First record of euendolithic biota from the basal part of Tal Group in Himachal Lesser Himalaya, India

All types of igneous, sedimentary and metamorphic rocks are susceptible to microbial weathering, including siliceous and calcareous rocks[1]. Disintegration of carbonate substrate by cyanobacteria is known both from freshwater and marine environment. The algae, which actively penetrate into the carbonate substrate, are known as euendolithic algae[2]. These algae dissolve the carbonates, penetrate into the carbonate substrate and form tubes which conform to the size of the algal filaments. The present communication records fossil euendolithic algae from the ooids in the black-bedded chert of Chert Member belonging to Deo Ka Tibba Formation (Lower Tal) of the Tal Group[3], exposed about 900 m southeast of Rayon (30° 37′55″ : 77°31′15″) in the southern limb of Nigalidhar Syncline, Sirmaur District, Himachal Pradesh (Figure 1 *a* and *b*). This member has yielded small shelly fossils of Meishucunian Zone-I (Early Cambrian) from Mussoorie and Garhwal synclines in the southeastern part of the Krol Belt[4,5].

Petrographic thin sections of black chert from the above area show the presence of ooids and brownish-yellow penetrating cyanobacterial remains comparable with known forms, viz. *Eohyella campbelliae*[6], *Eohyella rectoclada*[7] and *Oscillatoriopsis media*[8]. The slides are deposited in the museum of Birbal Sahni Institute of Palaeobotany, Lucknow.

Eohyella campbelliae Zhang and Golubic (Figure 2(v)). Cells aggregated in a colony, arranged in pseudoparenchymatic group, sheath not distinguished around the individual cells, cell size 2–6 μm long and 1.5–3.5 μm wide, spherical cell 3–5 μm, the apical cell larger than the basal cell.

The present form is comparable with the known *E. campbelliae*[6] preserved within the laminae of silicified stromatolites of the Lower Proterozoic sequence (1.7 Ga) of Dahongyu Formation, Changcheng Group, Hebei, northern China. A similar form has also been reported from the Doushantuo Formation, Wengan (Sinian), and Guizhou Province, southwest China[9]. This unnamed form is also recorded from East Greenland[10].

Eohyella rectoclada Green *et al.* (Figure 2 (i)–(iii)): Irregular pseudo filament (trichome) composed of spherical to cylindrical coccoidal cells; pseudo-branching

