CYANOBACTERIA, A TOOL FOR PLANETARY ENGINEERING

Abstract

Cyanobacteria, the prokaryote played a pivotal role in the formation of present-day earth. During the null and void times of earth with extreme climatic conditions there could be traced the presence of cyanobacteria and their mode of survival includes a number of reasons which is being discussed in detail through this paper. This review details into cyanobacterial evolution of photosynthesis and its stress adaptations and avoidance mechanisms. Furthermore, details into the key cause for evolution of life forms in the initial earth.

Keywords: Evolutionary Ecology, Cyanobacteria, Adaptations, Mars, Survival Strategies, Stress Avoidance Mechanisms, Photoprotective Substances, Life Beyond Earth.

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I. INTRODUCTION

Rothman (2017) notes that Earth survived catastrophic events before the evolution of life. Changes in atmospheric gases, climate, and the emergence of photosynthesis were correlated with the presence of oxygen (Kump, 2008). The "Great Oxygenation Event" was a prerequisite for these rapid events (Lyons et al., 2014), and cyanobacteria have been advocated as an ancient terrestrial form of life since primordial times (Drews, 2011; DiGregorio, 2007). The earliest fossil record of cyanobacteria dates back 3.5 million years, during the Precambrian period, and they likely played a significant role in producing oxygen in the atmosphere due to their photosynthetic capabilities (Schopf, 2000).

The viewpoint that cyanobacteria are an ancient form of terrestrial life is further substantiated by well-established algal fossil records, such as *Eosynechoccus amadeus* Hofmann 1976, the unicellular Cyanobacteria *Gloeothece coerulea* Geitler nom.rejic.1928, and silicified fossils of *the Palaeopleurocapsa* genus (Willmer and Rasser, 2022; Knoll, 2008). Additionally, cyanobacteria's wide range of tolerance in toxic environments (Parikh et al., 2006), exposure to ultraviolet radiation (Sinha et al., 1996), ability to thrive in Mars-like conditions (Baque et al., 2013), hot springs (Bhakta et al., 2016), saline and hypersaline environments (Sorensen et al., 2005a) further corroborate their primordial presence. Furthermore, their presence in ice-based ecosystems (Makhalanyane et al., 2015; Quesada and Vincent, 2012) and warmer deserts (Nienow, 2009) make them of particular interest.

Extensive reports have documented the presence of blue-green algae in the McMurdo ice shelves of Antarctica. *Phormidium frigidium* F.E.Fritsch 1912, *Phormidium murrayi* (West and G.S.West) Anagnostidis & Komarek.1988, and *Oscillatoria priestleyi* West and G.S.West 1911 are among the strains identified (Quesada and Vincent, 2012; Vincent, 2000; Vincent and Quesada, 1994). These strains have an optimum temperature that is higher than their existing environment, suggesting they may be cryosensitive but not cryotolerant. Additionally, approximately 250 strains of *Chroococcidiopsis* sp. have been identified in desert environments, including the Atacama Desert and Rose desert of McMurdo Dry Valley, Antarctica, which have been identified as Mars analogues due to their environmental conditions of cold and aridity (Warren-Rhodes et al., 2006). Mars analogues are simulated regions on Earth where one or more physiological factors are similar to those on Mars (Leveille, 2014).

The secret behind the adaptations of cyanobacteria to hostile environments and the rapidity of these adaptations remain unknown. Nevertheless, due to their billion years of evolution, cyanobacteria are considered to be the primary ancestors that independently originated life (Kulasooriya, 2011), which may have allowed them to develop adaptability to a broad range of harsh environments. Terrestrial algae are likely the most advanced group of algae, as their niches often experience frequent fluctuations in climatic factors like humidity, light, and temperature, in contrast to the more stable conditions of aquatic ecosystems. As such, they possess various biochemical and physiological adaptations, including changes in their structure and pigment pattern (Fritsch, 1922), reductions in growth (Warren-Rhodes et al., 2006), and changes in the cellular composition of macromolecules (Rindi, 2011). This review aims to shed light on the mechanisms of evolution and adaptation of terrestrial algae and provide examples of their ability to survive or even thrive in extreme niches.

