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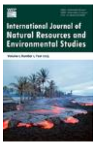
International Journal of Natural Resources and Environmental Studies
ISSN: 3006-2012 (Print), ISSN: 3006-0834 (Online) | Volume 8, Number 5, Year 2026
DOI: https://doi.org/10.62051/ijnres.v8n5.12
Journal homepage: https://wepub.org/index.php/IJNRES/index



A Review on Microbial Coal Biodegradation for Methane Production

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ABSTRACT

Coal biomethanation, as a green and low-carbon energy conversion technology, has shown significant application potential in coalbed methane (CBM) development. This paper systematically reviews the mechanisms and research progress of microbial coal biodegradation for methane production. The key processes, including hydrolysis, fermentation, hydrogen-producing acetogenesis, and methanogenesis, as well as their synergistic microbial interactions, are analyzed in detail. The characteristics of microbial community structures in coal seams are summarized, revealing that methane generation generally follows a metabolic pattern of “bacterial primary degradation coupled with archaeal terminal methanogenesis,” with hydrogenotrophic methanogens dominating in most basins. Furthermore, the progress of mixed microbial cultures combining indigenous and exogenous microorganisms for enhancing coal biogasification is reviewed. It is indicated that multi-source microbial consortia exhibit significant functional complementarity; however, their performance is influenced by factors such as community structure, environmental conditions, and interspecies interactions. Finally, current limitations in degradation mechanisms, functional microbial identification, and system stability are discussed, and future research directions are proposed, emphasizing the need for deeper mechanistic insights and microbial regulation strategies to promote the engineering application of coal biomethanation.

KEYWORDS

Coal biomethanation; Coalbed methane; Mixed microbial consortia; Methanogens; Microbial degradation; Anaerobic fermentation.

1. INTRODUCTION

Coal biomethanation technology has emerged in recent years as a green and low-carbon energy conversion approach with the advancement of biotechnology. It features a simple process, the ability to operate under ambient temperature and pressure, and relatively low cost [1, 2]. Compared with conventional catalytic methanation technologies, it shows significant advantages in terms of energy efficiency and environmental sustainability.

In the process of coal biomethanation, the structure of the microbial community is one of the key factors affecting coal degradation and methane production efficiency. Different microbial consortia exhibit significant variations in anaerobic fermentation performance, directly influencing the conversion efficiency of organic matter in coal. Studies have shown that microbial communities vary markedly across different regions, indicating that methanogenic consortia derived from different sources possess distinct coal-degrading capabilities. Although indigenous microorganisms are generally considered to be better adapted to the coal seam environment, some studies have demonstrated that exogenous microorganisms can be more effective in the bioconversion of coal to methane under certain conditions [3, 4].

2. RESEARCH PROGRESS ON BIOGENIC GAS

2.1. Classification of coalbed methane and definition of biogenic gas

Coalbed methane is a methane-dominated gas mixture that was long regarded as a mine hazard. It was not until the 1980s that it was re-recognized as a high-calorific-value clean energy source, which has since promoted extensive research on the process of coal conversion to biogenic methane. Based on the characteristics of coalbed methane in coal-bearing basins, coalbed methane can be classified into biogenic and thermogenic types. According to coal maceral composition and isotopic composition, it can also be divided into biogenic gas and thermogenic gas based on vitrinite reflectance[5]. Coalbed methane formed during the early coalification stages (such as the peatification and lignite stages) with relatively light carbon isotopic composition belongs to biogenic gas Thermogenic coalbed methane refers to methane-dominated hydrocarbon gases generated through a series of physical and chemical changes of organic matter in coal under relatively high reservoir pressure and temperature conditions during coalification, a process typically accompanied by the generation of some non-hydrocarbon gases and water. In contrast, biogenic coalbed methane is biogenic methane generated under specific geological settings, where aromatic, aliphatic and other macromolecular substances in coal are utilized by indigenous microorganisms in the coal seam and converted into simple small-molecule organic compounds, which are then utilized by methanogens to produce methane.

