



Short Communication

## Livestock Grazing and Greenhouse Gas Emission in Tibet

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### Abstract

The Tibetan plateau, the highest and largest plateau on earth, is experiencing more than twice of the average global warming rate. It is imperative to understand how livestock grazing, the most prevalent economic activity in Tibet, contributes to greenhouse gas (GHG) emissions in regards to global warming. Recent studies revealed intriguing results, which await a full interpretation of the underlying mechanisms.

### Keywords

Land use; Livestock grazing; Tibetan alpine grassland

### Introduction

The Tibetan plateau is the highest (average 4000 m asl) and largest (2.57 million km<sup>2</sup>) plateau on earth. It is characterized by a cold climate; low oxygen levels, strong ultra violet (UV) irradiation and poor primary productivity, and has a number of fragile alpine ecosystems. In recent decades, Tibet has witnessed strong effects from global warming, experiencing more than twice the average global warming rate [1]. This has raised substantial concerns for greenhouse gas (GHG) emissions and soil carbon instability, partly attributed to permafrost thaw. Livestock grazing is the most prevalent economic activity in Tibet, and two thirds of the Tibetan plateau is comprised of alpine grasslands [1]. Therefore, it is imperative to understand how livestock grazing in Tibet contributes to GHG emissions and soil carbon stocks in conjunction with global warming. Recent studies on the effects of current grazing regimes in the Tibetan alpine grasslands revealed complex results. Our study [2], and those of others, detected reduced CO<sub>2</sub> emissions and/or increased soil total organic carbon (TOC) under grazing compared with grazing exclusion sites [2-4]. However, there are also studies showing an increase [5] or no changes in GHG emissions from grazing [6]. Those conflicting observations await a full interpretation of the underlying mechanisms and implications. Soil microbial communities must be considered in elucidating the mechanisms and assessing the environmental impacts, owing to their pivotal roles in mediating soil biogeochemical cycling.

### Discussion

Most ecosystem models treat microbial community composition as a “black box”. However, understanding the mechanisms

underlying the microbial response is essential for improving model predictions, as microorganisms play key roles in biogeochemical cycles. Increasing evidence shows that abundances of microbial functional genes could be good indicators for potential geochemical processes. For example, abundances of microbial functional genes associated with carbon degradation were shown to correlate with CO<sub>2</sub> emissions in bare soils but not in soils with vegetation, suggesting that the microbial functional genes were linked to heterotrophic respiration [7]. In contrast, factors affecting ecosystem respiration ( $R_{eco}$ ) are complicated.

Livestock grazing can perturb ecosystem respiration through at least four mechanisms:

- (1) reduced vegetation can have negative effects on  $R_{eco}$  as autotrophic respiration decreases;
- (2) reduced vegetation increases soil temperature and thereby  $R_{eco}$ ;
- (3) low organic matter in grazing grasslands can reduce  $R_{eco}$  because microbial heterotrophic respiration is sensitive to the input of carbon from living plants; and
- (4) inputs of manure from livestock could increase  $R_{eco}$  by stimulating plant growth, microbial activity, labile carbon and nitrogen availability.

These factors intertwine, making it difficult to predict the net effect of grazing on  $R_{eco}$ . In our study [2], most microbial functional genes for organic carbon degradation were decreased by grazing and were correlated with the change in vegetation variables, most likely as a response to decreased carbon input from plants. This explains our observation of increased soil TOC and decreased  $R_{eco}$  from grazing.

We also showed that N<sub>2</sub>O emissions in the Tibetan alpine grassland were significantly and positively correlated with the abundance of *amoA* genes (encoding enzymes for ammonia oxidizing) and *ureC* genes (encoding a subunit of urease that converts urea to ammonia), but negatively correlated with the abundance of *nirS* genes (encoding nitrite reductase), suggesting that nitrification is the major process of N<sub>2</sub>O emission in this ecosystem [8,9]. The abundance of microbial genes related to nitrification increased, while that related to denitrification decreased [2], revealing potential alteration of soil nitrogen cycling from grazing. A recent grazing experiment in Tibet has consistently shown that the abundance of ammonia-oxidizing archaea (AOA) and bacteria (AOB) increased by 3.7 and 42 fold in grazing sites, while the abundance of *nirS*-harboring denitrifiers decreased [10]. The effects of grazing on ecosystems are not uniform due to different grazing management and local environment conditions. A study in Atlantic mountain grassland [11] showed that livestock grazing decreased soil respiration and microbial metabolic quotients at sites, but the effects on other grassland ecosystems may vary. For example, Inner Mongolian grasslands have lower soil water content, annual average temperature, vegetation biomass, and soil organic matter compared with Tibetan alpine grasslands. Many studies conducted in Inner Mongolia have found that grazing led to loss of soil organic carbon and nitrogen [12-16], partly owing to increased CO<sub>2</sub> and N<sub>2</sub>O emissions. Proper management grazing can sustain soil carbon sequestration and lower GHG emissions [17-19].

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## Conclusion

Livestock grazing in the Tibet alters aboveground vegetation and belowground microbial community composition, as well as soil variables and biogeochemical cycling. It is noted that grazing effects vary in different regions. Therefore, it is imperative to crack the “black box” of microbial communities to gain a mechanistic understanding of the effects of environmental changes. By linking process rates with microbial functional traits, we begin to achieve more accurate predictions of microbial responses that are amenable to ecosystem modeling.

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