II. THE KEY CAUSE FOR FORMATION OF LIFE ON EARTH

Questions related to the origin of earth is unresolved. It’s still suspicious among gravitational theory, gaseous hypothesis, nebular hypothesis, supernova, inter stellar, planetesimal hypothesis(Halliday A & Canup R, 2023). The key factor which mediates adaptation of first evolved life form in the molten initial days of earth is unaware. This review put forth a hypothesis for unearthing the key cause for evolution of life on earth. The very first hydrogen coated thermophilic cyanobacteria had survived under the extreme gravitational force, temperature and pressure of initial earth.

Molten lava could be a portion of earth’s interior core where rise and decline in temperature experience at different regions. In this heterogenous pressure, temperature condition thermophilic cyanobacteria would have found a habitable environment.

Molecular, biochemical and structural data of nitrogenase and hydrogenase enzymes contributed to the hydrogen metabolism by cyanobacteria. As the cyanobacteria possess key enzymes of hydrogen production ie is, nitrogenase; catalysing the reduction of nitrogen to ammonia with simultaneous production of hydrogen, uptake hydrogenase which take up hydrogen produced by nitrogenase and bidirectional hydrogenase for the uptake and release of hydrogen, this particular gas is the life promoting factor of thermophilic cyanobacteria in the initial earth(Tamagnini et al., 2002). There is a possibility of hydrogen to be the primary light element in the earth’s core (Hallsworth et al., 2023). The hydrogen gas is a poor conductor of heat and electricity(Schiller R, 2022), so the spongy covering of hydrogen gas is a protective covering for life in the initial earth. Other than conductivity, hydrogen gas is a radioprotectant and also non-toxic(Hu et al., 2020).The spongy covering became a favourable condition for the growth and survival of cyanobacteria. Other than hydrogen coating, additional adaptations that enables survival of cyanobacteria is reviewed shortly below.

1. **Evolution of Photosynthesis:** To commence photosynthesis in the anoxygenic condition of ancient earth, cyanobacteria utilized molybdenum, sulfur or iron as the electron donor (Stal, 2012). The presence of mass-independent fractionation of sulfur and molybdenum isotopes in sedimentary rocks is indicative of anoxygenic photosynthesis mediated by these elements (Arnold et al., 2004; Watanabe et al., 2009). An ancestral bacterium that oxidizes hydrogen peroxide by bacteriochlorophyll containing reaction centers may have been a precursor to oxygenic photosynthesis, as proposed by scientists (Blankenship and Hartman, 1998). In *Microcoleus chthonoplastes* Thruet ex Gomont 1892, both oxygenic and anoxygenic modes of photosynthesis have been reported, which could be a living evidence for the evolution of photosynthesis (Jorgensen et al., 1986; Stal, 2012).

   As oxygen started to accumulate in the Earth's atmosphere, greenhouse gases like methane gradually reduced (Zahnle et al., 2006; Pavlov and Kasting, 2002). Anoxygenic photosynthesis can be considered a prerequisite for reducing toxic gases, changing the potential of elements in the Earth, and depositing organic carbon. Photosynthetic organic molecules fixed in the thallus may become a part of humus when it decays, and the accumulation of layers of humus and sediments might have contributed to the weathering of rocks.

Cyanobacteria display diversity in their adaptation to light, which is attributed to the functional variation of their photosynthetic pigments. Chlorophyll is the pigment that becomes photochemically excited at the red limit of photosynthesis, between 680-700 nm (Lal, 2018). During the early stages of the Earth's history, the sun gradually increased its brightness (Gudel, 2007). At that time, cyanobacteria may have been exposed to low-frequency radio waves, infrared radiation, and visible light outside of the optical range, specifically 700-760 nm. It is unclear how chlorophyll a, b, and c functioned in such low-intensity light. Perhaps, under these conditions, cyanobacteria evolved pigments that absorb long-wavelength and low-energy light, such as chlorophyll d and f (Allakhverdiev et al., 2016).

