



TRANS-PACIFIC MICROBES RIDING THE EARTH'S JET STREAM: RESULTS FROM THE MT. BACHELOR OBSERVATORY



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ABSTRACT

Globally-dispersed airborne microorganisms are poorly understood. However, in spring 2011 at the Mt. Bachelor Observatory in North America (2.8 km above sea level), we captured sufficient microbial biomass in two transpacific air masses to permit a 16S ribosomal RNA microarray analysis. In each episode, we detected 2,800+ distinct microbial taxa. Transport across the Pacific Ocean from Asia was independently measured through meteorological/chemical data and microbial biogeography. Our results indicate that upper atmosphere winds can bridge microbial populations between distant continents. The presence, persistence and detectability of life in planetary atmospheres broadens the definition of habitable environments in the solar system (and beyond).



Annually, as much as 64 Tg of Asian aerosols are transported across the Pacific Ocean to North America [1].



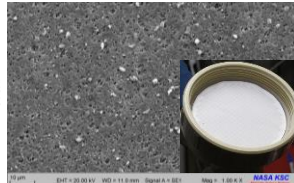
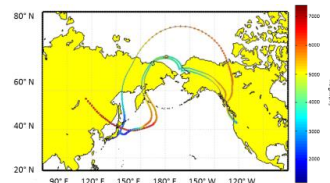
We collected samples from the Mt. Bachelor Observatory, a research station 2.8 km above sea level. In the springtime, windblown aerosols from Asia routinely reach the field site after crossing the Pacific Ocean in 7-10 days [2].

INTRODUCTION

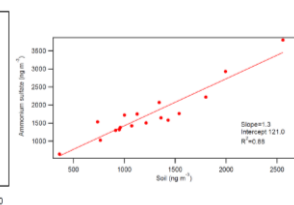
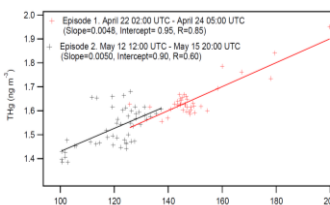
Lower troposphere air samples contain a substantial microbial component. Airborne microorganisms can spread genes to distant environments and even influence weather as cloud/ice condensation nuclei, but very little is known about microbial diversity and abundance at higher altitudes, where long-range atmospheric transport is more efficient. Mountaintop observatories can provide access to the upper troposphere [2] and lower stratosphere, making it feasible to capture enough biomass to employ modern molecular assays [1, 3].

METHODS

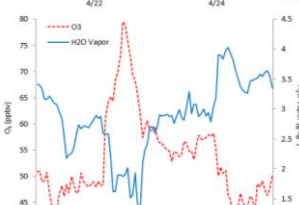
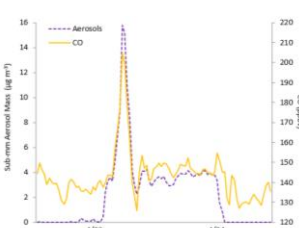
We collected samples from the Mt. Bachelor Observatory (MBO), a research station 2.8 km above sea level on the summit of an extinct volcano in central Oregon (43.98°N, 121.7°W). In the spring-time, windblown plumes of pollution, smoke, and dust from Asia routinely reach the field site after crossing the Pacific Ocean in 7 to 10 days [2]. Recently we described two major Asian long-range transport plumes with high concentrations of particulate matter (mostly dust, but also anthropogenic pollution) arriving at MBO [3]. Airborne bacterial concentrations were measured by qPCR, and rRNA sequencing was used to identify cultured species. Average bacterial genomes ranged from 1 to 4 m³ across the April episode and 2 to 7 m³ across the May episode, assuming that intact cells (containing 2 to 8 fg DNA) were captured. Several Gram-positive bacterial isolates were identified using culture-based recovery methods, but since so few species can actually be cultivated, we also examined the air samples with a more comprehensive molecular tool. Air samples (spanning 12-h intervals) from before, during, and after aerosol plume events were analyzed for microbial richness and abundance using a PhyloChip 16S rRNA microarray [1].



Polyethersulfone membrane filters used to collect atmospheric microorganisms [3].



