Why are mangroves degrading?

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A comparison has been made among 5 luxuriant and 25 degrading sampling sites in Pichavaram mangrove forests, for physico-chemical and biological variables. The data reveal that the causes of natural degradation of mangroves are mainly due to high salinity, low level of available nutrients, and poor microbial counts in the soil substrates.

MANGROVE forests are among the world's most productive ecosystems that protect coastal populations and support coastal fisheries and livelihood[1]. With continuing degradation and destruction of mangroves, there is a critical need to understand them better. To cite an example, Pichavaram is among one of the best-studied mangrove ecosystems in India; its area has already lost 75% of its green cover within the last century and of the existing forest area, only 10% has dense vegetation while the remaining 90% of the area has been degrading[2]. There is an urgent need to identify the causative factor(s) of natural degradation of mangroves in order to suggest remedial measures towards their restoration.

The study area (lat. 11°27′N; long. 79°47′E) is located between the Vellar and Coleroon estuaries (Figure 1). The mangrove area named as 'Pichavaram' occurs on 51 islets, ranging from 10 m^2 to 2 km^2, separated by intricate waterways, that connect the Vellar and Coleroon estuaries. The southern part near the Coleroon estuary is predominant with mangrove vegetation, while the northern part near the Vellar estuary is dominated by mud flats. The mangrove system covers an area of about 1100 ha, of which 50% is covered by forest, 40% by waterways and the remaining filled by sand-flats and mud flats.

The Vellar estuary opens into the Bay of Bengal at Parangipettai and links with the Coleroon River, which is a distributary of the River Cauvery. Mixing of three types of waters influences the mangrove area: (1) Neritic water from adjacent Bay of Bengal through a mouth called 'Chinnavaikkal', (2) Brackish water from the Vellar and Coleroon estuaries, and (3) Fresh water from an irrigation channel ('Khan Sahib canal'), as well from the main channel of the Coleroon River.

The tides are semi-diurnal and varying in amplitude from about 15 to 100 cm in different regions during different seasons, reaching a maximum during monsoon and post-monsoon and a minimum during summer. The rise and fall of the tidal waters is through a direct connection with the sea at the Chinnavaikkal mouth and also through the two adjacent estuaries. The depth of the waterways range from about 0.3 to 3 m.

In order to understand the stress factors, degrading mangroves were compared with luxuriant ones at Pichavaram. For this purpose, 25 degrading and 5 luxuriant sites were selected (Figure 1). From each site, soil samples were collected at a depth of 5–10 cm. The physico-chemical factors, floral and faunal resources were analysed.

The floral species were analysed for height and species composition as well as bacterial load (total heterotrophic bacterial counts). The faunal species such as prawns, crabs and fish were studied for their species composition and density.

The physico-chemical factors analysed were solar radiation, soil temperature, humidity, tidal amplitude, pH, electrical conductivity, levels of Na, K, N, P, Ca, Mg and trace elements (Pb, Cd, Cu, Co, Mn, Fe, Ni).

The following standard methods were used:

- Quantification of total heterotrophic bacteria by adopting pour plate method[3];
- Total organic carbon by chromic acid method[4];
- Measurement of temperature using a centigrade thermometer;
- Salinity using hand refractometer (Erma, Japan);
- Light intensity using a Lux meter (Digital TES-1332);
- Humidity using a hygrometer (Huger, West Germany);
- pH using a pH Pen (Hanna instruments, EN 50081-1);
- Electrical conductivity and total dissolved solid using a EC-TDS analyser (CM 183 Elico, India);
- Trace elements estimated using an Inductively Coupled Plasma Spectrophotometer (Japan);
- Sodium, potassium, calcium using a flame photometer (Elico Cl 22D, India);
- Nitrogen and phosphorus analysed in Sugarcane Breeding Research Institute, Cuddalore;
- Total sugar[5];
- Total amino acids[6];
- Tannin[7];
- Soil texture (Sieving method);
- Soil moisture (wet and dry weight base method); and
- Fishery resources (Cast net operation).

The objective of this work is to find out the stress factors that are responsible for degradation of mangroves, by comparing degrading mangroves with luxuriant ones. The data related to physico-chemical and biological aspects of the two different habitats are shown in Table 1.