Acaryochloris marina Miyashita and Chihara 2003, a unicellular cyanobacterium, has been found to have extended photosynthetic efficiency by containing 97% of chlorophyll d and only a small amount of chlorophyll a in one or two key positions (Loughlin et al., 2013; Miyashita et al., 2014). This species has been reported from various habitats such as coastal basins, Antarctic saline habitats, epilithic microbial mats on rocks, and as an epiphyte on red algae *Ahnfeltiopsis flabelliformis* (Kashiyama et al., 2008; Murakami et al., 2004). Chlorophyll d, with an absorption maximum at 711 nm, allows for photosynthesis beyond the red limit of photosynthesis (Chen et al., 2010), and thus can be considered an adaptation of this algae in terrestrial ecosystems. Similarly, cyanobacteria such as *Leptolyngbya* strain JSC1, Cyanobacteria strain KC1, and *Halomicronema hongdechloris* Chen, Li, Birch, and Willows 2012 carry out oxygenic photosynthesis in the near-infrared region due to their ability to use the red-shifted chlorophyll f pigment, which has an absorption range from 700-760 nm (Gan et al., 2015; Miyashita et al., 2014; Nurnberg et al., 2018; Trampe et al., 2020).

In cyanobacteria, the differential production of pigments is also influenced by environmental changes. For example, in Halomicronema hongdechloris Chen, Li, Birch, and Willows 2012 and cyanobacteria strain KC1, the ratio of chlorophyll f to chlorophyll a increased when cultures grown under white light were transferred to red light, while the ratio decreased when transferred from far red light to white fluorescent light (Chen et al., 2012; Miyashita et al., 2014). This pigment remodelling process can be considered an adaptation. Chlorophyll d and f are produced from chlorophyll a by oxidation, but their interconversion to chlorophyll a has not yet been discovered (Koizumi et al., 2005; Zahnle et al., 2006). It is possible that photoreceptors such as phytochromes or bacterial bicomponent signal transduction systems sense critical changes in sunlight and initiate the production of chlorophyll d and f.

Chlorogloeopsis fritschii A.K. Mitra and D.C. Pandey 1967 is known for its predominant level of adaptation through microsporine-like amino acids, in addition to chlorophyll d and f. Halder (2017) reported that this cyanobacterium grows in irregular superposed packets of colony, which acts as a self-shielding adaptation where cells on the periphery protect the underlying cells, creating an environment without visible light. This adaptation might be necessary for the proper functioning of chlorophyll d and f, as reported by Airs et al. (2014). Soil algae are more likely to be exposed to UV light, and *C. fritschii* synthesizes UV light-absorbing pigment in the form of microsporine-like amino acids, as observed in *Chlorogloeopsis* sp. PCC 6912 (Portwich and Garcia-Pichel, 1999).

Singh et al. (2010) utilized bioinformatics tools such as ORF finder and BLAST to analyze the genes responsible for the biosynthesis of microsporine-like amino acids (MAAs). The complete sequences of four species - *Anabaena* sp. PCC 7120, *A. variabilis* PCC 7937, *Synechocystis* sp. PCC 6803, and *Synechococcus* sp. PCC 6301 - were used for comparative analysis. The genes of interest were identified, and their nucleotide sequences were translated into corresponding amino acids using the ORF. A similarity search for related proteins was then conducted using BLAST, and phylogenetic trees were constructed.

Their analysis revealed that the unique combination of DHQS gene (YP_324358) and O-methyltransferase gene (YP_324357) responsible for the biosynthesis of MAAs was present only in *A. variabilis* PCC 7937, and not in the other three species. Moreover, during the phylogenetic analysis, the present study revealed evidence of horizontal gene transfer from cyanobacteria to dinoflagellates and from there to metazoa, which suggests the evolution of these genes from cyanobacteria to other organisms through the plastidic line.

