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Microbiological fingerprint of African dust deposition in alpine snow pack, Mont Blanc summit

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The biogeochemical effect of African dust transport has been reported mostly with respect to nutrient budget change in both terrestrial and aquatic ecosystems and global transport of microorganisms, including pathogens. However, its potential to seed or colonize the remote environments by transported microorganisms is poorly understood.

This study has focused on bacterial content and diversity of Saharan dust deposition from 2006, 2008 and 2009 in snow pack of Mont Blanc (MtBl) glacier as well as recognition of bacteria which could be involved in establishing microbiota in this icy environment.

Four snow samples recorded Saharan dust events from June 2006 (SDm06/2006 - 3,5 months aged), May and June 2008 (SDm05/2008 and SDm06/2008 - 1 month in between and 1 week aged each) and May 2009 (SDm05/2009 - 1 week aged) were collected at Col du Dome area (4250m a.s.l.). Bacterial community structure was assessed by ribotyping and subsequent sequencing of bacterial 16S rRNA genes. To exclude human-associated and laboratory contamination several controls were run in parallel updating our contaminant library. The obtained phylotypes were tested against this library keeping only those which successfully passed through this exam.

Of 176 selected clones from four clone libraries 29.8% were met in our contaminant library. The ‘true’ sequences were assigned to 57 phylotypes (>97.5% sequence similarity) originating mostly from soil. The prevalent phylotypes recovered were belonging to different bacterial divisions: Deinococcus-Thermus, Alpha-proteobacteria and CFB groups for SDm06/2006; Actinobacteria, Alpha-proteobacteria and CFB for SDm05/2008 and SDm06/2008; Actinobacteria and chloroplasts/plastids for SDm05/2009. Phylogenetic analysis of all phylotypes showed no shared species amongst all 4 dust layers in MtBl snow pack in 2006, 2008 and 2009. However, two phylotypes (Blastococcus saxobsidens sp. – 99%, Geodermatophilus obscurus sp. – 99%) were shared between 2008 and 2009 and one more (uncultured kaistobacter sp.) – between two events of 2008. Besides phylotypes met in our contaminant library several phylotypes were identified as related to human skin microbiome and plant pathogens.

Amongst microbes recovered from the snow with Saharan dust deposits several phylotypes were found may have the potential to colonize the snow pack of the glacier (average temperature - -11oC). All of them were previously discovered in cold ecosystems. In order to recover these ‘icy’ microbes in a culture the attempt was done with Deinococci but with no success.

As a conclusion drawn from this study it appears that microbial communities transported during Saharan dust events to terrestrial glacier vary widely in species composition with time and deposition time-series. Such variability likely results from features of dust mobilization in a source area, its transport and time-period of dust deposition in a snow. As to ‘icy’ phylotypes it seems they come up from a minor fraction which is different one event from another. Ongoing studies including microbial RNA analysis along with clean snow as a counterpart are in a progress.