

SINGAPORE ON THE GLOBAL MICROBIAL MAP



MetaSUB: the metagenomics and metadesign of the subways and urban biomes

A team of scientists from Singapore, led by Prof Niranjan Nagarajan at the Genome Institute of Singapore (GIS), has collaborated with the international MetaSUB consortium to build a global atlas of micro-organisms living in urban environments. This work was conducted over three years in 60 cities, with more than 4,700 samples analysed to create a geospatial microbial profile of cities – including >10,000 viruses and >1,000 bacteria that have not been described before. The study was published on 26 May in the journal *Cell*.



The team of scientists from GIS

In addition to shining unprecedented new light on global microbial diversity, the MetaSUB study showed that each city has its own unique microbial fingerprint, allowing samples associated with it to be identified with nearly 90% accuracy on average. Each cities' uniquely endemic microbes are a biodiversity resource that can be associated with its geographical location, elevation, average temperature, and other environmental characteristics.

For example, the key endemic microbes in Singapore include species such as (1) *Haloterrigena daqingensis*, an extremely saline-alkaline tolerant soil archaeon identified in Asia, (2) *Desulfovibrio magneticus*, a bacteria with magnetite crystals that can orient itself to Earth's magnetic field, (3) *Oceanimonas* sp. GK1, a salt-tolerant bacteria that can produce poly-hydroxybutyrate, a biodegradable polymer for use in medicine and packaging, (4) *Burkholderia seminalis*, a plant endophyte bacteria that produces antimicrobials against many pathogenic bacteria and fungi under drought conditions, (5) *Synechococcus* phage S-PM2, a virus that infects photosynthetic bacteria and can increase their light-harvesting capacity, (6) *Mesorhizobium* sp. WSM1497, a nitrogen-fixing endosymbiont of legumes, (7) *Halothiobacillus* sp. LS2, an important organism in global carbon and sulphur cycles because of its ability to depend entirely on inorganic compounds for its energy needs, (8) *Actinobacteria* bacterium IMCC19121, an important constituent of freshwater communities, and (9) *Klebsiella quasipneumoniae*, a recently described species that causes bloodstream infections.

Other notable observations from Singapore include a relatively moderate diversity of antimicrobial resistance genes compared to other cities, and limited viral diversity and exchange compared to other travel hubs in the world. The MetaSUB consortium continues to build on these and other observations in refining the global microbial map, with the upcoming global city sampling day on 21 June (<http://metasub.org/projects/gcsd>).