The data reveal that the luxuriant mangrove sites are rich in biodiversity of flora and fauna. In degrading sites, there is a reduction of 67.5% in floral species. The tree height is also lower by 83.4% in *Avicennia marina*, and by 78.8% in *Rhizophora mucronata*. However, there is a luxuriant growth of a salt march species, *Suaeda mari-*

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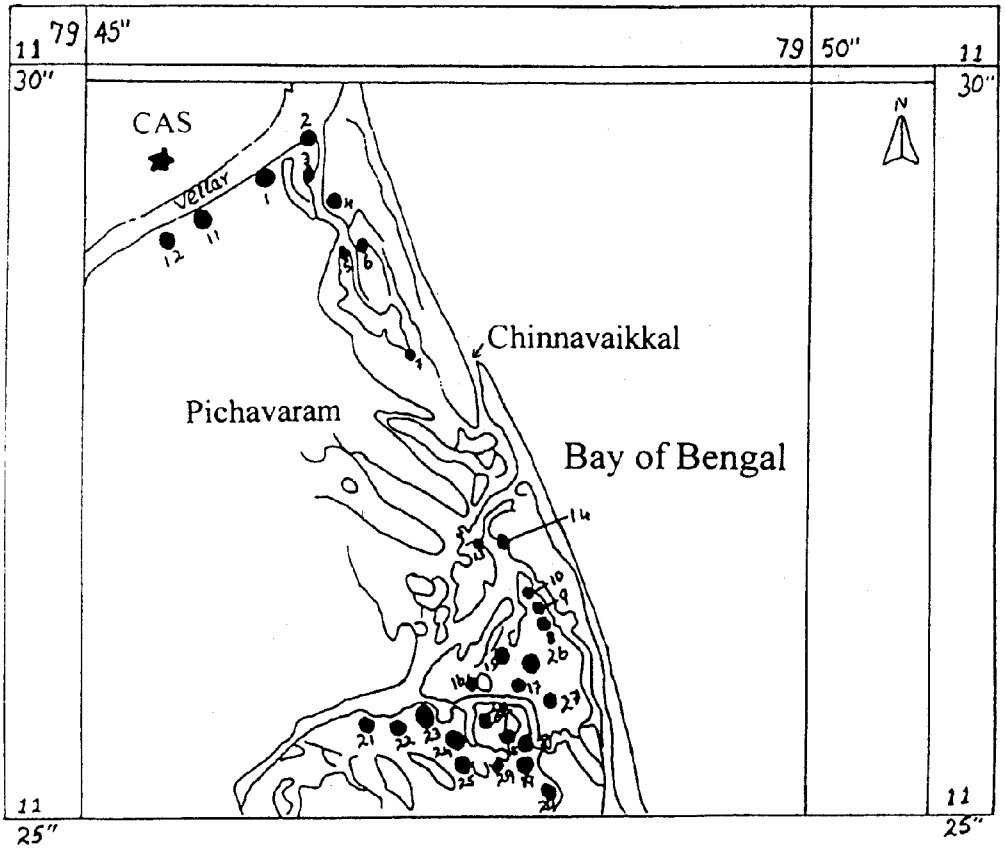

Figure 1. 25 degrading sampling sites (1–25) and 5 luxuriant sites (26–30).

tima, in degrading sites with a height increase by 17.3%. The *Suaeda* species may therefore, serve as indicator species of degrading mangrove sites.

The faunal resource in degrading mangroves is lower by 71.5% and its biodiversity by 59.1% than that in luxuriant mangroves. Prawn resource in degrading mangrove waters is lower by 56.7% than that in luxuriant ones; of which, *Metapenaeus* species are much lower by 86.1%. Fish in degrading site are lower by 55.1% and the crabs by 54.1% than those in luxuriant sites.

Level of organic solutes is lower in degrading mangrove habitats than in luxuriant site. For instance, total organic carbon is lesser by 28.5%, total sugars by 54.8%, and total amino acids by 34.5%. Due to low organic solutes, the total heterotrophic bacterial counts are lower by 85% in the degrading mangroves. There is also a reduction of soil nitrogen by 19.7%, phosphorus by 15.7%, and potassium by 19.9% in the degrading sites.