2. **Stress Avoidance Mechanisms:** During pioneer establishment on earth, they might have evaded stress conditions initially through avoidance mechanisms rather than resisting it. Phototaxis and gliding movement, the formation of microbial mat, individual thallus separation within algal mat are few stress avoidance mechanisms exhibited by the majority of cyanobacteria in the order Oscillatoriales.

- **Phototaxis and Gliding Movement:** Cyanobacteria are capable of phototaxis. *Synechocystis* sp. PCC6803 has a captivating phototaxis mechanism. They exhibit positive phototaxis movement towards light source whereas negative phototaxis away from deleterious ultraviolet light (Chau et al., 2015; Kim, 2017)driven by type IV Pili (Z. Chen et al., 2020) and further assessment of physiology or evolution behind phototaxis have pointed out either it may be changed in the direction of gliding movement as in *Phormidium uncinatum* Gomont ex Gomont 1892 (Carlos Tamulonis, 2011) or an inherent ability of all cells in the trichome to sense light like *Anabaena variabilis* Kutzing ex Bornet and Flahault 1886 which bend their trichome to U-shape in the direction of sunlight.(G. Choi et al., 2012)

  Locomotion of cyanobacteria those lacking the flagella is confusing! Though flagellar movement is impossible, instead they glide on the surface. The fact that gliding rate could be influenced by wavelength (Kim, 2017) and the direction of light (J. S. Choi et al., 1999) calls into question the mechanism of gliding. This mechanism in *Oscillatoria princeps* Vaucher ex Gomont 1892 that “gliding is produced by unidirectional waves of bending which act against substrate thus displacing trichome” (Halfen Lawrence & Castenholz, 1970)whereas one school of thought is polysaccharide extrusion through junctional pore is responsible for this movement in *Phormidium uncinatum* Gomont ex Gomont 1892 and *Anabaena variablis* Kutzing ex Bornet and Flahault 1886 (Hoiczyk & Baumeister, 1995)

- **Biofilim or Microbial Sheath:** One of the common stress avoidance mechanisms is communal living of members of different taxa into a microbial film or mat usually appear as certain laminated structures, few of their reports in extreme climatic conditions are Arctic (Quesada et al., 1999), saline (Sorensen et al., 2005b) and rice field (Sinha & Hader, 1996). Microbial mat of unicellular algae is reported in hypolithic rocks and caves (Stal, 2012) but filamentous colonial form like *Microcoleus chthonoplastes* Thuret ex Gomont 1892 become dense entangled mass on intertidal zone (Stal et al., 1985). Microbial mat manifest them firmly on exposed surface in spite of wave energy. Similarly, *Crinalium epipsammum* Winder, Stal & Mur 1992, a terrestrial cyanobacteria of filamentous habit, is reported from moving sand and sand dune. Microbial crust of *C.epipsammum* safeguard sand dune from erosion; (Mikhailyuk et al., 2019). In *Rivularia periodica* obenluneschloss,1991 shows tan coloured laminations on rocks, their crust contributes to biologically introduced calcification. The extra polymeric substances and sheath morphology changes with climate, so variation in calcification pattern observed in different climates (Willmer & Rasser, 2022).

Cyanobacterial members have their own preferred niches in this mat. For example, algal mat from mangrove sandy soil, in which a top layer of brownish coloured *Lyngbya aestuarii* Liebman ex Gomont 1892 and lower layer inhabited by *Microcoleus chthonoplastes* Thruet ex Gomont 1892, where former produce ultraviolet (UV) absorbing pigment that is scytonemin and latter get protected by virtue of overlying thallus (Karsten et al., 1998). Individualist thallus separation also observed in algal mat of Mc Murdo Iceshelf Antartica, *Oscillatoria priestleyi* West and G.S.West 1911, may be regarded as stress avoiders owing to their gliding locomotion even to low concentration of ultraviolet (UV) A and ultraviolet (UV) B and they may migrate to depth of mat. *Phormidium murrayi* (West ad G.S.West) Anagnostidis & Komarek 1988 are reported in the upper layers of this algal mat. They are nonmotile but nevertheless they are resistant to high energy radiation (Quesada & Vincent, 1997). In short, cyanobacteria in terrestrial habitat evolved to be in microbial mat for evading desiccation, ultraviolet (UV) light and so on.

