



## PATHOGENIC AND POLLUTING MICROBIAL LOAD AT ALANG-SOSIYA SHIP BREAKING YARD (ASSBY)

Jani, H.J.<sup>1</sup>; Ratna Trivedi<sup>2</sup>; Bhatt P.N.<sup>1\*</sup>

<sup>1</sup>DEPARTMENT OF ANALYTICAL CHEMISTRY, BHAVNAGAR UNIVERSITY, BHAVNAGAR, GUJARAT.

<sup>2</sup>DEPARTMENT OF MICROBIOLOGY, SHREE RAMKRISHNA INSTITUTE OF APPLIES SCIENCES, M.T.B. COLLEGE CAMPUS, ATHWALINES, SURAT, GUJARAT.

[drhitendra75@yahoo.com](mailto:drhitendra75@yahoo.com), [drratnatrivedi@gmail.com](mailto:drratnatrivedi@gmail.com)

### ABSTRACT:

Alang-Sosiya Ship Breaking Yard (ASSBY), is situated at 21°5' 21°29' north and 72° 5' 72° 15' east on the western Coast of Gulf of Cambay. Besides translocating commercial goods, the shipping trade inadvertently spreads many animal, plant and microbial species around the world. Ballast water pumped in from coastal waters mediates translocation of alien biota to new destinations. Wide physiological adaptability, species diversity and invidiousness of some bacteria to cause diseases in animals and plants call for investigations to decipher the deleterious effects brought about through ballast water exchange. The aim of the present study is to understand the seawater quality and distribution and contamination levels of microorganisms present in ASSBY.

**KEY WORD:** : ASSBY, pathogenic bacteria, indicator microorganisms.

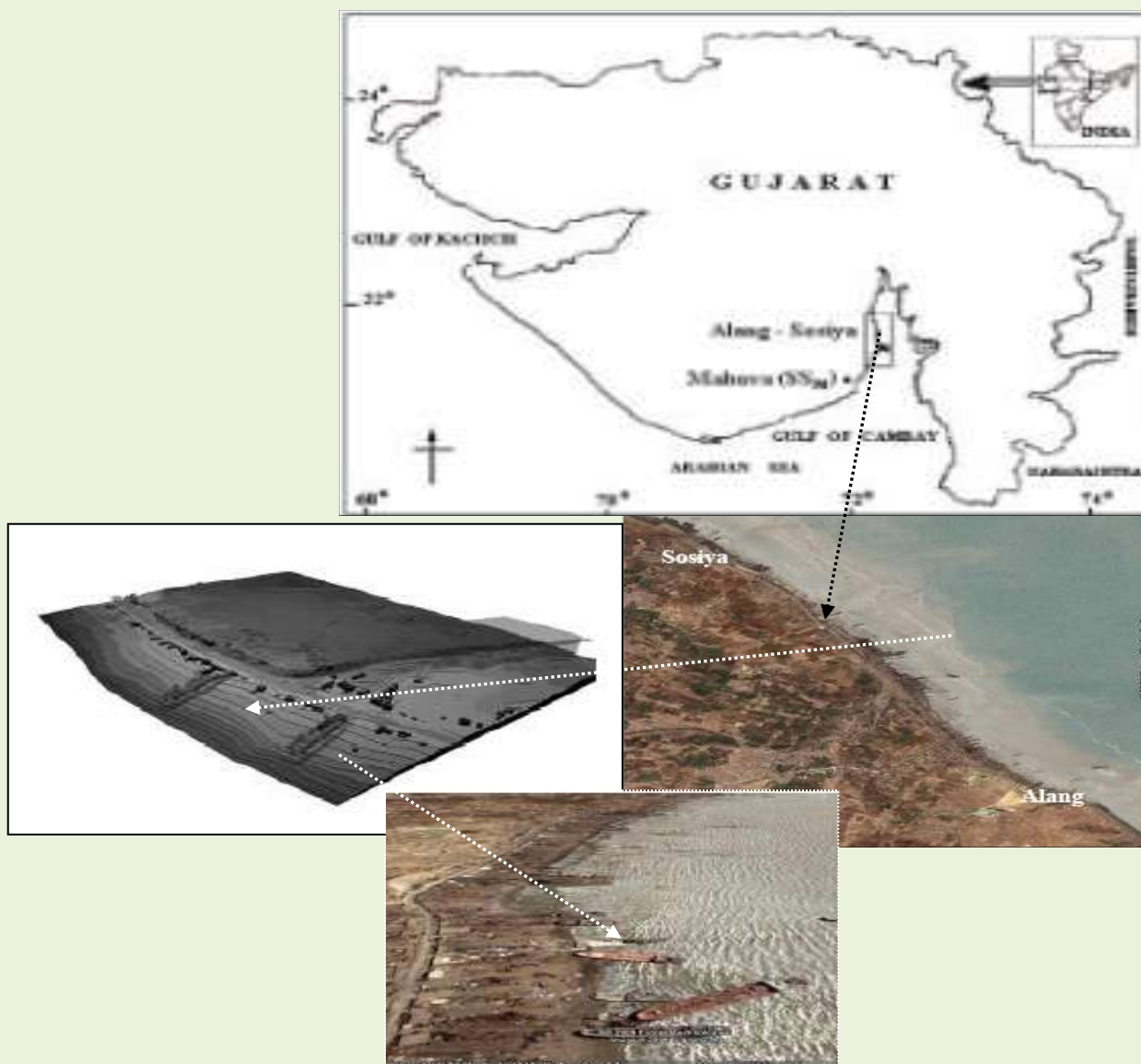
### INTRODUCTION:

