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A COMPLETE REVIEW ANALYSIS OF MICROORGANISMS STUDY IN RELATION TO GROUP I ELEMENTS OF MODERN PERIODIC TABLE

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ABSTRACT An attempt is made to understand the relationship between the biological world of microorganisms and Group I elements of periodic table. The study includes compilation of data from published research work relating the presence of microorganisms in a particular environment of element, production of elements such as Hydrogen through microorganism and also involvement of particular element and microorganism in metabolism and enzyme catalysed reactions. It is also observed that certain elements of Group I are inorganic, toxic and may not support the biological life of microorganisms. While there is vast data regarding involvement of microorganisms and elements, a few microorganisms in relation to Group I elements of the periodic table are covered in this article.

KEYWORDS : Microorganisms, Elements, Hydrogen, Lithium, Sodium, Rubidium

INTRODUCTION:

An attempt is made to understand the relationship between the biological world of microorganisms and Group I elements of periodic table. The study includes compilation of data from published research work relating the presence of microorganisms in a particular environment of element, production of elements such as Hydrogen through microorganism and also involvement of particular element and microorganism in metabolism and enzyme catalysed reactions. It is also observed that certain elements of Group I are inorganic, toxic and may not support the biological life of microorganisms. While there is vast data regarding involvement of microorganisms and elements, a few microorganisms in relation to Group I elements of the periodic table are covered in this article.

Role of Hydrogen in microorganism:

A brief discussion regarding the role of hydrogenase enzyme present in hydrogen oxidising bacteria is given below.

A diverse group of metalloenzymes[2,5] is represented by Hydrogensases[1]. The molecular reaction of converting dihydrogen into protons and electrons and also generation of dihydrogen in the reverse reaction is catalyzed by the hydrogenase.

$$H_2 \rightleftharpoons 2H^+ + 2e^- \quad (1)$$

$$H_2 \rightleftharpoons H^+ + H^- \quad (2)$$

The presence of a unique metal centre greatly increases the acidity of H_2 in this reaction resulting in the heterolytic splitting of the molecule and the nearby base further accelerates this reaction. The reverse addition of H^+ and H^- results in the regeneration of H_2. The presence of Hydrogenases in nature is abundant which include archaea, bacteria, and some types of eukarya[2,3,6–8].The classification of Hydrogenase is based on the active metal ion sites viz., [NiFe], [FeFe], and [Fe] present in the hydrogenase.[2,3,9,10]. A characteristic feature of the [NiFe] and [FeFe] hydrogenases is that the iron atoms are ligated by small inorganic ligands (CO and CN^-), which were first detected by FTIR spectroscopy.[11–13] These enzymes contain sulfur bridged bimetallic centers, typically with an open coordination site on one metal (Figure 1).

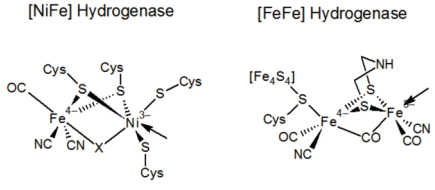

Figure 1: Structure of [NiFe] Hydrogenase and [FeFe] Hydrogenase

Hydrogenase and Hydrogen Metabolism in *Aquifex aeolicus* [14]

Aquifex aeolicus is from the order *Aquificales* and is isolated from a shallow submarine hypothermal system. This constitutes an important component of the microbial communities at elevated temperatures. It is a hyperthermophilic chemolithoautotrophic bacterium, which utilizes molecular hydrogen, molecular oxygen and inorganic sulfur compounds to flourish. *A. aeolicus* contains membrane-embedded [NiFe] hydrogenases as well as oxidase enzymes involved in hydrogen and oxygen utilization. *A. aeolicus* is a "knallgas" bacterium which needs hydrogen as electron donor and oxygen as electron acceptor for growth. It is a scarcely studied metabolic pathway. Hydrogenase I belonging to group 1 of [NiFe] hydrogenases containing respiratory enzymes is linked to the diheme cytochrome b^1. This enzyme is possibly involved in the oxygen reduction pathway in *A. aeolicus*. The first step of the bioenergetic pathway consists of an electron uptake from hydrogen by hydrogenase I and subsequent reduction of the quinone pool via the cytochrome *b* subunit. The electrons from the quinone pool probably pass through the membrane-attached cytochrome bc_1 complex toward a periplasmic cytochrome *c* finally reducing molecular oxygen by an oxidase enzyme (Fig. 1). At 70 °C a hydrogen-dependent reduction of exogenous cytochrome *c* was measured with detergent-extract membranes of *A. aeolicus* grown in the presence of elemental sulfur.