3. Morphological and Biochemical Adaptation

- **Adaptation in the Cell Envelop:** May be before the evolution of oxygenic photosynthesis, the absence of ozone layer might have forced cyanobacteria to adapt extreme ultraviolet (UV) radiation by making up a unique cell envelop. Even today, sustenance of these adaptations has contributed in withstanding the ultraviolet (UV) radiation on the terrestrial habitat where tolerance to desiccation is the only mean to survive. The colonization of terrestrial algae involves frequent encounter to harsh environment so thicker the envelop they produce better their adaptation to desiccation Cell wall characteristics of both gram-positive and gram-negative envelope meld together in cyanobacterial envelop (Bertocchi et al., 1990). According to (Hoiczyk & Baumeister, 1995), cell wall of gram-positive bacteria is multi layered with thickness ranging from 20 to 40 nm where as in gram- negative bacteria peptidoglycan layer is relatively thin ranging from 2 to 6 nm. The *Phormidium uncinatum* Gomont ex Gomont 1892 cell envelop thickness ranges from 15 to 35 nm and *Oscillatoria princeps* Vaucher ex Gomont 1892 has a diameter of more than 700 nm. Even though cyanobacteria possess cell wall thickness similar to gram positive bacteria, the former has a composition which is similar to gram-negative bacteria as it possesses an outer membrane and also lacks a typical component of gram-positive bacteria, that is the teichoic acid (Silhavy et al., 2010); (Hoiczyk & Hansel, 2000).

Lipopolysaccharide outer membrane, a unique feature of gram-negative bacteria is found in cyanobacteria. It is a straight double track structure with uniform width of 6 to 8 nm in *Phormidium uncinatum* Gomont ex Gomont 1892 (Hoiczyk, 1998). In addition to cyanobacterial o antigen, *Synechococcus* PCC6716 they also contain carotenoids, unusual fatty acids such as beta hydroxy palmitic acid which are anchored to underlying peptidoglycan (Schrader et al., 1981). Carotenoids protect cyanobacterial cell from high light intensity, particularly ultra violet (UV) range.

Cyanobacteria synthesis diverse external carbohydrate structures in response to different environment stimuli to retain cellular water. (Plude et al., 1991) reported pectin like polymer composed of 83% galacturonic acid synthesized by *Microcystis flos-aquae* C3-40. Similarly, *Phormidium uncinatum* Gomont ex Gomont 1892 and *Nostoc commune* Vaucher ex Bornet& Flahault,1886 sheath contain cellulose like homoglucan fibrils cross linked by minor monosaccharides (Hoiczyk, 1998) ; (Inoue-Sakamoto et al., 2017). Occurrence of different extra cell wall layers with specific function had reported in *Phormidium uncinatum* Gomont ex Gomont 1892. Cyanobacteria has an adaptation in switching their polysaccharide biosynthesis to different environment stimuli.

In *Nostoc commune* Vaucher ex Bornet & Flahault,1886 production of scytonemin and an oligosaccharide happens on differential exposure to UV Aand UV-B (Ehling-Schulz et al., 1997). ultraviolet (UV) A induces scytonemin biosynthesis whereas ultraviolet B induces Oligosaccharide mycosporine like amino acids so they suggest the existence of distinct photoreceptors that signals biosynthesis of these two pigments. Cell envelop of *Nostoc carneum* C.Agardh ex Bornet & Flahault 1886 possess reducing or antioxidant activity (Hussein et al., 2015). *N.commune* which contain aromatic pigments like scytonemin (Proteau et al., 1993) and oligosaccharide mycosporine like amino acids in the external smooth layer (Nazifi et al., 2015).

