



# Harmful Algal Blooms Associated Marine Bacteria: Composition and Potential

Ismail M Al Bulushi\*

Department of Food Science and Nutrition, Sultan Qaboos University, Oman

\*Corresponding author: Ismail M Al Bulushi, Department of Food Science and Nutrition, College of Agricultural and Marine Sciences, Sultan Qaboos University, Al Kod, Muscat, Oman, Tel: +968 24143619; Fax: +968 24413418, Email: isab@squ.edu.om; <https://orcid.org/0000-0002-2733-3644>

Mini Review

Volume 7 Issue 1

Received Date: February 21, 2022

Published Date: March 08, 2022

DOI: 10.23880/act-16000235

## Abstract

The frequency and recurrent of harmful algal blooms (HABs) has increased currently as an impact of the climate change. This phenomenon not only causes sea foods massive killing, but also changes the microbial composition seawater. Harmful algal blooms were found to introduce certain bacterial group and family of sea foods safety important to the sea environment such as *Enterobacteriaceae* and *Vibrio* sp. The potential of some introduced bacterial flora such as algicidal has been found. However, the pathogenicity of this flora to the seawater has not been explored. This mini review initially shows the natural composition of marine microflora and analyzes the composition of seawater microbial flora composition associated with HABs with a reference to the algicidal and pathogenicity potential of this flora.

**Keywords:** Harmful Algal Blooms; Pathogenicity; Algicidal Potential; Composition; Microflora

## Introduction

The safety and quality of sea foods are affected by different biological and chemical as well as the handling practices. Certain hazards such as pathogenic bacteria, heavy metals, biogenic amines and other chemical contaminants easily can be brought to the sea foods by marine environment and food handlers during handling. Marine environment is affected naturally by different phenomenon such as milky sea, bioluminescence, green flash, sea foam and brinicle [1], nevertheless, the harmful algal blooms (HABs) phenomenon has got the main attention among all natural phenomena that affected seas and oceans by food microbiologists, environment specialists and researchers worldwide due to its wide impacts on marine lives, coastal environment and possible impact on sea foods safety.

Harmful algal blooms or commonly known as red tide due to its impact on changing the colour of seas and oceans

is an old phenomenon occurs in seas, lakes and sea farms. However, the high frequent occurrence and intensification in the recent years were attributed to different factors such as increasing sea surface temperatures due to climate change, changing storm frequencies and salinity fluctuations [2]. Despite the mode of action, the immediate impacts of HABs were found to include massive fish and marine lives killing and closure of desalination stations [3-5]. Harmful algal blooms were found to be caused by different dinoflagellates worldwide such as *Alexandrium monilatum*, *Amphidinium carterae*, *Gymnodinium aureolum*, *Chrysochromulina polylepis*, *Prymnesium parvum*, *Cochlodinium catenatum*, *Cochlodinium polykrikoides* [3-9].

In sub-tropical seas such as the Sea of Oman, Arabian Sea and Red Sea, the main HABs causative was found to be *Noctiluca scintillans* [10-12]. This phenomenon associated with changes and introducing new microflora to seas and oceans to an extent that these changes need to be clearly

known due to its possible effect on seafoos safety. Therefore, this mini review initially shows the natural composition of marine microflora and analyze the composition of seawater microbial flora composition associated with HABs with a reference to the algicidal and pathogenicity potential of this new microbial flora.

### Natural Marine Microbial Flora

Marine fish harbours heterogeneous populations of microflora mainly bacteria. The type and count of the population depend on many factors such as environment, habit, handling and temperature, however, the nature of microflora in newly caught fish was found to be mostly depended on fish environment [13,14]. Among natural marine microflora, proteobacter have been widely found in deep and surface seawater. This group includes main classes namely alphaproteobacteria, betaproteobacteria, gammaproteobacteria, delpaproteobacteria, epsilonproteobacteria and zetaproteobacteria [15].

