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Biogeochemical activity in arsenic prone zone

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Abstract

The world's largest arsenic (As) mass poisoning have been reported from West Bengal, India in early eighties.. Arsenic as a Heavy metals are the natural constituents of the earth crust. The level of As have been found to be particular alarmining in India, Bangladesh, China, Taiwan, United states and many other countries. The health risks of As exposure due to the installation of thousand of shallow tube wells in Bengal Delta Plain (BDP) is known, However, microbial contamination of shallow aquifer is another important issue that can be linked with As mobilization and water quality. Different types of Bacteria influence As geochemistry by their metabolic pathway including oxidation, reduction, and mobilization reaction that highly regulates arsenic speciation in our environment. Herein, we further study the microbiological (bacteria, fungus & higher plant) population of ground waters with references various psycho-chemical parameters of ground water particularly arsenic (As) concentration.

Keywords: Arsenic; Microbiology; Geochemistry; Oxidation

Introduction

Arsenic contamination in ground water is a critical issue in West Bengal (India) and Bangladesh. Over the few decades, geogenic arsenic was highlighted in many regions of the world [1-4]. The most notable in South & Southeast Asia where 60 million people are affected by chronic arsenic poisoning [2]. Anthropogenic activities (fertilizer, arsenical pesticides, wooden poles preservative agents, mining waste, waste sewage sludge, and coal burning) and well drilling mobilize arsenic into the environment [2,4,5]. In Bengal Delta Plain (BDP), several biogeochemical process are also involved (i.e. chemical & redox change and bacterial Fe (III) reduction) in arsenic mobilization. This sub surface arsenic contamination of ground water not only affects human food chain (rice, vegetables, etc) but also human tissues. This endemic problem is most the important challenge to us [3,4].

Biogeochemical Process

Many researchers reported the role of iron reducing bacteria in arsenic mobilization [1]. Microbial reduction of Fe (III) by oxidation of organic carbon, leads to microbial decoupling reaction converting As(V) to, As (III) which is more toxic than As(V) [1]. Many fecal coliforms also involved in this decoupling reaction [6]. Some different class of fungi are capable of removing toxic arsenic compound from arsenic polluted environments. Most fungus store arsenic inside the cell cytosol with metal binding polypeptides e.g. metallothioneins or phytochelatins also called cell vacuoles. Fungus accumulates arsenic at their stationary phase of growth [7].

i. Depth dependent arsenic mechanism

Beside having soil of alluvial character, worlds largest Bengal delta plain (BDP) is, also a flood porn zone. Physico-chemical parameters of soil in this region has more pragmatic relation to arsenic mobilization. Many chemical parameters such as pH, Eh, Na^+, Ca^+, Mg^+, Fe_T, Fe (II) and also temperature has been reported to be positively co-related to arsenic mobilization [2-4].

ii. Oxidation and reduction process

The oxidation model demonstrates release of Arsenic from sulphide minerals by the reaction given below [8].

$$FeS_2\,(S) + 7/2\,O_2 + H_2O \leftrightarrow Fe^{2+} + 2SO_4^{2}- + 2H^+$$

$$FeAsS\,(S) + 13Fe^{3}+ + 8H_2O \leftrightarrow 14\,Fe^{2}+ + SO_4^{2}- + 13H+ + H_3AsO_4$$

The reduction model of arsenic also called reverse approach of the oxidation model involves co-precipitation of Arsenic with Fe/ Mn/-oxide/ Hydroxide [8].

$4FeOOH + CH_2O\text{-} PO_4$ (sorbed) $+7H^+ \rightarrow 4Fe^{2}+ + PO_4{}^{3}\text{-}$ (desorbed) $+6H_2O$

$2H_2AsO_4\text{-} + CH_2O + 5H+ \rightarrow 2H_3AsO_4 + HCO^3\text{-} + 2H_2O$

Future Scope

From the study it can be stated that the arsenic contamination has spread throughout the world and there is an urgency to fight against it. We hypothesize that microbes converts high toxic or carcinogen arsenite [As (III)] to arsenate [As (V)]. Also some applicable technique that can be used to analyze interaction between arsenic microbes (bacteria, fungus & higher plant) and physiological properties of subsurface and surface biodiversity.

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