Research

Regulation of denitrification at the cellular level: a clue to the understanding of $\text{N}_2\text{O}$ emissions from soils

Lars R. Bakken1,*, Linda Bergaust1, Binbin Liu2 and Åsa Frostegård2

1Department of Plant and Environmental Sciences, and 2Department of Chemistry, Biotechnology and Food Sciences, Norwegian University of Life Sciences, PO Box 5003, 1432 Aas, Norway

Denitrifying prokaryotes use NO$_3^-$ as terminal electron acceptors in response to oxygen depletion. The process emits a mixture of NO, N$_2$O and N$_2$, depending on the relative activity of the enzymes catalysing the stepwise reduction of NO$_3$ to N$_2$O and finally to N$_2$. Cultured denitrifying prokaryotes show characteristic transient accumulation of NO$_2^-$, NO and N$_2$O during transition from oxic to anoxic respiration, when tested under standardized conditions, but this character appears unrelated to phylogeny. Thus, although the denitrifying community of soils may differ in their propensity to emit N$_2$O, it may be difficult to predict such characteristics by analysis of the community composition. A common feature of strains tested in our laboratory is that the relative amounts of N$_2$O produced (N$_2$O/(N$_2$ + N$_2$O) product ratio) is correlated with acidity, apparently owing to interference with the assembly of the enzyme N$_2$O reductase. The same phenomenon was demonstrated for soils and microbial communities extracted from soils. Liming could be a way to reduce N$_2$O emissions, but needs verification by field experiments. More sophisticated ways to reduce emissions may emerge in the future as we learn more about the regulation of denitrification at the cellular level.

Keywords: nitrous oxide; soil; physiology; regulation; mitigation

1. DENITRIFICATION IN SOILS: A MAJOR SOURCE OF ATMOSPHERIC N$_2$O

Human activities have more than doubled the annual input of reactive nitrogen to the biosphere compared with prehistoric rates. This anthropogenic reactive N is primarily fertilizer N$_2$, biologically fixed N (in legume crops) and NO$_x$ from combustion. The ongoing amplification of the global N cycle has already altered the biogeochemical processes of natural ecosystems, their trophic dynamics and biological diversity [1]. The ultimate fate of anthropogenic nitrogen is a return to the atmosphere, either as N$_2$, N$_2$O or NO, which are the gaseous products of microbial red/ox-transformations of mineral nitrogen. The N-gas product-stoichiometry of these processes is controlled by the ecology and regulatory biology of the organisms involved, as modulated by environmental factors. A better understanding and quantification of these processes is urgently needed to improve our chances to minimize N$_2$O emissions [2]. The current accumulation of N$_2$O in the atmosphere accounts for approximately 9 per cent of estimated anthropogenic global warming and is recognized as the major factor causing destruction of stratospheric ozone [3]. The global N$_2$O emissions from cultivated soils have been estimated at 3.3 Tg N$_2$O yr$^{-1}$ [4], which is around 50 per cent of the estimated global anthropogenic N$_2$O emission. A substantial part of the remaining anthropogenic N$_2$O emissions (from water bodies and uncultivated areas) are driven by nitrogen losses from agroecosystems as well [5]. There is thus little doubt that terrestrial habitats (both cultivated and uncultivated) are one of the most important sources of atmospheric N$_2$O. Nitrification is probably a much more potent N$_2$O source than nitrification, as indicated by the low N$_2$O/NO$_3^-$ product stoichiometry of nitrification [6]. Tracer studies suggesting a major role of nitrification may possibly have confounded coupled nitrification–denitrification via nitrite [7]. Few tools are available to reduce the emissions from natural ecosystems, apart from reducing the inputs of anthropogenic reactive nitrogen. The effect of such reductions may be slow, however, owing to the long residence time of reactive nitrogen (as biomass and soil organic N) within the systems [8]. Cultivated areas, on the other hand, are intensively managed by drainage, cropping, tillage, liming, fertilization and use of agrochemicals. These operations should hold a potential for reducing the N$_2$O emissions, provided that we know how they affect the activity of the

* Author for correspondence (lars.bakken@umb.no).

One contribution of 12 to a Theo Murphy Meeting Issue ‘Nitrous oxide: the forgotten greenhouse gas’.
organisms responsible for N$_2$O production in the soil. Despite several decades of research on N$_2$O emissions, however, few (if any) practical ways to achieve substantial reductions of N$_2$O emissions have been invented.

