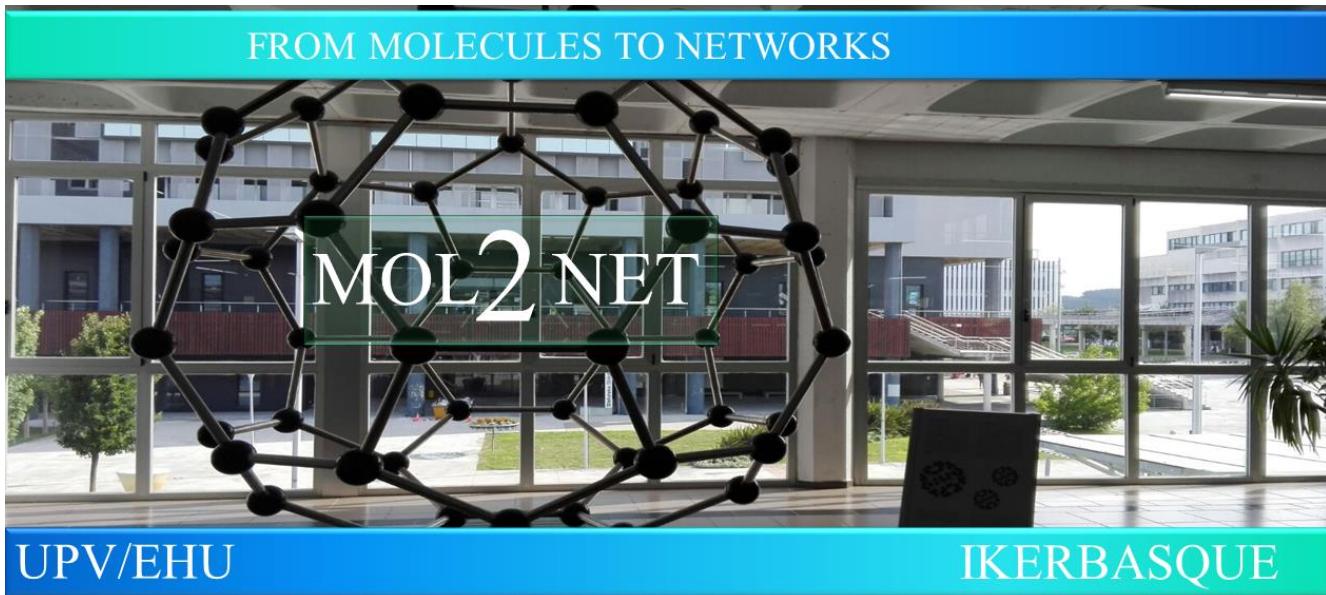




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### Bioremediation potential of glyphosate-degrading microorganisms in eutrophicated Ecuadorian water bodies