The light intensity in the degrading sites is higher by 41.6% due to poor tree canopy structures, leading to higher soil temperature by 12.8%. This results in evaporation of water, and concentration of salts, as is evident by an increase of salinity by 63.7%. Moreover, the soil tends to become sandy in degrading sites with lower water-holding capacity by 23.2% and lesser soil moisture by 25.4% than luxuriant site, which on the contrary are silt clay with high water holding capacity and moisture content.

Studies of forest structure reveal that timber resources are poor, mainly due to shorter canopies (10 m in *Rhizophora mucronata*; Table 1), as was also observed by other workers in the study area[2,8,9]. This compares unfavourably with the mangroves in South Sumatra (55 cm canopy height), Philippines (25–30 m), and Mexico (17 m)[10]. The brackish waters, which accumulate in the bowl-shaped mangrove soil substratum during monsoon, turn hyper-saline during summer, ultimately killing or retarding the growth of mangrove seedlings and those central areas become barren after some years. Such a situation is seen at degrading sites of Pichavaram, where the condition is hyper-saline. This problem becomes serious due to poor precipitation and poor flux of fresh waters and tidal waters[2].

It is clear from the data that the degradation of mangrove habitat is due to an array of factors mainly to high salinity, low level of available nutrients and poor microbial counts (Table 1). Hypersalinity induces stunted growth of *Avicennia marina* stands[11], reduces biomass in hydroponically grown *Bruguiera gymnorrhiza*[12], and causes denaturing of terminal buds in *Rhizophora mangle*

Table 1. Physico-chemical, and biological aspects of degrading and luxuriant mangrove habitats of Pichavaram forests

Variable	Mangrove habitat		% loss (–) or gain (+) due to degradation
	Degrading*	Luxuriant**	
Floral species (no.)	2.60 ± 1.8	8.00 ± 2.4	–67.5[a]
Tree height of *Avicennia marina* (m)	1.31 ± 1.0	7.90 ± 1.24	–83.4[a]
Tree height of *Rhizophora mucronata* (m)	2.12 ± 0.7	10.0 ± 1.6	–78.8[a]
Plant height of *Suaeda maritima* (m)	0.88 ± 0.2	0.75 ± 0.1	+17.3[b]
Faunal resource (no./5 hauls)	15.28 ± 5.94	53.6 ± 11.8	–71.5[a]
Faunal species (no./5 hauls)	5.73 ± 2.1	14.0 ± 0.6	–59.1[a]
Prawn resource (no./5 hauls)	18.26 ± 13.3	42.2 ± 10.7	–56.7[a]
Metapenaeus spp. (no./5 hauls)	3.57 ± 4.33	25.6 ± 10.8	–86.1[a]
Crab resource (no./5 hauls)	1.47 ± 1.4	3.2 ± 0.7	–54.1[a]
Fish resource (no./5 hauls)	4.22 ± 3.5	9.4 ± 3.2	–55.1[a]
Total organic carbon in soil (mg/g)	7.26 ± 2.8	10.16 ± 1.0	–28.5[b]
Total sugars in soil (mg/g)	0.14 ± 0.1	0.3 ± 0.1	–54.8[a]
Total amino acids in soil (mg/g)	6.14 ± 2.2	9.37 ± 0.7	–34.5[b]
Tannins in soil (mg/g)	0.81 ± 0.4	1.04 ± 0.1	–22.4[b]
Total heterotrophic bacteria in soil ($\times 10^3$/g)	268.3 ± 99.9	1797.1 ± 177.9	–85.0[a]
Total nitrogen (mg/kg)	59.6 ± 11.2	74.3 ± 3.1	–19.7[b]
Phosphorus (mg/kg)	15.73 ± 4.2	18.66 ± 2.5	–15.7[b]
Potassium (mg/g)	2.12 ± 0.7	2.65 ± 0.7	–19.9[b]
Calcium (mg/g)	1.26 ± 0.3	1.13 ± 0.1	+11.9[b]
Iron (ppm)	8655.7 ± 4838	10362.07 ± 2733.7	–16.5[b]
Copper (ppm)	7.85 ± 3.7	10.21 ± 28	–23.1[b]
Manganese (ppm)	72.8 ± 41.9	88.06 ± 34.1	–17.3[b]
Nickel (ppm)	12.39 ± 5.2	14.56 ± 31.1	–14.9[b]
Cobalt (ppm)	4.48 ± 1.7	5.14 ± 0.9	–12.8[b]
Cadmium (ppm)	2.0 ± 0.8	2.26 ± 0.5	–11.5[b]
Lead (ppm)	2.05 ± 0.9	2.32 ± 0.5	–11.6[b]
Zinc (ppm)	9.99 ± 4.3	13.11 ± 3.7	–23.8[b]
Light intensity (× 100 lux)	380.43 ± 153.61	268.6 ± 70.7	+41.6[a]
Soil temperature (°C)	31.87 ± 2.2	28.26 ± 0.9	+12.8[b]
Soil salinity (g/kg)	36.56 ± 13.63	22.33 ± 2.9	+63.7[a]
Electric conductivity (ms/cm)	57.42 ± 20.9	34.89 ± 4.5	+64.6[a]
Soil pH	7.63 ± 0.4	7.45 ± 0.2	+2.38[n]
Total dissolved solid in soil (ppt)	33.65 ± 15.6	17.85 ± 3.05	+88.51[a]
Coarse sand 0.5 mm (% of total)	3.38 ± 2.9	2.46 ± 1.7	+37.4[b]
Medium sand 0.25 mm (% of total)	22.2 ± 8.42	19.49 ± 10.1	+13.9[b]
Fine sand 0.125 mm (% of total)	41.4 ± 12.5	37.6 ± 5.1	+10.3[n]
Very fine sand 0.063 mm (% of total)	21.77 ± 7.1	21.67 ± 6.1	+0.5[n]
Course silt 0.037 mm (% of total)	12.39 ± 8.1	13.52 ± 7.9	–8.4
Silt and clay < 0.037 mm (% of total)	2.14 ± 1.2	3.26 ± 0.8	–34.4[b]
Water holding capacity (% of total)	46.26 ± 7.7	60.25 ± 2.6	–23.2[b]
Soil moisture (%)	31.49 ± 1.5	42.2 ± 6.8	–25.4[b]