Why is there so little progress? How can we improve our efforts? We suspect that one of the reasons for the current shortcoming of the research on N$_2$O emission is that there has been too little cross-talk between disciplines. Great progress has been achieved from studies of the biochemistry, regulatory biology and physiology of denitrifying prokaryotes over the last two decades, driven by molecular biology. Yet, too little of this knowledge has reached the agronomists/biogeochemists/earth scientists who have made great progress within their own fields. Most experiments within each of the disciplines mentioned are designed to solve ‘disciplinary’ problems, by scientists with only rudimentary understanding of how adjacent disciplines think and work, and their recent progress. We believe that better interaction and discussions between the disciplines hold a potential for progress in the search for ways to mitigate N$_2$O emission.

The present paper is an attempt to illustrate this potential, by reviewing recent progress in a series of experimental approaches dedicated to understanding the mechanisms at the cellular level which control the N$_2$O/(N$_2$ + N$_2$O) product ratio of denitrification. This ratio is of utmost importance for the earth sciences in their attempt to link N$_2$O emissions to the current amplification of the nitrogen cycle. Before diving into the microbiological investigations, we need to briefly recapitulate some research on N$_2$O emissions within the earth sciences.

### 2. FIELD EXPERIMENTS

N$_2$O emissions from agricultural soils have been studied intensively in numerous field trials on all continents, reviewed and analysed thoroughly by Stehfest & Bouwman [4]. Excess fertilizer N doses result in high emissions, but N$_2$O emissions correlate only poorly with the fertilizer N level when within realistic ranges. Numerous other factors are involved in controlling the N$_2$O emission from soils, which contribute to the huge spatio-temporal variation in emissions in field trials [4,9]. An unfortunate consequence of the spatio-temporal variation is that the power of statistical tests of such experiments is low, i.e. although the experimental treatments may have a real effect, there is a high risk of erroneously concluding that there was no effect (type II error). A number of management effects may have been erroneously rejected for this reason. A simple calculation of the confidence interval of the difference between contrasting treatments could reveal the pitfall; i.e. the substantial effect of a management could have existed without being detected as statistically significant. This is often neglected, possibly because it is frustrating to illuminate the low statistical power of the experiment.

Another problem with field trials is that the observations tend to be ‘anecdotal’ because the effects of specific operations on N$_2$O emissions are likely to be conditional, i.e. dependent on several other variables such as soil type, climate and other management operations. Drainage of the soils is a good example: drainage of paddy rice soils (drainage is often included in the annual management of such fields) will enhance the N$_2$O emission [10]; in farmed organic soils, the lowering of the water table (i.e. drainage) may or may not reduce N$_2$O emissions depending on other factors [11], whereas adequate artificial drainage to sustain a low water table depth throughout the whole year appears to reduce N$_2$O emissions from grassland soils [12]. Another example is tillage, which may result in higher or lower annual N$_2$O emissions, apparently depending on the climate and possibly a number of soil variables ([13] and references therein).

A third shortcoming of nearly all field experiments is that the N$_2$O/N$_2$ product ratio has not been measured, primarily because it has proved difficult to obtain reliable field measurements of N$_2$ production [14]. The acetylene inhibition method may be used, but is likely to underestimate denitrification owing to diffusion limitation [15] and acetylene-catalyzed oxidation of NO [16]. Tracer-based measurements are possible [17], but have not been used much because they are complicated, demanding continuous monitoring of both gas emissions and the tracer ($^{15}$N) concentration in the nitrate/nitrite pool of the soil. The scarcity of reliable measurements of N$_2$ production in field experiments is most unfortunate, since the N$_2$O/N$_2$ product ratios should be a target for designing mitigation options [2].

The potential benefit of measuring both N$_2$ and N$_2$O production is illustrated by two studies of intact soils from field experiments conducted by Zaman et al. [18,19], where they quantified both N$_2$O and N$_2$ production (the latter by the acetylene inhibition technique). They found that liming invariably reduced the N$_2$O/N$_2$ product ratio, and the effect on net N$_2$O emission was either nil [18] or positive (higher emission from limed soil [19]). Their quantification of N$_2$ production by the acetylene inhibition method may have been biased for the reason mentioned earlier (lack of steady-state conditions owing to restricted diffusion, and NO scavenging by acetylene). Nevertheless, their observation of an altered N$_2$O/N$_2$ product ratio is probably valid since we may assume that the bias is the same in all treatments.

