

Geographical variations of wanderer algae indicate the potential effects on biological and organic matter

Vinay Kumar Rao*

Department of Medical Genetics, JSS Medical College, Karnataka, India

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INTRODUCTION

Wanderer algae, also known as migratory algae, have attracted the attention of researchers worldwide and several studies have been conducted on their abundance, diversity and putative role in coastal environments. However, due to the small number of studies on migratory birds in the ocean, much more is unknown. Nonetheless, previous studies have revealed spatiotemporal variations in community structure and the influence of environmental factors, thereby providing indirect evidence for their role in the coastal and marine water columns. However, anecdotal reports do not provide a comprehensive understanding of the contribution of migrants to marine microbial food webs [1].

Algae typically possess a variety of extracellular enzymes, which are thought to convert Particulate Organic Matter (POM) to Dissolved Organic Matter (DOM), assist in POM megaaggregation, and contribute to the Biological Carbon Pump (BCP). It is Despite mounting evidence for the multiple roles of algae, marine ecosystem models have not yet accounted for algae as important heterotrophic components as well as bacteria. Over the past decade, some progress has been made in our understanding of the relationship between algae and other migratory organisms in marine ecosystems [2]. These studies show that fungal biomass decreases with depth and often resembles prokaryotic biomass or correlates with migrant biomass. So far, only bacteria are considered the most important heterotrophs in marine ecosystems in terms of biomass. Especially in the marine water column, is still tenuous. Therefore, redesigning marine ecosystem models by clarifying the nature of algae-bacteria relationships, integrating algae into marine food webs and filling gaps and connecting missing links requires a more comprehensive approach [3,4].

DISCUSSION

Fungal abundance patterns and their significance in the water column

Quantifying fungal abundance is important for understanding the role of fungi in the sea column. Algae have been found to be distributed throughout the SCS water column, from surface to deep water. It has been previously reported that fungal abundance decreases with water column depth and is mainly related to the PhytoWanderer abundance pattern. This may explain why the frequency of the receiving zone was higher than the other zones. Furthermore, it has been reported that the abundance of fungi in marine snow is high and is also associated with algal decline [5,6]. Therefore, the presence of algae throughout the water column may

Address for correspondence:

Vinay Kumar Rao,
Department of Medical Genetics, JSS Medical College, Karnataka, India
E-mail: orestis.tsonis@gmail.com

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result from association with sedimentary particles such as sea snow and algal debris. Compared with the non-light zone, the twilight zone showed higher frequencies than the light zone. This is likely due to the biogeochemical features of the Twilight Zone, such as the uptake of organic matter from the lit zone, the creation of hotspots of increased biodiversity, and ideal conditions for fungal colonization and survival [7]. Additionally, the Twilight Zone is home to a wide variety of life forms, including fish, crustaceans, jellies, bugs, and squid. Algae, pathogens and parasites of these marine organisms, can be found in this zone. Animal wastes that are rich in organic matter and sink from surface waters into faeces are also colonized by Twilight Zone algae. As algae are predominantly aerobic organisms, they may not be able to grow in deep water, resulting in low abundance in dark zones. It has also been reported that the bacterial density decreases with increasing depth. Overall, the results of this study suggest that depth is an important factor in determining differences in her SCS walking frequency [8,9].

The water column contains multiple energy sources, including sea snow, subsidence organic matter, cellular and structural components of dead organisms, and host organisms. A better understanding of migrant activity in the water column will help define the role of migrants in biogeochemical cycles. Based on metatranscriptomics data, a recent study reported mechanisms used by algae to cope with seasonal environmental stresses in coastal ecosystems. Marine sediment algae have been found to be metabolically active. The Mundia Microbiological Observatory

Time Series (MOTS) traverses the subtropical frontal zone of the Pacific Ocean east of New Zealand, and while the TARA ocean project operates at the surface and at various depths; our study focuses on the South China Sea waters. Similar to columns by bacterioWanderer provide the first evidence of metabolically active migrants. Furthermore, we report involvement of Walker in carbohydrate, protein and lipid metabolism in the water column of the SCS, suggesting a role for Walker in organic carbon turnover.

CONCLUSION

The presence of carbohydrate-degrading pathways, especially chitin, suggests that wanderers normally feed on this abundant polymer derived from crustaceans and zoo wanderer carcasses. Recently, the presences of polysaccharides and proteolytic ability in migratory birds have also been reported. Furthermore, we report the presence of a vitamin synthesis pathway in the Walker metagenome. This confirms previous reports suggesting the presence of algae as a source of vitamins in the deep sea, mainly in the absence of plant migratory organisms. In addition, L-amino acids have been reported to be released by grazing by plant wanderers, and the discovery of L-amino acid degradation pathways indicates degradation of plant wanderer remains by migrant societies. Overall, we suggest that wanderer metabolic capabilities are involved in marine biogeochemical cycles in a manner similar to that of bacterial wanderers.

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