*Values are the average of 25 sites **of 5 sites. [a]Values are significant at 1% and [b]at 5% level, and [n]not significant.

seedlings[13]. This also finds support to the fact that luxuriant mangrove forests are bestowed with either high annual direct precipitation and/or high surface water runoff from upland watersheds[14]. This is in accordance with Kathiresan *et al.*[15] who recorded a luxuriant growth of mangrove seedlings towards the monsoon month. The monsoon was associated with low salinity and high levels of nutrients. There was about 5-fold more of seedling growth and about 4-fold higher of leaf sprouting in monsoon (December) than those in summer months (April, July). The authors have attributed the luxuriant growth of mangroves to the monsoon runoff in the estuarine system that brings about profound changes such as lowering of salinity and increase in turbulence and nutrient levels. This also coincided with increased bacterial counts in the sediments, as observed by Kathiresan *et al.*[16], while monitoring a mangrove plantation that was artificially developed along the Ariyankuppam estuary along Pondicherry coast.

1. Kathiresan, K. and Bingham, B. L., *Adv. Mar. Biol.*, 2001, **40**, 81–251.
2. Kathiresan, K., *Hydrobiologia*, 2000, **430**, 185–205.
3. Chandramohan, D., in *Mangrove Microbiology, Role of Microorganisms in Nutrient Cycling of Mangrove Soil and Water*

(eds Agate, A. D., Subramanian, C. V. and Vannucci, M.), UNDP/UNESCO Regional project, 1988, pp. 61–84.
4. El Wakeel, S. K. and Riley, J. P., *J. Conseil Permanent Int. Pourl Explor. de la mer.*, 1956, **22**, 180–183.
5. Dubois, M., Gills, K. A., Hamilton, J. K., Roberts, P. A. and Smith, F., *Anal. Chem.*, 1956, **28**, 350–356.
6. Moore, S. and Steine, H., *J. Biol. Chem.*, 1948, **176**, 183–191.
7. Hagerman, A. E. and Butler, A. E., *J. Agric. Food Chem.*, 1978, **26**, 809–812.
8. Muniyandi, K., Ph D thesis, Annamalai University, Parangipettai, 1986, p. 215.
9. Kathiresan, K., Ramesh, M. X. and Venkatesan, V., *Environ. Ecol.*, 1994, **12**, 465–468.
10. Pool, D. J., Snedaker, S. C. and Lugo, A. E., Proceedings of the International Symposium on Biological Management of Mangroves, Honolulu, 1977, vol. 2, pp. 213–237.
11. Selvam, V., Mohan, R., Ramasubramanian, R. and Azariah, J., *Indian J. Mar. Sci.*, 1991, **20**, 67–69.
12. Naidoo, G., *Aqua. Bot.*, 1990, **38**, 209–219.
13. Koch, M. S. and Snedaker, S. C., *ibid*, 1997, **59**, 87–98.
14. Snedaker, S. C., in *Marine Geology and Oceanography of Arabian Sea and Coastal Pakistan* (eds Haq, B. V. and Milliman, J. D.), Van Nostrand Reinhold Co, New York, 1984, p. 255.
15. Kathiresan, K., Rajendran, N. and Thangadurai, G., *Indian J. Mar. Sci.*, 1996, **25**, 240–243.
16. Kathiresan, K., Rajendran, N. and Palaniselvam, V., *Indian J. Mar. Sci.*, 2000, **29**, 86–88.

