

Biohopanoids the
sedimentary rock
formation. hopanoids
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Biohopanoids are the lipid molecules found in many of the prokaryotic cell membrane, which are buried in the phospholipid bilayer. Hopanoids are similar to sterol molecules found in eukaryotic cells, which play a crucial role in rigidifying and maintaining the integrity of cell membrane (Talbot and Farrimond, 2007). Hopanoids are reported in some of Gram-stain-positive and Gram-stain-negative bacteria, cyanobacteria, purple non-sulfur bacteria, acetic acid bacteria, nitrogen fixing bacteria, methylotrophsmethanotrophs, sulphate reducing bacteria (SRB; Blumenberg et al., 2012; Blumenberg et al., 2006; Cvejic et al.

, 2000; Doughty et al., 2009; Hartner et al., 2005; Kannenberg et al.

, 1995; Ourisson et al., 1979; Ourisson et al., 1987; Rohmer et al.

, 1984; Saenz et al., 2012b; Talbot et al., 2008).

1. 1. 2 Geohopanoids Geohopanoids are the derivatives of biohopanoids which are formed by the diagenesis of biohopanoid (Tritza et al., 1999).

Diagenesis is a chemical and physical change occurs during the sedimentary rock formation.

Hopanoids are highly stable at extreme conditions like alkali, acidic and high temperature (McGarvey and Croteau, 1995; Shunthirasingham and Simpson, 2006). Therefore they are one of the very few compounds which survived in the process of rock and petroleum formation (Shunthirasingham and Simpson, 2006). The pentacyclic skeletons of the hopanoids are relatively stable. After the release of biohopanoids in nature, the BHPs get converted to a simpler product during sediment diagenesis (hopanols, hopanoic acids,

hopanes), but still, they retain the information about their parent compound (Shunthirasingham and Simpson, 2006).

1. 2 Distribution of hopanoids in bacteria Although the biosynthesis of hopanoid does not require dioxygen, it was thought that it is derived from aerobic organisms (Rohmer et al., 1984). Hence, hopanoids were considered as synthesized by bacteria in aerobic condition and indicative for oxygenated environments (Rohmer, 1999). However, few studies reported hopanoids from facultative anaerobic bacteria like *Rhodomicrobium* spp, *Rhodopseudomonas* spp, *Rhodospirillum rubrum* and *Zymomonas mobilis* (Miziorko, 2011; Neunlist et al., 1985; Rohmer et al., 1984; Talbot et al.

, 2007a). Recent studies showed that anaerobically grown *Geobacter metallireducens*, *G. sulfurreducens* and few species of the genus *Desulfovibrio* had hopanoids, but these bacteria can tolerate some oxygen (Blumenberg et al., 2006; Hartner et al., 2005). The occurrence of hopanoids from strictly anaerobic anammox bacteria which belong to phylum Planctomycetes were also reported (Hunter, 2007). These findings help to explain the occurrence of hopanoids in anaerobic environments as well (Banerjee and Sharkey, 2014; Bode et al.

, 2003; Volkman, 2003). Literature shows that 280 bacteria which represent 206 species, 117 genera and 10 major phyla were screened for hopanoid production (Berry et al., 1993; Blumenberg et al., 2006; Blumenberg et al., 2009; Hartner et al., 2005; Rohmer et al., 1984).

Around 168 bacteria which represents 60% of bacterial taxa tested were comprised of hopanoids (Talbot and Farrimond, 2007). Hopanoids were detected from various species belonging to diverse group such as Proteobacteria, Cyanobacteria, Actinobacteria, Acidobacteria, Planctomycetes, Firmicutes and majority of studies were focused on these groups. (Damsté et al., 2004; Rohmer et al., 1984; Talbot et al.

, 2007b; Talbot et al., 2008). However, the screening is strongly biased towards the specific taxonomic groups. The distribution of hopanoids is found to be heterogeneous; therefore the extent to which they are sterol surrogates is questionable. Hopanoids (diploptene (II), diplopterol (VI) and BHPs) were detected at all sampling depth of sediments (Blumenberg et al., 2010).

With the increasing in depth of sampling the amount of diagenetic product of hop-17(21)-ene (IV), hop-22(29)-ene (V) and 17 β (H), 21 β -homohopane (X) increases whereas the amount of diplopterol (VI) decreases with the depth. Bacteriohopanepolyols bacteriohopanetetrol (XXIII) and aminobacteriohopanetriol (XXIV) are dominant hopanoids in recent sediments. The occurrence of BHPs in sediment remains unchanged with increase in depth of sampling which suggests that BHPs are highly stable to diagenetic breakdown (Blumenberg et al.

, 2010). The BHPs are the putative precursor for diagenetically formed geohopanoids (hopanoidal alcohols, ketones, acids and hydrocarbons). Anhydrobacteriohopanetetrol (XXX) is abundant in sedimentary samples

which are the immediate diagenetic product of other BHPs (Blumenberg et al., 2010).

Many bacteria contain characteristic BHPs which are reported from modern and ancient sedimentary rocks and preserve the source specific information (Summons et al., 1999). Hence, hopanoids are used by geologists and paleobiologists for various paleoenvironmental reconstructions. But the knowledge about the source of sedimentary BHPs and changes in marine settings is limited.

1. 3 Lipid as biomarker Biomarker is a characteristic (molecule, gene or any trait) which carry information regarding the specific taxonomic group, metabolic process, physiological process or environmental condition. Various biological metabolites are used as biomarkers as they preserve the source specific information or can be linked to specific taxa.

Lipid molecules are one of the important molecular biomarker as it is highly stable to adverse conditions and mining of lipids from numerous species belonging to diverse taxa provide information to link there source of origin in environmental samples and geological records (Benz et al., 1983; Fischer et al., 2005). Therefore, it is important to understand the source of specific lipid and the degree of specificity which will help to assign significance of its environmental distribution. Initially, there was lack of knowledge about the genes involved in the biosynthesis of a biomarker in question; therefore a survey of diverse taxa for generic compounds and taxonomically unique molecules was used to determine the origins of biomarker lipids.

But with next generation sequencing approach thousands of genomes are getting sequenced, so the genomic approach