### 3. ECOSYSTEM MODELLING

Biogeochemical modelling of denitrification and its N$_2$O production are based on relatively crude models of the process and its regulation at the cellular level. Much effort has been invested in modelling the heat-, water- and not the least oxygen-transport within the soil matrix [20]. Less effort has been invested in refining the modelling of denitrifying community phenotype, which is a ‘black box’ in most models, based on relatively antique parameters for enzyme and growth kinetics. In addition, all soils are assumed to harbour the same community phenotype [9,21]. It appears bluntly wrong to assume that all community phenotypes are equal, as judged from investigations of community phenotypes of contrasting soils [22,23]. Despite these (and other) gross simplifications, the simulated annual N$_2$O emissions are often in reasonable agreement with measured values for contrasting soils [24] and for contrasting soil management scenarios [25], although the temporal variation is still a challenge [20,24].
Simplifications are necessary in biogeochemical ecosystem modelling, but it seems likely that the existing models could be improved through a dialogue between the modellers and the research community working with the genetic and physiological basis of denitrification. This is particularly true if the purpose of the modelling is to design ‘mitigation measures’, i.e. soil and fertilization routines that reduce the N₂O emissions. As stated previously, a reduction in the N₂O/(N₂ + N₂O) product ratio of denitrification should be a target when searching for mitigation measures. The existing models are possibly inadequate for this purpose, although this is unknown because we lack reliable data for N₂ production in field experiments to test their predictions. It would be arrogant (but possibly legitimate) to claim that when a nearly perfect match is found between measured and simulated annual N₂O emissions, the biogeochemical model is right for a number of wrong reasons. It is less arrogant (but fully legitimate) to claim that if used to simulate phenomena for which the models are not rigorously tested, their predictions are rather hypothetical.

Our impression is that field experiments and modelling of N₂O emissions have not made much progress regarding mitigation of N₂O emissions. This is reflected in several reviews of available mitigation options, which generally recommend operations that (i) secure synchronization of mineralization with the need for mineral N by growing crops and (ii) minimize the mineral N concentrations in the soil during off-season [26–31], which are not more than the general recommendations for good agronomic practice to minimize nitrate leaching [32]. A perpetuation of field experiments and modelling of N₂O emissions along the same track will probably not result in substantial progress regarding mitigations. That is not to say that such activities should be terminated. Field emission data are extremely important for several obvious reasons, and any hypothetical mitigation must be tested in field experiments. We are convinced that if there exist novel ways to reduce N₂O emissions, such mitigation options are more likely to be found through studies of the ecology and regulatory biology of denitrifying prokaryotes, with a deliberate focus on their ability to express N₂O reductase. We have dedicated ourselves to work along these lines, and the rest of this paper is a first attempt to summarize some of our findings.

4. N₂O FROM DENITRIFICATION DEPENDS ON REGULATION AT THE CELLULAR LEVEL

Denitrification is the stepwise reduction of NO₃ through NO₂, NO, N₂O to N₂, driven by four reductase enzymes NAR/NAP, NIR, NOR and N₂OR, respectively. This enables the organisms to sustain respiratory metabolism during oxygen limitation, with NO₃ as terminal electron acceptors. The denitrification proteome (NAR, NIR, NOR and N₂OR plus several other proteins) is synthesized in response to oxygen depletion, and is blocked by high oxygen concentrations (both transcriptional and post-transcriptional control [33]).

The transcription of the genes coding for the individual reductases is controlled by a network of transcriptional regulators and ancillary factors [34,35] which respond to intra- and extracellular signals among which are oxygen and N-oxides (NO and NO₂). Although important ‘nuts and bolts’ of this regulatory network have been unravelled for a few model strains, such as Paracoccus denitrificans, much remains to be discovered before we are able to fully understand the phenotypic response. For instance, we have found that phenotypic responses of various mutants of P. denitrificans suggest that the transcription of nar requires both FnrP and NarR (dual control), while the transcription of nosZ (coding for N₂OR) is equally effective with only FnrP (in response to oxygen depletion) or NNR (responding to NO) [36]. Another conspicuous finding regarding the regulation in P. denitrificans is that N₂OR is expressed much earlier than NIR and NOR (and possibly NAR), as illustrated in figure 1. Moreover, only a fraction of the cells are actually able to express NIR and NOR in due time before all the oxygen has been depleted [37,38]. We hypothesize that this is due to a stochastic initiation of the transcription of nir and nor, which then
regarding efficient reduction of NOx all the way to pH 7 demonstrates an outstanding performance to anoxic conditions (figure 2). The denitrification phenotype of \( P. \) denitrificans under nearly identical experimental conditions as Thauera expression of NIR and NOR, resulting in extremely conditions, it appears unable to perform a balanced and effective denitrification. But \( A. \) tumefaciens \( \textit{nosZ} \), with only minor emissions of both NO and N2O to emission of NO and N2O would be negligible. The natures of soils performed equally well, their contribution (less than 2 nmol flask \(^{-1}\)) of the strains reduced all NO3-N to N2. The transient accumulation of N2O is below the detection limit of the system which is approximately 2 nmol flask \(^{-1}\). Selected data from Bergaust et al. [37].

accelerates owing to product stimulation (NO accelerates transcription of both genes). In contrast, nearly 100 per cent of the cells appear to express N2OR, as judged from the specific rate of reduction of externally supplied N2O [37,38].

