

Figure 2. *Botryococcus* showing different stages of preservation. Solitary autospore ( $\times 960$ ); Two-chambered cup ( $\times 960$ ), Four-chambered cup ( $\times 900$ ), Botryoidal nature ( $\times 450$ ), Multicup aggregate ( $\times 900$ ); Abraded form ( $\times 400$ ).

sp., *Crybelosporites stylosus*, *Triporoletes reticulatus* and *T. radiates* (common occurrence) show a close resemblance with the *Triporoletes reticulatus* zone of this *Botryococcus*-bearing palynoassemblage from Kattarambakam.

Most of the fossil records of *Botryococcus* in India are from Eocene<sup>5-7</sup>, Miocene<sup>6-9</sup> and Pleistocene sediments<sup>10</sup>. Occurrence of this alga is also reported from Permian rocks of India<sup>11-14</sup>. The present

record of *Botryococcus* from the Lower Cretaceous (Late Albian) sediments from Kattarambakam is significant for it is the first record of this alga from Cretaceous of India.

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## Enechelon faults along West Coast of India and their geological significance

Subsequent to the advent of modern remote sensing technology, mapping and analysis of various lineaments and fractures and their correlation with geophysical and ground geological data have become a matter of great interest to geoscientists. The West Coast of India is one such region which has always attracted the attention of geoscientists and many have studied the region. The

significant amongst them are the studies by Jacob and Narayanaswamy<sup>1</sup>, Ramachandran<sup>2</sup> and Nair<sup>3</sup>. Jacob and Narayanaswamy<sup>1</sup> have observed that the Western continuity of the Palghat gap extends right up to 9° channel, separating Laccadives and Maldives. Ramachandran<sup>2</sup> has carried out very exhaustive analysis of lineaments by integrating total intensity aeromagnetic,

Bouger gravity anomaly and Landsat lineament data sets. On the basis of such an integration, he has identified four sets of lineaments in WNW-ESE to NW-SE, NNW-SSW, N-S to NNE-SSW and NE-SW directions.

Nair<sup>3</sup> has carried out structural interpretation for the entire West Coast of India and brought out certain newer information on the neotectonic activities





**Figure 1.** IRS 1A Satellite imagery mosaic of West Coast of Kerala showing Pleistocene faults. 1-6, lineaments/faults; □ Sinistral faults, A, Kasargod, B, Cochin, C, Cannanore; D, Mahe; E, Mysore; F, Kabbani river; G, Pandalayini; H, Ponnani river; I, Ootacamund massif.

In the present study, I have filtered out only the lineaments showing clear shifting of beds in the coastal landforms, which mostly fall in ENE-WSW direction.

The interpretation of IRS 1A satellite imagery data for the part of West Coast of Kerala and Karnataka, especially the area falling between Kasargod in the northwest and almost Cochin in the southeast (Figure 1), shows a set of ENE-WSW to NE-SW-trending sub-parallel lineaments, exhibiting clear sinistral shift of coastal landforms/shorelines in the area. Amongst these lineaments/faults, most of them are continuing even up to 700 to 800 km

in the continent with a clear northeasterly swing. They also continue up to Laccadives and Maldives in the southwest with ENE-WSW orientation (Figure 2).

1. The fault no. 1 trends in ENE-WSW direction with clear sinistral drag of beds in the coastal zone and coincides with the Lakshmithirtham lineament of Ramachandran<sup>2</sup>.

2. The ENE-WSW trending fault no. 2 of Cannanore region exhibits sinistral drag.

3. The fault no. 3 is again an ENE-WSW-trending linear feature, extending from Mahe in the West Coast to Mysore in Karnataka, with the swing towards

northeasterly. This sinistral coastal zone fault controls Kabbani river in the continental part and is described as Kabbani lineament with dextral strikeslip configuration by Katz<sup>4</sup> and Drury and Holt<sup>5</sup>.

4. The fault no. 4 shows sinistral shift of 5-6 km in the West Coast in Pandalayini area and merges with WNW-ESE trending Moyyar shear.

