



# Effect of salinity on soil respiration in relation to dissolved organic carbon and microbial characteristics of a wetland in the Liaohe River estuary, Northeast China

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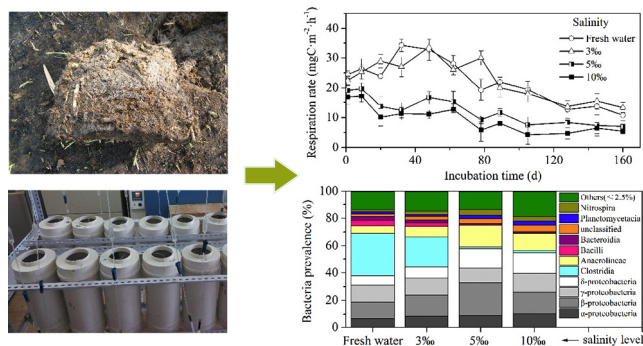
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## HIGHLIGHTS

- Effects of salinity on soil respiration were measured in an estuarine wetland.
- Salinity 5‰ decreased soil respiration rate.
- Soil respiration was related to microbial community structure rather than DOC.
- There may be a salinity threshold of soil respiration in brackish wetland.

## GRAPHICAL ABSTRACT



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## ABSTRACT

Increasing salinity has important impacts on biogeochemical processes in estuary wetlands, with the potential to influence the soil respiration, dissolved organic carbon (DOC) and microbial population. However, it is unclear how soil respiration is related to changes in the DOC and microbial community composition with increasing salinity. In this study, soil cores were sampled from a brackish wetland in the Liaohe River estuary and treated by salinity solutions at four levels (fresh water, 3‰, 5‰, and 10‰). Samples of gas, water and soil were collected to determine the respiration rates and microbial community structure of the soil and the DOC leaching from the soil. Compared to the low-salinity treatments (fresh water and 3‰), the high-salinity treatments (5‰ and 10‰) decreased the soil respiration rates by 45–57% and decreased the DOC concentrations by 47–55%. However, no significant differences were observed within the low-salinity treatments nor the high-salinity treatments. There is a positive correlation between the soil respiration rates and DOC concentrations in all treatments, but it does not indicate a genetic cause-effect relationship between them. The microbial community structure varied with the salinity level, with higher β- and δ-Proteobacteria abundance, as well as higher Anaerolineae, and lower Clostridia abundance in the high-salinity treatments. The respiration rates were slightly negatively related to the richness of Proteobacteria and positively related to the richness of Clostridia. This study suggests that there may be a salinity threshold (3–10‰) impacting the organic carbon loss from estuarine brackish wetlands. In addition, the response of soil respiration to increasing salinity may be mainly linked to changes in the microbial community composition rather than changes in the DOC quantity.

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## 1. Introduction

Estuarine wetlands, accounting for 3.4% of the global wetland area (Howe et al., 2009), play a critical role in supporting biodiversity conservation, providing a habitat for wildlife and protecting coastal water quality. Estuarine wetlands are also one of the important global carbon pools due to their sufficient capacity of carbon sequestration ( $250\text{--}500\text{ g C}\cdot\text{m}^{-2}\cdot\text{yr}^{-1}$ ) (Tobias and Neubauer, 2009). Soil respiration is one component of carbon cycles in wetlands, regulating the carbon sequestration of wetlands and influencing nutrient cycling in estuaries, as well as adjacent ecosystems (Jun et al., 2013). The global mean sea level will increase between 0.26 and 0.55 m and 0.45–0.82 m under the lowest and highest proposed greenhouse-gas concentration scenarios by 2100, respectively (IPCC, 2007; Hinkel et al., 2015). Rapid sea-level rise may subsequently increase the frequency of seawater intrusion farther into historically low-salinity estuary zones (Neubauer et al., 2013). This may further affect soil respiration in estuarine wetlands due to changes in biogeochemical processes caused by the increasing salinity (Chambers et al., 2014; Luo et al., 2017).

Estuarine wetlands are located where rivers enter the sea and the salinity of the soil is influenced by tides, which can regulate the physicochemical and microbial characteristics of wetland soils (Neubauer, 2013; Chambers et al., 2014). Generally, a higher ionic strength may cause non-salt-adapted microbial species to experience osmotic stress, interruptions in cellular function, and cell lysis (Wichern et al., 2006; Setia et al., 2010) and even a shift of the microbial community (Morrissey et al., 2014a). On the other hand, the abundant sulfate ( $\text{SO}_4^{2-}$ ) in seawater functions as electron acceptors for microbial respiration in tidal wetlands and contributes to the terminal mineralization of carbon (Weston et al., 2011; Marton et al., 2012). Additionally, cations in seawater (e.g.,  $\text{Na}^+$ ,  $\text{Mg}^{2+}$ ,  $\text{Ca}^{2+}$ , and  $\text{K}^+$ ) may quickly replace cations adsorbed in tidal wetland sediments, causing the availability of nutrients to increase and likely leading to changes in nutrient release (Weston et al., 2006). These biogeochemical changes are tightly related to carbon mineralization and nutrient cycling and are thus expected to have an important influence on soil respiration.