Scytonemin also has sun screening action in blue green algae (Rozema et al., 2002), and is isolated exclusively from extracellular sheath of cyanobacteria (Wada et al., 2013). Scytonemin is produced from intermediate compounds of shikimate pathway so this protective compound most likely to be appeared later in evolution (Derikvand et al., 2017); (Simeonov & Michaelian, 2019). *N.commune* colonies can be desiccated even for 87 years (Cameron, 1962) and those attached on sun-exposed faces of rocks are darker in colour because of scytonemin. The pigment profile of cyanobacterial crust isolated from desert samples reported that scytonemin concentration was elevated 2 to 6 times than chlorophyll *a* and lutein was also higher than chlorophyll *a* (Abed et al., 2010). In cyanobacteria, ultraviolet A radiation and scytonemin production are not distinct events, rather both of them occurred as a single cascade of events (Soule et al., 2016); (Pathak et al., 2019). Efficacy of scytonemin present in *Chlorogloeopsis* sp. strain 0-89-cgs is proven after photobleaching it with high ultraviolet-A radiation. Though radiation inhibited photosynthesis and detained growth in this terrestrial cyanobacterium, deposition of scytonemin on cyanobacterial sheath accustomed photosynthesis and growth, thus becoming resistant to photobleaching in due course(Garcia-Pichel et al., 1992).

- **Salinity and Osmotic Stress**Blue green algae are diverse with respect to the mechanism they evolved in stress condition especially under salinity and the accompanying osmotic stress. Halophilic archaea and bacteria adapt to saline condition by salt in strategy that is accumulation of large number of inorganic ions in the cytoplasm (Rodriguez-Valera, 1993). Biomolecules of these evolved strains are resistant to denaturation and they carry out their physiological function even under high ion concentration (Bayley & Morton, 1978)(Muller & Oren, 2003)

  Most organism including cyanophyceae evolved salt out strategy. This strategy has got different interpretations. One of the explanations is that they accumulate osmo-protectant initially and in the latter phase inorganic ions are transported across electrochemical gradients into cytoplasm (Pade & Hagemann, 2015). Other explanation is that, the excess ions in the cytoplasm are excluded by dint of Na^+ Cl^- pumb, Na^+ H^+ antiporters, Cl^-/H^+ antiporters and Na^+ ATPases. In *Aphanotheca halophytica* Fremy 1993, *Synechocystis* sp.PCC 6803, *A. marina* justify exclusion of ions from blue green algal cells (Fukaya et al., 2009)(Elanskaya et al., 2002) ;(Tsunekawa et al., 2009) ;(Wang et al., 2002)(Brown, 1976; Weinisch et al., 2018). Regarding salt out strategy, cyanobacteria exclude salt ions from the cytoplasm prior phase and simultaneously accumulate compatible solute.

  The Compatible solute concept was proposed by Brown (Brown, 1976). These low molecular compounds can be considered as the chemical chaperone of cells under multiple stress factors such as ultraviolet (UV) radiation, dehydration, high and low temperature, salt and pH. Cyanobacteria under saline stress in accordance with their compatible solutes had been assembled into three groups(Reed et al., 1986): low salt tolerant species such as *Nostoc* sp. PCC 7120 accumulating sucrose and or trehalose, moderate salt tolerant species similar to *Synechocystis* sp. PCC 6803 which synthesis glucosyl glycerol and third halophilic strains like *A. halophytica* which prefers glycine betaine (Erdmann, 1983); (Erdmann et al., 1992); (Pade & Hagemann, 2015) (Fulda et al., 1999).

