

12/04/2019

## QMEC: a tool for high-throughput quantitative assessment of microbial functional potential in C, N, P, and S biogeochemical cycling



In a new study in the journal *Science China Life Sciences* authors developed a quantitative-PCR-based chip, Quantitative microbial element cycling (QMEC), for quantifying the genetic potential of microbiota to mineralize soil organic matter at N, P and S.

From Pixabay.

Microorganisms are major drivers of elemental cycling in the biosphere substantially affecting carbon metabolism, organic matter degradation, nitrogen (N) efflux and phosphorus (P) mobilization in the processes may result in CO<sub>2</sub> elevation, greenhouse gases release, nutrient loading and water consumption influence ecosystems and humans. Determining the abundance of microbial functional traits involved in nutrients, including carbon (C), nitrogen (N), phosphorus (P) and sulfur (S), is critical for assessing microbial biogeochemical processes and their current global changes.

In a new study in the journal *Science China Life Sciences* authors developed a high-throughput quantitative Quantitative microbial element cycling (QMEC), for comprehensively profiling functional genes of the m

N, P, S and methane cycling.

Biogeochemical nutrient cycling consists of numerous steps, each mediated by various functional genes. Nutrient cycling is composed of several processes, including N fixation, nitrification, denitrification, ammonium oxidation, organic N mineralization and assimilatory and dissimilatory N reduction, with many functional genes involved. "The comprehensive evaluation of microbial functional potential in CNPS biogeochemical cycling requires obtaining quantitative data for all these genes, which is extremely laborious when using traditional methods to process many environmental samples", explains Dr. Bang-Xiao Zheng from CSIC-CREAF, Barcelona. The University of Helsinki.



*Figura 1. Global Ecology Unit.*

To address these limitations, the authors of this study (i) designed a set of primer pairs targeting functional genes involved in C, N, P, and S cycling and (ii) developed a high-throughput qPCR-based functional-gene chip detecting the simultaneous quantification of CNPS-cycling genes and further assessment of microbial biogeochemical dynamics and microbial responses to environmental changes. QMEC contains 36 primer pairs involved in C, N, P and S cycles, targeting 64 microbial functional genes for C, N, P, S and S. These primer pairs were characterized by high coverage (average of 18–20 phyla covered per gene) and (>70% match rate) with a relatively low detection limit (7–102 copies per run).

QMEC was successfully applied to soil and sediment samples, identifying significantly different structural diversities of the functional genes ( $P < 0.05$ ). QMEC was also able to determine absolute gene abundance. QMEC allows the simultaneous qualitative and quantitative determination of 72 genes from 72 samples in one run, comprehensively investigating microbially mediated ecological processes and biogeochemical cycles in contexts including those of the current global change", says Prof. Josep Peñuelas from CREAF-CSIC.

**Rosa Casanovas-Berenguer and Josep Peñuelas**

CREAF

Universitat Autònoma de Barcelona

[rosa.casanovas@creaf.uab.cat](mailto:rosa.casanovas@creaf.uab.cat)

### References

Zheng, B., Zhu, Y., Sardans, J., Peñuelas, J., Su, J. (2018). **QMEC: a tool for high-throughput quantitative assessment of microbial functional potential in C, N, P, and S biogeochemical cycling**. *Science China Life Sciences*. [10.1007/s11427-018-9364-7](https://doi.org/10.1007/s11427-018-9364-7)

[View low-bandwidth version](#)