ASSBY coast here enjoys certain distinct characters that make it conducive for forced ship beaching as well as dismantling. The tidal amplitude at the sheltered coastal area around ASSBY is usually in the range of 10-12 m.; the firm seabed and gentle seaward slope and mud free conditions make it ideal beaching condition. In addition this region has a semi arid climate (usually 7.4 – 47.3 degree C. with mean lowest at 21.9 and mean highest at 34.2 degree C, 558 mm mean rainfall with lot of dry days available which in turn generates continuous working hours and days throughout the year. <sup>1,3</sup>

Despite growing concern of bioinvasion and perceptible threats of disease-causing pathogens, direct studies on translocation of bacteria through ballast are rare, as well as the extent and implicit effects of the transfer of microorganisms in ballast water are not studied.

**MATERIALS AND METHOD:**

To quantify various groups of bacteria, water samples were collected during high tide and low tide from different locations. These sampling spots represented high-, moderate and low and off pollution zones in the ASSBY. Criteria for categorizing pollution gradients were: dissolved oxygen ( $< 2 \text{ mg l}^{-1}$  in high pollution zone), biological oxygen demand and nitrate-N General (total direct counts, total viable counts), pollution indicator (total coliforms, faecal streptococci) and different pathogenic bacteria were quantified using appropriate methods and specific media.



*Fig:1 ASSBY location and ship breaking*

## RESULTS AND DISCUSSIONS:

Table:1 : Seasonal variation of different bacterial populations (cfu/ml; mean  $\pm$  SD) in different pollution-gradient zone

