

Comparison of airborne microbial variations in air samples from Asian-dust source and arrival regions

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Aerosol dust is emerging as a significant vehicle for long-range transport of microorganisms. Nonetheless, many factors relating to this highly influential dispersal mechanisms remain unresolved, including the variation in dispersal bacterial communities during stochastic desert dust events, and the effect of aerosol transit over continental and oceanic surfaces to these communities. Here we elucidated bacterial 16S rRNA gene and fungal ITS-defined changes in airborne microbial communities at Asian-dust source regions (Gobi) and arrival regions (Japan) both lying along the trajectory for dust-event transport. Aerosols collected in the both regions generally reflected local origin from freshwater, marine, plant, or animal sources. In particular, dust events in the Gobi Desert increased these microbial cells and mineral particles to more than ten folds of concentrations. After dust-events occurrences in desert areas, the spore-forming microorganisms (bacteria: Bacillaceae, fungi: Davidiellaceae) and organic-aggregating bacteria (Cytophagaceae) showed high relative abundances, suggesting the survival of some microbes against strict atmospheric stressors over desert. These stress-resistance microbial populations were frequently dominated during Asian-dust events over Japan, which are located across China industrial area and Japan Sea. Presumably, atmospheric stressors over desert transit over deserts, anthropogenic polluted areas and oceanic waters strongly select for airborne microbial populations through atmospheric stressors.

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