5. The fault no. 5 trends in general NE-SW direction from Ponnani river mouth in the West Coast to Elagiri hills in the northeast. This also exhibits minor sinistral shift of beds along Ponnani river mouth. It controls the Bhavani river and delimits the southeastern and southern boundaries of Ootacamund massif and Biligirirangan hills respectively. In its northeastern proximity, it forms the western limit of Javadi hills.

6. The fault no. 6 is trending in NE-SW direction from Cochin in the West Coast to Coimbatore in the northeast where seismicity was reported in 1900 (ref. 6).

Most of the above observed sinistral strikeslip faults are found to extend right up to Laccadives and Maldives in the Arabian sea (Figure 2) and amongst these, the fault nos 5 and 6 are found to form 9° channel, separating Laccadives and Maldives. In addition to the above faults, few more sinistral strikeslip faults were also interpreted (fault nos 8, 9 and 10, Figure 2). All these faults trend in NE-SW direction in the continental part, take a swing towards west-southwesterly and finally ends in Laccadives and Maldives (Figure 2). Similar to fault no. 5, the fault no. 7 observed south of Alleppey continues as 8° channel in Laccadives, causing similar sinistral shifts of land in Laccadives. All the above discussed ten faults have gradually shifted not only the West Coast of Karnataka and Kerala but also Laccadives and Maldives into an enechelon pattern (Figure 2).

The above discussed six faults (nos 1 to 6, Figure 1) and the other (nos 7 to 10, Figure 2) system of faults have been demonstrated to be Precambrian dextral strikeslip faults in parts of Tamil Nadu and the adjacent states<sup>2,4,5,7</sup>.

Such Precambrian NE-SW-trending dextral faults swing towards west-southwesterly, with sinistral strikeslip configuration in Kerala and Karnataka coast and in Laccadives and Maldives according to the present observations (Figures 1 and 2).