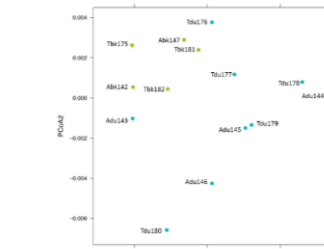
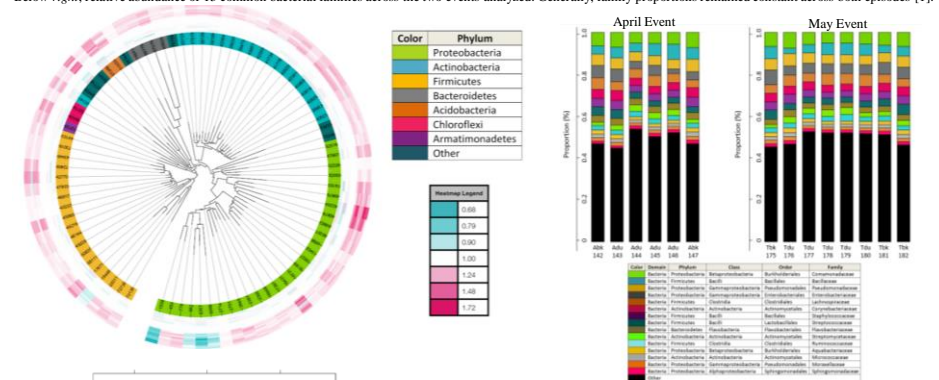
Enhancement ratios of total gaseous mercury (THg) and carbon monoxide (CO) during events was indicative of Asian long-range transport [1, 3]. Similarly, a high correlation coefficient between soil and NH₄SO₄ was observed, indicating the sampled air mass was aloft long enough (7-10 days) for thorough mixing [3].



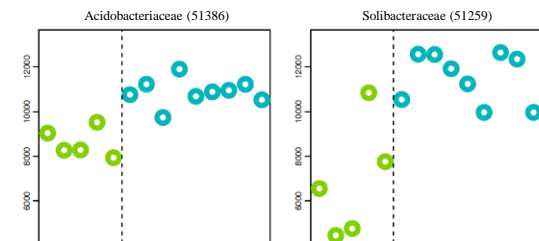
Common aerosols measured in April event to understand air mass transport history [3].

RESULTS

Below left, a circular tree (based on 16S rRNA gene alignment) displays taxonomic relationship of differentially abundant OTUs sampled during atmospheric plumes. Below right, relative abundance of 15 common bacterial families across the two events analyzed. Generally, family proportions remained constant across both episodes [1].



Principle coordinate analysis of background samples (green) and plume samples (blue). Partitioning shows similarity in taxa with air type (-du or -bk-), independent of plume timing (April or May). Adu143 and Tdu176 were transitional samples at plume onset.



PhyloChip HybScore plots depicting relative abundance changes across plume events. Only two atmospheric microbial taxa shown here but 2,800+ total OTUs were detected in each event [1].

CONCLUSIONS

We captured enough microbial biomass in two transpacific air plumes to permit a microarray analysis using 16S rRNA genes. Thousands of distinct bacterial taxa spanning a wide range of phyla and surface environments were detected before, during, and after each Asian long-range transport event. Interestingly, the transpacific plumes delivered higher concentrations of taxa already in the background air (particularly *Proteobacteria*, *Actinobacteria*, and *Firmicutes*). While some bacterial families and a few marine archaea appeared for the first and only time during the plumes, the microbial community compositions were similar, despite the unique transport histories of the air masses. Airborne microorganisms originate from the surface and must eventually return to it. Consequently, the atmosphere has generally been considered a conduit for life rather than a true ecosystem. However, our study revealed a microbial richness that rivals that of surface ecosystems and the presence of many phyla with adaptations for extended viability during atmospheric transport (e.g., spore-forming and Gram-positive bacteria). In addition, the potential for dynamic microbial interactions with the environment, such as *in situ* metabolism, the stimulation of cloud formation and precipitation, and selection pressures from UV radiation all justify further attention from the astrobiological community. The presence, persistence and detectability of life in planetary atmospheres broadens the definition of habitable environments in the solar system (and beyond). Whether atmospheric microbes can survive in the upper atmosphere of Venus or be detected through exoplanet atmospheric measurements is an area of emerging interest [4].

REFERENCES

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