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Motivation

Grasslands cover approximately 70% of agricultural soils worldwide and account for 53% of agricultural grounds in the Netherlands [1, 2]. Fertilization is an essential component of grassland management, used for increasing forage production and yield.

In the Netherlands, grasslands are often fertilized with animal manure [2], which serves as a vital source of nutrients crucial for plant growth and development. Manure is rich in nitrogen; excessive application contributes to emission of greenhouse gases, loss of nutrient through leaching and soil acidification [4]. To make agricultural practice more sustainable, nitrogen emission needs to be reduced.

Technological challenge

Microorganisms play important roles in soil nitrogen cycling [5], yet the impact of organic fertilization on grassland microbiomes remains understudied. Especially in Northern-Europe, research on this topic is still lacking. Therefore, insight is needed to unravel the influence of manure application on soil microbiomes, particularly the effect on microorganisms involved in the nitrogen cycle and their influence on plant nitrogen uptake and unwanted emissions to the environment.

By elucidating the effect of manure fertilization on the soil microbiome, this study aims to contribute to the establishment of efficient fertilization strategies and reducing nitrogen emission.

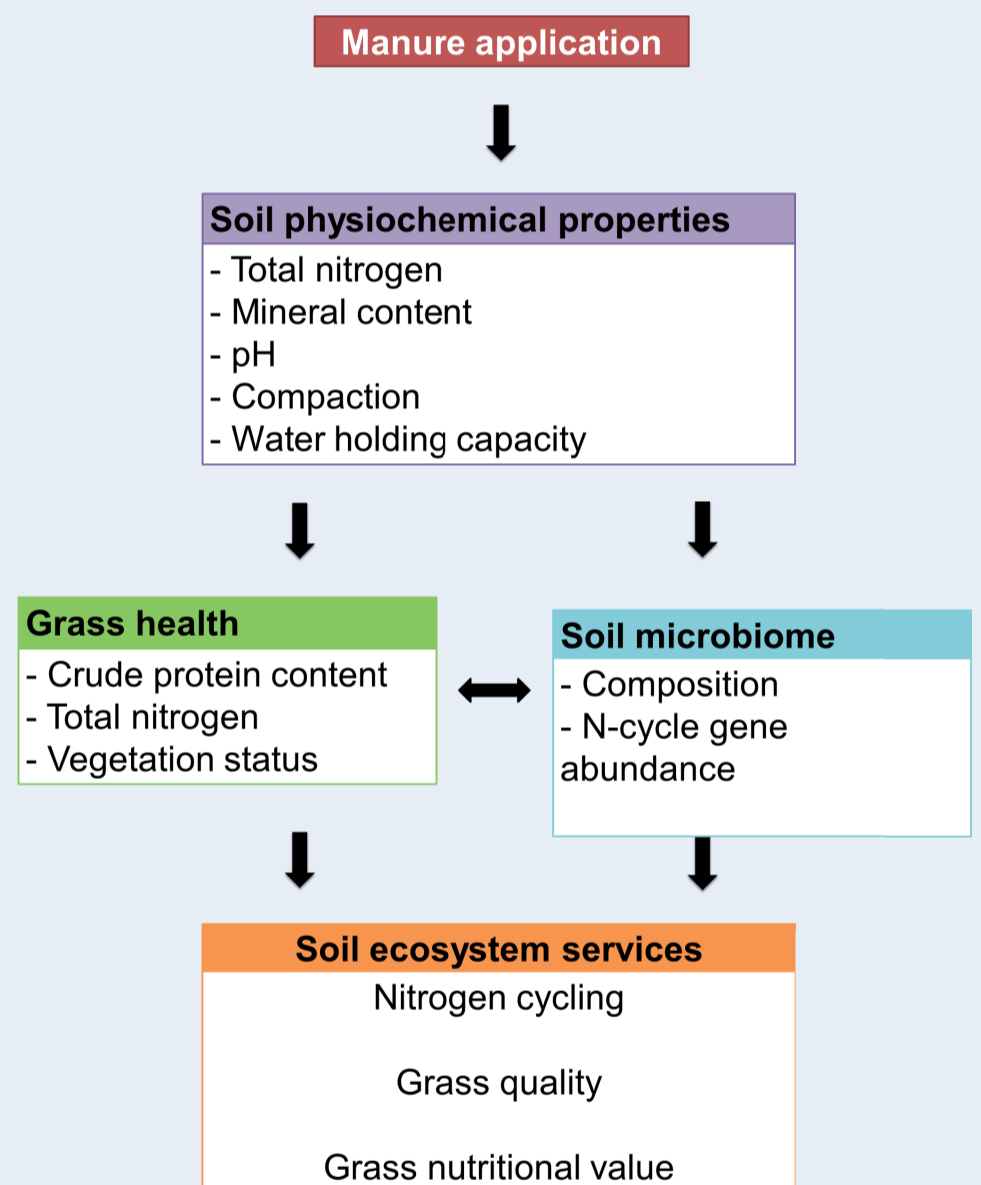
Research goals

The goals of this research is to investigate the effect of different forms of manure fertilization (slurry, digestate and composted) and two different application methods (injection and above ground spreading) on the grassland soil microbiome, with a particular focus on the nitrogen cycle.

This research aims to answer the following questions:

1. What is the impact of different organic fertilizers on composition and diversity of the soil microbial community in grasslands?

2. How does fertilizer injection influence the soil microbial composition and diversity compared to above ground application?
3. Can soil and grass nitrogen content be linked to nitrogen-cycle related gene abundance?



References

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