

Mediterranean aerosol radiative forcing and influence of the single scattering albedo

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Measurements of aerosol optical properties and surface shortwave irradiance carried out during 2004-2007 are used to estimate the aerosol direct radiative forcing at the surface at Lampedusa (35.5° N, 12.6° E), a small island in the central Mediterranean. Three different particle types are identified on the basis of their optical properties [1]: desert dust (DD), urban/industrial-biomass burning (UI-BB), and mixed aerosols (MA). The direct method [2] is used to estimate the surface shortwave forcing efficiency (FE_S), i.e. the forcing produced by aerosols with unit optical depth, for values of solar zenith angle, θ , between 20° and 75°. The absolute value of FE_S decreases with θ for all the aerosol types and varies between -185 and -81.7 Wm^{-2} for DD, -168 and -84 Wm^{-2} for UI-BB, -251 and -120.2 Wm^{-2} for MA, -208 and -106.5 Wm^{-2} for the whole dataset.

The ground-based measurements are combined with estimates of the aerosol single scattering albedo, ω , at 415.6 and 868.7 nm, at $\theta=60^\circ$ [3]. The forcing efficiency at $\theta=60^\circ$ of DD, UI-BB, and MA is derived for three intervals of the single scattering albedo ($0.7 \leq \omega < 0.8$, $0.8 \leq \omega < 0.9$, $0.9 \leq \omega \leq 1$) at 415.6 and 868.7 nm. The absolute value of FE_S decreases for increasing ω at 868.7 nm for all the aerosol types, while decreases with increasing ω at 415.6 nm for UI-BB and MA and increases for DD.

[1] Pace *et al.* (2006) *Atmos. Chem. Phys.* **6**, 697-713.

[2] Satheesh & Ramanathan (2000) *Nature* **405**, 60-63.

[3] Meloni *et al.* (2006) *Atmos. Chem. Phys.* **6**, 715-727.

Community-wide analysis of microbial genome signatures

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Metagenomics holds great promise for elucidating the roles of microorganisms in driving geochemical cycles. A key goal is to identify organisms underpinning specific processes and to place the roles of individual organisms into the context of microbial community function. A prominent challenge inherent to random shotgun sequencing of DNA from natural samples is assignment of metagenomic fragments to particular microbial species.

Here we explore the extent to which genomic nucleotide composition can be exploited to infer the origins of fragmentary DNA sequences in a natural microbial community. We analyzed metagenomic sequences derived from biofilms inhabiting acid mine drainage (AMD) in the Richmond Mine at Iron Mountain, CA. The dataset included composite genomes reconstructed for nine archaea, three bacteria, and numerous associated viruses, as well as thousands of unassigned fragments from strain variants and low-abundance organisms. Through simultaneous analysis of nucleotide composition-based clustering and high coverage, manually-curated genomic assemblies, we find that the genomes of coexisting microbes are distinguished by signatures of nucleotide composition at approximately the species to genus level. Clusters were resolved because intra-genome differences in nucleotide composition were small relative to inter-genome differences. In addition, our analysis revealed previously unknown genomic clusters corresponding to low-abundance organisms which appear to be involved in important community functions such as sulfur oxidation. An important conclusion is that shared environmental pressures and interactions among coevolving organisms do not obscure 'genome signatures' of nucleotide composition. Thus, genome signatures can be used to assign sequence fragments to populations, an essential prerequisite if metagenomics is to provide insights into the geochemical functions of microbial communities.