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Antibiotics and antibiotic resistance genes removal from leachate by aged refuse bioreactor on site removal

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The abuse of antibiotics caused the widespread of antibiotic resistome, which further raised the issue on public health. Leachate, generated during the landfill treatment of municipal solid waste, is the important hotspot of the antibiotics and Antibiotic Resistance Genes (ARGs) and no effective on-site treatment has been put forward for preventing ARGs dissemination until now. Herein, the aged refuse bioreactor was employed to remove antibiotics and ARGs from leachate, and the great removal performance was observed. For the detected antibiotics, the total removal efficiency was about 76.75%, and sulfanilamide and macrolide were removed with high efficiencies (>80%). Among the target ARGs, tetracycline and macrolide resistance genes (*tetM, tetQ and ermB*) were eliminated with 1.2-2.0 orders of magnitude. Mechanism study indicated that the occurrences of ARGs did not correlated with physicochemical parameters, but closely linked to the variations of the bacterial community structure. Network analysis revealed the potential host bacteria of ARGs in leachate, and redundancy analysis indicated the significant correlations between four genera and the distribution of ARGs, which implied that these key genera (including potential pathogens) drove the ARGs removal. Furthermore, the hydraulic loading test confirmed that the aged refuse bioreactor was capable of achieving high removal efficiencies even under shock loading for the higher loading was negative for the proliferations of potential ARGs hosts. This study suggested that the aged refuse bioreactor could be a promising way for antibiotics and ARGs on-site removal from leachate.

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mecA sequencing and SCCmec typing in methicillin resistant *Staphylococci*: A highly diversified element with new mutations in *mecA*

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Genetic mechanisms of methicillin resistance are still relevant in *Staphylococci*. The aim of this study is to assess the possible exchanges of staphylococcal cassette chromosome mec (SCCmec) between isolates of Methicillin-Resistant *Staphylococci* (MRS) and to check for known or new mutations in *mecA* DNA. A total of 35 MRS non repetitive isolates were recovered, including 20 *S. haemolyticus*, 7 *S. aureus*, 4 *S. sciuri*, 2 *S. saprophyticus*, and one isolate each of *S. xylosus* and *S. lentus*. Only 16 of the 35 strains were assigned to known SCCmec types: 7 SCCmec VII, 6 SCCmec IV and 3 SCCmec III, with possible horizontal transfer of the SCCmec VII from methicillin-resistant *S. haemolyticus* to methicillin-susceptible *S. aureus*. *mecA* genes sequencing in 10 selected isolates allowed description of nine punctual mutations, seven reported for the first time. The most frequent mutation was G246E, identified in isolates of methicillin-resistant *S. aureus*, *S. sciuri*, *S. saprophyticus* and *S. lentus*. These results emphasized the high degree of genetic diversity of SCCmec element in methicillin-resistant *Staphylococci* and describe new missense mutations in *mecA*, which might be important in understanding the evolution of methicillin and new β-lactams resistance.

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