



Conference Abstract

Exploring the use of new water quality indicators based on microbial communities

Luciana Griffero[‡], Emiliano Pereira-Flores[§], Belén González[§], Andrés Pérez[§], Cecilia Alonso[§]

[‡] Grupo Ecología Microbiana Acuática Centro Universitario Regional Este, Rocha, Uruguay

[§] Centro Universitario Regional Este, Rocha, Uruguay

Corresponding author: Luciana Griffero (lugrif@gmail.com)

Received: 03 Mar 2021 | Published: 05 Mar 2021

Citation: Griffero L, Pereira-Flores E, González B, Pérez A, Alonso C (2021) Exploring the use of new water quality indicators based on microbial communities. ARPHA Conference Abstracts 4: e65420.

<https://doi.org/10.3897/aca.4.e65420>

Abstract

The growing concern for the quality of water in aquatic ecosystems makes it essential to develop new indicators that allow evaluating and predicting their state against anthropogenic impact. Microorganisms are able to reflect quickly changes in their habitat, through both its taxonomic and functional characteristics, and that is why they are in consideration as indicators of environmental quality (*1).

The objective of this work was to identify attributes of the composition and functionality of microbial communities, to be evaluated as an indicator of water quality, focusing on emerging pollutants (ECs). For that, ECs and bacterial communities were analyzed along the basins of two coastal lagoons encompassing an anthropogenic gradient, looking for taxonomic and functional indicators. Taxonomic indicators were looked using Illumina sequencing of 16S RNAr gene V4 region followed by identification of amplicon sequence variants (ASVs) and taxonomic annotation. In the case of functional indicators, shotgun sequencing was used added to identification and annotation of open reading frames (ORFs). Clustering techniques were implemented to define groups of sites based on the concentration of different categories of ECs. Then, the indicator value analysis (IndVal) (*2) was performed to identify taxonomic and functional traits that could be used as indicators of those groups. Finally, each sample was assigned to the corresponding group based on the indicators.

A first analysis involved the search of taxonomic indicators for all the set of samples including three groups of sites of low, medium and high impact of emerging contamination. It was possible to find indicators with a very high IndVal value for the three groups of samples. All indicators were based on the co-occurrence of three ASVs belonging to several of the most abundant bacteria phyla (Actinobacteria, Bacteroidetes, Cyanobacteria, Planctomycetes, Proteobacteria). The bacterial indicators correctly assigned 100% and 93% of the samples to their corresponding group for streams and lagoons respectively.

Then, a comparison between taxonomic and functional indicators using a subset of 41 samples was made, including two groups of samples: high and low-medium impact. Both the taxonomic and functional indicators showed high IndVal values for the high and low impact groups, being the highest in the case of functional genes Table 1. The high impact group was perfectly predicted for both taxonomic and functional indicators. The low-medium impact group was perfectly predicted by the functional indicators and 85% of the samples were correctly assigned by the taxonomic indicators.

Table 1. Taxonomic and functional indicators for high and low-medium impacted group		
Taxonomic indicators	Identity	IndVal
Group 1 (High impact)	Malikia + Solitalea + Cloacibacterium normaense +Arcobacter cryaerophilus	0.75
	Aquabacterium + Chloroplast + Chloroplast+ Alphaproteobacteria	0.75
	Solitalea + Flavobacterium + Prevotella copri + Chloroplast	0.5
Group 2 (low to medium impact)	SAR11_clade + SAR92_clade	0.6
	SAR11_clade + Malikia	0.33
	Malikia + Flavobacterium	0.3
Functional indicators	Identity	IndVal
Group 1 (High impact)	Glycosyl hydrolase family 48 + Ethanolamine utilisation protein EutQ + DNA-J related protein	1
Group 2 (low to médium impact)	Ribulose bisphosphate carboxylase large chain, catalytic domain + D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain + C2H2-type zinc finger	0.94

In conclusion, widespread availability of NGS technology allows for deep characterization of microbial diversity, enabling the use of robust ecological tools. Taking into account the high indval and prediction values, taxonomic and functional bacterial indicators appear as promissory candidates to evaluate for aquatic systems monitoring and conservation strategies.

Keywords

InDval Taxonomic and funtional indicators Next Generation Sequencing Emerging contaminants

Presenting author

Luciana Griffero

Presented at

1st DNAQUA International Conference (March 9-11, 2021)

Hosting institution

Centro Universitario Regional Este

Endnotes

- *1 Caruso G, La Ferla R, Azzaro M, Zoppini A, Marino G, Petochi T, et al. Microbial assemblages for environmental quality assessment: Knowledge, gaps and usefulness in the European Marine Strategy Framework Directive. *Critical Reviews in Microbiology* 2016; 42: 883-904.
- *2 Dufrene, M. and P. Legendre. 1997. "Species Assemblages and Indicator Species: The Need for a Flexible Asymmetrical Approach." *Ecol Monogr* 67(3):345–66.