Gammaproteobacteria includes fish safety important genera such as those belong to *Enterobacteriaceae* like *Salmonella* sp., *Escherichia* sp. and polluted seas pathogens such as *Vibrio* sp. and quality important hydrogen-producing bacterial genera such as *Shewanella* sp. [16]. Gammaproteobacteria were found to dominate the proteobacterial flora of seawater in many studies [17-21]. Pathogenic Gammaproteobacteria such as *Salmonella* sp. and *Vibrio parahaemolyticus* have been found as the main causative of food poisoning outbreaks associated with fish and other seafoods. For instance, data of fish-associated foodborne disease outbreaks in the United States, 1998-2015 revealed that *Salmonella* sp. caused the largest outbreaks (50%) in fish with the main fish types implicated tuna (37%), mahi-mahi (10%), and grouper (9%) [22]. Moreover, *Vibrio parahaemolyticus* was found to be the main causative of some food poisoning outbreaks associated with oysters in US and Spain [23,24].

### Harmful Algal Blooms Associated Bacterial: Floral Composition and Potential

Bacterial floral association with HABs was mainly studied on the basis of the algicidal potential of some bacteria associated with different HABs. In this respect, certain bacterial species such as *Hahella* sp., *Pseudoalteromonas peptidysin*, *P. carrageenovora*, *Exiguobacterium* sp., *Pseudoalteromonas* sp. *Zobellia* sp., *Cellulophaga lytica*, *Planomicrobium* sp., *Bacillus cereus*, *Micrococcus luteus*, *Marinomonas* sp., *Stakelama* sp., *Porphyrobacter* sp., and *Albirhodobacter* sp. have shown algicidal activities against certain dinoflagellates such as *Prorocentrum donghaiense*, *Gymnodinium catenatum*, *Microcystis aeruginosa*,

*Gymnodinium catenatum*, *Cochlodinium polykrikoides* [25-30].

Other studies however, focused on the analyses of the composition of seawater bacteria associated with HABs. For instance, among Gammaproteobacteria, *Enterobacteriaceae* were found in seawater associated with 4 dominant harmful dinoflagellates causing blooms of *Cochlodinium polykrikoides*, *Dinophysis caudata*, *Prorocentrum arenarium* and *Protoperidinium* in UAE [31]. Moreover, *Vebrio cholerae* was found during *Lingulodinium polyedrum* bloom, *Aeromonas* sp. and *Shewanella* sp. were found during *Microcystis* sp. bloom, *Sphingomonas alaskensis*, *Xanthomonas* sp. and *Porphyrobacter* sp. during *Microcystis aeruginosa* blooms, *Ochrosphaera* sp., *Isochrysis* sp. and *Synechococcus* sp. during *Lingulodinium polyedrum* blooms, *Vibrio toranzoniae*, *Ruegeria pelagia* and *Psychrobacter adeliensis* during *Skeletonema costatum* blooms [25-36].

In fact, unpolluted seas and oceans are generally not an appropriate environment for pathogenic *Enterobacteriaceae* member such as *Salmonella* sp. and *Vebrio cholerae* as for instance in *Salmonella* sp. case, salt can cause osmotic shock which could lead to cell death [37]. Thus, the association of pathogenic *Enterobacteriaceae* and *Vibrio* sp. with HABs in some studies [31,38] could raise the concerns about the safety of seas and sea foods caught in HABs zones.

It can be understood from the previous studies that despite analyzing the composition of the HABs associated bacteria and elucidating the diversity of this flora, none of these studies have shown any potential of this flora relates to the safety of the seawater HABs zone where most the important seafoods such as shellfishes are caught in or closed HABs zone [32-36].

In conclusion, HABs do change the microbial flora of seawater and do introduce new flora. Despite the diversity of HABs associated bacterial flora, only algicidal potential has been explored and known, however, the pathogenicity and seawater safety aspect of this newly introduced flora has not been attempted.