The data regarding aerobic, thermophilic, hydrogen-oxidizing bacteria have been discussed[15]. The aerobic, facultive chemolithotrophs reported include *Hydrogenomonas thermophilus*[16], *Pseudomonas thermophila K-2*[17], *Pseudomonas hydrogenothermophila*[18], *Flavobacterium autothermophilum*[18] and *Bacillus schegelii*[19,20].

The anaerobic and methane producing bacteria, *Methanobacterium thermoautotrophicum* [21] which is thermophilic, obligately chemolithoautotrophic and hydrogen oxidizing has been reported. Facultative lithoautotrophs are aerobic, hydrogen-oxidizing bacteria (both mesophiles and thermophiles) which are found growing heterotrophically on several types of organic compounds. Therefore, the hydrogen-oxidizing bacteria are assumed to form a physiological group containing no obligate chemolithoautotrophs, in contrast to other chemolithoautotrophic bacterial groups. Six newly isolated strains of aerobic, thermophilic, hydrogen-oxidizing bacteria which are obligate chemolithoautotrophs are studied for their phenotypic and chemotaxonomic characteristics[15]. Table I gives name and type of few Hydrogen oxidising bacteria.

facultative lithoautotrophs

Table I: Hydrogen oxidising bacteria

S No	Microorganism	Type	Reference
1.	*Aquifex aeolicus*	Hyperthermophilic chemolithoautotrophic bacterium	14
2	*Hydrogenomonas thermophilus*	Aerobic, thermophilic, hydrogen-oxidizing bacteria	16
3	*Pseudomonas thermophila K-2*	Aerobic, thermophilic, hydrogen-oxidizing bacteria	17
4	*Pseudomonas hydrogenothermophila*	Aerobic, thermophilic, hydrogen-oxidizing bacteria	18
5	*Flavobacterium autothermophilum*	Aerobic, thermophilic, hydrogen-oxidizing bacteria	18

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6	*Bacillus schegelii*	Aerobic, thermophilic, hydrogen-oxidizing bacteria	19,20
7	*Methanobacteriirm thermoautotrophicum*	Thermophilic, obligately chemolithoautotrophic, and hydrogen oxidizing	21

Hydrogen producing bacteria[22]:

Cyanobacteria are photoautotrophic microorganisms [23-38] that use two sets of enzymes to generate hydrogen gas. The first one is **Nitrogenase** and it is found in the heterocysts of filamentous cyanobacteria when they grow under nitrogen limiting conditions. Hydrogen is produced as a by-product of fixation of nitrogen into ammonia. The reaction consumes ATP and has the general form:

$$16ATP + 16H_2O + N_2 + 10H^+ + 8e^- \xrightarrow{\text{Nitrogenase}} 16ADP + 16Pi + 2NH_4^+ + H_2 \text{ [24]}$$

A Nitrogenase enzyme consists of two parts, one is dinitrogenase and the other is dinitrogenase reductase. Dinitrogenase breaks apart the atoms of nitrogen. Dinitrogenase reductase plays the specific role of mediating the transfer of electrons from the external electron donor (a ferredoxin or a flavodoxin) to the dinitrogenase [39-41].

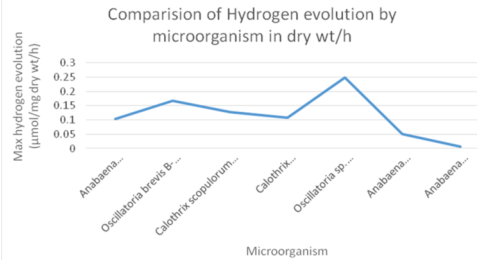
The other hydrogen-metabolizing/producing enzymes in cyanobacteria are **Hydrogenases**; they occur as two distinct types in different cyanobacterial species. One type of them, uptake hydrogenase [42], has the ability to oxidize hydrogen and the other type of hydrogenase is reversible or bidirectional hydrogenase and it can either take up or produce hydrogen.

$$H_2 \xrightarrow{\text{Hydrogenase}} 2H^+ + 2e^-$$

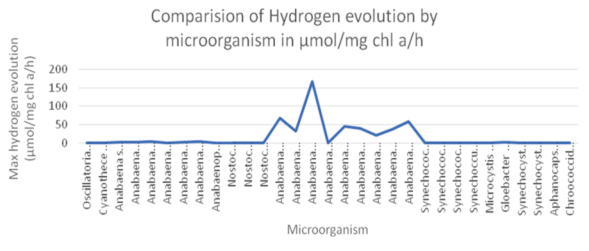
Around 14 cyanobacteria genera produce hydrogen under a wide range of culture conditions[42], most of which having the ability to produce hydrogen are shown in Table 2 which is followed by two comparison graphs I and 2 showing the maximum evolution of hydrogen.