2.2. Further classification of biogenic coalbed methane and microbial enhancement technology (MECBM)

Studies have shown that coal has the potential for secondary biogenic gas generation. Based on previous research, and according to differences in generation time, parent material sources, and geological conditions, biogenic coalbed methane can be further divided into primary biogenic coalbed methane and secondary biogenic coalbed methane[6]. The technology of injecting anaerobic microbial communities and their required nutrients into coal seams to enhance coalbed methane production, namely microbial enhanced coalbed methane (MECBM) technology, holds potential for increasing coalbed methane resources. The introduction of microorganisms can improve coal seam permeability, thereby facilitating coalbed methane extraction. This technology has achieved certain success in pilot tests carried out in some basins in Australia. Relevant field tests have also been conducted in the Huaning Block in Yunnan and the Zheng-1 Block in the Qinshui Basin in China, achieving certain production enhancement goals[7, 8]. Further experimental studies have found that methanogenic communities have a certain permeability-enhancing effect on coal, leading to the preliminary proposal of the concept of biologically enhanced coal seam permeability. Biogenic methane, according to its formation pathways and origins, can also be classified into primary and secondary types. When a coal seam possesses the nutrients necessary for methanogen growth and reproduction, and is under suitable conditions of temperature, pressure, oxidation-reduction potential, and pH, methanogens can degrade coal and generate a methane-dominated gas mixture through a series of anaerobic fermentation reactions. This gas mixture is referred to as biogenic coalbed methane, or simply biogenic methane.

2.3. Biogenic methane generation pathways, coal degradation mechanisms, and influencing factors

Currently, various aspects of biogenic methane have received extensive attention from researchers worldwide. In some basins, the total amount of coalbed methane extracted far exceeds the total resources discovered during the exploration phase, further highlighting the resource contribution of biogenic methane. There are two main generation pathways for biogenic methane in coal seams: one is through carbon dioxide reduction, and the other is through fermentation of methyl compounds such as acetate[9]. The subsequent introduction of the concept of secondary biogenic methane indicates that secondary biogenic gas can account for a significant proportion of total resources in some high-permeability enrichment areas. Studies have shown that biogenic methane exists in almost all low-rank coal basins, with biogenic methane having been successively discovered in coal seams in Australia, Poland, New Zealand, and in regions such as Shanxi, Xinjiang, Anhui, and Yunnan in China. The presence of methanogens in coal seams is crucial for biogenic methane generation[10-13]. Experiments have confirmed that microorganisms are capable of degrading coal, and low-rank coal can be converted into methane using either exogenous microbial strains or indigenous microorganisms from coal samples[14]. The mechanisms of coal biodegradation mainly include enzymatic attack, microbial chelation, and basal metabolism[15]. In addition, biogenic methane generation is influenced by multiple factors, such as coal seam thickness, salinity, microbial communities, organic matter in coal, coal macerals, pH, and oxidation-reduction potential. The hydrocarbon generation capacity of a coal seam can be measured by organic matter abundance, which is closely related to coal seam thickness. Among coal macerals, vitrinite is more easily degraded and utilized by microorganisms for conversion into methane compared to raw coal and liptinite. The presence of volatile organic compounds in coal is conducive to increasing biogenic methane production. Increased salinity typically leads to a decrease in methane yield and concentration, while methane generation is maximized at pH 8, with either acidic or alkaline conditions reducing methane production[16]. Oxidation-reduction potential also significantly affects the reproduction rate of methanogens, with lower potential conditions being more favorable for biogenic gas generation, achieving the highest methane concentration at a specific potential value[17].

3. RESEARCH PROGRESS ON MAIN MICROORGANISMS IN COAL-TO-BIOMETHANE CONVERSION

3.1. Coal degradation stages by microorganisms and types of methanogens

Studies have shown that coal is a complex mixture composed of various compounds including aromatic, heterocyclic, and aliphatic compounds, and cannot be directly utilized by methanogens. The generation of biogenic methane requires the synergistic action of multiple microorganisms (including bacteria, archaea, and fungi) to degrade the complex macromolecular organic substances in coal into simple small-molecule compounds that can be utilized by methanogens. The microbial degradation of organic matter in coal consists of four stages: the hydrolysis stage, the fermentation stage, the acetogenesis stage, and the methanogenesis stage.