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Molecular cloning and phylogenetic analysis of the ribosomal protein S19 from amphioxus *Branchiostoma belcheri tsingtaunese*

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An amphioxus cDNA, *AmphiS19*, encoding the ribosomal protein S19 was isolated from the gut cDNA library of *Branchiostoma belcheri tsingtaunese*. The cDNA contains a 444 base pair (bp) open reading frame, flanked by a 27 bp 5′ untranslated region and a 138 bp 3′ untranslated region. The ORF encodes a putative 147 amino acid protein with a calculated molecular mass of 16,222 Da. Alignment of the complete amino acid sequences of 14 eukaryotic S19 revealed that AmphiS19 exhibited >71.0% similarity to all known vertebrate homologues and <59.9% to those of the other eukaryotes, including invertebrates. The phylogenetic analysis based on the amino acids of invertebrate and vertebrate S19 proteins showed that the amphioxus protein was at the base of a clade of vertebrate S19 proteins, indicating that amphioxus is not only the sister group of extant vertebrates but also the basal lineage of chordates.

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RIBOSOMES are organelles that mediate the sequential addition of amino acids to the carboxyl end of the growing polypeptide chain, according to the blueprints encoded by the mRNA[1]. Each ribosome consists of two subunits. The eukaryotic 80S ribosome is composed of a large subunit – 60S, and a small one – 40S, while the prokaryotic 70S ribosome has a large subunit – 50S, and a small one – 30S. The large subunit contains three ribosomal RNAs (rRNAs), 5S, 5.8S and 28S, in eukaryotes, but only two, 5S and 23S in prokaryotes. The small subunit contains a single rRNA in both types of organism: an 18S rRNA in eukaryotes and a 16S rRNA in prokaryotes. Both eukaryotic and prokaryotic small subunits comprise several dozen ribosomal proteins. The proteins of the small subunit are called S1, S2... and those of the large subunit are called L1, L2...[2,3]. The ribosomal proteins have been largely identified and their sequences determined. Many ribosomal proteins have been shown to bind specific regions of rRNA. Ribosomal proteins catalyse ribosome assembly and stabilize rRNA tertiary structure, adapting the structure of the ribosome for optimal function[3]. The sequences of most eukaryotic ribosomal proteins have counterparts in prokaryotic ribosomal proteins, suggesting that they might derive from common ancestral nucleotide sequences present before the divergence of eukaryotes and prokaryotes, and be well-conserved throughout evolution[4]. However, it has been recently shown that the possibility of the phylogenetic utility of the ribosomal proteins cannot be ruled out[5].

The eukaryotic S19, a core protein that is associated with the 18S rRNA of the 40S small subunit generally contains 143 to 156 amino acids[6–8]. There are no known counterparts in prokaryotes, mitochondria and chloroplast, and therefore this protein appears to be a recent addition to the eukaryotic ribosomal protein repertoire[9]. The genes encoding eukaryotic ribosomal protein S19 have been identified extensively in species, including animals, plants, and fungi[7,8,10–13]. Amphioxus, a cephalochordate, is the closest living relative to the vertebrate, and has been widely known as the most important animal to study the origin and evolution of vertebrates[14]. To date, more than one hundred of genes have been cloned and sequenced in amphioxus such as the *Hox*[15], *Insulin-like* (*ILP*)[16], *Cdx*[17], and *AmphiF-spondin*[18]. However, the