

Toilet waste provides knowledge about diseases' global transmission routes

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Analysis and genome sequencing of disease-causing microorganisms and antimicrobial resistance bacteria in toilet waste from international aircraft could be a first step towards global surveillance of infectious diseases and identification of how they are transmitted between countries. The analysis was conducted by researchers from the National Food Institute, Technical University of Denmark, and DTU Systems Biology and is published in the scientific journal *Scientific Reports*.

Globally, [infectious diseases](#) account for approximately 22% of all deaths and experts expect this figure will increase over the coming years. In addition to the serious consequences to those who fall ill, infectious diseases put huge pressure on health care spending and they can trigger restrictions on the trade of goods and on the way people travel around the world.

Current international disease surveillance systems are mainly based on reports made by doctors after treatment of infected patients. As a consequence, disease-causing microorganisms and resistance bacteria have time to spread and make large population groups sick before they are detected.

There is currently only very limited information about the global occurrence and transfer of antimicrobial resistance and infectious diseases.

Researchers at the National Food Institute and DTU Systems Biology are working to develop faster methods to detect and respond to outbreaks of disease globally by using genome technology, which allows for a disease-causing microorganism's entire DNA profile to be mapped out at one time. The researchers are also working to establish an international platform that will allow for the exchange of data generated.

Important knowledge in aircrafts' septic tanks

International aircraft are known as important transmission routes for infectious diseases. Consequently, the researchers used genome technology to analyze toilet waste from 18 aircraft that arrived at Copenhagen Airport from nine destinations in South and North Asia as well as North America.

The toilet waste was analyzed for all known [antimicrobial resistance](#)

genes as well as a number of disease-causing microorganisms.

"According to forecasts, almost one and a half billion people will travel internationally by plane in 2016. Our work has shown that there is great potential in making airports sites where we can quickly collect data on [resistance genes](#) and certain microorganisms ," Professor Frank Møller Aarestrup from the National Food Institute explains.

The researchers analyzed the total DNA that was purified from the toilet waste using the latest sequencing technology and big data analysis.

"DTU is one of the world's leading research centers in the field of bioinformatics, and at DTU Systems Biology we have one of the world's largest computers dedicated to life science. This study shows that in the long run we can combine the collection of biological samples with total sequencing and fast data analysis while at the same time monitoring all known and perhaps unknown organisms rather than looking for one organism at a time as we have done until now," Professor Thomas Sicheritz-Pontén from DTU Systems Biology explains.

Differences between continents

Tetracycline-, macrolide- and beta-lactam-resistance genes were the most abundant in all samples.

Analysis also showed geographical differences. As such, there was a greater variation in the resistance genes in the samples from South Asia, North Asia and all the samples from Asia combined compared with samples from North America. When it comes to the microorganisms, there were fewer *Clostridium difficile* bacteria in samples from South Asia than from both North Asia and North America, while the incidence of *Salmonella enterica* was greatest in samples from South Asia.

More information: Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance, *Scientific Reports* 5, Article number: 11444 (2015) [DOI: 10.1038/srep11444](https://doi.org/10.1038/srep11444)

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