Table 2: Cyanobacteria genera producing oxygen.

S.No	Microorganism	Type	Max hydrogen evolution	Ref. no
1	*Anabaena cylindrica* B-629	Marine cyanobacteria	0.103 µmol/mg dry wt/h	23
2	*Oscillatoria brevis B-1567*	Marine cyanobacteria	0.168 µmol/mg dry wt/h	23
3	*Calothrix scopulorum 1410/5*	Marine cyanobacteria	0.128 µmol/mg dry wt/h	23
4	*Calothrix membrnacea B-379*	Marine cyanobacteria	0.108 µmol/mg dry wt/h	23
5	*Oscillatoria* sp. Miami BG7	Marine cyanobacteria	0.250 µmol/mg dry wt/h	24
6	*Oscillatoria limosa*	Marine cyanobacteria	0.83 µmol/mg chl a/h	25
7	*Cyanothece* 7822	Marine unicellular cyanobacteria	0.92 µmol/mg chl a/h	26
8	*Anabaena* sp.PCC 7120	Heterocystous cyanobacteria	2.6 µmol/mg chl a/h	27
9	*Anabaena cylindrica* IAMM-1	Heterocystous cyanobacteria	2.1 µmol/mg chl a/h	27
10	*Anabaena variabilis* IAMM-58	Heterocystous cyanobacteria	4.2 µmol/mg chl a/h	27
11	*Anabaena cylindrica* UTEX B 629	Heterocystous cyanobacteria	0.91 µmol/mg chl a/h	27
12	*Anabaena flos-aquae* UTEX 1444	Heterocystous cyanobacteria	1.7 µmol/mg chl a/h	27
13	*Anabaena flos-aquae* UTEX LB 2558	Heterocystous cyanobacteria	3.2 µmol/mg chl a/h	27
14	*Anabaenopsis circularis* IAM M-13	Heterocystous cyanobacteria	0.31 µmol/mg chl a/h	27
15	*Nostoc muscorum* IAM M-14	Heterocystous cyanobacteria	0.60 µmol/mg chl a/h	27
16	*Nostoc linckia* IAM M-30	Heterocystous cyanobacteria	0.17 µmol/mg chl a/h	27
17	*Nostoc commune* IAM M-13	Heterocystous cyanobacteria	0.25 µmol/mg chl a/h	27
18	*Anabaena variabilis* AVM13	Heterocyst filamentous	68 µmol/mg chl a/h	28
19	*Anabaena variabilis* PK84	Heterocyst filamentous	32.3 µmol/mg chl a/h	29
20	*Anabaena variabilis* PK84	Heterocyst filamentous	167.6 µmol/mg chl a/h	30
21	*Anabaena variabilis* PK84	Heterocyst filamentous	0.11 µmol/mg chl a/h	31
22	*Anabaena variabilis* ATCC 29413	Heterocyst filamentous	45.16 µmol/mg chl a/h	30
23	*Anabaena variabilis* ATCC 29413	Heterocyst filamentous	0.05 µmol/mg dry wt/h	32
24	*Anabaena variabilis* ATCC 29413	Heterocyst filamentous	39.4 µmol/mg chl a/h	29
25	*Anabaena variabilis* 1403/4B	Heterocyst filamentous	20 µmol/mg chl a/h	33
26	*Anabaena azollae*	Heterocyst filamentous	38.5 µmol/mg chl a/h	30
27	*Anabaena variabilis* PK17R	Heterocyst filamentous	59.18 µmol/mg chl a/h	30
28	*Anabaena variabilis* SPU 003	Heterocyst filamentous cyanobacteria	5.58 nmol/mg dry wt/h	34
29	*Synechococcus* PCC 6830	Non-nitrogen-fixing unicellular cyanobacteria	0.26 µmol/mg chl a/h	35
30	*Synechococcus* PCC 602	Non-nitrogen-fixing unicellular cyanobacteria	0.66 µmol/mg chl a/h	35
31	*Synechococcus* PCC 6307	Non-nitrogen-fixing unicellular cyanobacteria	0.02 µmol/mg chl a/h	35
32	*Synechoccus* PCC 6301	Non-nitrogen-fixing unicellular cyanobacteria	0.09 µmol/mg chl a/h	35
33	*Microcystis* PCC 7820	non-nitrogen-fixing unicellular cyanobacteria	0.16 µmol/mg chl a/h	34
34	*Gloebacter* PCC 7421	Non-nitrogen-fixing unicellular cyanobacteria	1.38 µmol/mg chl a/h	34
35	*Synechocystis* PCC 6308	Non-nitrogen-fixing unicellular cyanobacteria	0.13 µmol/mg chl a/h	35
36	*Synechocystis* PCC 6714	Non-nitrogen-fixing unicellular cyanobacteria	0.07 µmol/mg chl a/h	35
37	*Aphanocapsa montana*	Non-nitrogen-fixing unicellular cyanobacteria	0.40 µmol/mg chl a/h	35
38	*Gloeocapsa alpicola* CALU 743	Unicellular non-diazotrophic cyanobacteria	0.58 µmol/mg protein	36
39	*Chroococcidiopsis thermalis* CALU 758	Unicellular non-nitrogen-fixing	0.7 µmol/mg chl a/h	26
40	*Mycrocystis* PCC 7806	Unicellular/colony embedded in matrix	11.3 nmol/mg prot/h	27
41	*Microcoleus chthonoplasts*	Mat-building cyanobacteria	1.7 nmol/mg prot/h	34



