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

Human populations worldwide are increasingly confronted with infectious diseases and antimicrobial resistance spreading faster and appearing more frequently. Knowledge regarding their occurrence and worldwide transmission is important to control outbreaks and prevent epidemics. Here, we performed shotgun sequencing of toilet waste from 18 international airplanes arriving in Copenhagen, Denmark, from nine cities in three world regions. An average of 18.6 Gb (14.8 to 25.7 Gb) of raw Illumina paired end sequence data was generated, cleaned, trimmed and mapped against reference sequence databases for bacteria and antimicrobial resistance genes. An average of 106,839 (0.06%) reads were assigned to resistance genes with genes encoding resistance to tetracycline, macrolide and beta-lactam resistance genes as the most abundant in all samples. We found significantly higher abundance and diversity of genes encoding antimicrobial resistance, including critical important resistance (e.g. bla<sup>CTX-M</sup>) carried on airplanes from South Asia compared to North America. Presence of Salmonella enterica and norovirus were also detected in higher amounts from South Asia, whereas Clostridium difficile was most abundant in samples from North America. Our study provides a first step towards a potential novel strategy for global surveillance enabling simultaneous detection of multiple human health threatening genetic elements, infectious agents and resistance genes.

General information
Publication status: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, Metagenomics, National Food Institute, Research group for Genomic Epidemiology, Research Group for Diagnostic Engineering
Number of pages: 9
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Scientific Reports
Volume: 5
Article number: 11444
ISSN (Print): 2045-2322
Ratings:
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.3 SJR 2.034 SNIP 1.589
Web of Science (2015): Impact factor 5.228
Web of Science (2015): Indexed yes
Original language: English
Keywords: Genome informatics, Microbial ecology, Infectious-disease diagnostics, Infectious diseases
Electronic versions:
srep11444.pdf
DOIs:
10.1038/srep11444
Source: FindIt
Source-ID: 275553958
Research output: Contribution to journal › Journal article – Annual report year: 2015 › Research › peer-review