### References

1. <https://www.marineinsight.com>.
2. Fu F, Tatters A, Hutchins D (2012) Global change and the future of harmful algal blooms in the ocean. *Mar Ecol Prog Ser* 470: 207-233.
3. Richlen M, Morton S, Jamali E, Rajan A, Anderson D, et al. (2010) The catastrophic 2008-2009 red tide in the Arabian Gulf region, with observations on

- the identification and phylogeny of the fish-killing dinoflagellate *Cochlodinium polykrikoides*. *Harmful Algae* 9(2): 163-172.
4. Jiang X, Tang Y, Lonsdale D, Gobler C (2009) Deleterious consequences of a red tide dinoflagellate *Cochlodinium polykrikoides* for the calanoid copepod *Acartia tonsa*. *Mar Ecol Prog Ser* 390: 105-116.
  5. Vargas-Montero M, Freer E, Jiménez-Montealegre R, Guzmán J (2006) Occurrence and predominance of the fish killer *Cochlodinium polykrikoides* on the Pacific coast of Costa Rica. *Afr J Mar Sci* 28(2): 215-217.
  6. Tang Y, Gobler C (2009) Characterization of the toxicity of *Cochlodinium polykrikoides* isolates from Northeast US estuaries to finfish and shellfish. *Harmful Algae* 8(3): 454-462.
  7. Gobler C, Berry D, Anderson R, Burson A, Koch F, et al. (2008) Characterization, dynamics, and ecological impacts of harmful *Cochlodinium polykrikoides* blooms on eastern Long Island, NY, USA. *Harmful Algae* 7(3): 293-307.
  8. Landsberg J (2002) The effects of harmful algal blooms on aquatic organisms. *Rev Fish Sci* 10(2): 113-390.
  9. Kim CS, Lee SG, Kim HG (2000) Biochemical responses of fish exposed to a harmful dinoflagellate *Cochlodinium polykrikoides*. *J Exp Mar Biol Ecol* 254(2): 131-141.
  10. Madhu N, Jyothibabu R, Maheswaran P, Jayaraj K, Achuthankutty C, et al. (2012) Enhanced chlorophyll a and primary production in the northern Arabian Sea during the spring intermonsoon due to green *Noctiluca scintillans* bloom. *Mar Biol Res* 8(2): 182-188.
  11. Al-Azri A, Piontkovski S, Al-Hashmi K, Goes J, Gomes H, et al. (2010) Chlorophyll a as a measure of seasonal coupling between phytoplankton and the monsoon periods in the Gulf of Oman. *Aquatic Ecol* 44(2): 449-461.
  12. Mohamed Z, Mesaad I (2007) First report on *Noctiluca scintillans* blooms in the Red Sea off the coasts of Saudi Arabia: consequences of eutrophication. *Oceanologia* 49(3): 337-351.
  13. Al Bulushi I (2009) Gram-positive bacteria in sub-tropical marine fish and their mesophilic spoilage potential. PhD Dissertation, The University of Queensland, pp: 240.
  14. Shewan J (1977) The bacteriology of fresh and spoiling fish and the biochemical changes induced by bacterial action. The conference on handling, processing, and marketing of tropical fish. UK, pp: 51-56.
  15. (2022) Proteobacteria: Overview of Proteobacteria.
  16. (2022) Gammaproteobacteria.
  17. Franco DC, Signori CN, Duarte RT, Nakayama CR, Campos LS, et al. (2017) High prevalence of Gammaproteobacteria in the sediments of Admiralty Bay and North Bransfield Basin, Northwestern Antarctic Peninsula. *Front Microbiol* 8: 153.
  18. Suh S, Park M, Hwang J, Kil E, Jung S, et al. (2015) Seasonal dynamics of marine microbial community in the South Sea of Korea. *PLoS One* 10(6): e0131633.
  19. Yamamoto M, Takai K (2011) Sulfur metabolisms in epsilon- and gamma-Proteobacteria in deep-sea hydrothermal fields. *Front Microbiol* 2: 192.
  20. Obernosterer I, Catala P, Lami R, Caparros J, Ras J, et al. (2008) Biochemical characteristics and bacterial community structure of the sea surface microlayer in the South Pacific Ocean. *Biogeosciences* 5: 693-705.
  21. Lysnes K, Torsvik T, Thorseth I, Pedersen R (2004) Microbial populations in ocean floors basalt: results from OPD LEG 187. *Proceedings of the Ocean Drilling Program, Scientific Results 187: 1-27.*
  22. Barrett K, Nakao J, Taylor E, Eggers C, Gould L (2017) Fish-associated foodborne disease outbreaks: United States, 1998-2015. *Foodborne Pathog Dis* 14(9): 537-543.
  23. McLaughlin J, De Paola A, Bopp C, Martinek K, Napolilli N, et al. (2005) Outbreak of *Vibrio parahaemolyticus* gastroenteritis associated with Alaskan oysters. *N Engl J Med* 353(14): 1463-1470.
  24. Lozano-Leon A, Torres J, Osorio C, Martinez-Urtaza J (2003) Identification of tdh-positive *Vibrio parahaemolyticus* from an outbreak associated with raw oyster consumption in Spain. *FEMS Microbiol. Lett* 226(2): 281-284.
  25. Zhang H, Peng Y, Zhang S, Cai G, Li Y, et al. (2016) Algicidal effects of prodigiosin on the harmful algae *Phaeocystis globosa*. *Front Microbiol* 7: 602.
  26. Kristyanto S, Kim J (2016) Isolation of marine algicidal bacteria from surface seawater and sediment samples associated with harmful algal blooms in Korea. *Korean Journal of Microbiology* 52(1): 40-48.
  27. Tian C, Liu X, Tan J, Lin S, Li D, et al. (2012) Isolation, identification and characterization of an algicidal bacterium from Lake Taihu and preliminary studies on its algicidal compounds. *J Environ Sci* 24(10): 1823-

