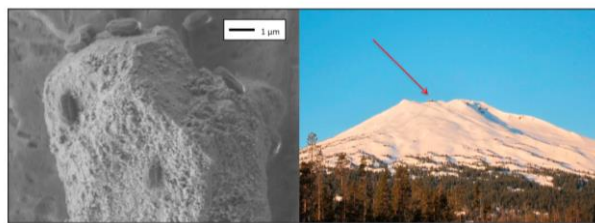


TRANSPACIFIC MICROBES RIDING THE EARTH'S JET STREAM: RESULTS FROM THE MT. BACHELOR OBSERVATORY. D. J. Smith¹, D. A. Jaffe², D. W. Griffin³, M. N. Birmele⁴, H. J. Timonen², A. C. Schuerger⁵, J. Hee², and M. S. Roberts⁶, ¹NASA Ames Research Center, Space Biosciences Division, david.j.smith-3@nasa.gov, ²University of Washington, Science and Technology Program, djaffe@uw.edu, ³U.S. Geological Survey, dgriffin@usgs.gov, ⁴NASA Kennedy Space Center, Sierra Lobo, michele.n.birmele@nasa.gov, ⁵University of Florida, schuerg@ufl.edu, ⁶Center for the Advancement of Science in Space, michael.s.roberts@nasa.gov.

Introduction: Air samples from the lower troposphere contain a substantial microbial component that originates from a variety of marine/terrestrial sources. Airborne cells 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 (i.e., global dispersal) is more efficient. Mountaintop observatories can provide access to the upper troposphere and lower stratosphere, making it feasible to capture enough biomass to employ modern molecular assays [1].



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 springtime, 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 [3], we described two major Asian long-range transport plumes with high concentrations of particulate matter (mostly dust, but also anthropogenic pollution) arriving at MBO. Airborne bacterial concentrations were measured by quantitative PCR, and rRNA sequencing was used to identify cultured species. Average bacterial genomes ranged from 1 to 4 m⁻³ across the April episode and 2 to 7 m⁻³ 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, our goal was to reexamine the air samples with a more comprehensive molecular tool testing the hypothesis that transpacific plumes deliver rich microbial populations to North America.

Microbes were collected on sterile polyethersulfone filters (pore size, 0.8 µm) connected to an air-sampling device at MBO [3]. Briefly, a high-volume pump

pulled ~0.5 m³ min⁻¹ of air through individual filters over 12-h intervals, and then samples were removed from the device and stored at -80°C. During sampling periods, meteorological and atmospheric chemistry data were collected for aerosol elemental composition (e.g., ammonium sulfate [NH₄SO₄], soil, and trace metals), carbon monoxide (CO), ozone (O₃), water (H₂O) vapor, total gaseous mercury (THg), temperature, atmospheric pressure, wind speed, and direction.

Results and Conclusions: In spring 2011 at MBO, 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 support the idea that the atmosphere might be considered an ecosystem in its own right [4]. The presence, persistence and detectability of life in planetary atmospheres broadens the scope for the search for life in the solar system (and beyond).

References:[1] D. J. Smith et al. (2013) *AEM*, 79, 1134–1139. [2] Weiss-Penzias et al. (2006) *J. Geophys. Res.*, 111, D10304. [3] D. J. Smith et al. (2012) *Microb. Ecol.*, 64, 973–985. [4] D. J. Smith (2013) *Astrobiology*, 13, 981–990.