The peculiar patterns of regulation in \( P. \) denitrificans explains why this organism emits only traces of N2O (less than 2 nmol flask \(^{-1}\)) during transition from oxic to anoxic conditions (figure 2).

The denitrification phenotype of \( P. \) denitrificans at pH 7 demonstrates an outstanding performance regarding efficient reduction of NOx all the way to N2, with only minor emissions of both NO and N2O (less than 2 nmol N2O flask, or less than 0.004% of all NO3-N reduced to N2). If the denitrifying communities of soils performed equally well, their contribution to emission of NO and N2O would be negligible. The performance of \( P. \) denitrificans appears to be exceptional, however. A strain that has been studied in equal detail in our laboratory is the soil bacterium \textit{Agrobacterium tumefaciens} [39]. This organism is unable to reduce N2O to N2 because it lacks \textit{nosZ}, i.e. the gene coding for N2OR. Strains which lack \textit{nosZ} occur within many genera of denitrifying prokaryotes, and if organisms with such truncated denitrification apparatus were dominating in soils, it would obviously result in high N2O/(N2+N2O) product ratios of denitrification. But \( A. \) tumefaciens contrasts with \( P. \) denitrificans in another conspicuous way: when confronted with a rapid transition from oxic to anoxic conditions, it appears unable to perform a balanced expression of NIR and NOR, resulting in extremely high emissions of NO, as illustrated in figure 3.

We have also analysed the denitrification regulatory phenotype (DRP) of a number of reference strains and recently isolated strains within the genus \textit{Thauera} under nearly identical experimental conditions as that for \( P. \) denitrificans shown in figure 2 [40]. One of the strains lacked \textit{nosZ} and produced 100 per cent N2O, while the seven other strains had all the necessary genes to make a complete denitrification from NO3 to N2. A common feature of all the \textit{Thauera} strains was robust control of NO at nanomolar levels, very similar to \( P. \) denitrificans (5–35 nM in the liquid phase). They deviated grossly, however, regarding the transient accumulation of both NO2 and N2O. Some of the strains reduced all NO3 to NO2 before expressing NIR and NOR, whereas others accumulated negligible amounts of NO2. The strains were also different regarding the transient accumulation of N2O, ranging from 0.06 to 5 per cent of all NO3-N finally reduced to N2. The results are summarized in figure 4, together with their phylogenetic relationship based on 16S rDNA.

There exists a plethora of similar studies where the transient accumulation of N2O has been studied in a similar way for complex communities [41,42], biofilms [43] and in cultured denitrifiers [44–54]. It is difficult to summarize these results in a consistent way, since the experimental conditions are widely different from one experiment to the other. But the general impression is that the denitrification phenotypes of prokaryotes are profoundly different regarding their ‘intrinsic’ propensity of emitting N2O, as assessed by the amounts of N2O accumulating transiently when switching from oxic to anoxic respiration. These differences between denitrification phenotypes are most probably owing to differences in the regulatory network controlling the transcription of their denitrification genes (and possibly post-translational regulation). Thus, we propose a term ‘DRP’ [38], which is a set of variables that characterize the organisms ability to perform a balanced and effective transition from oxic to anoxic respiration with marginal emissions of intermediates.

Assuming that denitrifying bacteria are profoundly different regarding their DRPs, a crucial question is whether these characteristics are in any way related to phylogeny of the organisms. If such relationships exist, the analysis of denitrification community DNA would possibly enable us to predict characteristics of the community phenotype, although the task would be far from trivial owing to interactions via the intermediates NO2 and NO. Further on, the phylogeny of the DRP could also shed some light on the evolution of the various DRP traits and their fitness value.

However, we have scant knowledge about the phylogeny of various DRP traits, since this has hardly been studied at all in the past. The results already mentioned for the closely related strains within \textit{Thauera} [40] demonstrated surprisingly different DRPs among such closely related strains, both regarding their transient accumulation of NO2 and N2O, but not for NO. The allocation of these DRPs within the phylogenetic tree does not suggest any systematic relationship between phylogeny and the various DRP traits.

