Title: Low functional redundancy in stochastically assembled bacterial communities

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Stochastic community assembly (*e.g.,* random dispersal, ecological drift) is recognized to play a role in the taxonomic composition of microbial communities, however, its effects on the functional properties of communities have often been overlooked. Indeed, functional redundancy, *i.e.* the ability for different taxa to perform similar functions, uncouples taxonomic composition from functioning, thus, communities with different taxonomic structure can still be functionnally equivalent, alleviating the impacts of stochastic assembly on community functioning. We tested the effects of stochastic assembly on the functional gene composition of lake water bacterial communities grown at identical environmental conditions. Using a genome-centric metagenomic approach, we investigated whether (i) taxa dispersal limitation resulted in "functional dispersal limitation", (ii) we could predict the functional properties (*i.e.,* consumption of glucose and cellobiose) from the functional gene repertoire and (iii) assembly mechanisms could be elucidated from gene distribution. "Functional dispersal limitation" was not the cause of the lack of consumption of cellobiose in some of the communities, and we could not predict the functional properties from the functional gene repertoire. However, stochastic assembly was reflected in the gene distribution and comparing different functional categories, we observed a remarkable consistency across scales of diversity (α, β and γ) showing higher dissimilarity among genomes in genes related to the interaction with the environment than in genes tied to basic functions like DNA replication. This diversity pattern was persistent when analysing 28 000 bacterial genomes randomly sampled from the Genome Taxonomy Database (GTDB), exposing a global pattern across bacterial functional genes.