Bulletin of Environment, Pharmacology and Life Sciences Bull. Env. Pharmacol. Life Sci., Vol 12 [8] July 2023 : 437-442 ©2023 Academy for Environment and Life Sciences, India Online ISSN 2277-1808 Journal's URL:http://www.bepls.com CODEN: BEPLAD REVIEW ARTICLE OPEN ACCESS

Faunal Diversity in Coal Mine: A Global Review

Anjana Chaudhuri¹, Shikha shrivastava ²'Divya Kumudini Minj³

Govt V.Y.T, P.G, Autonomous College Durg Chhattisgarh Indira Gandhi PG College Vaishali Nagar College Durg Chhattisgarh ², Govt VYT P. G Autonomous College Durg Chhattisgarh ³ Email <u>id-anjana.korba@gmail.com</u>¹

ABSTRACT

Coal water can be important sources of micro fauna since the environment are suitable for the growth of microorganisms. There are several reasons to investigate biodiversity of micro fauna. Coal fields located in the effect of *in situ* stress It increase as fall of the nearby rocks become more.so efficient workers are needed for this work. The study of coal mine biodiversity is not new. The study of coal mine biodiversity in underground coal mine is not very popular subject, but some works have been done earlier by some scientists and workers. The present study is a review of work done in field of faunal diversity in coal water in coal mine. KEY WORDS: Micro fauna, Acid mine, microsphere. Archaeal,

Received 23.05.2023

Revised 12.06.2023

Accepted 24.07.2023

INTRODUCTION

Coal water can be important sources of microfauna since the environment are suitable for the growth of microorganisms. There are several reasons to investigate biodiversity of microfauna. The microbial ecology, comparative microbial biodiversity from coal water sample collected from various. nearby coal fields can done. Few works have been done in field of coal mines and microorganisms which are mentioned below under review of literature. Under Coal Mine Act 1957 various rules and precaution must be following to work in coal mine.

By studying the temperature of Britain's coalfields, a median geothermal gradient of 24.1°C km–1 was calculated for the British coalfields [56]. Moreover, the Mine water drainage from coal mining is transforming productivity of agricultural lands to unproductivity wasteland. Soil of rice paddy field and productivity are adversely j comparing them with non-mined land.[43]

ACID MINE WATER OF BITUMINOUS COAL MINE:

The study of coal mine biodiversity is not new. The study of coal mine biodiversity in underground coal mine is not very popular subject, but some works have been done earlier by some scientists and workers. Acid mine water of bituminous coal mines of Monongalia country, west Virginia have microorganisms have active role in the mine water and also formation of sulphuric acid within the mine may due to them.[3] The effect of abandoned mine drainage on stream and responses to remediation in both the anthracite and bituminous coal mining in Pennsylvania (USA) .Micro invertebrate communities in AMD stream was different from reference stream .[30].

MICROFAUNA:

E. coli is also present in acid streams were used as a suggestive index of probable disease transmission. [4]. Microbial content is more in acid contaminated as compared to non-contaminated streams from same geographical area sand and acid- tolerant heterotropic microorganisms is also low. Most gram positive aerobic and anaerobic died out very rapidly in acid water instead iron ,sulphur oxidizing were bacteria present.[5].The microbial communities in an acid stream and found the after the stream moves from underground to the surface, rapidly evolves into distinct community close to that in the downstream storage pond.[23].Dominant microbial species in acid mine drainage receiving toxic in coal mine of Wetland [19].The age assigned to the microfauna is Oligocene- microcene and the assemblage has affinity with tertiary fauna.[29]

Large variety of microorganisms adapted to extreme environment of acid mine water.[38]. The microbial communities present in two under coal mines in the Bowen Basin, Queensland, Australia, present in pumped water from the actively mined areas, as well as pre and post mining formation waters .The

changing ground water flow dynamics and the introduction of oxygen in the mud surface has increased microbial biomass and diversity. The diversity of microorganisms and their functions in AMD ecosystems focused their bio technological applications in bio mining and AMD bioremediation according to their capacities [39] New data on AMD microbial ecology and evolution especially dynamic of microbial diversity community functions and population genome[4]. The early stage of biofilm formation in Rio Tinto (SW Spain) on extremely acidic environment and analysed diversity colonization rates and seasonal variation and the lower diversity found in extreme conditions in term of pH and heavy metal concentration.[20]

The general trends concerning the diversity and Eco physiology of eukaryotic acidophilic microorganisms and highly acidic environments are usually inhabited by algae, amoebas ,ciliates, heliozoan and rotifers.[32]. Diversity of microscopic Eukaryotes diversity that developed in acid mine drainage also found a limited diversity of archaea, bacteria and viruses were found. They suggested that environmental pressures and interplay between the members of these communities limits Species diversity at all trophic levels.[22] Composition and structure of microbial communities in acid mine drainage and bacterial ,Archaeal and micro eukaryotic were found.[24].Microorganisms that were expose to the pollutants in the environment of metal/metalloid have the tendency to fight the metal stress by various mechanisms [26],[Chemosynthetic bacteria population ,Acidothio bacillus ,Ferroxidan predominate in coal refuge gob piles [27].

