

Paratypes: Four otoliths (IITR/SB/252-256).

Horizon and locality: Dark-green shale below the top lignite seam, Vastan lignite mine, Surat District, Gujarat.

Etymology: Named after Dr Dirk Nolf (Belgium), in recognition of his research on fossil otoliths.

Diagnosis: Overall shape somewhat trapezoidal with extended postero-ventral region; inner face slightly convex; outer face much more convex; greatest thickness at the centre; ventral rim somewhat rounded and characteristically longer than dorsal rim; posterior rim oblique; anterior rim obliquely straight; sulcus with a larger ostium than cauda; anterior end of sulcus close to, but totally disconnected from ostial rim; shallow but distinct depression above the sulcus.

Remarks: This species is not closely comparable to any known fossil gobiids and probably belongs to an extinct genus.

Genus *Gobiidarum vastani* n.sp.

Material: Approximately 150 otoliths.

Holotype: IITR/SB/257, right otolith.

Paratypes: Eight otoliths (IITR/SB/258-265).

Horizon and locality: Dark-green shale below the top lignite seam, Vastan lignite mine, Surat District, Gujarat.

Etymology: Named after the type locality Vastan, Surat District, Gujarat.

Diagnosis: Shape sub-quadrangular; height and length nearly equal; maximum thickness of otoliths in the lower half; outer

face markedly more convex than inner face; ventral rim broadly rounded and slightly longer than dorsal rim; prominent postero-dorsal angle present on the dorsal rim; upper half of both anterior and posterior rims with a characteristic notch; posterior constriction more prominent; sulcus located anteriorly along the midline but totally disconnected from anterior margin; ostium expanded antero-ventrally; shallow depression present just above the sulcus.

Remarks: This species resembles 'Gobiidae sp.2' from the Middle Eocene Nanggulan Formation of Java<sup>5</sup>, but the latter species can be easily distinguished by its centrally located sulcus.

The present find is paleobiogeographically significant because it represents the oldest record of the family Gobiidae in the world. Taken together with the presence of gobiids in the middle Eocene of Kutch and Java, it clearly shows that the traditional idea of an 'explosive' appearance of this family at the Eocene-Oligocene boundary was probably an artifact of the fossil record, and that the gobiids were already an important group in the early Eocene coastal marine fish ecosystems in India. This probably holds true for several other groups of perciform fishes whose otolith-based fossil records have so far been known mainly from Europe, but which are strikingly diverse in modern Indo-West Pacific marine faunas. Ongoing study of the Vastan and Kutch otolith associations is expected to

provide further insight into the nature of early history of these groups.

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SUNIL BAJPAI\*  
VIVESH VIR KAPUR

*Department of Earth Sciences,  
Indian Institute of Technology,  
Roorkee 247 667, India*

*\*For correspondence.  
e-mail: sunilfes@iitr.ernet.in*

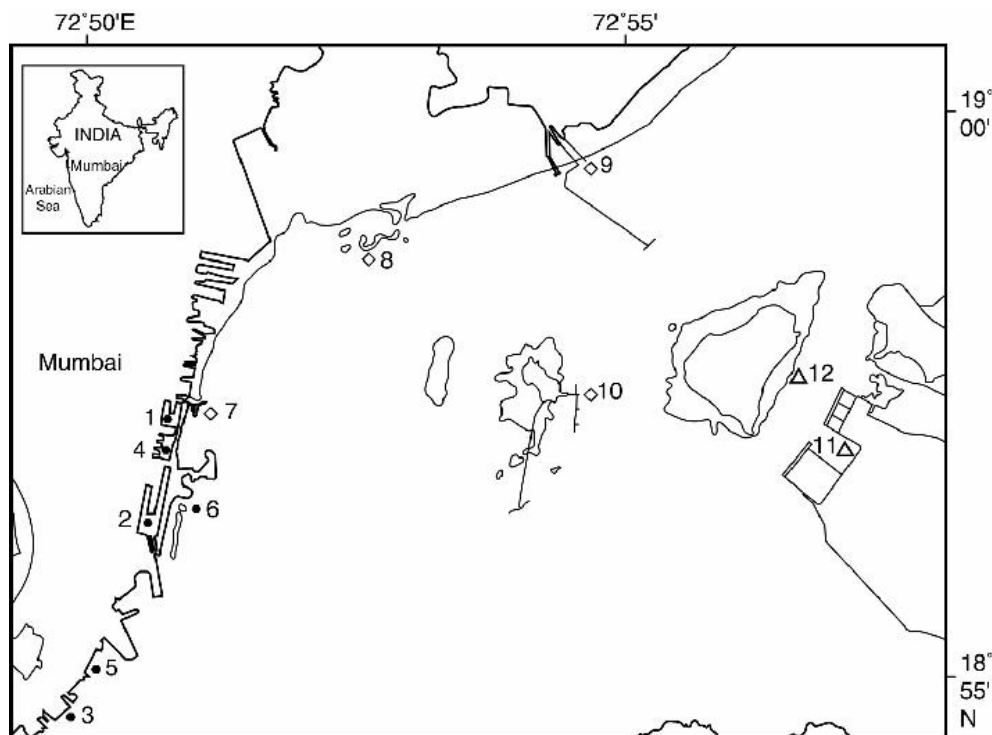
## Abundance of pollution indicator and pathogenic bacteria in Mumbai waters