To sum up, it seems clear that denitrification phenotypes are profoundly different regarding their propensity to emit N2O, assessed by their transient accumulation of N2O when initiating denitrification
in response to oxygen depletion. They are also very different regarding their transient accumulation of nitrite (NO\textsubscript{2}). We have too few rigorous comparative investigations to draw conclusions on the possible relationship between these phenotypes and taxonomy/phylogeny, but the study of closely related strains of \textit{Thauera} do indicate that we may expect to find as much variation within taxonomic groups as between them. This would mean that characterizing the composition of denitrifying communities by metagenomic sequencing of genes coding for 16S rRNA or functional denitrification genes has limited value as a predictor of the communities' propensity to emit N\textsubscript{2}O. It would not imply, however, that no relationship will be found between the community composition and its propensity to emit N\textsubscript{2}O. Attempts have been made, with variable success, in ecophysiological studies of N\textsubscript{2}O formation [55–58]. Although such approaches cannot be expected to reveal causal relationships between genetic composition and phenotype of soil microbial communities, they may serve as hypothesis-generating observations. In order to find causal relationships, we may have to dive deeper than to phylogeny, possibly by identifying regulatory gene sequences that characterize various DRPs across phyla.

5. DENITRIFICATION IS AFFECTED BY pH

A recurring observation in ecological studies of denitrification has been that the product ratio of denitrification is strongly affected by pH [59,60]. Soils have inherently different pH depending on their parent mineral material modulated by biological processes, and the N\textsubscript{2}O/(N\textsubscript{2}+N\textsubscript{2}O) product ratio appears to be negatively correlated with pH within the normal range for agricultural soils (pH 5–8).
This would indicate that liming slightly acidic soils could be a way to reduce N₂O emissions, but this has been effectively ignored until recently. Why did it take so long time to discover this? Possibly for two reasons. One is that the immediate response to the knee-jerk reaction of many microbial ecologists is a drastic increase in N₂O emission [61], most probably because it causes a transient enhancement of net N mineralization and nitrification. A second reason may be that the mechanism causing the observed pH effect on the N₂O/N₂ product ratio of denitrification was not well understood.

How can the pH affect the N₂O/N₂ product ratio of denitrification? Our studies of the model strain P. denitrificans [37] shed some light on this:

— At pH 7, P. denitrificans emits nearly no N₂O when switching from oxic to anoxic denitrification in batch cultures.
— Lowering the pH of the medium resulted in increasing transient accumulation of N₂O, and at pH 6, it produces nearly 100 per cent N₂O (no N₂O reductase activity).
— The lack of N₂O reductase activity at pH 6 was not caused by low relative transcription rate of nosZ compared with that of the other denitrification genes; the ratio between mRNA copy numbers for nosZ and that for nirS was practically unaffected by pH (figure 1).
— Neither is it due to a particularly narrow pH range for the activity of the N₂O reductase enzyme (compared with that of the other denitrification enzymes): N₂O reductase expressed at pH 7 was functioning well at pH 6 when tested in vivo.

Our tentative conclusion is that low pH hinders the synthesis of a functional N₂O reductase enzyme, most probably by interfering with the assembly of the enzyme in the periplasm (which is the location of the functional enzyme).

6. CONCLUDING REMARKS
Our investigations demonstrate that the N₂O/(N₂+N₂O) product ratio of denitrification is
pervasively controlled by pH, be it in pure cultures of denitrifying bacteria or in soils. Our in-depth studies of the model strain *P. denitrificans* showed that the effect is primarily owing to interference with the assembly of the enzyme, rather than a narrow pH range for the N₂O reductase enzyme. The recurring observations of similar pH effect on denitrification in soils indicate that it is a general phenomenon in nature. The findings suggest that the ongoing soil acidification of agricultural soils by intensification of agriculture and excessive use of N-fertilizers, as convincingly demonstrated for China [64], may enhance the N₂O emissions drastically. We hypothesize that careful adjustment of pH in agricultural soils will reduce N₂O emissions from slightly acidic soils. This needs to be tested rigorously in field trials, however. More sophisticated ways to reduce N₂O emissions may emerge in the future as we learn more about the ecology and the regulatory biology of denitrifying prokaryotes.

REFERENCES


36 Bergaust, L., van Spanning, R., Frostegård, Å. & Bakken, L. R. In press. Expression of nitrous oxide reductase in Paracoccus denitrificans is regulated by oxygen and nitric oxide through FnrP and NNR. Microbiology (doi:10.1099/mic.0.554148-0)


40 Liu, B., Mao, Y., Bakken, L. R. & Frostegård, Å. In preparation. A comparative analysis of genotypes and denitrification phenotypes of strains within the genus Thauera.