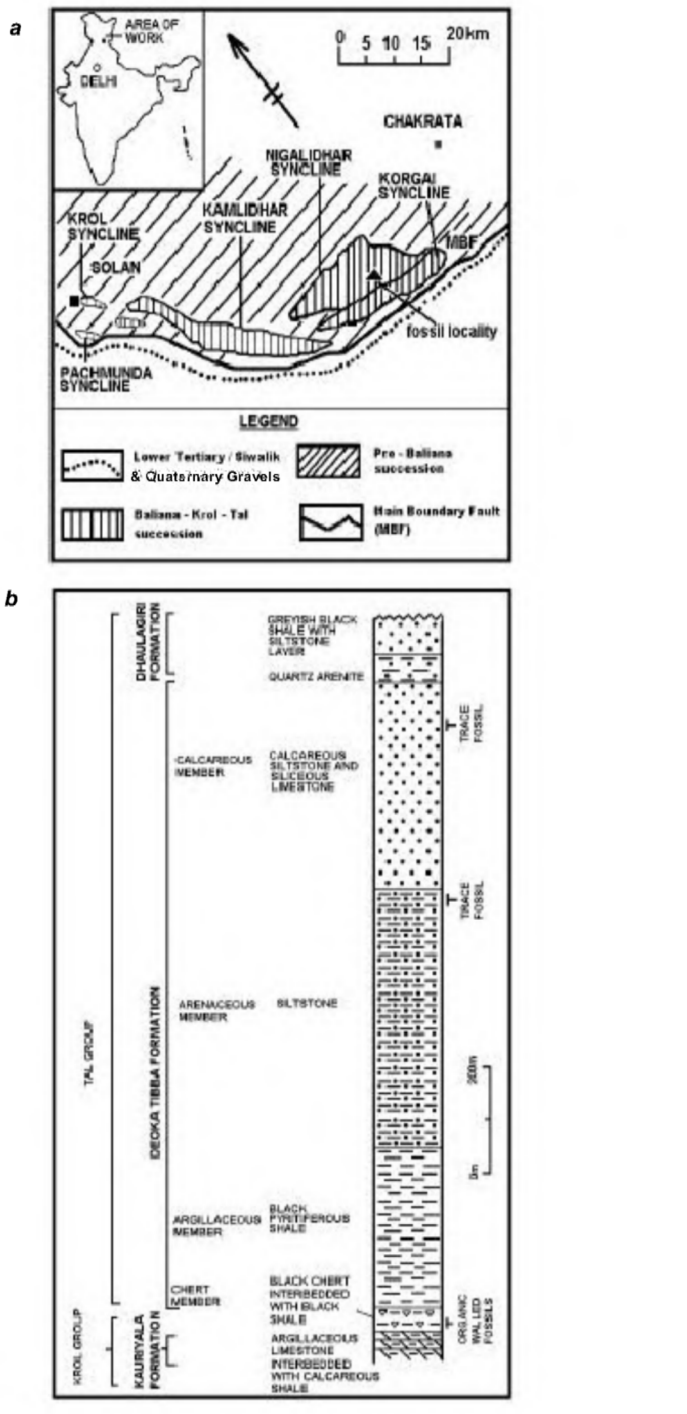

Figure 1. ***a***, Sketch geological map of Baliana–Krol–Tal succession of Krol Belt, Himachal Lesser Himalaya showing fossil locality (modified after Shankar *et al.*[3] and Auden[20]). ***b***, Stratigraphic column of Tal Group[3] exposed in Rayon–Koti Dhaman section, southern limb of Nigalidhar Syncline, Sirmaur District, Himachal Pradesh showing fossiliferous horizon.

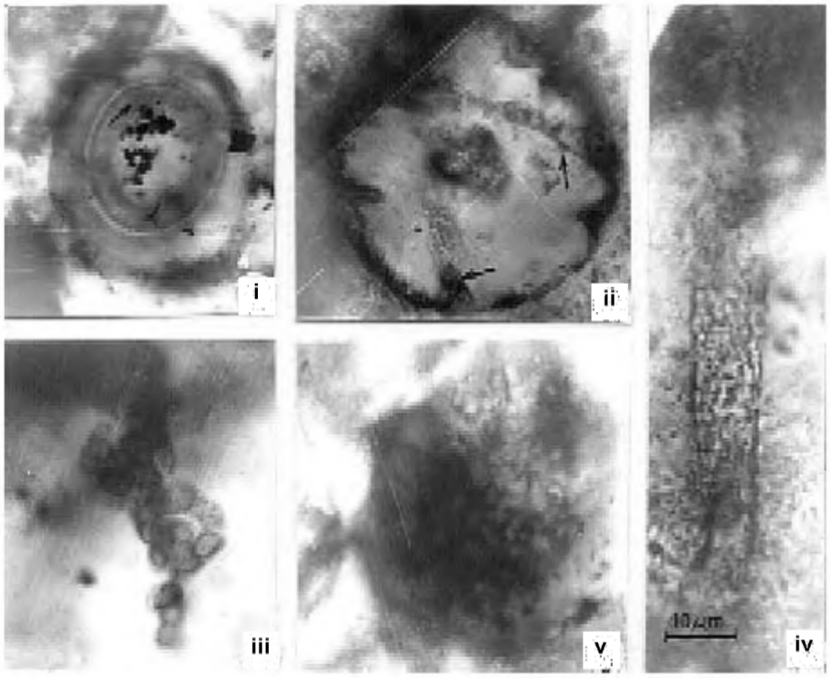

Figure 2. (i) Ooid having concentric ring with euendolithic cyanobacterial algae *Eohyella rectoclada* Green *et al.* 1988; × 400. Arrows show coccoidal microfossil entering the ooid. (ii), Solitary ooid having euendolithic cyanobacterial algae *E. rectoclada* Green *et al.* 1988 and *Oscillatoriopsis media* Mendelson & Schopf; × 400. Arrows show filamentous microfossil entering the ooid. (iii), *E. rectoclada* Green *et al.* 1988; × 400. (iv), *O. media* Mendelson & Schopf; × 1000. (v), *Eohyella comphellii* Zhang and Golubic; × 400.