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. From the ca. 12 billion tones of annual translocation of

ballast water by bulk cargo ships, increasing numbers of non-indigenous organisms have become established in new locations around the world<sup>1</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. In addition to a variety of macro-bio-invaders<sup>2,3</sup>, many bacteria can survive long duration in the ballast tanks<sup>4</sup>.

Upon ballast release, alien species/strains capable of competing with their resident counterparts become established. Therefore, concerns on locations where exchange takes place and the possible effects of alien organisms taken in during exchanges on the receiving port (including the open ocean), need critical evaluation.

With ca. 5000 ships berthing annually, the Mumbai Port is among the busy ones. Bulk cargo importing/exporting and oil-importing ships possibly exchange ca. 50



**Figure 1.** Sampling locations in Mumbai harbour, Mahul creek, Jawaharlal Port area. Locations in most polluted zone (indicated by circles) are: 1, Princess Dock; 2, Indira Dock; 3, Sassoon Dock; 4, Victoria Dock; 5, Apollo Bunder; 6, Berth 20. Locations in moderately polluted zone (indicated by diamonds) are: 7, Ferry Wharf; 8, Mahul Creek; 9, New Pirpau Point and 10, Jawahar Dweep. Locations in less polluted zone (indicated by triangles) are: 11 Jawaharlal Nehru Port Trust (JNPT) and 12, near Elephanta island. A control site (not shown in the map), at 18°57'N and 72°46'E located ca. 25 km southwest of Princess Dock was sampled during all three collections for this study.

million tons of ballast water within the precincts of this port. To quantify various groups of bacteria, water samples were collected during November 2001 (post-monsoon), April (pre-monsoon) and October 2002 (monsoon) from different locations (Figure 1). These sampling spots represented high- (Princess Dock, Indira Dock, Sassoon Dock, Victoria Dock, Apollo Bunder, Berth 20, and Ferry Wharf), moderate- (Mahul Creek, New Pirpau Point and Jawahar Dweep) and low- (Jawaharlal Nehru Port Trust (JNPT) and off Elephanta island) pollution zones in the Mumbai harbour–Mahul creek–JNPT confluence. Criteria for categorizing pollution gradients were: dissolved oxygen ( $< 2 \text{ mg l}^{-1}$  in high pollution zone), biological oxygen demand ( $\geq 4.5 \text{ mg l}^{-1}$  in high pollution zone) and nitrate-N ( $\geq 0.35 \text{ mg l}^{-1}$  in high pollution zone). General (total direct counts, total viable counts), pollution indicator (total coliforms, faecal streptococci) and eight different pathogenic bacteria were quantified using appropriate methods and specific media. Further, typical colonies of *E. coli* O157 (from *E. coli* O157 agar) and

*Shigella* from xylose lysine desoxycholate agar were sero-typed using antisera by following manufacturer's (Difco) instructions. Over 65% (67 of 102 isolates) of the tested colonies counted as *Shigella*-like organisms were found to be serotypes of *Shigella-Alkaligenes* Dispar group. Similarly, 85% (85/97) of *E. coli* O157 colonies agglutinated with the antiserum (*E. coli* O antiserum O157). From a previous fatty-acid fingerprint analysis, it was found that nearly 65% (8 of the 12 tested) isolates of *Vibrio parahaemolyticus*-like organisms from TCBS medium proved to be strains of *V. parahaemolyticus*. Thus, assuming a moderate 50% colonies counted as 'like organisms' actually belonging to the species we looked for, the abundance of eight pathogenic bacteria during pre-monsoon (March–May; sampled in April), monsoon (June–October; October) or post-monsoon (November–February; November) are available (Table 1).

