



White Rann of Kachchh harbours distinct microbial diversity reflecting its unique biogeography

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Highlights

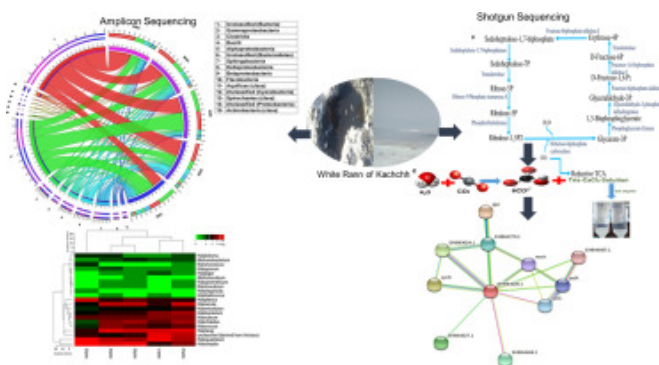
- Metagenomic study of unique desert ecosystem of White Rann of Kuchchh was performed.
- White Rann has thick cover of salts with wide day/night temperature differences.
- The prokaryotic community was dominated by bacteria followed by archaeal species.
- The community was aerobic and oligotrophic, having ability for sulphur respiration.
- The indigenous bacteria was found to possess carbonic anhydrase gene.

Abstract

The understanding of sub-surface soil microbial diversity is limited at both saline and hypersaline ecosystems, even though salinity is found to affect the microbial community in aqueous and terrestrial environment. In this study, a phylo-taxonomy analysis as well as the functional

characteristics of microbial community of flat salt basin of White Rann of Kachchh (WR), Gujarat, India was performed along the natural salinity gradient. The high throughput sequencing approach has revealed the numerical abundance of bacteria relative to the archaea. Salinity, TOC, EC and sulphate concentration might be the primary driver of the community distribution along the transect at WR. The much anticipated effect of salinity gradient on the microbial composition surprisingly turned out to be more speculative, with little variance in the community composition along the spatial distance of WR. The metabolic pathways involved in energy metabolism (like carbon, nitrogen, sulphur) along with environmental adaptive genes (like osmotic and oxidative stress response, heat and cold shock genes clusters) were abundantly annotated from shot-gun metagenomic study. The carbonic anhydrase harbouring bacteria Bacillus sp. DM4CA1 was isolated from WR, having a catalytic ability for converting the gaseous carbon dioxide in presence of calcium carbonate into calcite at 25 % higher rate as compared to non-harbouring strains. The enzyme has a role in multiple alternative pathways in microbial metabolism. With the array of results obtained, the study could become the new reference for understanding the diversity structure and functional characteristics of the microbial community of terrestrial saline environment.

Graphical abstract



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Introduction

In recent past, microbial ecology has moved beyond the descriptive analysis of microbial community pattern, trying to establish a correlation between edaphic factors and microbial diversity (Rath et al., 2019; Antwis et al., 2017). Yet, challenges exist, to understand the underlying dynamics that shapes the communities in response to environmental changes. The cumulative evidences have suggested that, besides pH, salinity is co-determinant for shaping the microbial communities across the biomes. In the global aquatic system, salinity has been the primary determinant and strongly correlated with microbial diversity and community composition. However, in the terrestrial (soil) ecosystem, microbial diversity has been predominantly associated with difference in soil pH (Lauber et al., 2009).

In spite of having a large proportion of saline soil (in a terrestrial environment), the understanding of the effect of salinity on soil microbial communities is still in its infancy level at many stages. In fact, it could be difficult to disentangle the effect of other variables which may co-vary along with salinity.

For example, soil with increasing salinity is often found to decrease the organic matter input in the habitat along with differences in soil pH (Wong et al., 2008; Rengasamy, 2010; Setia et al., 2013). Further, understanding the ecology of the desert microbiome is tedious because of the high degree of diversity and spatial heterogeneity (Prosser, 2015). However, microbiome at deserts or saline environments possesses a signature microbial community with a unique functional dynamics, which not only dominates, but also perpetuate sufficiently to impart visible characteristics to such habitats while regulating the biogeography of that ecosystem.

Among the five great provinces (i.e. for dry climates) across the continents, the tropical desert in the Asian continent extends in India from Rajasthan to Gujarat known as 'Thar Desert', wherein Gujarat it is known as Rann of Kachchh (Kutch). The Rann of Kachchh has an unusual geomorphic terrain. It has a unique environment with the fact that the region has a long coastline of Arabian Sea on one side and salt desert on the other side. Due to the seasonal saline marshy region, the salt concentration reaches the saturation level. Therefore, the part of the desert over the years has been covered with salt crystals and completely devoid of soil particles, with no-vegetation, sub-categorically known as 'White Rann of Kachchh'. Topographically, the White Rann is a 'bowl-shape' depression, which has a unique biotic province and gene pool of the semi-arid biogeographic zone in the sub-continent, without any counterpart across the globe (Reddy et al., 2016; Khonde et al., 2011). It is a flat salt basin covered by 4 to 5 in. of thick salt crust followed by dark black coloured sediment (clayish) supported by rocks beneath them.

