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EBNet
Environmental Biotechnology

18th International Symposium on Microbial Ecology (ISME), Lausanne, 14-19 August 2022

Ecological modelling of microbial communities in engineering systems: microbial immigration and functional trait-defined heterotrophic guilds
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(& Co-author for oral presentation: ‘Revealing the complex dynamics of antimicrobial resistance genes immigrating from sewers to activated sludge’)

POSTER ABSTRACT

Ecological modelling of microbial communities in engineering systems: microbial immigration and functional trait-defined heterotrophic guilds

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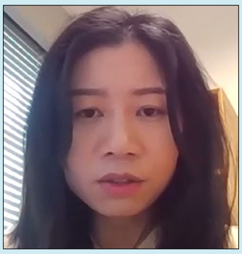

Abstract

Activated sludge is one of the most widely applied biological engineering systems worldwide. The microbial communities in activated sludge are selected by controlling engineering process parameters for organic degradation and nutrient removal functions, but the selection mechanisms and intervention from external factors are not well understood. Here we aim to develop quantitative ecological models and evaluate two types of ecological phenomena: microbial immigration, and functional guilds of heterotrophs. Both are commonly observed but poorly explained in engineering systems.

Firstly, we present a quantitative model to evaluate mass-flow microbial immigration to engineering systems using process parameters and microbial community data. Each species’ growth rate and immigration rate can be estimated from the model. It predicted that zero- or negative-growth-rate heterotrophs still contributed to the substrate consumption at considerable percentages. Secondly, based on the heterotrophic-specialist model, we differentiated trophic (readily and slowly degradable substrates) heterotrophic guilds. Using biomarkers RNA and storage compound polyhydroxyalkanoates which were tested prior across nine full-scale systems, flow cytometry cell sorting and amplicon sequencing were used to reveal the compositions and genetic functional traits (e.g. *rrn* copy number) of different heterotrophic guilds. This model predicts heterotrophic substrate-guild-trait links at finer resolutions.

Putting together the two models, the link between microbial immigration and heterotrophic functional guilds was revealed and new hypotheses were generated. Microbial immigration carries fast growers to activated sludge which may affect our fundamental understanding of community growth and functions. These models will be helpful to improve engineering system design and modelling and are applicable to natural systems.

Use the QR code to view Bing’s video on her poster presentation.