



Permissiveness of Microbial Community from Wastewater Treatment Plant towards IncP-1 Plasmid

Li, Liguang; Dechesne, Arnaud; Smets, Barth F.; Madsen, Jonas Stenlørkke; Sørensen, Søren J.

Publication date:
2017

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):

Li, L., Dechesne, A., Smets, B. F., Madsen, J. S., & Sørensen, S. J. (2017). *Permissiveness of Microbial Community from Wastewater Treatment Plant towards IncP-1 Plasmid*.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Permissiveness of Microbial Community from Wastewater Treatment Plant towards IncP-1 Plasmid

Liguan Li¹, Arnaud Dechesne¹, Barth F. Smets^{1,*}, Jonas Stenløkke Madsen², Søren J. Sørensen²

¹Department of Environmental Engineering, Technical University of Denmark, Denmark

²Department of Biology, University of Copenhagen

[*bfsm@env.dtu.dk](mailto:bfsm@env.dtu.dk)

Abstract

Horizontal gene transfer (HGT), especially conjugal plasmid transfer, is one of the key drivers in global antibiotic resistance transmission. To predict the fate of antibiotic resistance gene (ARG), the transfer and host range of ARG carrying plasmids in relevant microbial communities needs to be understood. Wastewater treatment plants (WWTPs) are a potential conduit of ARG transfer between human intestinal and environmental bacteria, and WWTPs are being examined as potential hot spot of antibiotic resistance dissemination. In this study, a comprehensive assessment of antibiotic resistance transmission was performed in activated sludge (AS) of WWTP. Utilizing the well-established fluorescent reporter system, plasmid permissiveness in AS microbial communities were evaluated by transfer frequency using microscopic image analysis and by host range identification through combining flow-cytometry sorting and 16S rRNA gene amplicon sequencing. Under mimic sewer conditions (e.g., synthetic wastewater as growth medium), we challenged the sampled AS communities (Danish WWTP Mølleaværket, Lyngby-Taarbæk) with model plasmids from three subclades in IncP-1 compatibility group (pKJK5 (ϵ), pB10 (β -1) and RP4 (α)) which were harbored by two different host strains - *Escherichia coli* MG1655 and *Pseudomonas putida* KT2440. The results showed that different donor-plasmid combinations had distinct transfer frequencies in the AS microbial communities, ranging from 3.39×10^{-5} to 5.05×10^{-4} T/R (transconjugant/recipient) (0.3 to 5 T per 10,000 R), with the most efficient transfer realized in *E. coli* (pKJK5). Unexpected broad host range across plasmid-host pairs was revealed in phylogenetic profile of transconjugant communities with total 308 exact sequence variants distributed over 13 phyla, including major group *Proteobacteria* (mainly by *Enterobacteriales* and *Pseudomonadales* in *Gammaproteobacteria*) and a few rare phyla in Gram-positive groups (e.g., *Actinobacteria* and *Firmicutes*), indicating that 'long-distance' transfer across phylogenies and Gram-positive/negative might be frequent under environmental conditions.