Fate of tetracycline, sulfonamide and fluoroquinolone resistance genes and the changes in bacterial diversity during composting of swine manure

Ammaiyappan Selvam, Delin Xu, Zhenyong Zhao, Jonathan W.C. Wong*

Sino-Forest Applied Research Centre for Pearl River Delta Environment, Hong Kong Baptist University, Kowloon Tong, Hong Kong

1. Introduction

Antibiotics are used in animal husbandries for both prophylactic and therapeutic purposes. However, 30–90% of the administered antibiotics are excreted through urine and feces as non-metabolized parent compounds and these non-metabolized antibiotics in the animal manure become a significant source of antibiotics and cause the development of antibiotic resistant microorganisms in the environment (Heuer et al., 2011). Consequently, there are concerns about the transfer of antibiotic resistance determinants to pathogens that may reduce the efficiency of antibiotic therapy to both human and animals (Barton, 2000). Development of resistance to antibiotics in microbes is a highly complex process and yet not completely understood even in clinical environments. But it was demonstrated that antibiotics even at sub-inhibitory concentrations affect cell functions and change the genetic expression of virulence factors or the transfer of antibiotic resistance (Salyers, 2002). The frequency of bacteria carrying antimicrobial resistance genes seems to be especially high for pigs as compared to cattle or sheep which correlates with the amounts of antibiotics used in the husbandry of these animal species (Enne et al., 2008; McKinney et al., 2010; Schweiger et al., 2009). High usage of antibiotics put a pressure on the thriving microbes to evolve resistance for the specific environment. Besides, continuous prophylactic use of antibiotics would also facilitate the development of antibiotic-resistant bacteria in animals that in turn act as a potential source of antibiotic resistance genes in the environment. Furthermore, animal manure promoted horizontal transfer of antibiotic resistance genes in soil were reported previously (Smalla et al., 2000). More details on the source of antibiotic resistance genes (ARGs) in soils and related impacts on the microbial dynamics can be found from the recent review by Heuer et al. (2011). Despite the numerous reports on the presence and dissemination of manure-driven ARGs, their fate during the composting was never reported, although composting was demonstrated to reduce the levels of antibiotics significantly (Arikan et al., 2009; Dolliver et al., 2008; Hu et al., 2011; Selvam et al., 2012; Wu et al., 2011). As a promising bioremediation technology, composting has been applied to remove antibiotics from animal manures recently. During composting, the presence of a wide variety of complex organic compounds will encourage the development of a wide diversity and high population of microorganisms (Diaz et al., 1993). Usually, microorganisms dominating within the contaminated environment are those capable of utilizing and/or surviving toxic contamination. For their survival, they must possess appropriate mechanism for the tolerance; in case of antibiotics, presence of antibiotic resistance genes (ARGs) was implicated. On one hand removal of antibiotics from the animal manures is important; while, on the other hand the ARGs must also be eliminated to prevent their accumulation in soil.

DNA-based method, like real-time PCR (polymerase chain reaction), is being used increasingly in microbial ecology to quantify the functional gene markers within the environment (Smith and Osborn, 2009), owing to the feasibility of quantifying both cultivable and non-culturable bacteria. There are studies concerning the

* Corresponding author. Tel.: +852 34117056; fax: +852 34112355.
E-mail address: jwcwong@hkbu.edu.hk (J.W.C. Wong).

0960-8524/$ - see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biortech.2012.03.045