Bacterial group	Pollution gradient											
	High season			Moderate season			Low season			Control site season		
	Pre-monsoon	Monsoon	Post-monsoon	Pre-monsoon	Monsoon	Post-monsoon	Pre-monsoon	Monsoon	Post-monsoon	Pre-monsoon	Monsoon	Post-monsoon
General population												
TDC	8887571 $\pm$ 544425	373614.3 $\pm$ 31810.2	3854286 $\pm$ 228986	3222667 $\pm$ 31675.4	15091260 $\pm$ 2495415	2480000 $\pm$ 199753	6549333 $\pm$ 300322	298666.7 $\pm$ 67987.74	3740000 $\pm$ 215990	3740000	6005000	359000
TVC	401731.4 $\pm$ 6012.4	974617.1 $\pm$ 16523	15089 $\pm$ 853.57	127220.8 $\pm$ 2189.63	957500 $\pm$ 68905.8	3146.6 $\pm$ 270.71	588333.3 $\pm$ 46530.6	632852 $\pm$ 64484.9	13106.7 $\pm$ 57.91	14700	72500	60750
TC	126615.3 $\pm$ 214777.8	36893 $\pm$ 453.5	3764.0 $\pm$ 302.86	3100 $\pm$ 395.38	8893.33 $\pm$ 686.89	6823.33 $\pm$ 1141.14	10168.77 $\pm$ 1206.14	1120.0 $\pm$ 101.52	776.67 $\pm$ 106.28	250	2350	150
VLO	24546.43 $\pm$ 5349.66	7737.17 $\pm$ 603.37	5782.9 $\pm$ 429.55	4850.07 $\pm$ 350.75	6227.89 $\pm$ 179.42	7666.67 $\pm$ 493.29	10441.67 $\pm$ 9345.33	3019.76 $\pm$ 304.72	4183.33 $\pm$ 223.07	2050	2000	250
TS	10097 $\pm$ 330.73	15955 $\pm$ 3839.67	19971.2 $\pm$ 330.63	4322.88 $\pm$ 93.42	532.5 $\pm$ 890.16	3143.33 $\pm$ 4905.98	657.67 $\pm$ 30.34	8083.33 $\pm$ 1212.53	4376.00 $\pm$ 746.87	30	90	195
Specific pathogen												
ECO157	3607.86 $\pm$ 578.99	2507.54 $\pm$ 32.73	1525.25 $\pm$ 18.99	2255.87 $\pm$ 433.01	1251.56 $\pm$ 11.46	712.33 $\pm$ 111.6	66.67 $\pm$ 11.55	83.33 $\pm$ 14.43	136.93 $\pm$ 22.79	8	0	0
VC	20207.14 $\pm$ 4308.88	3948.60 $\pm$ 384.49	63.87 $\pm$ 44.99	361.67 $\pm$ 337.87	200 $\pm$ 82.55	283.33 $\pm$ 91.43	10025.67 $\pm$ 996.53	121.83 $\pm$ 103.55	256.0 $\pm$ 14.11	12	20	3
VP	4289.29 $\pm$ 1049.36	139.14 $\pm$ 177.14	56.43 $\pm$ 69.32	66.67 $\pm$ 11.54	436.67 $\pm$ 34.30	170.67 $\pm$ 156.55	143.33 $\pm$ 24.83	49.96 $\pm$ 26.52	353.98 $\pm$ 37.33	1	0	22
SH	234.45 $\pm$ 36.34	150.67 $\pm$ 55.22	317.85 $\pm$ 33.64	122.33 $\pm$ 23.34	431.45 $\pm$ 30.64	658.33 $\pm$ 43.63	214.33 $\pm$ 64.67	153.23 $\pm$ 56.44	113.33 $\pm$ 36.34			
SA	41282.9 $\pm$ 560.20	1716.4 $\pm$ 146.87	1017.1 $\pm$ 126.24	3408.33 $\pm$ 497.37	1933.33 $\pm$ 199.08	1300.45 $\pm$ 100.37	5007.5 $\pm$ 498.75	916.67 $\pm$ 101.04	72.5 $\pm$ 11.43	10	0	0.5
FS	10033.21 $\pm$ 2448.35	121.4 $\pm$ 10.89	155.43 $\pm$ 59.76	1633.33 $\pm$ 270.15	405.91 $\pm$ 45.48	393.33 $\pm$ 31.01	33340 $\pm$ 3510.35	166.67 $\pm$ 28.87	101.67 $\pm$ 9.75	7	0	0.3
AH	330.63 $\pm$ 33.05	428.57 $\pm$ 60.82	80.57 $\pm$ 17.18	306.67 $\pm$ 36.33	333.33 $\pm$ 57.73	126.87 $\pm$ 19.41	211.67 $\pm$ 40.17	109.63 $\pm$ 17.86	53.09 $\pm$ 8.41	0	0	0
CA	1175.57 $\pm$ 443.28	355.78 $\pm$ 308.31	152.09 $\pm$ 34.65	367.33 $\pm$ 195.34	1123.33 $\pm$ 149.59	38.09 $\pm$ 0.54	1093.33 $\pm$ 885.46	68.33 $\pm$ 59.66	34.33 $\pm$ 5.69	0	18.9	0

