Nexus between anaerobic digestion of animal waste and antibiotic-related pollutants: A critical review

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Abstract

Anaerobic digestion (AD) of animal waste is a sustainable technology for renewable energy production. However, antibiotics widely used in livestock are often excreted in significant amounts (17–90 %), affecting biogas production and promoting the spread of antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) which pose serious public health risks. This review critically discusses the intricate interplay among AD, antibiotics, ARGs, and MGEs focusing on mechanisms, microorganisms, and enzymes involved. Antibiotics exhibit contrasting effects on methane production, from inhibition to non-effect or even stimulation. Moreover, the removal efficiency of antibiotics, ARGs, and MGEs varies based on the antibiotic's type, concentration, and characteristic and AD parameters. Key antibiotic removal pathways include dechlorination, hydrolysis, demethylation, and various modifications of functional groups such as amino, formyl, acetyl, and hydroxyl groups. Enzymes like acetate kinase, laccase, esterase, acetyltransferases, and dehydrogenases play crucial roles in antibiotic biodegradation. Genera like *Methanomethylovorans*, *Methanothrix*, *Desulfomonile*, and *Syntrophaceae* could biodegrade antibiotics like erythromycin, sulfamethoxazole, and ampicillin at concentrations 10–250 μg l^{-1}. Strategies like pretreatment, post-treatment, co-digestion, and carbonaceous material supplementation are proposed to enhance pollutant removal efficiency and energy recovery. Finally, challenges and future research directions are outlined to enhance AD's effectiveness in managing antibiotic pollutants and advancing waste-to energy sustainability.

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HIGHLIGHTS

- Interactions among AD, antibiotics, ARGs, and MGEs were comprehensively discussed.
- Antibiotic residue repercussions on anaerobic digestion performance are discussed.
- Effects of antibiotic properties and AD parameters on antibiotics, ARGs, MGEs removal.
- Discussed: mechanisms, microorganisms, enzymes affecting antibiotic, ARG, MGE in AD.

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ABSTRACT

Anaerobic digestion (AD) of animal waste is a sustainable technology for renewable energy production. However, antibiotics widely used in livestock are often excreted in significant amounts (17–90 %), affecting biogas production and promoting the spread of antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) which pose serious public health risks. This review critically discusses the intricate interplay among AD, antibiotics, ARGs, and MGEs focusing on mechanisms, microorganisms, and enzymes involved. Antibiotics exhibit contrasting effects on methane production, from inhibition to non-effect or even stimulation. Moreover, the removal efficiency of antibiotics, ARGs, and MGEs varies based on the antibiotic's type, concentration, and characteristic and AD parameters. Key antibiotic removal pathways include dechlorination, hydrolysis, demethylation, and various modifications of functional groups such as amino, formyl, acetyl, and hydroxyl groups. Enzymes like acetate kinase, laccase, esterase, acetyltransferases, and dehydrogenases play crucial roles in antibiotic biodegradation. Genera like *Methanomethylovorans*, *Methanothrix*, *Desulfomonile*, and *Syntrophaceae* could biodegrade antibiotics like erythromycin, sulfamethoxazole, and ampicillin at concentrations 10–250 μg l^{-1}. Strategies like pretreatment, post-treatment, co-digestion, and carbonaceous material supplementation are proposed to enhance pollutant removal efficiency and energy recovery. Finally, challenges and future research

Abbreviations: AD, Anaerobic digestion; AcoD, Anaerobic co-digestion; ARGs, Antibiotic resistance genes; ARB, Antibiotic-resistant bacteria; C/N, Carbon to nitrogen ratio; COD, Chemical oxygen demand; CIP, Ciprofloxacin; CLA, Clarithromycin; CTC, Chlortetracycline; CH_4, Methane; DOC, Doxycycline; ENR, Enrofloxacin; ERY, Erythromycin; FFC, Florfenicol; HGT, Horizontal gene transfer; HRT, Hydraulic retention time; HT, Hydrothermal treatment; MGEs, Mobile genetic elements; MLs, Macrolides; McrA, Methyl coenzyme M reductase gene; MLSB, Macrolide, lincosamide, and streptogramin B; MDL, Method detection limit; NOR, Norfloxacin; OTC, Oxytetracycline; QNs, Fluoroquinolones; SRT, Solid retention time; SIR, Substrate to inoculum ratio; SAs, Sulfonamides; SMZ, Sulfamethizole; SDZ, Sulfadiazine; SMX, Sulfamethoxazole; SDD, Sulfadimidine; SDM, Sulfadimethoxine; SMN, Sulfamethazine; TS, Total solid; TC, Tetracycline; TYL, Tylosin; TMP, Trimethoprim; VS, Volatile solid; VFAs, Volatile fatty acids.

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