

Water mass properties and circulation in the Cape Basin – A multiproxy approach

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Highly resolved profiles of Th/U-isotopes and CaCO₃ concentrations from the southern Cape Basin (ODP Leg 177, Site 1089, 4620 m) are presented covering the past 310 kyr. The ²³⁰Th-profiling method is applied to quantify sediment focussing, and to calculate vertical ²³²Th-fluxes and preserved fluxes of calcium carbonate. The flux of ²³²Th is used as a proxy for dust input [1]. The ²³²Th based dust record from the Sub-Antarctic South Atlantic shows a good covariation with Antarctic dust data [2] although a different signal dynamics points to a non linear amplifier affecting the dust transport to Antarctica. The preserved flux of CaCO₃ at Site 1089 shows a clear variability on glacial interglacial timescales documenting significant changes in the corrosiveness of bottom/deep waters. Authigenic U is commonly present at Site 1089. Since this site is located in an open Ocean area (low productivity) and sediment focussing was high but constant, we interpret the authigenic U signal at Site 1089 as a proxy for the oxygen content of bottom waters. A combination of our results with other proxies (benthic δ¹³C and fragmentation index [3], and mineralogical parameters [4], allows a congruent reconstruction of water mass properties and circulation in the Cape Basin on glacial/interglacial timescales. Based on this multi proxy approach we conclude that that during glacial times the conveyor circulation was weak, and the abyssal Cape Basin was filled with less corrosive and aged deep waters. A correlation/phase analysis suggest the following see-saw scenario: benthic δ¹³C values increase (decrease) first, then the Agulhas Current strengthens (weakens), the fragmentation index of forams rises (falls) before the preserved CaCO₃ flux decreases (increases), and finally authigenic Uranium is not accumulated/released (accumulated).

[1] Winckler *et al.* (2008) *Science* 320, 93. [2] Lambert *et al.* (2008) *Nature* 452, 616. [3] Hodell, Gersonde, & Blum (2002) *Proc. ODP, Sci. Results*, 177. [4] Kuhn & Diekmann, (2002) *Palaeogeography Palaeoclimatology Palaeoecology* 182, 287.

Distribution and potential impacts of biological ice nucleators in the atmosphere

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At subzero temperatures warmer than -40°C, aerosol particles in clouds initiate freezing through the heterogeneous nucleation of ice, which can trigger the processes leading to precipitation. A diverse range of natural and anthropogenic particles are capable of initiating the ice phase, but the most active naturally occurring ice nuclei (IN) are biological in origin and have the capacity to catalyze freezing at temperatures near -2°C. The abundance and distribution of the most active IN in the atmosphere (i.e., biological IN) have been described in only a very limited way, their diversity and ecological/biological sources have not been systematically investigated, and their role in precipitation generation and the global climate remains speculative. However, biological particles have been shown to be abundant in atmospheric aerosols and there is evidence that some bacteria may serve as IN in clouds. Species of ice nucleating bacteria or biological IN in general have been detected in snow and rain from a variety of global locations, and ~95% of the immersion IN active at temperatures warmer than -10°C are inferred to originate from bacteria and/or biological cells. Based on the widespread distribution of biological IN in the atmosphere, they are likely to encounter the appropriate conditions to affect processes leading to precipitation. Aerosol-cloud simulation models imply that high loads (10 per liter at -20°C; under conditions of water saturation) of biological IN may influence the average concentration and sizes of crystals in clouds, horizontal cloud coverage in the free troposphere, precipitation at the ground, and incident solar insolation at the surface. Unearthing a 'weak feedback' between sources of biological IN (e.g., plants and surface ecosystems) and cloud atmospheric processes has implications for deciphering functional biological mechanisms which influence the climate system and understanding global dissemination strategies of phytopathogens and other microorganisms.