Environmental Pollution 158 (2010) 1119–1126

Contents lists available at ScienceDirect

Environmental Pollution

journal homepage: www.elsevier.com/locate/envpol

Review

Progress in decontamination by halophilic microorganisms in saline wastewater and soil

Xuliang Zhuang [a,b,*], Zhen Han [a,c], Zhihui Bai [a], Guoqiang Zhuang [a], Hojae Shim [d]

[a] Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, 18 Shuangqing Road, Haidian District, Beijing 100085, China
[b] Bureau of Science and Technology for Resources and Environment, Chinese Academy of Sciences, Beijing 100864, China
[c] Graduate University of Chinese Academy of Sciences, Beijing 100049, China
[d] Department of Civil and Environmental Engineering, Faculty of Science and Technology, University of Macau, Macau SAR, China

Review on the decontaminative capabilities of halophilic microorganisms in saline wastewater and soil.

ARTICLE INFO

Article history:
Received 23 April 2009
Received in revised form
13 January 2010
Accepted 18 January 2010

Keywords:
Decontamination
Halophilic microorganisms
Saline soil
Saline wastewater

ABSTRACT

Environments with high-salt concentrations are often populated by dense microbial communities. Halophilic microorganisms can be isolated from different saline environments and different strains even belonging to the same genus have various applications. Wastewater and soil rich in both organic matter and salt are difficult to treat using conventional microorganisms typically found in wastewater treatment and soil bioremediation facilities. Studies on decontaminative capabilities and decontamination pathways of organic contaminants (i.e., aromatic compounds benzoate, cinnamate, 3-phenylpropionate, 4-hydroxybenzoic acid), heavy metals (i.e., tellurium, vanadium), and nutrients in the biological treatment of saline wastewater and soil by halophilic microorganisms are discussed in this review.

© 2010 Elsevier Ltd. All rights reserved.

1. Introduction

Environments with NaCl concentrations approaching saturation are often populated by dense microbial communities (Oren, 2002). Although mostly isolated from the salted food, their natural habitats are hypersaline waters containing intermediate levels of salt concentration and hypersaline soils (Rodríguez-Valera, 1986). According to Kushner (1978), several physiological groups of microorganisms and their requirement of particular salt concentration for the best growth are considered: (1) nonhalophiles (less than 0.2 M NaCl); (2) halotolerant (nonhalophiles tolerating high-salt concentrations); (3) slight halophiles (0.2–0.5 M NaCl); (4) moderate halophiles (0.5–2.5 M NaCl); (5) extreme halophiles (2.5–5.5 M NaCl). Many microorganisms are nonhalophiles or nonhalotolerant that cannot inhabit in high-salt environments. Halophilic microorganisms can be isolated from different saline environments, and different strains even belonging to the same genus are shown with various applications (Table 1).

The two main groups of microorganisms adapted to hypersaline environments are halophilic archaea and halophilic bacteria (Garcia et al., 2004). Many works (Asker and Ohta, 1999; Joo and Kim, 2005; Mevarech et al., 2000; Oren, 1986; Trüper and Galinski, 1990) have been done on ecology, taxonomy, biosynthesis, production of compatible solutes (such as amino acids, sugars, and betaines), canthaxanthin, halophilic enzymes using halophilic bacteria, and proteomics of halophilic archaea.

Saline and hypersaline environments are frequently contaminated with organic compounds as a result of industrial activities (Oren et al., 1992). In the biological treatment of such conditions, the microorganisms conventionally used show only poor degradative efficacy due to the highly saline conditions and the exposure to low-level, non-point sources of toxic contaminants. Halophilic microorganisms possess wide biotechnological applications and their abilities to degrade various environmental contaminants cannot be ignored. Many reports indicated that bacteria living in hypersaline environments may have a greater potential in degrading pollutants than previously assumed (Nicholson and Fathepure, 2005). For instance, a moderately halophilic bacterial consortium has been identified degrading polycyclic aromatic hydrocarbons (PAHs) in a marine environment (Arulazhagan and Vasudevan, 2009). Three strains among 27 strains of halophilic and halotolerant bacteria isolated from the effluents of textile industries showed remarkable abilities in decolorizing the widely used

---

* Corresponding author at: Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, 18 Shuangqing Road, Haidian District, Beijing 100085, China. Tel.: +86 10 62923562; fax: +86 10 62923563;
E-mail address: xlzhuang@rcees.ac.cn (X. Zhuang).

0269-7491/$ – see front matter © 2010 Elsevier Ltd. All rights reserved.
doi:10.1016/j.envpol.2010.01.007

Table 1
Microbial taxonomy of halophilic microorganisms reviewed.