We categorized all those pathogenic groups with  $\geq 50 \text{ cells ml}^{-1}$  as those of high intensity. All pathogenic groups we looked for were high during all three sea-

sons throughout the study area. In contrast, at a control site (Figure 1) 25 km from the docks, many were  $\leq 10 \text{ cells ml}^{-1}$  (Table 1). Their preponderance ( $\geq 200$  colonies  $\text{g}^{-1}$  dried wt) was discernible throughout the year in samples of sediments, plankton and marine macrophytes (Table 2). Total counts of bacteria ( $10^9$ – $10^{10} \text{ l}^{-1}$ ) in Mumbai waters far exceeded the numbers reported from Chesapeake Bay<sup>4</sup>, which receives an estimated  $1.2 \times 10^{10} \text{ l}$  or more of foreign ballast. Total coliform counts, in the range of  $10^3$ – $10^4 \text{ ml}^{-1}$  are 2–3 orders higher in comparison with the Hong Kong harbour<sup>5</sup> or Seine River and its estuary<sup>6</sup>. In general, owing to large outfalls of sewage and a variety of industrial effluents from Mumbai Metropolis, the Mumbai harbour–Thana creek–Bassein creek confluence supports high microbial activity, and abundance (both pathogenic and other allochthonous) and ecologically versatile bacterial groups<sup>7–9</sup>. Although several other disease-causing organisms might be present, our results are useful to recognize high density of bacterial pathogens causing cholera (enterotoxigenic *E. coli* O157 and *Vibrio chol-*

**Table 1.** Seasonal variation of different bacterial populations (numbers ml<sup>-1</sup>; mean ± SD) in different pollution-gradient zones of Mumbai harbour and control site mean counts (numbers ml<sup>-1</sup>) ca. 25 km offshore from Mumbai harbour

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

*erae*), gastroenteritis (*V. parahaemolyticus*, *Campylobacter* spp.), salmonellosis (*Salmonella* spp.), shigellosis (*Shigella* spp), aeromonad septicaemia (*Aeromonas hydrophila* group), meningitis and other streptococcal conditions (*Streptococcus* spp) in the study area.

Quantifying bacterial groups is of pertinence in ballast management of ships since a peculiar problem in ship-stability 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) ballast water within the harbour 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. Inside the ballast tanks, 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>.

All four strains of potent pathogens we isolated from these waters survived for ten or more weeks (Table 3) when held in filtered sea-water microcosms set up to represent the ballast-intake waters. 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 envi-

**Table 2.** Different bacterial populations (numbers  $\times 10^3$  g dry wt<sup>-1</sup> sample) in sediment, animal and plant samples collected from Mumbai harbour

Bacterial type*	Animal and plant sample			
	Sediment	Barnacle	Zooplankton	<i>Chaetomorpha</i>
General population				
TVC	2240970	1427900	2087601573	446428693
TC	1.792	100.52	4382	428.57
VLO	208.41	282.30	25040	3830.36
TS	5.602	1.14	200.32	0.183
Specific pathogen				
EC O157	191.83	0.0057	2472.70	100
VC	75.07	256.73	7512	11473.22
VP	15.87	147.79	35056	1790.18
SA	21.22	133.87	23788	0.205
SH	16.96	11.38	169.02	2.28
FS	28.46	24.27	525.84	24062.51
AH	0.381	0.128	9.39	0.48
CB	27.90	920.28	275.44	38705.37

\*Refer to Table 1 for expansion of abbreviations. Since the differences between seasons were not pronounced, data presented here are mean of all sediment ( $n = 24$ ), animal ( $n = 3$  each) and plant (*Chaetomorpha*,  $n = 3$ ) samples collected during different sampling seasons.

**Table 3.** Persistence of direct viable bacterial numbers (DVN; counts ml<sup>-1</sup>) in 2.5 l microcosms containing natural, filtered seawater without added carbon and energy sources. DVN determined following Kogure *et al.*<sup>17</sup>

Bacterial species	Starvation duration (days)			
	0	28	60	75
<i>Pseudomonas aeruginosa</i>	$7.93 \times 10^5$	$2.93 \times 10^4$	$9.09 \times 10^3$	$7.74 \times 10^3$
<i>Salmonella</i> sp.	$6.39 \times 10^5$	$1.20 \times 10^4$	$4.04 \times 10^3$	$1.98 \times 10^3$
<i>Escherichia coli</i> O157	$4.21 \times 10^5$	$2.48 \times 10^4$	$3.03 \times 10^3$	$2.35 \times 10^4$
<i>Vibrio cholerae</i>	$1.62 \times 10^5$	$1.33 \times 10^4$	$6.07 \times 10^3$	$2.71 \times 10^3$

ronment. 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.

