Early trajectories of microbial communities and organic matter during colonization in artificial freshwater ecosystems

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Résumé

The trajectory of microbial colonization within newly formed aquatic ecosystems is still not well documented. In particular, we do not know the importance of trophic status and environmental conditions on this trajectory. One main hypothesis is based on the competitive exclusion of microbial species along an environmental gradient according to their nutritional strategies: "Specialist" species should colonize stable and thus mature ecosystems, while "generalist" ones should appear in "young" ecosystems where a larger pool of resources is available. This would lead to the replacement of "generalist" species, that would be more tolerant to environmental perturbations, by "specialist" ones relative to well defined ecological niches (mostly the organic matter and nutrients). To explore this hypothesis, we realized a 1-year survey of the microbial colonization within the 16 artificial ponds of the PLANAQUA platform (PLAteforme expérimentale Nationale d'écologie AQUAtique, CEREEP-France), during their first impoundment. For eight of them an enrichment in mineral N and P was performed at the beginning of the phytoplankton growth to stimulate a eutrophication phenomenon. We explored whether the microbial communities and the organic matter, in term of quality, quantity, taxonomical and functional richness, were synchronized, and whether simulation of eutrophication modified these trajectories. To do so, we determined the abundance

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[*] Intervenant

and the taxonomical and functional diversity of the major microbial groups (phytoplankton, bacteria, archaea and virus), in combination with the diversity of dissolved organic matter (cDOM spectral analysis) and classical *in situ* multi-parameters. Altogether, these data suggest that microbial communities of these new artificial ecosystems rapidly converged toward those of natural freshwater ecosystems. Our results provide new insight into colonization process and community assembly mechanisms, and underlie the role of the microbial loop in the stability of aquatic ecosystems.

Mots-Clés: freshwater macrocosm, early microbial succession, eutrophisation