Graph 1: Comparison of Hydrogen max evolution by microorganism in dry wt/h unit



Graph 2: Comparison of Hydrogen max evolution by microorganism in µmol/mg chl

Role of Lithium in microorganism:

Lithium is not generally used biologically by bacterial cells and, in fact, show some toxicity at moderate to high concentrations [43]. Lithium toxicity varies among microorganisms. Lithium is used for the selective growth of bacteria such as *Bifidobacterium spp*[44]. In *E. coli*, lithium detoxification is partly mediated by Li^+ efflux via an Na^+/H^+ antiporter [45]. Li^+ can substitute for Na^+ in the cotransport of amino acids and some sugars in some bacteria [46,47,48,49,50,51,52]. Lithium can also replace Na^+ in driving the flagellar motor of vibrio aliginolyticus [53]

Role of Sodium in microorganism:

Litter components and soil organic matter biodegradation is a crucial step which involves microorganisms as well as soil animals. The terrestrial decomposer communities are usually dominated by fungi microbial biomass. These contribute in the cycling of both macronutrients and trace elements[54],[55],[56]. Fungal rhizomorph tissues contained significantly greater concentrations of Ca, K and Na. Fungal sporocarps contain greater concentration of Cu, K, Na and P. Significant concentration of Ca, Cu, Fe, K, Mn, N, Na and P in fungi in a Jeffrey pine ecosystem and in tropical forests. Na concentrations present in both rhizomorphs and sporocarps is shown in Table 3

Table 3: Sodium concentrations in rhizomorphs and sporocarps

S.No	Organic Material	Location	Sodium conc. In ppm
1	White pine forest floor [57]	N. Carolina	2- 23 [57], [58]
2	Fungal Hyphae [59]	N. Carolina	------
3	Fungal rhizomorphs [57]	N. Carolina	251-557
4	Fungal sporocarps [57]	N. Carolina	94-246
5	Jeffrey pine needles [55,60]	Nevada	265
6	Fungal rhizomorphs [55,60]	Nevada	219-3415
7	Fungal fruiting bodies [55,60]	Nevada	250-900
8	Hardwood forest floor [57]	N. Carolina	2-28 [57], [58]
9	Fungal Hyphae [59]	N. Carolina	--------
10	Fungal rhizomorphs [57]	N. Carolina	127-157
11	Fungal sporocarps [57]	N. Carolina	687-961
12	Hardwood forest floor [56]	Tennessee	130-450
13	Fungal rhizomorphs [56]	Tennessee	385-315
14	Fungal sporocarps [56]	Tennessee	380-420
15	Fungal rhizomorphs [55,60]	Central	616-29,125
16	Fungal sporocarps [55,60]	S. America	210-2313

Role of Potassium in microorganism:

The morphology of anaerobic microorganism under high salinity is balanced by potassium and it shows long term effect. Potassium addition improves the dehydrogenase activity and bacterial cell viability[51]. In different strains various organic acids are produced by Potassium solubilizing microorganisms (KSMs). KSMs which are rhizospheric microorganisms solubilize the insoluble potassium (K) to soluble potassium for plant growth and yield. Potassium solubilization is carried out by a large number of saprophytic bacteria and fungal strains (*Aspergillus spp*. And *Aspergillus terreus*)[52]which is shown in Table 4.

