

Bacterial Diversity Change of the Surface Seawater from Dunedin, New Zealand to Australian Antarctic Ridge (AAR)

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PURPOSE

To investigate the richness and biogeographical distribution pattern of bacterial communities in the South Pacific Ocean (from Dunedin, NZ to AAR)

ABSTRACT

The prokaryotic microbial diversity of surface seawater from the Dunedin, New Zealand to the Australian-Antarctic Ridge (AAR), the largest unexplored expanse of the global mid-ocean ridge system was analyzed by pyrosequencing method. Seawater samples were collected from twenty five stations during the expedition of ice breaker ARAON in the early 2011. The temperature of seawater dropped from 12.9°C to 2.8°C and similarly the salinity decreased from 34.2 to 33.8 as he latitude goes up from 47° to 62°. The total 27,566 bacterial pyrosequencing reads were collected in this study and they were clustered into 84 to 160 phylotypes by 97% similarity cutoff. Most of phylotypes were affiliated to *Bacteroidetes*, *Alphaproteobacteria*, and *Gammaproteobacteria*. The minor phyla were included *Betaproteobacteria*, *Cyanobacteria*, and *Verrucomicrobia*. The *Alphaproteobacteria* decreased while *Bacteroidetes* increased as the latitude is higher. Interestingly the *Cyanobacteria* was observed in the seawater collected from at the latitude lower than 55°S. The change of composition in the bacterial community may be correlated with the change in environmental factors.

METHODS

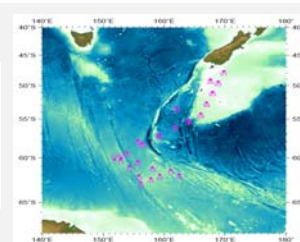
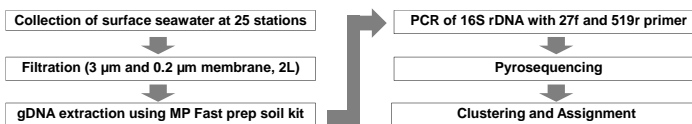


Fig. 1 Sampling site

RESULTS

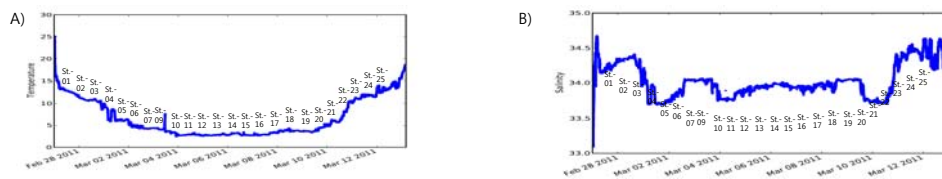


Fig. 2 Change of environmental factors A) Temperature B) Salinity

The temperature of seawater dropped from 12.9°C to 2.8°C and similarly the salinity decreased from 34.2 to 33.8 as he latitude goes up from 47° to 62°.

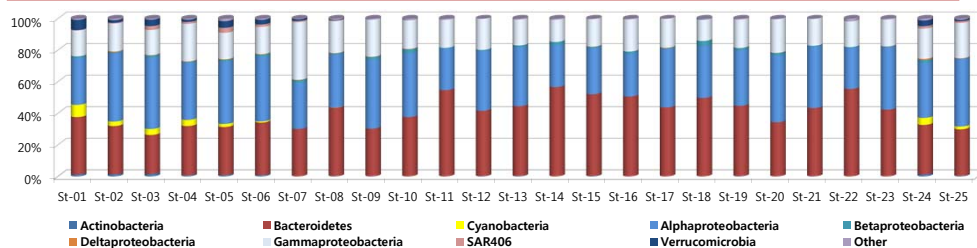


Fig. 3 Bacterial community composition

Most of phylotypes were affiliated to *Bacteroidetes*, *Alphaproteobacteria*, and *Gammaproteobacteria*. The minor phyla were included *Betaproteobacteria*, *Cyanobacteria*, and *Verrucomicrobia*. The *Alphaproteobacteria* decreased while *Bacteroidetes* increased as the latitude is higher. *Cyanobacteria* was observed in the seawater collected from at the latitude lower than 55°S.

| Cluster name | St-01 | St-02 | St-03 | St-04 | St-05 | St-06 | St-07 | St-08 | St-09 | St-10 | St-11 | St-12 | St-13 | St-14 | St-15 | St-16 | St-17 | St-18 | St-19 | St-20 | St-21 | St-22 | St-23 | St-24 | St-25 |
|--------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Cluster 1 | 15.7 | 23.3 | 25.6 | 21.5 | 20.9 | 22.8 | 15.1 | 18.6 | 28.3 | 19.1 | 16.7 | 17.5 | 14.0 | 7.0 | 6.6 | 10.5 | 16.5 | 13.8 | 16.6 | 21.5 | 18.6 | 18.6 | 9.7 | 15.8 | 22.1 |
| Cluster 2 | 4.5 | 3.3 | 3.6 | 3.1 | 4.3 | 3.1 | 4.9 | 5.5 | 8.0 | 7.1 | 9.3 | 7.8 | 6.1 | 1.8 | 5.1 | 4.5 | 5.2 | 4.5 | 6.9 | 11.8 | 5.3 | 5.3 | 8.6 | 2.1 | 4.4 |
| Cluster 3 | 1.4 | 0.4 | 0.8 | 0.1 | 0.2 | 0.9 | 2.1 | 3.3 | 5.1 | 6.9 | 10.4 | 6.6 | 5.4 | 5.1 | 3.3 | 9.1 | 13.7 | 7.5 | 8.2 | 7.7 | 8.2 | 2.6 | 0.1 | 0.0 | 0.0 |
| Cluster 4 | 0.3 | 1.1 | 0.8 | 0.8 | 1.1 | 2.0 | 3.0 | 4.8 | 3.9 | 8.0 | 4.2 | 7.4 | 6.4 | 9.7 | 8.1 | 5.6 | 8.6 | 7.8 | 5.1 | 7.8 | 8.0 | 8.0 | 5.5 | 0.7 | 0.8 |
| Cluster 5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 1.2 | 1.6 | 2.1 | 3.4 | 9.8 | 12.4 | 6.4 | 9.5 | 9.9 | 7.6 | 7.7 | 7.8 | 6.9 | 2.2 | 7.4 | 7.7 | 0.3 | 0.0 | 0.0 |

Fig. 4 Change in major OTUs

The composition of the most frequent OTU, Cluster 1 assigned to SAR 11 (*Alphaproteobacteria*) decreased as the latitude goes up.

CONCLUSION

These results suggested that the change of composition in the bacterial community may be correlated with the change in environmental factors.