

能登半島上空へと長距離輸送される大気バイオエアロゾル ～北極域および中国乾燥地帯～

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Phylogenetic analysis of bacterial communities included in free tropospheric bioaerosol transported from Chinese desert and North Asia

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Long-range transport of airborne microorganisms through the troposphere plays an important role in microbial dispersal and has significant impacts on biological ecosystems, human life, and atmospheric processes in downwind areas. However, microbial communities in the troposphere have rarely been investigated because the direct collection of microbial cells at high altitude requires sophisticated sampling techniques. In this study, air sampling using an aircraft was performed over the Noto Peninsula in Japan, where the tropospheric winds carry aerosol particles from continental areas. Air samples were collected at 800m and 3000 m at four sampling dates during which air masses originated from the Gobi Desert and the North Asia (eastern Siberia and Hokkaido) and wind directions were from the west (west air samples) and north (north air samples), respectively. The west air samples had higher levels of aerosol particles, and microorganisms from the sample grew in culture media containing up to 15% NaCl, whereas the north air sample showed no microbial growth in the same media. All isolates obtained from the NaCl-amended cultures were identical to *Bacillus subtilis*. The 16S rDNA clone library of west air samples was mainly composed of one phylotype of *B. subtilis* in Firmicutes and Bacteroidetes with the sequences of Firmicutes phylotype corresponding to that of the cultured *B. subtilis* sequence. The clone library of north air samples consisted primarily of two phyla, Actinobacteria and Proteobacteria, which are known to dominantly inhabit low temperature environments of North Asia. Presumably, tropospheric wind direction contributes to the dynamics of airborne bacterial communities at high altitudes.

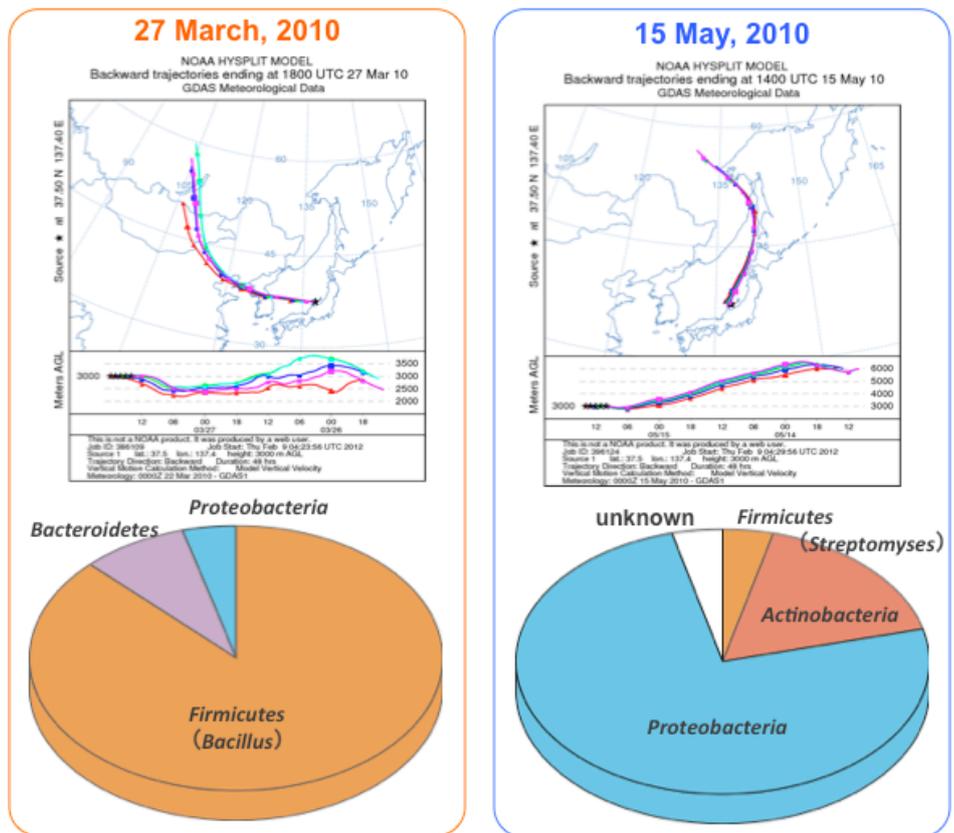


Figure 1. Upper figures indicate three-day backward trajectories of aerosols that arrived Suzu City on March 27th, 2010 and May 15th, 2010. Down figures indicated bacterial composition analyzed using the partial sequences of 16S rDNA amplicons that were obtained from the clone libraries of each air sample

References

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