In the future of ballast-water-management arena, assessment of incidence of as many individual pathogenic groups (including their genetic differences) as possible would be necessary, as we have done in this study. Owing to the involvement of different geographic locations, cargo types, shipping routes, accidental deballasting into restricted oceanic/coastal areas and some other navigational aspects,

there will be a need to know as many details as possible, in particular of human pathogens, including viruses. Although innumerable microbial species in the past might have gone out or, have been brought in, the densities of many human pathogens found during this study are alarmingly high. A note of caution however, is that ships deballasting into this already poor quality environment might have been and could be adding pathogens from other regions of the world. Invasion of pathogenic microorganisms from other locations would worsen the situation here and expose the native biota already under stress to a new domain of biological threats affecting fishing and recreation, among other activities. Our seasons-based analyses of a variety of samples from Mumbai Port 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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N. RAMAIAH\*  
VRUSHALI KOLHE  
A. SADHASIVAN

*National Institute of Oceanography,  
Dona Paula,  
Goa 403 004, India*

\*For correspondence.

e-mail: ramaiah@darya.nio.org

## Falling Late Holocene sea-level along the Indian coast

The global rise in the sea-level, which accompanied the melting of great ice sheets of the last glacial episode, started ca. 14 ka BP and continued with minor oscillations till the present sea-level was reached. There are three main schools of thought as regards the sea-level changes during the last 6 ka BP, viz. (i) the sea-level underwent relatively large fluctuation repeatedly from 1.5 m below to 3 m above the present level<sup>1</sup>; (ii) the sea-level has been lower than the present but has maintained a continuous rising trend, with an ever decreasing amplitude, before reaching its present level<sup>2</sup>, and (iii) the sea-level rose above the present level ca. 5 ka BP and oscillated between 2 m above and the present level<sup>3</sup>.

The third suggestion of high sea-level during the post last glacial period was based largely on the presence of marine terraces on Pacific islands. Substantial evidences of sea-level stands during the last 6 ka BP, as measured over large portions of the Southern Hemisphere, are now available<sup>3</sup>. A review of data, obtained from different places in the non-glaciated and tectonically stable regions of the Southern Hemisphere, shows that during this period the sea-level had oscillated. In the tectonically stable New South Wales coast of Australia, numerous marine shells found above present-day sea-level and associated with beach rocks up to 3.5 m above sea-level, indi-

cate relative fall in sea-level during Late Holocene, with minor oscillations<sup>3</sup>.

On the Arabian Peninsula, the Holocene sea transgressed inland approximately 7 ka BP that continued until 4 ka BP. Since then, regression set in, which has led to progressively seaward development of intertidal and supratidal zones<sup>4</sup>. There are beach terraces located 1–3 m above the present high-level marks on the Arabian side of the Gulf, which were formed as a result of Late Holocene transgression. There is no important tectonic movement in the entire Arabian Peninsula, with the exception of weak uplifts in some areas<sup>5</sup>.

The sea-level change curves for the Holocene of Indian coastal areas are far from clear. From the available data, previous workers<sup>6–9</sup> have drawn slightly differing curves. However, according to these researchers, the sea-level was much below (~90 m) the present msl about 14.5 ka BP. It rose to around –70 m about 10 ka BP at a fast rate and then slowed down considerably till it reached the present level about 7 ka BP. Beyond 7 ka BP till ca. 4 ka BP, a steady, rising sea-level trend was maintained<sup>9,10</sup>. The sea-level reached 2–4 m higher than the present about 5–6 ka BP<sup>11</sup>. It continued to rise further till about 4.5 ka BP. Since then, the sea-level has been falling as demonstrated by the occurrence of old tidal flats inland to the newer tidal flats. Even

the shifts of the coastal dunes, younging towards the sea coast, lead to the same conclusion of the emergence of the coast in recent times<sup>12</sup>.

A gastropod shell, *Cerithium*, obtained from lagoonal marls of old tidal flats at an altitude of about 1 m above the High Tide Level (HTL), and exposed about 8 km from Porbandar on the Porbandar–Veraval Highway (Porbandar district, Gujarat) has been dated by <sup>14</sup>C method to be 4080 ± 90 yrs BP (Sheila Kusungar, PRL, Ahmedabad; pers. commun.).

Recently, we collected several invertebrate shells and a few semi-fossilized coral heads from the youngest part of Unit IV (algal rudstone) of Aramda Reef Member, Chaya Formation exposed in Mithapur, Jamnagar district, Gujarat<sup>13</sup> (Tej Bahadur, unpublished Ph D thesis, University of Rajasthan). Aramda Reef Member has been interpreted as coral–algal reef facies of lagoon environment<sup>13</sup>. Although Unit IV is exposed extensively in Mithapur, the marginal lagoonal sediments were trenched out from the area near Bala Hanuman temple in Mithapur. This represents the youngest part of Unit IV. The shells include unaltered, well-preserved gastropods (*Trochus*, *Turbo*, etc.) and bivalves (Placunids and Cardids). The gastropod shell, *Turbo*, sent to Woods Hole Oceanographic Institute, USA for <sup>14</sup>C dating by AMS (Accelerator Mass Spectrometry) method, has yielded