

P294

Salinity affects microbial community structure in saemangeum reclaimed land

Kiyoon Kim, Sandipan Samaddar, Shamim Ahmed, Choudhury Aritra Roy and Tongmin Sa*

Department of Environmental and Biological Chemistry, Chungbuk National University, Cheongju, South Korea

Abstract

Saemangeum reclaimed land is a part of Saemangeum Development Project. Most of the persistent problems of Saemangeum reclaimed land remain to be related to soil salinity. Soil salinity is a major abiotic factor related to microbial community structure and also fungi have been reported to be more sensitive to salinity stress than bacteria. The aim of this study was conducted to investigate the effect of soil salinity levels on the microbial communities in Saemangeum reclaimed land using 454 pyrosequencing analysis. Soil samples were collected from 12 sites in Saemangeum reclaimed land. For pyrosequencing, 27F/518R (bacteria) and ITS3/ITS4 (fungi) primers were used containing the Roche 454 pyrosequencing adaptor-key-linker (underlined) and unique barcodes (X). Pyrosequencing was performed by Chun's Lab (Seoul, Korea) using the standard shotgun sequencing reagents and a 454 GS FLX Titanium sequencing System (Roche, Inc.). In the soil samples, Proteobacteria (bacteria) and Ascomycota (fungi) shows the highest relative abundance in all the soil sample sites. Proteobacteria, Bacteroidetes, Plantomycetes, Gemmatimonadetes and Parcubacteria were shown to have significantly higher abundance in high salinity level soils than low salinity level soils, while Acidobacteria and Nitrospirae has significantly higher relative abundance in low salinity level soils. The abundance of fungal, Ascomycota has the highest relative abundance in soil samples, followed by Basidiomycota, Chlorophyta, Zygomycota and Chytridiomycota. Basidiomycota, Zygomycota, Glomeromycota and Cerozoa were show significantly higher relative abundance in low salinity level soils. The principal coordinate analysis (PCoA) and correlation analysis shown to salinity-related soil parameters such as E_{Ce}, Na⁺, SAR and EPS were affected to bacterial and fungal community structure. Proteobacteria, Bacteroidetes, Plantomycetes exhibited significantly positive correlation with soil salinity, while Acidobacteria exhibited significantly negative correlation. In the case of fungal community, Basidiomycota and Zygomycota were seen show significantly negative correlation with salinity related soil parameters. These results suggest that provide understanding effect of soil salinity on microbial community structure and correlation of microbial community with soil parameters in Saemangeum reclaimed land.

Keywords: Soil salinity, Bacterial and fungal community, Saemangeum, Pyrosequencing

Corresponding author*

Tongmin Sa

Address: Chungdae-ro 1, Seowon-Gu, Cheongju, Chungbuk 28644, South Korea

Tel: +82-43-261-2561, Fax: +82-43-271-5921

E-mail: tomsa@chungbuk.ac.kr