Dissolved organic carbon (DOC) is a very active fraction in soil organic matter and is sensitive to changing environmental factors (Tobias and Neubauer, 2009). The increasing salinity decreases the desorption capacity of tidal wetland sediments because the ionic strength is higher in seawater than in tidal wetland sediments (van Dijk et al., 2015) and consequently affects DOC release and retention in soil (Rashad et al., 2010). Chow et al. (2003) reported that the DOC concentrations in soil water of peatland were higher in low saline solutions than those in high saline solutions. They suggested that the polyelectrolytes of humic substances may stretch configurations due to mutual repulsion of the negative charges on dissociated or ionized functional groups. In contrast, some studies showed that DOC contents increased with salinity in sandy clay loam and tidal freshwater marsh soils due to cation exchange and/or changes in water inundation (Mavi et al., 2012; Wang et al., 2017). DOC is derived from biotic and abiotic processes (Kalbitz et al., 2000) and, thus, may be related to soil respiration (Yang et al., 2006; Chow et al., 2006).

Salinity is an important factor regulating soil respiration by impacting microbial community structures and activities (Edmonds et al., 2009; Hagemann, 2011; Rath and Rousk, 2015). Salt stress resulting from the low osmotic potential can alter the microbial activity (Chowdhury et al., 2011a), and high salinity can reduce the size of microbial communities due to an inability to adjust to high salt concentrations (Li et al., 2011; Morrissey et al., 2014b). Some studies have shown that the richness of  $\beta$ -Proteobacteria,  $\gamma$ -Proteobacteria and  $\varepsilon$ -Proteobacteria can alter with salinity change in wetland soils (Desta et al., 2014; Tang et al., 2012). A study for coastal and riparian wetlands in the Yangtze River estuary has shown that salinity had a negative effect on the abundance of  $\beta$ -Proteobacteria and a positive effect on  $\alpha$ -Proteobacteria (Hu et al., 2014). Under salinity change, a shift of the

microbial community may cause changes in the microbial metabolism as more energy is devoted to osmoregulation and adjustment to the salt environment (Nie et al., 2011). However, only few studies have demonstrated relations between soil respiration and microbial communities as responses to salinity changing (Hu et al., 2014; Xi et al., 2014).

Although previous studies have addressed the effects of salinity on soil respiration, it is unclear how soil respiration relates to changes in DOC concentration and microbial communities with increasing salinity. In this study, we examined soil respiration, DOC concentrations and microbial community structure in a brackish wetland of Liaohe River estuarine by using an incubation with microcosms at the four salinity levels (fresh water, 3‰, 5‰ and 10‰). The goals of this study were to provide a better understanding of how salinity affects soil respiration and its relation to DOC release and microbial community composition in estuarine wetlands under salinity change. We hypothesized that 1) there would be obvious effect of salinity on soil respiration, DOC concentrations and microbial community structure in soils and 2) the effect of salinity on soil respiration would be related to DOC concentrations and microbial community structure.

## 2. Materials and methods

### 2.1. Study site

The Liaohe River estuarine wetland is located in the northern region of Liaodong Bay, northeast China. Wetlands dominated by *Phragmites australis*, *Suaeda heteroptera* and tidal flats are successively distributed in the area (Zhao, 1999). *Phragmites australis* wetlands, which cover >70% of the total area of the Liao estuarine, have a vegetation cover of >90%. The soil profile (0–30 cm depth) in *Phragmites australis* wetlands is composed of an organic horizon above and an eluvial horizon below. We chose a *Phragmites australis* wetland ( $40^\circ 55' 40.02''\text{N}$ ,  $121^\circ 45' 24.88''\text{E}$ ), approximately 4.2 km from the coast, as the study site. At the site, the thickness of the organic horizon is approximately 13 cm deep and the eluvial horizon lies beneath it. The soil properties are shown in Table 1.

### 2.2. Soil core sampling and experimental design

At the study site, a total of fifteen soil cores, 16 cm in diameter and 30 cm long, were randomly collected from the *Phragmites australis* wetland in early spring (April 2014) when the water level was below the ground surface to allow for the retrieval of intact soil cores. The collected soil cores were placed in polyvinyl chloride (PVC) tubes, 16 cm in diameter and 45 cm long, and transported to the laboratory. In the laboratory, twelve soil cores were used for microcosm experimentation to determine the soil respiration rate and DOC concentration, and three soil cores were used for soil property analysis (Table 1). Each microcosm bottom was sealed using a cover, where two pipes were installed to connect to a Mariotte's bottle and a suction flask (Fig. 1). The Mariotte's bottle was used to supply the salt solution, and the suction flask was used to extract the water from the microcosm. A fine glass screen and a silica sand layer of 3-cm thick were successively placed on the bottom to avoid losing soil particles during soil water extraction. All microcosms were preincubated for one week with wetland water to restore the microbes in the soil. During incubation, the volume of water in the microcosms was approximately 2800 ml. At the end of the preincubation period, the water was extracted from the microcosms to remove the initial dissolved matter in the soil. Then, the microcosms were randomly selected as the fresh water (FW), 3‰ ( $S_3$ ), 5‰ ( $S_5$ ) and 10‰ ( $S_{10}$ ) salinity treatments. Each treatment was replicated three times. The fresh water treatment was obtained by adding deionized water, and the salinity treatments were amended with 3‰, 5‰ and 10‰ salt solutions. The corresponding electrical conductivities (EC,  $25^\circ\text{C}$ ) of the salt solutions were approximately  $5.4\text{ mS}\cdot\text{cm}^{-1}$ ,  $10.5\text{ mS}\cdot\text{cm}^{-1}$  and  $18.6\text{ mS}\cdot\text{cm}^{-1}$ . These levels fall into the salinity range of the soil solution in freshwater wetland (<0.5‰), brackish wetland (0.5–5‰) and salt wetland (>5‰)

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