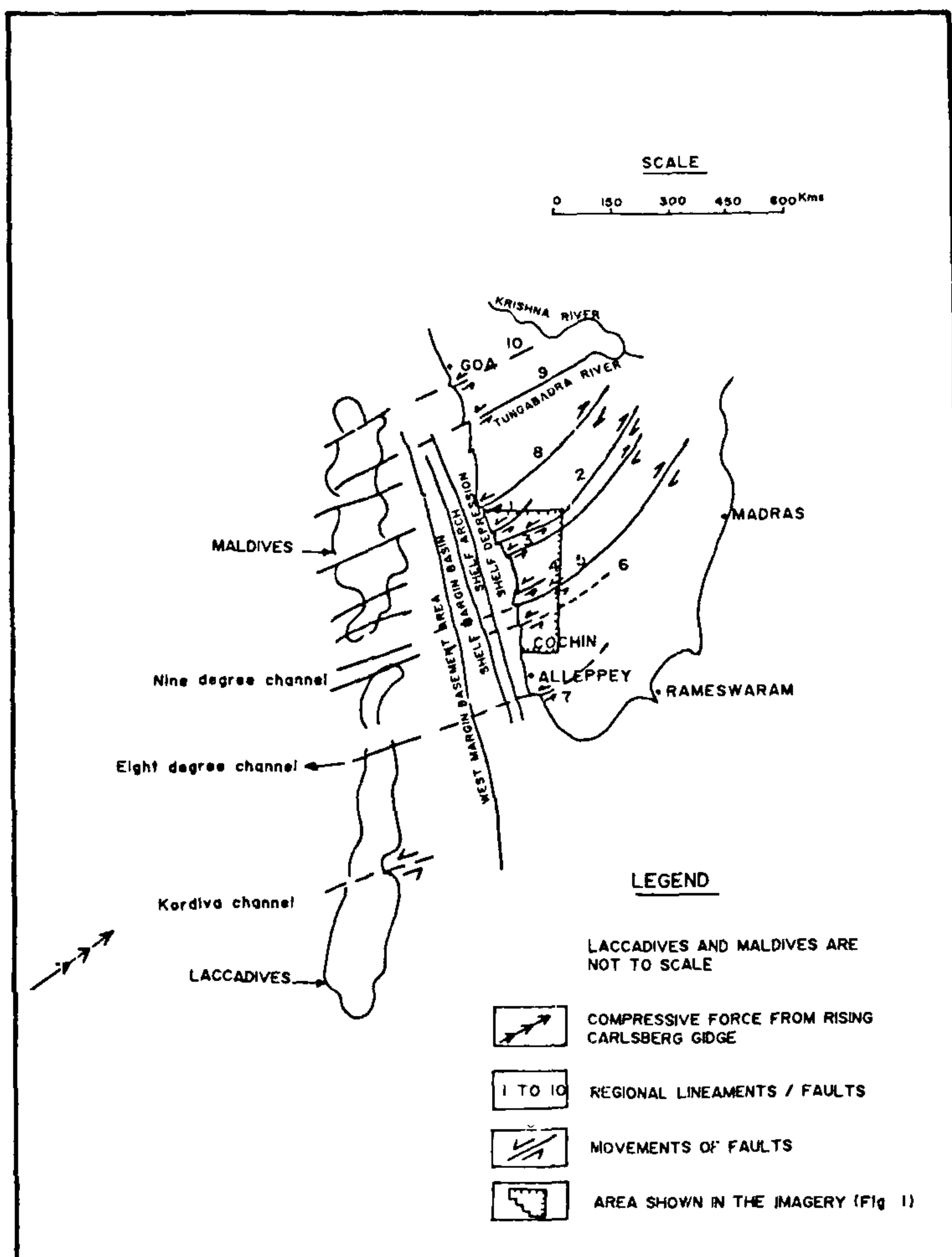


Figure 2. Off-shore and on-shore tectonic features of West Coast.

Nair<sup>8</sup> has also demonstrated clear Holocene earth movements along a few ENE-WSW faults in the coastal plains and also in the surf zone of Kerala coast in the form of lagoons, submerged platform, etc. He also extended few sets of ENE-WSW-trending Holocene faults right up to Laccadives and Maldives.

But, Jacob and Narayanaswamy<sup>1</sup> have extended the Palghat fault up to 9° channel in Laccadives and Maldives. On the contrary, the present study and also the studies by Nair<sup>8</sup> advocate the possibility of extending only the ENE-WSW-trending fault right up to 9° channel and similarly the other faults up to Laccadives and Maldives. Ramasamy and Balaji<sup>7</sup> have once again found that almost all the

ENE-WSW-trending faults of Kerala and Karnataka are Pleistocene sinistral faults. Thus, it indicates that all the Precambrian NE-SW-trending regional dextral strikeslip faults of the continental part have been transformed into Pleistocene sinistral faults in the West Coast.

Ramasamy *et al.*<sup>9</sup> have demonstrated an E-W-trending cymatogenic arch between Mangalore in the West Coast and Madras in the East Coast. Subrahmanya<sup>10</sup> too found an upward along Mangalore and Madras alignment.

The integration of such an E-W-trending cymatogenic arch with present set of ENE-WSW to NE-SW-trending sinistral strikeslip faults indicates that

these ENE-WSW trending sinistral faults of Kerala are referable to Left lateral wrenches<sup>11</sup>. And if so, the E-W-trending Mangalore and Madras arch and the sinistral strikeslip faults might have been formed due to the northerly directed compressive force which may be related to the movement of Indian plate towards Tibetan plate.

The possibility for such northerly directed compressive force as a source to Mangalore-Madras arch has also been suggested by Ramasamy *et al.*<sup>9</sup>.

An alternate model is also possible to explain these sinistral faults. Lepichon<sup>12</sup> has observed that the Carlsberg ridge is raising at the rate of 1 to 30 cm per year, thereby causing northeasterly directed force towards Indian subcontinent. Radhakrishna<sup>3</sup> has observed NNW-SSE-trending onshore Quaternary fractures in the West Coast of India and attributed the same to an ENE-WSW-trending post-trappean compression.

Ghosh and Zutshi<sup>14</sup> have identified a number of NNW-SSE-trending continental depressions, continental shelf arches and shelf margin basins (Figure 2). All these observations suggest that the West Coast region is being subjected to ENE to northeasterly directed force due to the rise of Carlsberg ridge.

This might have caused not only on-shore and offshore NNW-SSE-trending arches, deeps and flexures but also would have transformed the pre-existing Precambrian dextral faults into sinistral ones. However, the morphology and the dynamics of such coastal faults need deeper studies for a better understanding of post-collision tectonics.

