

## Publication

## Gone with the Wind: Microbial Communities Associated with Dust from Emissive Farmlands

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Dust is a major vehicle for the dispersal of microorganisms across the globe. While much attention has been focused on microbial dispersal in dust plumes from major natural dust sources, very little is known about the fractionation processes that select for the "dust microbiome." The recent identification of highly emissive, agricultural land dust sources in South Africa has provided the opportunity to study the displacement of microbial communities through dust generation and transport. In this study, we aimed to document the microbial communities that are carried in the dust from one of South Africa's most emissive locations, and to investigate the selective factors that control the partitioning of microbial communities from soil to dust. For this purpose, dust samples were generated at different emission sources using a Portable In-Situ Wind Erosion Lab (PI-SWERL), and the taxonomic composition of the resulting microbiomes was compared with the source soils. Dust emission processes resulted in the clear fractionation of the soil bacterial community, where dust samples were significantly enriched in spore-forming taxa. Conversely, little fractionation was observed in the soil fungal communities, such that the dust fungal fingerprint could be used to identify the source soil. Dust microbiomes were also found to vary according to the emission source, suggesting that land use significantly affected the structure and fractionation of microbial communities transported in dust plumes. In addition, several potential biological allergens of fungal origin were detected in the dust microbiomes, highlighting the potential detrimental effects of dust plumes emitted in South Africa. This study represents the first description of the fractionation of microbial taxa occurring at the source of dust plumes and provides a direct link between land use and its impact on the dust microbiome.

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