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三组微生物菌群分解油菜秸秆的消化液性质比较

## Properties of digestive solution during anaerobic degrading rape straw by three different microbial communities

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## 中文摘要:

利用微生物对秸秆进行酸化前处理能够有效提高秸秆甲烷发酵效率。该文以探索不同微生物菌群对秸秆消化过程的影响为目的,利用3组不同的菌群(纤维素分解菌群M C1、纤维素分解菌群WDC2以及牛粪菌群(CD))消化油菜秸秆,通过监测消化液的性质变化,评价不同菌群对油菜秸秆酸化前处理的效果。结果表明,菌群WDC2、MC 1、CD均能有效地提高油菜秸秆消化效率(油菜秸秆分解率分别为46.77%、44.28%和43.40%),相比于未加入外源菌的对照处理,分解率提高12.21%~15.58%。WDC2和MC 1能有效地提高消化液中的化学需氧量(COD),在分解的48 h,2组菌群的 COD比未加入外源菌群处理分别提高9.13%和7.83%。CD不能提高培养液中的COD含量。此外,相比与MC1与CD,WDC2能够更好的维持培养液内的可溶性糖含量。可见, 3组菌群均能够促进油菜秸秆消化分解,纤维素分解菌群WDC2具有更好的油菜秸秆分解活性和COD溶出能力,优于其他2组菌群。

## 英文摘要:

Straw acidification pre-treatment by microorganisms can improve efficiency of methane fermentation. In order to explore the effect of different microbial communities (cellulose-degrading community MC1, cellulose-degrading community WDC2 and cattle dung microbial community (CD)) were used to acidify rape straw. Effect of acidification pre-treatment on rape straw was evaluated by detecting properties changing of digestive solution during digestion process of rape straw. The results indicated that community MC1, WDC2 and CD could improve the efficiency of rape straw digestion effectively (degradation rates of rape straw were 46.77%, 44.28% and 43.40% respectively), and degradation rate increased by 12.21%-15.58% comparing with control treatments of no adding exogenous bacteria. Community MC1 and WDC2 could effectively improve COD content in the digestive solution. In 48h of digestion, COD content in solution digested by the two communities increased by 9.13% and 7.83%, respectively compared with treatments without adding exogenous bacteria. Cow manure microbial community had no capability of improving COD content in the digestive solution. In addition, compared with community MC1 and cow manure, community WDC2 could better maintain soluble sugar content in the digestive solution. Therefore, three microbial communities are cable to digest rape straw, cellulose-degrading community WDC2 has better digestion activity of rape straw and COD-producing capability comparing with community MC1 and CD.

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