



High-throughput sequencing analysis of the bacteria in the dust storm which passed over Canberra, Australia on 22-23 September 2009

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Following a prolonged drought in Australia in the first decade of the 21st century, several dust storms affected the heavily populated East coast of Australia. The largest such storm occurred on 22-23 September 2009 and had a front of an estimated 3000km. A 24hr average PM10 concentration of over $2,000\mu\text{g}/\text{m}^3$ was recorded in several locations and an hourly peak of over $15,000\mu\text{g}/\text{m}^3$ was recorded (Leys et al. 2011).

Over two time periods duplicate aerosol samples were collected on 47mm diameter cellulose nitrate membranes at a location removed from anthropogenic influences. One set of samples was collected in the afternoon the dust event started and another was collected overnight. Additionally, overnight rainfall was collected in a sterile bottle. DNA was directly extracted one membrane from each time point for molecular cloning and high throughput sequencing, while the other was cultivated on Tryptic Soy Agar (TSA).

High throughput sequencing was performed using the 454 Titanium platform. From the three samples, 19,945 curated sequences were obtained representing 942 OTUS, with the three samples approximately equal in number. Unclassified Rhizobiales and *Stenotrophomonas* were the most abundant groups which could be attributed names. A total of 942 OTUs were identified (cutoff = 0.03), and despite the temporal relation of the samples, only eleven were found in all three samples, indicating that the dust storm evolved in composition as it passed over the region. Approximately 800 and 500 CFU/m³ were found in the two cultivated samples, tenfold more than was collected from previous dust events (Lim et al, 2011). Identification of cultivars revealed a dominance of the gram positive Firmicutes phylum, while the clone library showed a more even distribution of taxa, with Actinobacteria the most common and Firmicutes comprising less than 10% of sequences.

Collectively, the analyses indicate that the concentration of cultivable organisms during the dust storm dramatically relative to calm conditions. A diverse and variable population of microorganisms were present reflecting the vast source and dynamic nature of the storm.