TDC, Total direct count; TVC, Total viable counts; TC, Total counts; VLO, *Vibrio*-like organism; TS, Total streptococci; EC, *Escherichia coli* O157; VC, *Vibrio cholerae*; VP, *Vibrio parahaemolyticus*; SH, *Shigella* sp.; SA, *Salmonella* sp.; FS, *Streptococcus faecalis*; AH, *Aeromonas hydrophila*; CA, *Campylobacter* spp.; TDC was determined by acridine orange direct count following Hobbie *et al.*<sup>16</sup>. The following specific media were used for enumerating different populations of bacteria; nutrient agar for TVC; McConkey agar for TC and EC; thiosulphate citrate bile salts sucrose agar for VLO, VC and VP; xylose lactose deoxycholate agar for SA and SH; *E. coli* O157 agar for *E. coli* O157; Hi-Crome salmonella agar for SA and EC; M enterococcus agar for TS; *Aeromonas* isolation agar for AH; Blood-free *Campylobacter* selectivity agar for CA and bile esculin azide agar for FS. Typical colonies on these media were counted as like organisms and 50% were considered as actual ones using inferences from serotyping (representative) exercise. Standard microbiological methods and media were employed for this study<sup>18</sup>.

## DISCUSSION:

Quantifying bacterial groups is of pertinence in management ASSBY since a peculiar problem and concern is that one cannot move an empty vessel offshore for ballast intake. Since utmost importance is to be paid to maintain the stability of the ship, most oil tankers and cargo vessels need to take in (or discharge) water within the zone anywhere in the world. Thus, when the harbour water, which is abundant in pathogens both from urban sewage and previous ballast-discharges is pumped in, the loading of ballast tanks with a cocktail of potent pathogens is imminent. Attachment of pathogenic bacteria to living amoebae, many stages of shellfish larvae<sup>10,11</sup>, dinoflagellate cysts to exoskeletons of chitin-bearing copepods, plankton and seaweeds

contribute significantly to their survival for several days to months<sup>12,13</sup>, as is also evidenced by monitoring direct viable fractions (° metabolically active fractions). They can also survive unattached for weeks, and upon deballasting, are dispersed<sup>10</sup> and can establish in new destinations<sup>13</sup>. We observed similar trend in artificial, natural and diluted sea-water microcosms as well (unpublished observations). These results affirm the persistence of allochthonous microflora in the marine environment. Despite the annual variations, our observations during different seasons help recognize the high abundance of both indicators (total coliforms and total streptococci) and many human pathogenic bacteria. As already known for different species of bacteria<sup>4,12</sup>, small numbers of all pathogens we examined, surely surviving in sea water for one to several weeks<sup>14,15</sup>, when taken in with ballast water would disperse to other regions through ballast movement. Our seasons-based analyses of a variety of samples from ASSBY area make evident the perpetual presence of a plethora of potential human pathogens. Avoidance of ballast water exchange in areas with loads of pathogenic bacteria is a better option to reduce risks of microbial bioinvasion. We stress that the results from this study need not be viewed only from the immediate economic gains viewpoint, but be taken serious note of for long-term safety and for the benefit of future posterity. It is not impossible to establish clean water harbours by adapting technological advances, strict monitoring and compliance of the upkeep of environment in its near nascence.

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