It is apparent that very little is known about microbial diversity and geomicrobiological and biogeochemical potential of the flat salt basin of White Rann of Kachchh. In such an ecosystem, because of high evapotranspiration, salt accumulation becomes an important stress factor and high salinity reduces the water potential which may result in a quick decline in growth rate affecting the native microbial community dynamics. Therefore, it becomes imperative to explore the microbial diversity and their functional capabilities in extreme stress environments such as high salinity (Horneck et al., 2010; Narayan et al., 2018). We hypothesized that, the microbial community assemblage along with the diversity, changes with change in natural salinity gradient.

To test this hypothesis, a study was designed to define the microbial community (i.e. bacteria and archaea through taxonomic identification and phylogenetic characterization) of flat salt basin using amplicon sequencing of phylogenetic marker gene (16S rRNA) using Illumina platform. One limitation of 16S rRNA gene study is that it cannot directly link the phylogeny to function(s) and vice-versa and thus for annotating and understanding the functional potential of this native microbial community shot-gun metagenomic approach was applied. Here, an attempt was also made to establish that community assemblage at White Rann was whether influenced by deterministic or stochastic processes or by both. Additionally, the carbonic anhydrase harbouring bacterial strain was isolated from White Rann and partially characterized for its enzymatic activity.

Section snippets

Sample collection and physicochemical analysis

Soil samples (salt crystals or salt pans 8–10 cm thick, along with dark coloured water) were collected from transect of few kilometres within the White Rann of Kachchh [(WR); 23°51'11.4696"N

69°29'6.3312"E] (Fig. 1). Five sampling sites were randomly selected in equi-distance and three samples from each site were sampled by digging a rough rectangular pit of 8–10 cm wide and depth. Samples were immediately transported to the lab and metagenomic DNA was extracted within 24 h. These samples were ...

Physicochemical properties

The five samples of salt crust or salt crystals from WR showed a wide salinity gradient from 238 to 630 ppt, with a narrow pH (7.45 to 7.97), a range of TOC (0.67 to 2.08%) and a wide range of EC (70 to 136 (ms/ppt)mScm⁻¹). The results from Table 1, indicatively suggested the prevailing of a wide range of environmental conditions at WR. Thus, the varied environmental conditions might have influenced the microbiome assemblage at WR. Salinity at WR was the combined effects of five major ions in ...

Discussion

At White Rann, the ecosystem is unique, hypersaline with arid desert climatic conditions, intense sun exposures, wide gap between day and night temperatures, high evaporation-precipitation ratio which reinforces to have the discrete microbial community at such habitats. The study sites were characterized with the increasing salinity and electrical conductivity with less change in pH. Importantly, on contrary to the common observations, the total organic carbon content increases with increase in ...

Conclusion

Through this study, it can be deduced that the microbial ecosystem at White Rann was oligotrophic, where multiple phenotypes might co-exist together depending upon the nutrient availability and prevailing local environmental stress. The salinity which was in the range of 238–630 ppt along with the sulphate (16100–23,460 mg/l) might have a significant role during community assemblage at White Rann. The study was initiated with an anticipation of strong impact of salinity gradient on microbial ...

CRedit authorship contribution statement

KJ & DM conceived the concept of the study. PS preformed the experiments and drafted initial manuscript. KJ, VS & DM refined and edited the manuscript. All authors read and approved the final manuscript. ...

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. ...

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...In addition, the non-dominant genera *Desulfovibrio* and *Clostridium* *sensu stricto* ($0.001 < p \leq 0.01$) increased significantly (relative abundances increased to 1.13% and 1.17%, respectively). *Tolumonas* is an SOB bacterium, and the decrease in its relative abundance slows down the oxidation of S_2^- (Han et al., 2020; Singh et al., 2021). *Desulfobacter* (Chaudhary et al., 2023; Jonkers et al., 2005; Wang et al., 2022; Zhang et al., 2023b; Zhou et al., 2021), *Desulfovibrio* (Chaudhary et al., 2023; Jonkers et al., 2005; Wang et al., 2022; Zhou et al., 2021), and *Clostridium* *sensu stricto* (Takahashi et al., 2010; Wang et al., 2019b; Xu et al., 2021) are SRB, which promoted more SO_4^{2-} to be reduced to S_2^-

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