions.

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