不同優勢菌科 *Clostridiaceae* 菌相比例養豬場污泥對高 COD 廢水降解效能分析

Analysis of the Degradation Performance of *Clostridiaceae* with Different Abundances in Swine Farm Sludge for High-COD Wastewater

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摘　要

養豬場糞尿水中含有豐富且多樣化的微生物菌相，由於各場廢水處理的操作條件與水質特性不盡相同，所產生的污泥在菌群組成上亦存在差異。然而，文獻顯示養豬場厭氧污泥中大多以 *Clostridiaceae* 為優勢菌科，其具備分解葡萄糖等有機物之能力，能將大分子有機物轉化為小分子，並進一步產生氫氣（H_2）、丁酸及二氧化碳（CO_2）等中間產物與氣體，對有機物降解發揮關鍵作用。可得知菌群特性得以作為後續進行菌相調控與選擇性應用的重要依據，未來若將養豬場污泥植種應用於工業廢水處理，亦可依據工業端多樣化的有機污染物降解需求，選擇合適來源之污泥及菌群進行植種，以提升廢水處理效能並增進系統運作之穩定性。

因此為驗證 *Clostridiaceae* 實際處理效能，本研究針對三場不同養豬場進行污泥菌群組成分析，顯示三場污泥中均可觀察到 *Clostridiaceae* 為主要優勢菌科。為進一步評估其對高濃度有機廢水的降解效能，本研究選用 COD 為主要污染物來源之綜合廢水處理廠作為測試對象，該廢水處理廠主要處理來源為樹脂廠、化工廠及石化廠之製程廢水，廢水中含有大量醛類、醇類、樹脂及塑膠類有機物，屬於典型高 COD 廢水，厭氧進流水之 COD 濃度約為 1,500 至 1,600 mg/L。試驗中選用上述三場養豬場污泥進行植種，並於實驗室設置模擬實廠之廢水處理槽，進行水質與菌相分析，以探討功能性優勢菌科對污染物去除之影響。結果顯示，三場養豬場污泥中 *Clostridiaceae* 之菌相佔比分別為 38%、22% 及 20%，且 *Clostridiaceae* 佔比較高之組別於高 COD 廢水處理下展現出更佳的有機物去除效能，試驗組別 COD 降解率最高之試驗組別較工業端自場廢水處理提升 19.5%。

關鍵詞：優勢菌群，植種污泥，菌相分析，廢水處理效能分析

Abstract

The wastewater from swine farms contains a rich and diverse microbial community. Due to differences in operational conditions and wastewater characteristics at each farm, the microbial composition of the resulting sludge also varies. However, literature indicates that anaerobic sludge from swine farms is predominantly composed of Clostridiaceae, which has the ability to degrade organic compounds such as glucose. Clostridiaceae can break down large organic molecules into smaller ones, further producing intermediate metabolites and gases such as hydrogen (H_2), butyric acid, and carbon dioxide (CO_2), playing a key role in organic matter degradation. This microbial characteristic thus provides an important basis for subsequent microbial community regulation and selective application. In the future, if swine farm sludge is used for seeding industrial wastewater treatment systems, suitable sludge sources and microbial communities can be selected according to the diverse organic pollutant degradation requirements of industrial wastewater, thereby improving treatment efficiency and enhancing the operational stability of the system.

Therefore, to verify the actual treatment performance of Clostridiaceae, this study analyzed the microbial composition of sludge from three different swine farms, showing that Clostridiaceae was the dominant bacterial family in all three samples. To further evaluate its degradation efficiency for high-strength organic wastewater, a comprehensive wastewater treatment plant with COD as the main pollutant was selected as the test target. This plant primarily treats process wastewater from resin plants, chemical plants, and petrochemical plants, which contains significant amounts of aldehydes, alcohols, resins, and plastics, representing typical high-COD industrial wastewater. The influent COD concentration for the anaerobic treatment stage ranged from approximately 1,500 to 1,600 mg/L. Sludge from the three swine farms was used for seeding experiments, and pilot-scale reactors simulating the actual plant were set up in the laboratory to analyze water quality and microbial communities, investigating the impact of the functional dominant bacterial family on pollutant removal. The results showed that the relative abundance of Clostridiaceae in sludge from the three swine farms was 38%, 22%, and 20%, respectively. The group with the higher Clostridiaceae abundance exhibited better organic matter removal efficiency under high-COD wastewater treatment conditions, achieving a COD removal rate up to 19.5% higher than that of the original industrial wastewater treatment system.

Keywords:Dominant Microbial community，Seeding sludge，Microbial community analysis，Wastewater treatment performance analysis