

# **Characterization of airborne microbial aerosols during a long-range transported dust event in Eastern China: bacterial community, influencing factors, and potential health effects**

**Ying Rao<sup>1,2,3#</sup>, Heyang Li<sup>2,4#</sup>, Mingxia Chen<sup>5</sup>, Qingyan Fu<sup>6</sup>, Guoshun Zhuang<sup>1\*</sup>, Kan Huang<sup>1,7,8\*</sup>**

<sup>1</sup>Center for Atmospheric Chemistry Study, Shanghai Key Laboratory of Atmospheric Particle Pollution and Prevention (LAP<sup>3</sup>), Department of Environmental Science and Engineering, Fudan University, Shanghai, 200433, China

<sup>2</sup>Third Institute of Oceanography, Ministry of Natural Resources, Xiamen 361005, China

<sup>3</sup>Health Center of Minnan Normal University, Zhangzhou 363000, China

<sup>4</sup>Fujian Provincial Key Laboratory of Marine Ecological Conservation and Restoration, Xiamen 361005, China

<sup>5</sup>Department of Biological technology and Engineering, HuaQiao University, Xiamen 361021, China

<sup>6</sup>Shanghai Environmental Monitoring Center, Shanghai, 200030, China

<sup>7</sup> Institute of Eco-Chongming (IEC), Shanghai 202162, China

<sup>8</sup>Institute of Atmospheric Sciences, Fudan University, Shanghai 200433, China

#Co-first author

\*Corresponding author

E-mail: huangkan@fudan.edu.cn; gzhuang@fudan.edu.cn

Table S1. The bacteria that exhibited significant differences among the three groups at the genus level

<b>Genus name</b>	<b>Grouop1</b> <b>Mean±Sd(%)</b>	<b>Group2</b> <b>Mean±Sd(%)</b>	<b>Group 3</b> <b>Mean±Sd(%)</b>	<b>Pvalue</b>
Moraxella	0.001±0.002	0.013±0.004	0.048±0.032	<0.05
Pedobacter	0.133±0.016	0.227±0.023	0.346±0.098	<0.05
Methylorosula	0.013±0.001	0.028±0.006	0.092±0.058	<0.05
Nitrosomonas	0.010±0.005	0.032±0.008	0.085±0.043	<0.05
Microvirga	0.415±0.126	0.824±0.147	0.541±0.001	<0.05
Rubrobacter	0.468± 0.032	0.625±0.066	0.317±0.017	<0.05
Nostoc	0.056±0.035	0.471±0.050	0.018±0.003	<0.05
Gemmatimonadaceae	0.160±0.015	0.258±0.031	0.113± 0.005	<0.05
SubsectionIII	0.104±0.033	0.329±0.119	0.036±0.015	<0.05
CL500-29_marine_group	0.019±0.015	0.139±0.036	0.079±0.021	<0.05
Cystobacteraceae	0.016±0.009	0.155±0.126	0	<0.05
Actinobacteria	0.009±0.005	0.147±0.057	0	<0.05
Xanthobacteraceae	0.013±0.006	0.117±0.070	0.004±0.006	<0.05
Illumatobacter	0.019±0.008	0.086±0.047	0	<0.05
DA101_soil_group	0	0.071±0.061	0	<0.05
Psychrobacter	0.790±0.119	0.480±0.083	1.783±0.160	<0.05
Acetobacteraceae	0.236±0.049	0.123±0.010	0.164±0.033	<0.05
Limnobacter	2.955±1.075	1.546±0.421	1.999±0.256	<0.05
Bryocella	0.037±0.040	0.009± 0	0	<0.05
P-102	0.033±0.013	0.006±0.002	0	<0.05
WCHB1-69	0.008± 0.002	0	0	<0.05
Oceanisphaera	0.005± 0.002	0	0	<0.05