As a naturally occurring element, the abundance of uranium in the environment is very low. Anthropogenic activities, including fossil fuel combustion, uranium ores mining and enrichment for nuclear weapon manufacturing, and electricity generation in nuclear fueled power plants, has released significant amount of uranium into the environment. As a result, uranium contamination is a worldwide phenomenon. According to the US Department of Energy (DOE), there are about 2,000,000 acres in 30 states that are contaminated with uranium [1].

In contaminated groundwater, Uranyl [U (VI)] is the dominant uranium species, which is highly soluble and mobile in the subsurface environments. Uranium is toxic to humans, as well as animals, due to its radioactive and heavy metal nature. To prevent the spread of uranium in the environment, is an emerging challenge to environmental scientists. Many microbes are proved to be capable of reducing highly soluble U(VI) to sparingly insoluble U(IV) form, and precipitate the reduced uranium as mineral uraninite. These microbial processes might be an ideal solution to clean-up uranium contaminated environments, because of their relatively low cost and minimum environmental disruption. Unlike the biodegradation of toxic organic pollutants, bioremediation of uranium largely depends on reducing its bioavailability in the environment. The best documented uranium bioremediation strategy is immobilization, which includes bioreduction and/or bioprecipitation. Phylogenetically, diverse species of Bacteria are found to be able to reduce U(VI) to U(IV), and those bacteria are dominated by Fe(III)-reducing bacteria (FeRB) and sulfate-reducing bacteria (SRB) [2]. Uranium in the contaminated environment might also be immobilized, by binding to microbial extracellular polysaccharides (EPS) and other molecules containing negatively charged functional groups, such as hydroxyl, carboxyl, or phosphate, a process termed as biosorption.

Microbial reduction of uranium is still a hot topic in the field of bioremediation. Novel bacteria have been isolated and characterized for U(VI) reduction, and the molecular genetic mechanisms, e.g. enzymes, electron transfer system, and uranium transport system involved in microbial reduction of U(VI), have been studied [2]. Some researchers have surveyed whole genome transcription profile of some bacteria, hoping to identify genes and/or gene clusters that might be important for uranium residence and bioprecipitation [3]. Recently, significant efforts have been paid to in situ microbial bioremediation, which include electron donor addition, indigenous microbial community characterization, and evaluation of long-term bioremediation effectiveness [4]. Next-generation sequencing and functional gene array techniques have been successfully applied in microbial uranium bioremediation [5]. On the other hand, biosorption might be a promising approach to remediate uranium contaminated environments, since some bacteria and microbial assemblages have shown to have the capability to adsorb uranium from aqueous phase [6]. According to the data available to date, it seems that an ideal uranium bioremediation strategy, largely depends on a thorough understanding of the microbiological, ecological, geochemical features of the selected contaminant site.

Although, major progress on microbial bioremediation of uranium contamination has been made, there are still some challenges in microbial bioremediation of uranium, which may be summarized as following:

1. Instability of the microbial reduced uranium form U(IV). It could be re-oxidized back to U(VI), in presence of Fe(III) mineral and free O₂. How to maintain the stability of the reduced form, is a major challenge when using reductive precipitation strategy to remediate U(VI).

2. Poor understanding of the mechanisms of biosorption. Additional efforts need to be paid, towards a better understanding of principles behind biosorption, especially in uranium biosorption by biofilm, a promising but complex microbial system for uranium bioremediation.

3. Limited data is available, regarding microbial bioremediation of uranium, at a systems biology level. This could be done, by combining two and more of the newly developed metagenomic tools, e.g. 454-pyrosequencing, functional gene array, proteomics, transcriptomics and metabolomics.

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