JAS2015 Vol. 93 No. 3, p. 1039-1051

猪体外发酵模型和电镜扫描表明酶制剂可促进DDGS中纤维-淀粉-蛋白复合物的降解

R. Jha, T. A. Woyengo, J. Li, M. R. Bedford, T. Vasanthan and R. T. Zijlstra

原文链接：https://www.animalsciencepublications.org/publications/jas/abstracts/93/3/1039

本试验研究了复合碳水化合物酶单独酶解或其与蛋白酶合用对玉米DDGS和小麦DDGS猪体外消化模型的影响。三个DDGS样品，小麦DDGS样品1（wDDGS1），小麦DDGS样2（wDDGS2）、玉米DDGS样1（cDDGS），试验开始前先经胃蛋白酶和胰蛋白酶处理进行预消化。酶解产物再加入矿物缓冲液，并在体外发酵模型，试验为3×3因子设计，三个样品，三个发酵模型（添加新鲜猪粪便发酵、或再增加复合碳水化合物酶、或再增加复合碳水化合物酶和蛋白酶）。测定72小时内产气量。同时测定挥发性脂肪酸（VFA）含量。DDGS样品和发酵酶解后的产物通过激光共聚焦显微镜测定其组成，并使用扫描电子显微镜检查法观察其内外结构。干物质基础下，wDDGS1, wDDGS2, 和cDDGS分别含蛋白35.5%、43.4%和29%，淀粉2.23%、0.51%、6.40%，含可利用赖氨酸0.82%、0.80%、0.89%，含非淀粉多糖24.8、22.5、23.0%。玉米DDGS总产气量和VFA含量高于小麦DDGS(P < 0.05)。复合碳水化合物酶可增加玉米DDGS的总产气量和小麦DDGS1的VFA产量(P < 0.05)，但是不影响小麦DDGS样2的产气量和VFA产量。在复合碳水化合物酶基础上添加蛋白酶可以降低3个DDGS样品的总产气量和VFA产量，增加支链VFA的产量。激光共聚焦显微镜和扫描电子显微镜检测结果表明DDGS主要是抗性淀粉和非淀粉复合物在生产过程中聚合而成。在体外经猪粪便发酵后，酶解DDGS的颗粒总的来说较未酶解样品要小。总的来说玉米DDGS颗粒孔隙较小麦DDGS更多，其更容易发酵。小麦DDGS2的可发酵性低于小麦DDGS1，表明发酵的效率取决于颗粒的多孔性和DDGS的来源。蛋白酶降低复合碳水化合物的酶解效率。

Enzymes enhance degradation of the fiber–starch–protein matrix of distillers dried grains with solubles as revealed by a porcine in vitro fermentation model and microscopy

R. Jha\*†, T. A. Woyengo\*, J. Li\*22, M. R. Bedford‡, T. Vasanthan\* and R. T. Zijlstra 3\*

Website link: https://www.animalsciencepublications.org/publications/jas/abstracts/93/3/1039

Effects of treating corn and wheat distillers dried grains with solubles (DDGS) with a multicarbohydrase alone or in combination with a protease on porcine in vitro fermentation characteristics and the matrix structure of the DGGS before and after the fermentation were studied. Three DDGS samples (wheat DDGS sample 1 [wDDGS1], wheat DDGS sample 2 [wDDGS2], and corn DDGS [cDDGS]) were predigested with pepsin and pancreatin. Residues were then subjected to in vitro fermentation using buffered mineral solution inoculated with fresh pig feces without or with a multicarbohydrase alone or in combination with protease in a 3 × 3 factorial arrangement. Accumulated gas production was measured for up to 72 h. Concentration of VFA was measured in fermented solutions. The matrix of native DDGS and their residues after fermentation was analyzed using confocal laser scanning microscopy and scanning electron microscopy to determine internal and external structures, respectively. On a DM basis, wDDGS1, wDDGS2, and cDDGS contained 35.5, 43.4, and 29.0% CP; 2.23, 0.51, and 6.40% starch; 0.82, 0.80, and 0.89% available Lys; and 24.8, 22.5, and 23.0% total nonstarch polysaccharides, respectively. The in vitro digestibility of DM for wDDGS1, wDDGS2, and cDDGS was 67.7, 72.1, and 59.6%, respectively. The cDDGS had greater (P < 0.05) total gas and VFA production than both wheat DDGS. The wDDGS2 had lower (P < 0.05) total gas production than wDDGS1. Multicarbohydrase increased (P < 0.05) total gas production for cDDGS and total VFA production for wDGGS1 but did not increase gas or VFA production for wDDGS2. Addition of protease with multicarbohydrase to DDGS reduced (P < 0.05) total gas and VFA productions and increased (P < 0.05) branched-chain VFA regardless of DDGS type. Confocal laser scanning microscopy and scanning electron microscopy revealed that DDGS were mainly aggregates of resistant and nonfermentable starchy and nonstarchy complexes formed during DDGS production. After in vitro fermentation with porcine fecal inoculum, particles of enzyme-treated DDGS were generally smaller than those of the untreated DDGS. In conclusion, cDDGS had a more porous matrix that was more fermentable than the wheat DDGS. The wDDGS2 was less fermentable than wDDGS1. Multicarbohydrase increased fermentability of cDDGS and wDDGS1 but not wDDGS2, indicating that its efficacy in DDGS is dependent on matrix porosity and DDGS source. Protease hindered efficacy of multicarbohydrase.