Summary:

1. Pre-drought system (April): Nitrogen fixation genes dominant, lots of necromass (qPCR vs. RT-qPCR)
2. Mid-drought system (August): high microbial activity (RNA content) and biomass turnover (qPCR vs. RT-qPCR), highest quantity of B-amo gene copies
3. Late-drought system (October): increase in DNRA + ANRA-associated genes, 5.4 mm rain on date of sample collection but still drought conditions (02.10.2018)

Pre-drought system (April): Nitrogen fixation genes dominant, lots of necromass (qPCR vs. RT-qPCR)

* After onset of extreme drought event nifD genes decreased by 25.21% in alpine peatlands on Zoige pleateau, did not impact denitrification genes nirK and nirS (Yan 2023)
* Soil nitrogen fixation rates increased with nifH gene copies, both positively correlated with soil water content in Zoige Pleateau peatlands, degradation = less nitrogen fixation (<https://doi.org/10.1016/j.scitotenv.2020.141084>)
* ‘In our study, microbial communities of rewetted fens were largely similar to communities of undrained fens, also suggesting substantial recovery by rewetting… however, there was also a high variability in recovery among rewetted fens. Subsequent correlative analyses revealed that a higher microbial lcommunity dissimilarity was observed in rewetted fens in which soil organic matter contents were relatively low, i.e. with an estimated organic matter content less than ca. 70%’ (<https://doi.org/10.1038/s41396-020-0639-x>)
* ‘N-related microbial enzyme activities such as nitrogenase, aminopeptidase and urease) were weakly impacted by temperature increase but increased with drought’ (in global peatland climate change meta study) (https://doi.org/10.1016/j.soilbio.2023.109287)

Mid-drought system (August): high microbial activity (RNA content) and biomass turnover (qPCR vs. RT-qPCR), highest quantity of B-amo gene copies

* The sources of nitrogen for the microbial biomass can be the plant residue itself, the mineral N already present in soil or recently mineralized, and the recycling soil biomass (Interactions between decomposition of plant residues and nitrogen cycling in soil )
* AOB abundance more responsive to N addition (6x) than AOA (<https://doi.org/10.1016/j.soilbio.2016.05.014>)
  + Both AOA and AOB amoA gene abundances responded positively to N addition, suggesting that elevated N supply generally increases soil ammonia-oxidizing microbial abundance. However, across all studies, AOB mean log response ratios to N additions were over 6 times greater than those of AOA. This indicates that AOB abundances are substantially more responsive to increases in N availability, although because of differences in cell sizes and specific activities ([Prosser and Nicol, 2012](https://www.sciencedirect.com/science/article/pii/S0038071716300840" \l "bib67)) this may not necessarily reflect comparable changes in activity between AOA and AOB.
* AOA more competitive at low substrate concentrations (source from introduction) – however, soil NH4 was not significantly dynamic in either site (get numbers)
* Increased decomposition (due to oxygen exposure) as water table falls – microbial necromass decomposes (decrease in qPCR values)
  + ‘approx‐ imately 11%–27% of soil nitrogen is bacterial necromass nitrogen’, particularly in peptidoglycan of bacterial cell walls (DOI: 10.1111/gcb.14781)
    - Free N-acetyl-glucosamine and glucosamine were here considered to mainly originate from decomposition of fungal chitin, since peptidoglycan mainly decomposed to muropeptides which contained glucosamine in a ratio to muramic acid at 6.7 (±1.1) (<https://doi.org/10.1016/j.soilbio.2019.107660>)
    - . As we expected, protein decomposition was the major contributor to total soil organic N fluxes, ranging between 65 and 95%. (as above)
  + Decay of necromass releasing peptidoglycan amino acids (i.e. muramic acid) as the system shifts from anoxic to oxic could be responsible for a flux in organic nitrogen that AOB could be better able to utilize than AOA due to its lower substrate affinity
  + Necromass N mineralization significantly increases under elevated temperatures (and so does necromass N pool itself) (DOI: 10.1111/gcb.15206)
  + Impact of drought negligible in meta-study on Muramic-N ([**https://doi.org/10.1111/gcb.16676**](https://doi.org/10.1111/gcb.16676)) – potential delay vs. short experiment may not capture impacts, and drought studies limited to grassland + forest
  + Evidence for most necromass turnover in top 0-5 cm in grassland soils (<https://doi.org/10.1038/s43247-022-00439-0>)
  + Possible evidence of microbial ‘mining’ of N from necromass substrates under low N and high NAG (n-acetyl-glucosamine) conditions (<https://doi.org/10.1016/j.soilbio.2019.05.017>)
    - No evidence for NAG uptake in AOB or NOB in lab biofilm (10.1128/AEM.70.3.1641–1650.2004)

Late-drought system (October): increase in DNRA + ANRA-associated genes, 5.4 mm rain on date of sample collection but still drought conditions (02.10.2018)

* DNRA:
  + Global mean DNRA rate significantly higher in paddy soils than forests/grasslands/croplands, precipitation is main stimulator (<https://doi.org/10.1021/acs.est.1c07997>)
    - Evidence for N2O emissions decreasing with increasing DNRA
    - Soil saturation and its effect on oxygen levels is the most important factor controlling DNRA
  + ‘Taken together, the oxidation status and the C/NO3- ratio appear to be the most important factors regulating the importance of DNRA in soil, while the effect of pH was not consistent’ (10.5194/bg-8-1779-2011)
    - ‘Dessimilatory NO3- reduction to ammonium (NH4+) (DNRA)’
* nirB codes DNRA and ANRA (10.1016/j.scitotenv.2020.139710), nrfA is unique to DNRA and is primary marker + had no significant changes during the study period so likely change is from ANRA
  + Thus, under these conditions (relatively high concentrations of nitrate or nitrite, > 2mM), Nir is required for nitrate and nitrite assimilation (vs. nrf) (doi.org/10.1007/s00203-018-1590-3)
    - . These results suggest that at low nitrate concentrations, Nir is responsible for assimilating nitrite along with production of a small amount of free ammonium. At high nitrate concentrations, Nir is not producing excess ammonium; instead most of the nitrite is secreted into the media and has little effect on the growth of cells.
  + Possible response for hypoxia in tomato and soybean roots (0.4161/psb.23578, 10.1016/j.jplph.2007.10.016)
  + *nasA required for nitrate assimilation (0021-9193/95/$04.0010)*
  + nirB – NADH-dependent nitrite reductase (ch. 17)
    - nasA – nadh-dependent nitrate reduction (ch. 17)