Table 4: Predominant Acids & Salts produced by Microorganisms

S. No	Microorganism	Predominant acid & salts produced	References
1	*Penicillium frequentans*, *Clasdosporium*	Oxalic, Citric, Gluconic Acids	53
2	*Paenibacillus mucilaginosus*	Tartaric, Citric, Oxalic	54,55
3	*Aspergillus niger*, *Penicillium* sp	Citric, Glycolic, Sucinnic	56
4	*B. megaterium*, *Pseudomonas* sp., *B. subtilis*	Lactic, Malic, Oxalic, Lactic	57
5	*B. megaterium*, *E. freundii*	Citric, Gluconic	57
6	*Arthrobacter* sp., *Bacillus* sp., *B. firmus*	Lactic, Citric	58
7	*Aspergillus fumigatus*, *Aspergillus candidus*	Oxalic, Tartaric, Citric, Oxalic	59
8	*Pseudomonas aeruginosa*	Acetate, Citrate, Oxalate	60,61
9	*B. mucilaginosus*	Oxalate, Citrate	62
10	*Pseudomonas* spp.	Tartaric, Citric	63

Role of Rubidium in microorganism:

Few evidences suggest that Rubidium may substitute in microbial metabolism for K, and it may involve with neuro pathway mechanism[64].

Role of Caesium in microorganisms:

An innovative caesium transporting bacterial pump is said to be beneficial in radioactivity decontamination process. Rhodopsin is a marine bacterium, which usually pumps sodium, lithium across the cell membrane[65]. This has led to the study of light driven caesium pump. It was able to introduce a range of mutations at two positions within the rhodopsin protein from *Krokinobacter eikastus*, which is important for its pump activity. When *E.coli* expressed the mutated protein, the concentration of different ions in solutions in which they were suspended was observed. This indicates successful pump activity.[66] A number of microorganisms can uptake caesium. Uptake is influenced by various factors such as the operational mode (batch or continuous flow systems), biomass immobilization, pH and particularly the presence of other monovalent cations, such as K^+ and Na^+. Microorganisms with particularly high affinity for Cs^+ are isolated. Removal of caesium by biotechnological methods has potential application in bioremediation of radionuclides contaminated environment.[67] The urge for microbe – Cs interaction is due to the continued release of caesium radioisotopes into the environment. Microbial Cs^+(K^+) uptake is mediated by monovalent cation transport systems located on the plasma membrane. Cs^+ has equal or greater affinity than K for transport in certain microorganisms. The external cations such as Cs^+, K^+, Na^+, $NH_4^+$and H^+ influence microbial Cs^+ accumulation. It is generally accompanied by an approximate stoichiometric exchange for intracellular K^+. The presence of Cs^+ in cells is not growth inhibitory but rather the loss of K^+. The high microbial tolerance to Cs^+ is due to sequestration of Cs^+ in vacuoles or changes in the activity and or specificity of transport systems mediating Cs^+ uptake[68]

CONCLUSION:

As such the analysis of microorganisms in relation to Group I element provides us with enormous scope in vast fields. The Hydrogen producing bacteria draws good scope for biofuel with its Hydrogen production. Microorganisms involving sodium can be applied for effective biodegradation of organic waste. The role of potassium in the study of Anaerobic microorganisms under highly saline conditions and for good bacterial cell viability can be explored in detail. The conversion of insoluble potassium to soluble potassium by certain microorganisms can be used to enhance cultivation in better way for plant growth. It is generally observed that microorganisms are not much involved with Lithium, Rubidium and Caesium, but some selective microorganisms do interact with these metals which are very essential for bioremediation of radionuclides contaminated environment. Enormous work has been done on the synthesis and study on the novel pharmacophore groups for their antimicrobial activity. The author's recent work on this line may be cited as an example. On this line an understanding of the relation between each chemical element and their interaction with microorganism will provide greater scope in the application of CADD oriented drug development activities.[69] A review regarding the interaction of microorganisms with group II elements of periodic table is in progress.

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Conflict of Interest:

The author has no conflict of interest. Shall Abide by the norms of the publishing journal.

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