Metagenomic Analysis of Toilet Waste from Three Different Income Areas in Bangkok, Thailand



Burden of disease index



Model for surveillance system

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Infectious

disease, AMR

Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance

Metagenomic analysis of viruses in toilet waste from long distance flights—A new procedure for global infectious disease surveillance

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viruses

-South Asia having significantly higher viral species richness as well as higher abundances of Salivirus A, Aichivirus A and Enterovirus B, compared to samples originating from North Asia and North America

-high numbers of Rotaviruses in airplanes departing from Islamabad

9 countries, 18 long-distance flights Article | Open Access | Published: 08 March 2019

Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage

Rene S. Hendriksen, Patrick Munk, Patrick Niage, Bram van Bunnik, Luke McNally, Oksana Lukjancenko Timo Röder, David Nieuwenhuijse, Susanne Karlsmose Pedersen, Jette Kieldgaard Thomas Lanken Conradsen Clausen, Josef Korbinian Vogt, Pimlapas Leekitcharoen de Schans, Tina Zuidema, Ana Maria de Roda Husman, Simon Rasmussen, Sewage Surveillance project consortium, Clara Amid, Guy Cochrane, Thomas Sicheritz-Ponten, Heike Schmitt, ... Frank M. Aarestrup 🗠 (+ Show authors

Nature Communications 10, Article number: 1124 (2019) Cite this article 59k Accesses | 320 Citations | 432 Altmetric | Metrics



aircrafts' septic tanks

AMR gene abundance strongly correlates with socio-economic, health and environmental factors, which we use to predict AMR gene abundances in all countries in the world

https://www.nature.com/articles/s41467-019-08853-3 https://www.quora.com/Can-commercial-planes-dump-their-toilet-waste-in-the-sea

-S. enterica and Norovirus were also detected in higher amounts from South Asia.

-C. difficile was most abundant in samples from North America.

https://www.nature.com/articles/srep11444

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6331095/

Factors affecting biological agents in wastewater

<u>Adv Appl Microbiol</u>, 2008; 65: 249–269. Published online 2008 Nov 20. doi: <u>10.1016/S0065-2164(08)00609-6</u> PMCID: PMC7112011 PMID: <u>19026868</u>

Pathogen Surveillance Through Monitoring of Sewer Systems

Ryan G. Sinclair,*1 Christopher Y. Choi,† Mark R. Riley,† and Charles P. Gerba*

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Factors that affect concentration of the biological agent in sewage

Site of replication in the host GI, upper respiratory, nose, skin, internal organs

Duration of release from the host

Concentration in the source

Incidence of disease in the population

Water use per capita

Season

Survival in the sewer system

Summary concept



Public Health Support



Public health action

early warning decisions / mitigation strategies / policy healthcare infrastructure

More data over time, more reliable Networking

Objective

• To investigate and compare the abundance and diversity of bacteria and antimicrobial resistance (AMR) from toilet wastes of three different income areas in Bangkok.



Site selection

collects toilet waste from 3 different income areas

Low income (L) (< 10,000 THB / monthly / household) More diversity pop. effect; commuting merchant, worker Middle income (M) (Low middle & Upper middle income) More diversity pop. effect

High income (H) Less diversity pop. effect



Sampling sites





Laboratory works : data analysis and visualization



Genomic_QC



1_Phylum

49 phyla





948 mapped ARG genes



FPKM (Fragments Per Kilobase of Million reads) is a unit commonly used to quantify (estimate) the levels of genes (abundance) in a microbial community.

2_ResFinder (cont.)

948 mapped ARG genes

"erm.F._3_M17808", "sul2_2_AY034138", "tet.Q._1_L33696", "sul1_9_AY963803", "tet.C._2_AY046276", "tet.W._5_AJ427422", "tet.36._1_AJ514254"



income



4575 mapped ID







4_Virulence factors

1013 mapped protein functions



4_Virulence factors (cont.)

Virulence_proteinfunction_FPKM



"heat.shock.survival.AAA.family.ATPase.ClpK..thermal.stress.survival",
"Unknown.protein.function",
"Tellurium.ion.resistance.protein",
"Microcin.C",
"Colicin.E1",

Virulence_protein_function

$heat. shock. survival. {\sf AAA. family. ATP ase. Clp K thermal. stress. survival the stress survival stress survival stress survival stress survival stress stre$	
Unknown.protein.function	
Tellurium.ion.resistance.protein	
Microcin.C	
Colicin.E1	
Ferric.aerobactin.receptor	
Glutamate.decarboxylase	
Outer.membrane.protein.complement.resistance	
Bacteriocin.microcin.B17	
enterotoxin.N	
Enterobactin.siderophore.receptor.protein	
Type.1.fimbriae	
${\it High.molecular.weight.protein. 2. non.ribosomal.peptide.synthetase}$	
Avian.Ecoli.haemolysin	
Siderophore.receptor	

type.3.fimbrial.major.subunit

Enteroaggregative.immunoglobulin.repeat.protein Outer.membrane.lipoprotein.YHD.fimbriael.cluster lipoprotein.Nlpl.precursor Chaperone.YHD.fimbriael.cluster AraC.negative.regulator serine.protease.autotransporters.of.Enterobacteriaceae..SPATE. Major.pilin.subunit.YHD.fimbriael.cluster Protein.TraJ..Positive.regulator.of.conjugal.transfer.operon. leukocidin.D.component enterotoxin.I intimin.like.adhesin.FdeC Usher.YHD.fimbriael.cluster Aerobactin.synthetase Outer.membrane.protease..protein.protease.7. Others

Summary

- AMR genes : abundance 4 in high-income population
- Virulence factors : abundance 🐥 in high-income population

















