



## **Can we trust current estimates for biological nitrogen fixation?**

Jean-Philippe Bellenger (1) and Anne Kraepiel (2)

(1) Université de Sherbrooke, Department of Chemistry, Sherbrooke, Qc, Canada (jean-philippe.bellenger@usherbrooke.ca),

(2) Princeton University, Department of Chemistry, Princeton, NJ, USA (kraepiel@Princeton.edu)

Biological nitrogen fixation (BNF) consists on the reduction of atmospheric dinitrogen (N<sub>2</sub>) into bioavailable ammonium. This reaction accounts for up to 97% of nitrogen (N) input in unmanaged terrestrial ecosystems. Closing the N budget is a long standing challenge in many ecosystems. Recent studies have highlighted that current methods used to assess BNF are affected by critical biases. These findings challenge our confidence in many N budgets and call for a profound reconsideration of our methodological approaches.

Beside these methodological issues, our ability to properly assess BNF might be further altered as a result of a misconception regarding the importance of BNF enzymatic diversity in nature. BNF is catalyzed by the enzyme nitrogenase (Nase) for which three isoforms have been identified so far; the molybdenum (Mo), vanadium (V) and iron-only (Fe) isoforms. Currently BNF is mostly considered to primarily depend on the Mo isoform. The contribution of the alternative Nases (V and Fe isoforms) to BNF in natural habitats has been mostly overlooked. However, recent findings have challenged this traditional view of the Nases hierarchy (Mo isoform predominance) with deep implications for BNF assessment in the field.

Here, I will present an overview of recent findings, provided by various research groups, challenging current methods used to assess BNF. I will also present a summary of recent studies highlighting the importance of alternative Nases in nature. I will finally illustrate how altering our view on the Mo-Nase predominance can deeply affect our confidence in current BNF estimates.

I will conclude by presenting new methodological approaches that will contribute to significantly improve our ability to understand and estimate BNF in the field by improving our capacity to access BNF spatio-temporal variability and enzymatic diversity.