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Microbial communities established on Mont Blanc summit with Saharan dust deposition

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Dust originating from the Sahara desert can be uplifted during storms, transported across the Mediterranean towards the Alpine region and deposited during snowfalls. The microbes associated with dust particles can be involved in establishing microbiota in icy environments as well as affect ecosystem and human health. Our objective was to use a culture-free DNA-based approach to assess bacterial content and diversity and furthermore, to identify 'icy' microbes which could be brought on the Mont Blanc (MtBl) summit with Saharan dust and became living in the snow. Saharan dust fallout on MtBl summit from one event (MB5, event June 2006) vs. control libraries and that from another event (May 2008) were collected in Grenoble (SD, 200 m a.s.l.) and at Col du Dome (MB-SD, 4250 m a.s.l.). Soil from Ksar Ghilane (SS, Saharan desert, Tunisia, March 2008) was taken for overall comparison as a possible source population. Fresh snow falling in Grenoble (85) was collected as example of diversity in this area.

To assess the microbial diversity 16S rRNA gene libraries (v3-v5 region) were constructed for corresponding dust-snow samples (MB5, SS, SD, 85 and MB-SD) along with clear snow samples and several controls. For both MB5 and MB-SD samples full-gene technique was evoked in attempt to differentiate reproduced bacteria from damaged DNA. Before sequencing the clones were rybotyped. All clone libraries were distinct in community composition except for some single phylotypes (or closely related groups) overlap.

Thus, clone libraries from two different events that were collected at Col du Dome area within 2 year interval (MB5 and MB-SD) were different in community composition except one of the abundant phylotype from MB-SD library (Geodermatophilus sp.) which was shared (98% sequence similarity) with single representative from MB-5 library. These bacteria are pigmented and radiation-resistant, so it could be an indicator of desert origin for our sequences. For MB5 library two Deinococcus-Thermus phylotypes (46.2%) along with A-Proteobacteria and CFB were dominated while for MB-SD library two Actinobacteria phylotypes (29%) with another A-Proteobacteria phylotype were copious. This testify that two dust events are principally different in species composition meaning that any other events can also be different in microbes transferred from Sahara to MtBl summit. Of three other gene libraries (SD, SS and 85) selected as 'supporting' gene pools for MB-SD two libraries (SD and 85) were strictly different from MB-SD while SS library showed two phylotype groups shared with MB-SD. Among them, one A-Proteobacteria phylotype have been detected in unrelated dust event (Polymenakou et al., 2008). It's worth noticing that one numerous A-Proteobacteria phylotype from MB5 library was closely related (97%) to another numerous phylotype from 85 (Grenoble snow fallout) library despite the events were separated geographically and split in time. Such phylotypes could be present in atmosphere elsewhere. Amongst microbes detected in MtBl dust layers libraries four separate minor phylotypes (three cyanobacteria and Deinococcus sp1) were found in MB5 and two minor phylotypes (uncultured actinobacteria, uncultured alphaproteobacteria) - in MB-SD which could be living (keep safe) in ice and snow. All of them were early discovered in cold ecosystems. Seems to be despite the dominant phylotypes recovered in both dust event gene libraries might have a high chance to be established in a snow as populations the minor phylotypes in the dust microbial load are more important in habiting the snow with dust-providing nutrients. In order to recover the cultures of 'icy' microbes identified by sequence the attempt was done with Deinococci but we didn't succeed.

The full gene and partial gene sub-libraries of the MB5 sample showed different results with respect to observed phylotypes. For example, 'cold-loving' Cyanobacteria phylotypes were detected only in full gene library while one phylotype related to abundant Deinococcus sp was detected mostly by partial gene PCR approach. This provides extra evidence for microbes (Cyanobacteria spp.) which indeed can be living in snow that follows from their full-size gene sequences. When microbes are dead (DNA is degraded in snow with time like ancient DNA) someone has more possibility to be recovered by partial gene sequences.

Several phylotypes related to human (Streptococcus sanguinis, Acinetobacter johnsonii and Helcococcus sp.) and plants pathogens (Sphingomonas melonis, Pseudomonas sp) were detected in association with studied dust events. Based on these primary results another view concerning the microbial transport from Sahara desert to the terrestrial glacier can be drawn. The dust fallout could provide just nutrients than dominant microbial seeds while minor phylotypes can be brought from elsewhere.