  Sucrose and trehalose considered as a general osmo-protectant to desiccation and salinity, in *N. muscorum* on the top of sucrose and trehalose, proline over accumulation enhanced salt tolerance (A. K. Singh et al., 1996), in hyper saline species in addition to glycine betaine, secondary compatible solute such as glutamate betaine reported (Mackay et al., 1984). Generally, genes which codes for the enzyme that synthesise these compatible solutes have been identified however none of the genes which codes for trehalose and glucosyl glycerol have detected in *Microcystis aeruginosa* and *Prochlorococcus* sp. (Klahn et al., 2010); (Pade & Hagemann, 2015). We presume either there may be some multifunctional enzyme that exhibit pleiotropy under salt stress or else there may be some receptors like phytochrome, cryptochrome or bicomponent signalling to initiate biosynthesis of compactable solutes not included in the genome.

There seems an immense disparity between *Synechococcus* and *Synechocystis* species in terms of osmo protectant and adaptation to stress condition though both of them are unicellular cyanobacteria. *Synechocystis* accumulate glucosyl glycerol and is halotolerant (Marin et al., 1998) can with stand elevated concentration of salinity whereas *Synechococcus* accumulate proline and is regarded as salt shocked strain (Fulda et al., 1999). Under majority of the stress condition *Synechoccus* up-regulate the respiratory genes and down-regulate the photosynthetic one. On the contrary, both set of genes are downregulated in the latter (Billis et al., 2014).Physiology and adaptation of cyanobacteria varies with species. In real sense compatible solutes has a cascade of action that varies with species.

III. CONCLUSION

The ability of cyanobacteria to transform the Earth's atmosphere through the production of oxygen is a remarkable feat that has paved the way for the evolution of life as we know it. Moreover, the study of cyanobacteria can potentially provide insights into the possibility of life beyond Earth. Through research and experimentation, it has been shown that some strains of cyanobacteria are capable of surviving in extreme conditions similar to those found on other planets. The potential application of cyanobacteria in terraforming other planets and supporting life in space exploration further highlights their significance in the field of astrobiology. Overall, the study of cyanobacteria and their adaptations provides an interesting avenue for both biotechnology and space exploration**.**

IV. DISCUSSION

The study of cyanobacteria has been limited due to the lack of resources available for the analysis of their phylogenetic evolution. With only 35 completely sequenced genomes out of approximately 2,500 species, more exploration into genome-level analysis is necessary to identify significant genes that result in the distinct shikimate pathway and mutant development (Nicolaisen et al., 2010). However, bioinformatics applications have the potential to facilitate this research and provide insight into the metabolic processes of cyanobacteria.

The ability of cyanobacteria to thrive in outer space has significant implications for the search for extraterrestrial life. The first EXPOSE-E mission demonstrated the viability of vegetative cells of Chroococcidiopsis sp. under space vacuum and extra-terrestrial ultraviolet spectrum (Cockell et al., 2011; Billi et al., 2011). Further research has been conducted on the desert strain of Chroococcidiopsis in simulated Mars conditions on Earth (Warren-Rhodes et al., 2006) and in the Biofilm Organisms Surfing Space (BOSS) and Biology and Mars Experiment (BIOMEX) of the EXPOSE-R2 mission of Russia (Baque et al., 2013). These developments suggest that interplanetary transport and settlement of life beyond Earth may be possible through the lithopanspermia theory. However, further research is needed to understand the climate of other planets and how algal biotechnology can contribute mutant strains of microalgae that can survive in these conditions.

In addition to facilitating the search for extra-terrestrial life, the study of cyanobacteria also has practical applications. Genome-scale metabolic models can be constructed with a completely annotated genome sequence of cyanobacteria, providing insight into all the possible biosynthesis that occurs within the species (Ducat et al., 2011). Mathematical models can then be used to predict metabolic rates and behaviour, allowing for the development of more efficient and effective biotechnological applications of cyanobacteria.

Inshort, the study of cyanobacteria has the potential to significantly impact both our understanding of life beyond Earth and our ability to develop practical applications in biotechnology. With further exploration of genome-level analysis and the use of bioinformatics, we can gain insight into the metabolic processes of cyanobacteria and develop models that predict their behaviour. This information can then be used to develop more efficient and effective biotechnological applications of cyanobacteria.

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