Variation of bacterial biodiversity from saline soils and estuary sediments present near the Mediterranean Sea coast of Camargue (France)

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Salinity is an important environmental factor influencing microbial community composition. To better understand this influence, we determined the bacterial communities present in 17 different sites of brackish sediment (underwater) and soil (surface) samples from the Camargue region (Rhône river delta) in southern France during the fall of 2013 and 2014 using pyrosequencing of the V3?V4 regions of the 16S rRNA genes amplified by PCR. This region is known for abundant flora and fauna and, though saline, 30% of rice consumed in France is grown here. We found that bacterial abundance in 1 g of soil or sediment, calculated by qPCR, was higher in sediments than in surface soil samples. Members belonging to the Proteobacteria, Bacteroidetes, Chloroflexi and Firmicutes phyla dominated the bacterial communities of sediment samples, while members belonging to the Proteobacteria, Bacteroidetes, Gemmatimonadetes, Actinobacteria, Firmicutes and Acidobacteria