The hydrolysis and fermentation stages are carried out by hydrolytic and fermentative bacteria such as Bacteroides, Clostridium, Eubacterium, Bifidobacterium, Butyivibrio, and Gram-negative rods[18]. Through hydrolysis and fermentation, the functional groups or covalent bonds in coal are broken, degrading complex macromolecular polymers into organic compounds such as long-chain alkanes, long-chain fatty acids, and monocyclic aromatic hydrocarbons. These are further degraded into intermediate products including short-chain alkanes, volatile fatty acids, alcohols, phenols, and aromatic compounds. In the acetogenesis stage, acetogenic bacteria convert the intermediate products obtained from the hydrolysis and fermentation stages (such as long-chain fatty acids, aromatic compounds, and amino acids) into H2, CO2, acetic acid, etc., providing substrates for the growth and metabolism of methanogens in the next stage. In the methanogenesis stage, methane is generated primarily from acetic acid, hydrogen, and carbon dioxide produced in the previous stages. The main functional microbial community in this stage is methanogens, which are microorganisms capable of utilizing simple substances to generate methane. They are generally divided into three types: hydrogenotrophic methanogens (carbon dioxide-reducing methanogens), acetoclastic methanogens, and methylotrophic methanogens. The importance of methanogens in the community structure lies in the fact that they are the only microorganisms capable of metabolically producing methane[19, 20].

3.2. Studies on microbial diversity in coal seams

With the widespread application of 16S rRNA gene sequencing technology, increasing attention has been directed to characterizing microbial communities in coal seams. Early investigations revealed that coalbed water from northern Japan harbored methanogens predominantly affiliated with hydrogenotrophic Methanoculleus and methylotrophic Methanolobus, along with minor populations of Methanobacterium and Methanosarcina, indicating the presence of biogenic coalbed methane in this region[21]. In the Illinois Basin, methanogenic communities were dominated by hydrogenotrophic Methanocorpusculum, with hydrogen-reduction methane serving as the principal source[22]. In the Ordos Basin, bacterial communities were primarily composed of Proteobacteria and Actinobacteria, while methanogens were dominated by Methanosarcina and Methanoculleus[23]. Similarly, water samples from Illinois showed bacterial dominance by Bacteroidetes, Proteobacteria, and Firmicutes, accompanied by methanogens of the genera Methanobacterium and Methanococcus.

In the Gippsland Basin, water samples exhibited bacterial communities dominated by Proteobacteria and Firmicutes, with Methanobacterium as the predominant methanogen[24]. Studies also identified methylotrophic and hydrogenotrophic methanogenic archaea in coal seams of southeastern Montana. An investigation of Chinese mining areas revealed that bacterial communities were largely dominated by Proteobacteria and Firmicutes, while methanogens were primarily represented by Methanobacterium, Methanolobus, and Methanoculleus[25]. Notably, microbial diversity and abundance were significantly higher in regions with confirmed biogenic coalbed methane. Analysis of water samples from the Huaibei mining area uncovered a wide range of methanogens, including Methanoregula, Methanobacterium, Methanomethylovorans, Methanolobus, and Methanomassiliicoccus, the latter of which had not been previously reported in coal-associated communities, substantially filling a knowledge gap.

In the Qinshui Basin, methanogens in produced water were predominantly composed of Methanobacterium, Methanomicrobium, and Methanolobus, with hydrogenotrophic methanogens as the dominant type[26, 27]. Gene sequencing of coalbed water from the Erlian and Hailaer Basins showed that methanogens in Erlian samples were dominated by Methanocalculus and Methanobacterium, whereas those in Hailaer samples were mainly represented by Methanobacterium and Methanosarcina, with hydrogenotrophic methanogenesis being the predominant pathway in both regions.

4. LITERATURE REFERENCES

4.1. Comparison of methanogenic performance between indigenous and exogenous microorganisms

Theoretically, indigenous microbial communities in coal seams are likely best adapted to the coal seam environment, whereas exogenous microorganisms have limited survivability under such conditions and may therefore not contribute significantly to biogenic gas enhancement. It has been shown that both indigenous and exogenous microorganisms exhibit coal degradation and methanogenic capabilities under laboratory conditions, with indigenous microbial communities being more suitable for application in microbial enhanced coalbed methane technology[28]. However, other studies have demonstrated that the addition of exogenous methanogenic communities to native methanogenic microbial communities in coal results in a higher methane generation rate than when only nutrients are supplemented[29].