- 1831.
28. Kim M, Jeong S, Lee S (2008) Isolation, identification, and algicidal activity of marine bacteria against *Cochlodinium polykrikoides*. *J Appl Phycol* 20(1): 1069-1078.
  29. Skerratt J, Bowman J, Hallegraef G, James S, Nichols P (2002) Algicidal bacteria associated with blooms of a toxic dinoflagellate in a temperate Australian estuary. *Marine Ecology Progress Series*, 244: 1-15.
  30. Lovejoy C, Bowman J, Hallegraef G (1998) Algicidal effects of a novel marine *Pseudoalteromonas* isolate (class Proteobacteria, gamma Subdivision) on harmful algal bloom species of the genera *Chattonella*, *Gymnodinium*, and *Heterosigma*. *Appl Environ Microbiol* 64 (8): 2806-2813.
  31. Khan M, Qalandri K, Sankaran A, Adnani L, AlAlami U (2014) Monitoring of phytoplankton species and associated bacterial populations in the coastal water of United Arab Emirates. *International Conference on Desalination Environment and Marine Outfall System, Oman*.
  32. Ismail M, Ibrahim H (2017) Phytoplankton and bacterial community structures and their interaction during red-tide phenomena. *Ocean Science Journal* 52(3): 411-425.
  33. Shi L, Cai Y, Kong F, Yu Y (2011) Changes in abundance and community structure of bacteria associated with buoyant *Microcystis* colonies during the decline of cyanobacterial bloom (autumn-winter transition). *Ann Limnol Int J Lim* 47(4): 355-362.
  34. Limei S, Yuanfeng C, Hualin Y, Peng X, Pengfu L, et al. (2009) Phylogenetic diversity and specificity of bacteria associated with *Microcystis aeruginosa* and other cyanobacteria. *J Environ Sci* 21(11): 1581-1590.
  35. Mouriño-Pérez RR, Worden AZ, Azam F (2003) Growth of *Vibrio cholerae* O1 in red tide waters off California. *Appl Environ Microbiol* 69(11): 6923-6931.
  36. Fandino L, Riemann L, Steward G, Long R, Azam F, et al. (2001) Variations in bacterial community structure during a dinoflagellate bloom analyzed by DGGE and 16S rDNA sequencing. *Aquat Microb Ecol* 23(3): 119-130.
  37. Keerthirathne TP, Ross K, Fallowfield H, Whiley H (2016) A Review of temperature, pH, and other factors that influence the survival of *Salmonella* in mayonnaise and other raw egg products. *Pathogens* 5(4): 63.
  38. Greenfield D, Gooch Moore J, Stewart JR, Hilborn ED, George BJ, et al. (2017) Temporal and environmental factors driving *Vibrio Vulnificus* and *V. Parahaemolyticus* Populations and their associations with harmful algal blooms in South Carolina detention ponds and receiving tidal creeks. *Geohealth* 1(9): 306-317.