Superkingdom	Phylum	Class	Order	Family	Genus	Strain
Bacteria	Actinobacteria	Actinobacteria (class) Actinobacteridae (subclass)	Actinomycetales (order) Micrococcineae (suborder)	Micrococcaceae	Nesterenkonia	*Nesterenkonia* sp. strain MF2
	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	*Bacillus cereus*, *Bacillus flexus*
				Bacillales Family XII. Incertae Sedis	Exiguobacterium	*Exiguobacterium homiense*
				Noctuoidea	Halobacillus	*Halobacillus trueperi*
				Staphylococcaceae	Salinicoccus	*Salinicoccus* sp. strain QW6
					Staphylococcus	*Staphylococcus aureus*
		Clostridia	Halanaerobiales	Halanaerobiaceae	Halanaerobium	*Haloanaerobium congolense*, *Halonaerobium lacusrosei*, *Haloanaerobium praevalens*, *Haloanaerobium alcaliphilum*
				Halobacteroidaceae	Halanaerobacter	*Haloanaerobacter chitinovorans*
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Ochrobactrum	*Ochrobactrum* sp.
		Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	Pseudoalteromonas	*Pseudoalteromonas* sp.
			Enterobacteriales	Enterobacteriaceae	Enterobacter	*Enterobacter cloacae*
			Oceanospirillales	Halomonadaceae	Halomonas	*Halomonas campisalis*, *Halomonas organivorans*, *Halomonas* sp strain GTW, *Halomonas elongata*
			Pseudomonadales	Pseudomonadaceae	Pseudomonas	*Pseudomonas aeruginosa*
			Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	*Stenotrophomonas maltophilia*
Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Haloarcula	*Haloarcula* sp. strain D1, *Haloarcula vallismortis*, *Haloarcula hispanica*
					Haloferax	*Haloferax* sp. D1227, *Haloferax volcanii*, *Haloferax mediterrani*
Eukaryota, Viridiplantae (kingdom)	Chlorophyta	Chlorophyceae	Chlamydomonadales	Dunaliellaceae	*Dunaliella*	*Dunaliella* sp.

azo dyes (Rauf and Ashraf, 2008), and four halotolerant and/or halophilic denitrifying bacteria capable of degrading trimethylamine under both aerobic and denitrifying conditions were newly isolated from coastal sediments and wastewater contaminated by marine water (Kim et al., 2003). Halophilic archaea can also grow on *p*-hydroxybenzoic acid (Cuadros-Orellana et al., 2006) and aromatic substrates as the sole carbon and energy source, as in *Haloferax* sp. D1227 which was isolated from the oil brine contaminated soil (Fu and Oriel, 1998). Since the *ortho* degradation pathway for degrading benzoate and salicylate has been found in *Halomonas campisalis*, an alkaliphilic and moderate halophile, by detecting metabolites (catechol and *cis*,*cis*-muconate) (Oie et al., 2007), the degradation mechanism of halophilic microorganisms becomes not hard to figure out. It has been suggested the ability to degrade toxic compounds is a widespread feature among halophilic microorganisms.

2. Halophilic reaction mechanism

In order to survive at high-salt concentrations, halophilic microorganisms have to maintain an osmotic balance with their external environment. In recent years, detailed investigations have been sought to understand three major theories:

(1) The highly negative surface charge of halophilic proteins makes them more soluble and renders them more flexible at high-salt concentrations, conditions under which non-halophilic proteins tend to aggregate and become rigid (Mevarech et al., 2000). Most enzymes of halobacteria are active and stable at high-salt concentrations and lose activities at salt concentrations lower than 2 M (Pieper et al., 1998).

(2) Halophilic bacteria include a heterogeneous physiological group of microorganisms belonging to different genera. For the successful adaptation at high-salt conditions, they actively extrude Na^+ and maintain the internal ion concentration through Na^+/H^+ antiporters (Ventosa et al., 1998). To prove this theory, *Escherichia coli* cell which lacked all of the major Na^+/H^+ antiporters was used. After the encoding gene was cloned from halophilic bacteria, it could grow in medium containing 0.2 M NaCl or 10 mM LiCl (Zou et al., 2008).

(3) During salt stress, most halophilic and halotolerant bacteria are able to accumulate compatible solutes from their environment or synthesize such compatible solutes as sugars, amino acids, glycine betaine, trehalose, and ectoine (Trüper and Galinski, 1990). A fragment of the glycine betaine transporter betH gene, showing 56% identity to the OpuD of *Bacillus subtilis* which belongs to the betaine/carnitine/choline transporter (BCCT) family, was obtained from the genome of *Halobacillus trueperi* and this gene helped it accumulate glycine betaine under the condition of high osmolarity (Lu et al., 2004).

Therefore, halophilic bacteria could survive in the environment with high-salt concentrations. Owing to their dual characteristics of being halophilic and degrading contaminants, halophilic bacteria possess a huge application value of treating saline wastewater and contaminated saline soil.

Download English Version:

https://daneshyari.com/en/article/4426083

Download Persian Version:

https://daneshyari.com/article/4426083

Daneshyari.com