BACTERIA

Sampling done from nine different mines. About 32 bacterial strains with different colour margin, elevation and opacity isolated with from varying depths of Dara Adam Khel located in the Federally Administrated Tribal area of Pakistan. The bacterial strain represents gene pool that may be further analysed for bio mediation, biodegradation and antimicrobial plant growth promoting abilities.[42]Coal mine generated Wasteland of Ranijanj, Bihar, India coal soil sample have heterophic gram negative phosphate population. Certain groups of sulphur cycle bacteria found in coal bearing strata of a coal strip mine at Decker, Montana and in mining areas in north-eastern Wyoming. This did not multiply in mine water environments. The hydrocarbon sulphide produced by these organisms contributed to heavy metal precipitation in the sedimentation pond [6]. The microbial communities inhibiting a site acid mine drainage AMD have relevance to microbiology bioleaching and to understanding of geochemical and Sulphur cycle.[12] Coalmine drainage in the North Eastern Coalfield Margarita ,Assam (India), the acidity mainly arises from the oxidation of pyrites of coal. Thiobacillus Ferroxidan found to accelerate the sulphur leaching rate from coal and is indigenous to mine drainages[8.]Bacterial population throughout the ground water flow system associated with Nickel rim mine tailings impoundment Ontario Canada.[13]. Bacteria of fresh water coal mine spoils have to produce antimicrobial Compound [28]. Microbial methanogenesis and community structure from coal seam aquifer located 843 -907 m below ground level in Northern Japan. Anova analysis provides evidence for a change in the genetic diversity at archaea population s that are dominated by methanogens.[21]. Dominance by a small no. of bacteria AMD microbial biofilm communities contain a notable variety of coexisting and closely related Euryarchaea. There result expand genomic information for this order archaea.[31]. The bacterial community from on AMD tailings pond using both classical culturing and modern direct sequencing technique Acidothiobacillus and Acidophilus were isolated.33]. From coal mine remains have metal/metalloid pollutions to surface ground water and the bioremediation is achieved by bacteria consortism.[57]. Effect soil properties The conclusion drawn were the randomness of the soil dumping increase the heterogeneity of mines soil properties which raise the complexity of reclamation practice, negative and positive result of mining.[54]. Significant amounts of bio methane were generated from coal by the addition of grassland soil microbial communities these discovery contributed to a global microbial diversity in coal mine environment and made a contribution to knowledge of the synthetic microbiology with regard o effective methanogenic microbial consortia for coal degradation.[51] Archaea kingdom in coal mines play important role in geochemical cycle a for coal beneficiation.[48] **ROTIFERS:**

Rotifers collected in spring and summer from two lakes of Ohio which receive acid mine drainage. The most abandoned rotifers Keatella and Brachionus species showed broad tolerances to pH[7]. In Coal mine water reservoir of Eastern Poland have nine planktonic species of rotifers, were found, two of these were dominating namely Brachionus angularis and B. Rubens. They were regarded as typical indicators of eutrophic waters containing Chlorides and sulphate and were responsible for their occurrence.[9]. Coalmine waters with high conductivity limit species diversity, affect the structure and greatly reduce the density of planktonic rotifers [25].

The structure of the rotifer communities determined the most important environmental factors that are significantly affect their structure in river influenced by salty mine water discharge. Among electrical conductivity, temperature and concentration of phosphate, increase in electrical conductivity due to mine water decrease density of rotifers.[52]. Certain bacteria are potentially contributing to a microbiologically

mediate Acid Mine Drainage system by remediation process.[53] Among the minor groups, protozoa(Alveolata,Amoebozoa) a green algae (Chlamydomonas),and dominant group of prokaryotes was(Alphaproteobacteria)present in acid drainage water of a quarry used for the mining of brown coal [55].