Further investigations have explored whether a composite microbial community, consisting of coal seam microorganisms mixed with mangrove sediment microorganisms, could enhance natural gas production[30]. The results indicated that co-cultivation of microorganisms from different sources increased biogenic methane yield from lignite. Methanogenic communities contain diverse microbial populations, among which functional microorganisms play a significant role in enhancing methane production and are a major factor influencing methane yield. The selection and mixed cultivation of microbial populations with different functions is considered one of the primary approaches for obtaining functional consortia.

After years of research, it is generally accepted that microorganisms struggle to utilize the aromatic structures present in coal, which limits biogenic methane formation. To enhance the biodegradation capacity of mixed consortia toward the aromatic structures in coal, researchers have enriched a fungal-methanogenic consortium capable of degrading coal and a functional fungal consortium specialized in degrading aromatic compounds, and have proposed a compounding strategy for methane enhancement[31]. It was confirmed that the efficient consortium obtained after compounding significantly increased methane production. On this basis, to further elucidate the mechanism of coal degradation and methane production by the compounded high-efficiency consortium, experiments on anaerobic lignite degradation and methane generation were conducted, with investigations into the evolution of community structure, intermediate metabolites, and coal structural characteristics[32]. The results showed that the proportion of aromatic-degrading bacteria in the compounded consortium was relatively high, and their aromatic degradation capability was outstanding, which promoted rapid methane generation. Therefore, compounding can specifically enhance the degradation of particular components in coal, thereby improving overall coal degradation efficiency.

In another study focusing on the screening of methanogenic consortia and the anaerobic degradation of petroleum hydrocarbons, with the aim of enhancing oil recovery and achieving bioconversion of residual oil to gas, the results showed that the newly formed consortium obtained by mixing selected strains exhibited superior methanogenic performance compared to the individual consortia before mixing[33]. Mixing indigenous and exogenous microbial samples followed by acclimation cultivation also yielded consortia with higher gas production efficiency.

4.2. Controversy over co-cultivation of microbial consortia and screening of functional communities

Whether co-cultivation of different microbial consortia promotes microbial degradation remains a subject of debate. A study focusing on hydrolytic bacteria investigated the coal degradation characteristics of individual strains and mixed microbial agents. The results indicated that coal samples treated with either individual strains or mixed agents generally exhibited reduced specific surface area and total pore volume[34]. Overall, co-degradation tended to weaken the degradation capacity of dominant strains and, to some extent, inhibited microbial coal degradation. A comprehensive metagenomic study comparing seven different environmental communities revealed that all anaerobic communities contained genes for all known methanogenesis pathways[35]. However, the abundances of these genes varied considerably across different environments, and they were encoded by distinct methanogenic archaea. In experiments aimed at screening dominant methanogenic consortia, to enable the microbial communities in the acclimation system to adapt to artificial culture conditions, an anaerobic activated sludge rich in methanogens was progressively acclimated by gradually increasing the ratio of culture medium to bacterial suspension in an oxygen-depleted sodium acetate medium. Through this stepwise acclimation process, multiple dominant methanogenic consortia were ultimately obtained.

5. CONCLUSION

This review systematically summarizes the research progress on biogenic coalbed methane, including its classification, generation pathways, degradation mechanisms, microbial diversity, and consortium regulation strategies. The main conclusions are as follows:

(1) Coalbed methane is classified into biogenic and thermogenic types.

(2) Biogenic coalbed methane is divided into primary and secondary types; MECBM technology can improve permeability and enhance methane production.

(3) Biogenic methane is generated via CO2 reduction or acetate fermentation, and coal biodegradation involves four stages.

(4) Dominant methanogenic genera include Methanobacterium, Methanoculleus, Methanolobus, and Methanosarcina, with hydrogenotrophic methanogenesis being the predominant pathway.

(5) Indigenous microbes are theoretically better adapted, but exogenous addition or mixed cultivation can also enhance methane production.

(6) The effect of co-cultivation remains controversial.

(7) Future research should focus on microbial interactions, optimization of compounding strategies, and synergistic enhancement between indigenous and exogenous microorganisms.

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