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## Interpretation of nucleotide/protein sequence data: Some pitfalls

Identification of unknown genes and their products by computer search have received high priority among molecular biologists. However, since biologists are not always computer analysts at the same time, there always exists a finite probability of making errors in analysing sequences and in interpretation of data which can easily be avoided with some advice from computer analysts. We would like to highlight some of the precautionary measures that need to be taken to avoid the inherent pitfalls in sequence data and their proper interpretations.

The worst and a very common source of errors in DNA sequences is the contamination of vector sequences arising during cloning and subcloning of DNA fragments. In 20,000 sequences in the GenBank 63 alone, more than 50 instances of cloning vector contamination have been detected<sup>1</sup>. In a smaller number of cases the anomalous sequences might have arisen during editing, but in a majority of the cases, large blocks of vector sequences contaminated the actual sequence. Incorporation of anomalous sequences, particularly in the coding regions, not only hinders the recognition of low-level homologies and consensus sequences, but can also exhibit false similarities with other sequences, leading to erroneous conclusions. An example of such an error is in the nucleotide sequence of the *recA* gene of *Vibrio cholerae*<sup>2</sup> published from our laboratory. While careful sequencing of both strands and comparison of the sequence-based restriction maps with the map of the cloned DNA fragments might eliminate the problem, vector contamination can be easily and

quickly detected and removed using computer programs that are now available<sup>1</sup>. The contamination can also be removed by comparing the sequence with the dataset of vector sequences available at the GenBank.

'Frameshift' is another frequently occurring error in DNA sequences<sup>3,4</sup>. This happens when a base is either missed or added during reading of sequencing gels. Posfai and Roberts<sup>5</sup> have detected many such errors in EMBL (release 24) and GenBank (release 56) using the program DETECT, which examines alternative reading frames from related proteins. The program BLASTX<sup>4,6</sup> based on BLAST<sup>7</sup> algorithm can also predict frameshift errors by comparing the translated nucleotide sequences from all six reading frames with a protein database. When the similarity to a protein switches from one frame to another in the same strand of the query sequence, there is definitely a frameshift error in the sequence<sup>4</sup>. However, with the simultaneous translation and alignment algorithms, proteins with >30% sequence identity can be reliably recognized even in the presence of 1% frameshifting error rates and 5% base substitution rates<sup>8</sup>.

In nucleotide sequence analysis, unknown complete or partial open reading frames (ORFs) are often encountered along with the sequence of the gene of interest<sup>4,6</sup>. These ORFs, overlooked in most cases by the investigators, might represent useful functions. Two computational approaches are now used either independently or in combination to determine whether the overlooked putative ORFs are indeed bonafide genes<sup>3,4,6</sup>.

The first is an intrinsic approach, which distinguishes the coding regions from the non-coding ones on the basis of the statistical analysis of some parameters of the sequence without referral to any other sequence<sup>4,6,9,10</sup>. The software that has been extensively used for this purpose in human genome sequence analysis<sup>2</sup> is GRAIL<sup>11</sup>, which utilizes the sensor-neural network approach to evaluate the intrinsic properties of the DNA sequence like frame bias, dinucleotide fractal occurrence, etc. This approach can also be used in the analysis of small genome after proper modification. Using the GenMark method based on phased Markov Chain model, Borodovsky *et al.* predicted expressed ORFs in the unannotated regions of *Escherichia coli* genomic DNA from EcoSeq6 database<sup>12</sup>. The second approach for predicting genes is extrinsic and involves comparison of the putative deduced amino-acid sequence with protein sequence databases and searching for motifs<sup>4,6</sup>. If the deduced amino-acid sequence of the putative ORF shows 'significant' similarity to one or more proteins in the database, it is almost certain that the putative ORF represents a bonafide gene. It may be pseudo- or cryptic gene, but is definitely not a part of non-coding region<sup>4</sup>. Using these two approaches, a large number of new genes in the unannotated regions of *E. coli* genome have been identified and searches for genes that have escaped detection so far in several other organisms are in progress.

To search for homology of a newly generated protein sequence with other sequences, i.e. databank one or the other alignment programs are used<sup>7,13-15</sup>. If