may be due to slippage of the apical or intercalary cell; maximum length 120 µm; cells barrel to rectangular due to preservation; cells aggregated in a colony; sheath not distinguished around the individual cells; cell size: 2–12 µm long and 1.5–8 µm wide; the apical cell larger than the basal cell.

The present form is morphologically comparable with *E. rectoclada*[7] from the oolites and pisolites of the Upper Proterozoic Eleonore Group, Central East Greenland. An unnamed form comparable to extant *Hyella gigas*[11] was earlier recorded[10,12] from the ooids of Eleonore Bay Group of Upper Proterozoic sequences (East Greenland) and Backlundtoppen Formation of Spitsbergen. The present fossil taxa *E. rectoclada*[7] morphologically compares with this extant genus. This type of form showing concentric ring and cortex was also recorded earlier from the Upper Proterozoic sediments of Eleonore Bay Group, Central and East Greenland[13] and is also comparable with the forms recorded in the modern sediments of Bahamas. Absence of baeocytes may be either due to stable cyclic environmental condition during the deposition or this may be a juvenile stage of this form.

Oscillatoriopsis media Mendelson and Schopf (Figure 2 (ii) and (iv)): Trichome (incomplete) solitary, slightly curved, unbranched, uniseriate, 110 µm in length; cells barrel-shaped, 5–6 µm in length and 10 µm in width; cells dark brown in colour, surface granular, homogenously filled with fine carbonaceous matrix.

The present form is morphologically comparable with the known *O. media*[8] from Yudoma, Siberia (625 Ma) and Upper Riphean of Shorikha and Burovaya, Turukhansk, Siberia[14] as well as the recorded similar form[15] having controversial affinities, belonging to genus *Siphonophycus*[16] from the Upper Precambrian sediments of Grand Canyon Group, Arizona.

The recovered biotic assemblage of endolithic microorganisms is preserved in the ooids and is seen penetrating the surface to reach the centre of the ooids and sometimes even cuts across them (Figure 2 (i)). Structurally well-preserved specimens of *Eohyella* and *Oscillatoriopsis* (Figure 2 (ii)) are seen penetrating into an ooid in thin section, indicating the boring nature of the microorganisms. Similar endolithic microorganisms penetrating ooids are known from present-day Bahamas Sea[17].

Cyanobacteria belonging to Oscillatoriales and Pleurocapsales are most tolerant and change their habit according to environment from oxic to anoxic, and their optimum growth occurs between 6.5 and 8.00 ph. At present, in the Bahamas Sea these forms grow from 100 to 700 m depth. They change their habit from heterotrophy to autotrophy in accordance with depth, due to changes in nitrogen concentration and availability of oxygen[18]. Pisolites/oolites with similar microfossils have been reported from Svalbard and Greenland[7,12,13]. Depositional environment for these ooides and microorganisms has been interpreted as supra-tidal to subtidal.

Thus, the present microorganisms show their involvement in the destruction of the carbonate (ooids that were subsequently silicified)[19], which may have been made possible through their physiological activities. The observation and critical analysis of the recovered euendolithic fossils indicate the formation of ooids in subaerial to supratidal environment and subsequent deposition of these ooids in subtidal environment, which is conducive for the growth of these euendolithic microorganisms.

