
The good, the bad and the novel extremophile candidate phyla from Lake Dziani Dzaha

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Résumé

Extreme environments are major sources of previously unknown microbial diversity and are useful systems to investigate limits of life, microbial biogeography and ecology as well as

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adaptation and evolution of microbial lineages. Recovery of metagenome assembled genomes (MAGs) of uncultured microbial populations from extreme environments has revealed many novel lineages and expanded our vision of the tree of life and the ecological roles of uncultured microorganisms. Applying this approach on the hypoxic, hypersaline and hyperalkaline waters of Lake Dziani Dzaha (Mayotte), we identified four novel extremophile candidate phyla sibling to *Elusimicrobia* and *Omnitrophota* within the Planctomycetota–Verrucomicrobiota–Chlamydiota (PVC) superphylum. While these lineages belonged to the rare biosphere of the lake compared to the predominant *Limnospira* and *Picocystis* photosynthetic primary producers, genomes mining revealed contrasted catabolic capabilities across these lineages and energetical metabolism based on hydrogen utilization and extracellular electron transfers for two phyla, suggesting original syntrophic interactions with other members of the lake community. By contrast, potentially extracellular giant proteins were identified in the genome of another novel phylum, as observed in predatory ultrasmall *Omnitrophota.* Domain analysis of these giant proteins revealed the presence of multiple carbohydrate binding domains similar to pectin lyase domains in association with intrinsically disordered protein regions allowing conformational malleability. In addition, disaggregase domain was also identified, suggesting that these giant extracellular proteins could be involved in extracellular dissociation and degradation of pectin-rich packed cells such as the predominant trilobe shaped Chlorophytes *Picocystis salinarum.* Our results provided genomic evidence for unusual interspecies interactions in Lake Dziani Dzaha, supporting the ecological concept of a gradient of microbial interactions.

Mots-Clés: Genomics, extreme environment, uncultivated