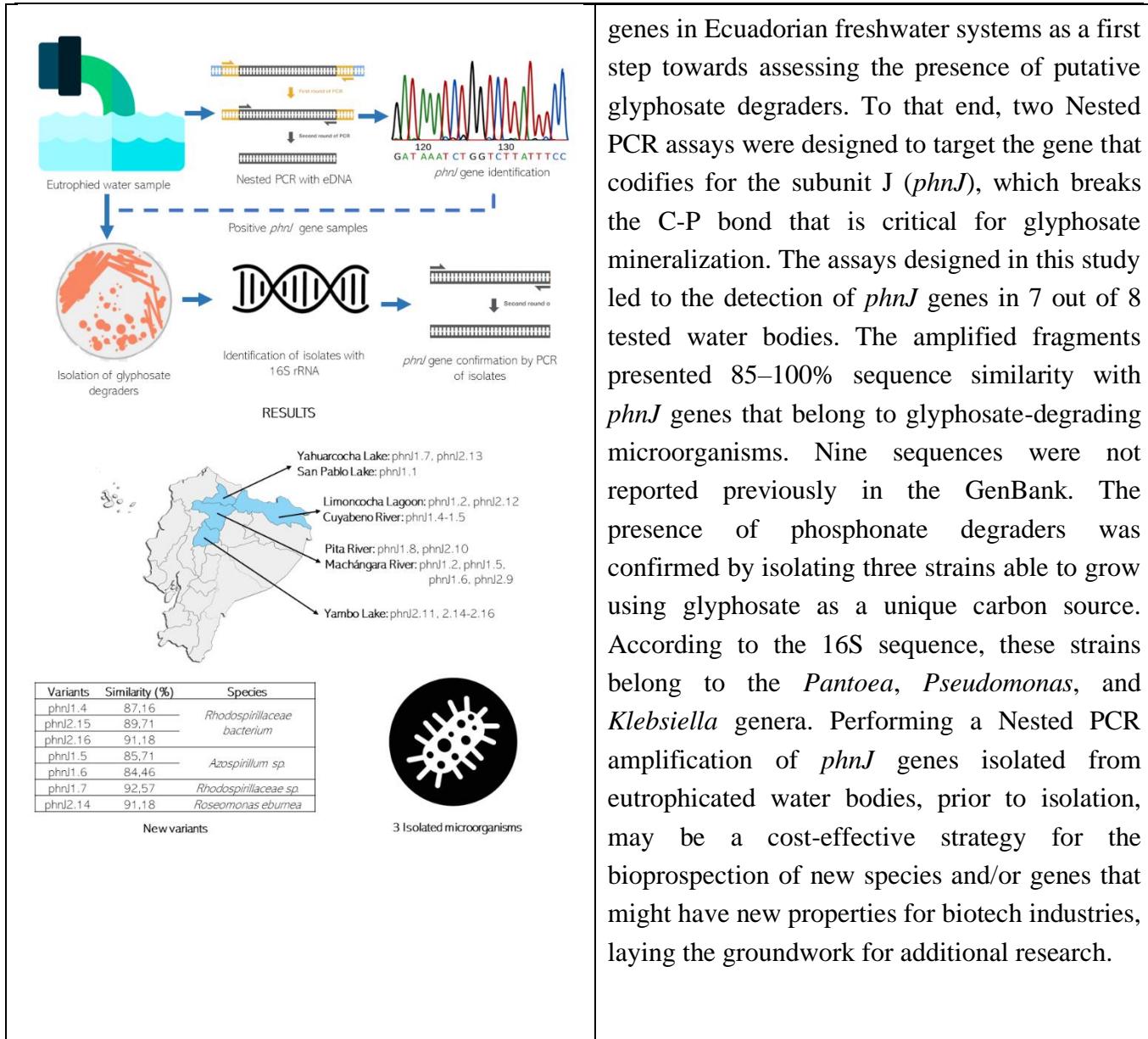
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Graphical Abstract	Abstract
	<p>Phosphonate compounds are the basis of many xenobiotic pollutants, such as Glyphosate (N-(phosphonomethyl-glycine). Only prokaryotic microorganisms and the lower eukaryotes are capable of phosphonate biodegradation through C-P lyase pathways. Thus, the aim of this study was to determine the presence of C-P lyase</p>



genes in Ecuadorian freshwater systems as a first step towards assessing the presence of putative glyphosate degraders. To that end, two Nested PCR assays were designed to target the gene that codifies for the subunit J (*phnJ*), which breaks the C-P bond that is critical for glyphosate mineralization. The assays designed in this study led to the detection of *phnJ* genes in 7 out of 8 tested water bodies. The amplified fragments presented 85–100% sequence similarity with *phnJ* genes that belong to glyphosate-degrading microorganisms. Nine sequences were not reported previously in the GenBank. The presence of phosphonate degraders was confirmed by isolating three strains able to grow using glyphosate as a unique carbon source. According to the 16S sequence, these strains belong to the *Pantoea*, *Pseudomonas*, and *Klebsiella* genera. Performing a Nested PCR amplification of *phnJ* genes isolated from eutrophicated water bodies, prior to isolation, may be a cost-effective strategy for the bioprospection of new species and/or genes that might have new properties for biotech industries, laying the groundwork for additional research.

## References

- Hernández-Alomía, F., Ballesteros, I., & Castillejo, P. (2021). Bioremediation potential of glyphosate-degrading microorganisms in eutrophicated Ecuadorian water bodies. Saudi Journal of Biological Sciences. <https://doi.org/10.1016/j.sjbs.2021.11.013>