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Diverse genetic bases of Indian polyembryonic and monoembryonic mango (*Mangifera indica* L) cultivars

Mango is one of the most important fruit crops in India. It is known to have been cultivated in India since the last 4000 years. Almost all cultivars belong to the species *Mangifiera indica*, family Anacardiaceae. *M. indica* is native to India and occurs abundantly in forests and cultivated areas. Hence, it is difficult to differentiate true wild forms from cultivated ones. The commercially grown cultivars have arisen through seedling selections made for different fruit characters like colour, taste, flavour, size, etc. Later, these cultivars have been vegetatively propagated and cultivated in a wide area[1]. Mango cultivars are classified into two groups: monembryonic type or Indian type and polyembryonic type or Indo-Chinese type[2]. In India, majority of the cultivated types are monoembryonic. Surprisingly, polyembryonic types were grown only in southern India, especially in coastal parts of Kerala, Karnataka and Goa.

Emergence of multiple seedlings from a single seed is referred to as polyembryony. This was observed in 59 families, 158 genera and 239 species[3]. In mango, Sachar and Chopra[4] observed nucellar embryos in nineteen mango varieties. Using crosses of polyembryonic and monoembryonic cultivars and their segregating hybrids, Arnon *et al.*[5] demonstrated that polyembryony in mango is controlled by a single dominant gene. Polyembryonic and monoembryonic types are intercrossable, and cultivation of polyembryonic varieties is confined to the west coast adjacent to the Western Ghats, which is one of the hot spots of biodiversity. Keeping this in view, the present study was carried out to examine whether these two classes have a common or different genetic base using Random Amplified Polymorphic DNA (RAPD) and chloroplast DNA Restriction Fragment Length Polymorphism (RFLP) analysis.

In this study, ten polyembryonic and monoembryonic cultivars each traditionally grown in the west coast of southern India were used to determine the genetic relatedness among them using RAPD markers (Table 1). DNA isolation and RAPD analysis were carried out as described by Ravishankar *et al.*[6]. We have employed 19 random primers which amplified 153 polymorphic and 33 monomorphic markers.

Eight mango cultivars from each of these groups were used for chloroplast DNA RFLP analysis. The primers ORF 106-rbcL and GIF-GI460 were used to amplify chloroplast-specific DNA fragments[7,8]. They amplified around 3.1 kb and 1.5 kb fragments respectively. ORF 106-rbcL products were restriction-digested with six enzymes, *Eco*RI, *Bam*HI, *Xba*I, *Xho*I, *Taq*I *and Pst*I. Digested PCR fragments were separated on 2% agarose. Except *Pst*I, no other enzyme digested PCR-amplified fragments. *Pst*I digestion produced similar bands. Therefore, data from restriction digestion of ORF-rbcL fragment were not used for statistical analysis. For GIF-G1460 products, 15 enzymes were used for restriction digestion. *Bam*HI, *Hae*III, *Hind*III, *Hinf*I, *Msp*I, *Pst*I, *Taq*I and *Xba*I were able to digest amplified DNA. Restriction enzymes *Bgl*II, *Dra*I, *Eco*RI, *Eco*RV, *Kpn*I, *Pvu*II, and *Xho*I did not digest GIF-G1460 amplified fragments. Bands on agarose gel were scored as in the case of RAPD. Data from RAPD markers and chloroplast DNA RFLP markers were used for cluster analysis and principal component analysis (PCA), separately[9]. For cluster analysis, squared Euclidian distances were calculated for pair-wise differences among cultivars and based on minimum variance algorithm, the dendrogram was constructed[10].

Dendrogram analysis of RAPD and chloroplast DNA RFLP data clearly grouped the cultivars into two based on

Table 1. Polyembryonic and monoembryonic cultivars used in this study

Serial no.	Polyembryonic cultivar	Serial no.	Monoembryonic cultivars
P1	Peach	M1	Rumani
P2	Kurukkan	M2	Raspuri
P3	Mylupilian	M3	Totapuri
P4	Vellaikulumban	M4	GoaMankurd
P5	Muvandam	M5	Alphonso
P6	Bappakai	M6	Xavier
P7	Nekkare	M7	Kadari
P8	Olour	M8	Padari
P9	Chandrakaran	M9	Suvarnarekha
P10	Starch	M10	Banganapalli