TITLE: MOBILOME OF MANGROVE SEDIMENTS

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Mangroves are important coastal ecosystems found in transition zones between marine and freshwater ecosystems showing characteristics of both of them. This biome is an interesting model ecosystem for studying microbial stress tolerance and adaptive mechanisms. An important but still poorly comprehended mechanism associated with adaptation of microorganisms is horizontal gene transfer (HGT), mediated mainly by plasmid exchanges. Overall, methodologies that access the structure and function of microbial groups in mangroves and the descriptions of the plasmids that host genes related to major changes in this system are important tools to enhance the knowledge on adaptations as drivers of processes in this diverse environment. This study aims to properly describe the mobilome found on mangrove sediments, combining sequence-based analyses with advanced triparental conjugative transfer experiments. The frequency of plasmid transfer was higher on oil-contaminated mangrove sediments when compared with pristine mangrove. The promA plasmids group was the prevalent on mangrove samples, and its abundance was constant between samples. IncP-1, Incp-W and Incp-Q plasmids groups were not detect on mangrove sediments. It was developed a set of primer with target on *par*A site of promA group, a hotspot of gene insertion. On this hotspot was identified a dioxigenase gene on oil-contaminated mangrove. One plasmids of each area (oil-contaminated and printine) was isolated. The sequencing of these plasmids and the plasmidome (all plasmids obtained from total plasmids extraction from sediments) are being developed. The data give support for a better understand of microbial community adaptation in mangrove soils, possibly indicating to how extent the found plasmids might be involved in systematic mechanisms and crucial processes for adaptation, maintenance and operation of the ecosystem.

Keywords: horizontal gene transfer; plasmids; microbiome; adaptation; evolution

Development Agency: FAPESP, CNPq, CAPES