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Tropical Air Microbiome Analysis Reveals Daily Cycle, Environmental Drivers

Oct 25, 2019 | [staff reporter](#)

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NEW YORK – A team from Singapore and Brazil has started characterizing the microbial genes and representatives in air samples collected over time from a tropical environment in Singapore, identifying day-to-night swings in microbiome diversity and content.

"[T]he majority of the dynamics in taxa composition occur within [24 hours], but not across days, weeks, or months," first author Elena Gusareva, a post-doctoral researcher at the Nanyang Technological University's Singapore Centre for Environmental Life Sciences Engineering, and her colleagues wrote in their *Proceedings of the National Academy of Sciences* paper, noting that "[e]nvironmental parameters are the main drivers for the observed phenomenon, with temperature being the most important one."

The researchers used metagenomic sequencing to assess nearly 800 samples collected every two hours over almost a week at three-month intervals for more than a year at a tropical site in Singapore. Along with relatively high fungal representation in the air samples, they uncovered reproducible cycles in communities, with microbial diversity reaching a peak during the day and bacterial abundance apparently declining at night.

With deep metagenomic sequencing, the researchers assessed the microbial representatives and gene collections present in 795 samples collected at an outdoor site during the sampling period, representing a dozen samples each day for five-day cycles spread three months apart. Over this period, they noted, the sampling site went through two monsoon seasons as well as dry seasons.

Using some 330 million reads generated from these samples, the team identified a core set of 725 microbial species that turned up consistently over time, though only a fraction of the metagenomic sequences — between 9 and 17 percent — were successfully matched up with known microbial taxa.

Overall, the air microbiome showed pronounced microbial diversity, particularly during the day, and contained a large number of fungal representatives, the researchers reported. More than 80 percent of the reads in the samples corresponded to fungal representatives, for example, while almost 15 percent appeared to come from bacteria. Archaea were represented by less than 0.1 percent of reads, while 2.6 percent of reads seemed to stem from plant species. Even after adjusting for the relatively large size of the fungal genomes, the team estimated that an average of almost 38 percent of cells in the samples came from fungi.

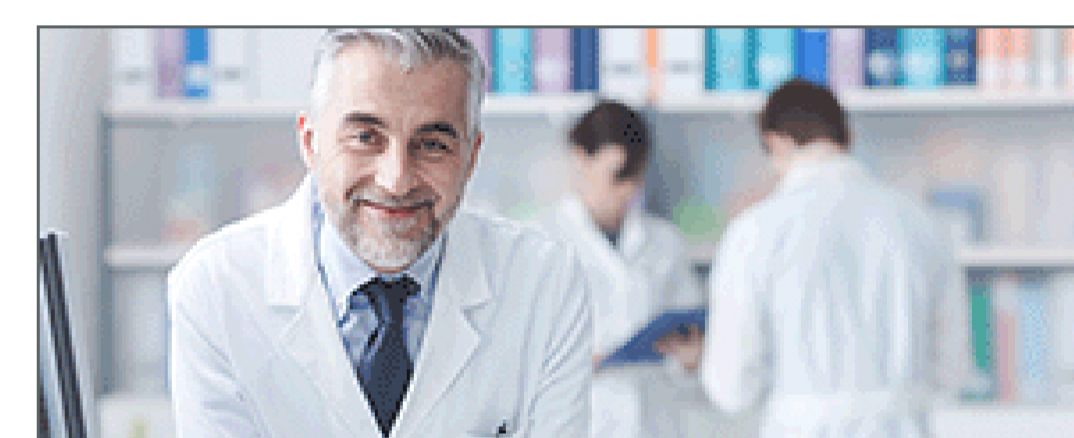
"Unlike terrestrial or aquatics, where prokaryotes are prevalent, the tropical airborne biomass was dominated by DNA from eukaryotic phyla," the authors reported. "Specific fungal and bacterial species were strongly correlated with temperature, humidity, and [carbon dioxide] concentration, making them suitable biomarkers for studying the bioaerosol dynamics of the atmosphere."

By comparing the air microbiomes with those described previously in microbial communities in soil and water samples, though, the team did see some consistent themes, including apparent driver roles for environmental factors in the rise and fall of various microbial representatives in the microbiomes and the interactions between them.

Moreover, the authors suggested that the same experimental and analytical strategies outlined in the study "will inform future environmental surveys that will investigate the spatial dynamics and natural variability of airborne microbial communities."

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