PROTOZOA:

Unidentified flagellates protozoa and flagellate carboxylated microsphere in sandy organelle in contaminated aquifer sediments field and laboratory useful as analogs investigating several abiotic aspects of flagellates transport behavior in ground water.[10].The diversity of microorganisms including obligatory acidophillic ,eukaryotes such as fungi, yeasts ,algae and protozoa are stable environment with constant pH.[11]. *Euglena mulabilis* a benthic photosynthetic protozoan is variably abandoned in effluent channel that contain acid mine drainage, discharging from coal mine but sulphate is highly concentrated *Euglena mulabilis* are largely absent suggested adverse effect on beneficial Fe mediating acidophilic protozoans.[14] Acid Mine Drainage system represented one of the most unfavourable habitats for microorganisms due to its low pH and high concentrations of metals. Compared to to bacteria and fungi, soil protozoa remain limited numerous occurrences between protozoa and bacterial or fungal taxa showed bio-interaction among them. [59]. The composition of micro biome of acid drainage water of a quarry used for the mining of brown coal Among the minor groups, protozoa (Alveolata,Amoebozoa) a green algae (Chlamydomonas),and dominant group of prokaryotes.

Acid Mine Drainage may contaminate surrounding ecosystem Communities of autotrophs and heterotrophic archaea and bacteria catalyse iron and sulphur oxidation determine release of metal and sulphur to environment acid mine drainage communities have limited no. of metabolically available reaction.[15]Indigenous microorganisms are responsible for accelerating sulfide mineralization mobilizing metals. Other catalyse reductive processes that essentially reverse this reaction and ameliorate polluted mine waters [16].

Acid Mine Drainage microbial communities like microbial eukaryotes form a biofilm structure they produce dissolved carbonate ions, which are likely important for the growth of chemo lithoautotrophic acidophlic prokaryotes.17 epiphytic eukaryotic community as well as evaluate the influence of different physiochemical characteristic of water in biodiversity structure and population. [18]. Microbial communities (methanogens and anaerobic fermentation bacteria) in the coal and water in a representative small production coal mine of central China responsible are for biogenic methane formation. Themost abundant genera in coal and mine water were Rheinheimera and Hydrogenophaga[34]. Biodiversity , pattern of spatial and temporal distribution of bacterial communities , linked to changes in The physiochemical conditions in acid mine water.[35] By different metabolic network at the organization level of Bacterial, archaea and eukaryotic diversity play important role in Acid Mine Drainage ecosystem [36].

Mine impacted, anoxic groundwater with high concentration springs and a weeps associated with iron oxide mounds and deposits which were colonized by iron oxidizing microorganisms that remove most of dissolved iron at low pH efficiently remove most efficiently iron at low pH.[37].Environmental oxidation and microbial metabolism drive production in acid mine drainage in microbial community of bacterial archaeal eukaryotes due to geochemical and seasonal characteristics is fundamental to AMD monitoring and remediation .[41]The microbial diversity within all domains of life in the different microhabitat at Los Rueld underground mine (N W Spain]detected by bacterial function [44].

CONCLUSION

Deep sea fauna is known but underground fauna is still unknown as the mine form a window to a deeper Earth 1000m below the Earth surface it is best to study fauna biodiversity inhibiting in the uncommon biodiversity as no sunlight reaching the inner depth of mine the existence of fauna is questionable but during some pilot studies. Some examples of fauna has been found. The water quality present in the water flowing under coal mine is quite different from the water found on the surface as the river , pond , lake so it will be interesting to study the fauna biodiversity found in the depth of coal mine. In the coal mine the water body formed of coal and the roof also is rock mass of coal biodiversity and food chain is different and interesting to be known.

FUTURE ISSUE

Though many workers have studied the coal mine water, but there is scarcity of studies from Indian coalmines.

1. Only few studies regarding Micro fauna inhibiting in coalmine water Ecosystem have been explored. Physiological matters would help to understand ecosystem of under coal mine. Tolerance level of microorganisms can be observed.

2.Coal water is itself a micro habitat so new microorganisms may be explored besides investigation of microbial ecology of mine water, influences of mine water on micro fauna can be observed

3.Deep Sea fauna is known but underground fauna is still unknown as the mine form a window to a deeper Earth 1000m below the Earth surface it is best to study fauna biodiversity inhibiting in the uncommon biodiversity as no sunlight reaching the inner depth of mine the existence of fauna is questionable but during some pilot studies. Some examples of fauna have been found.

4. The water quality present in the water flowing under coal mine is quite different from the water found on the surface as the river, pond, lake so it will be interesting to study the fauna biodiversity found in the depth of coal mine.

5. In the coal mine the water body formed of coal and the roof also is rock mass of coal biodiversity and food chain is different and interesting to be known.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interests regarding the publication of this paper.

ACKNOWLEDGEMENT

We are thankful to department of Zoology V.Y.T.P.G College, Durg, Chhattisgarh India for providing well equipped laboratory and library.

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CITATION OF THIS ARTICLE

Anjana C, Shikha S, Divya K M. Faunal Diversity in Coal Mine: A Global Review. Bull. Env. Pharmacol. Life Sci., Vol 12 [8] July 2023: 437-442