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基于16SrRNA基因序列分析梅花鹿瘤胃细菌多样性

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Bacterial Diversity in Rumen of Sika Deer (*Cervus nippon*) Based on 16S rRNA Sequences Analysis

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摘要 本试验旨在对以柞树叶为主要粗饲料来源的梅花鹿瘤胃细菌多样性进行分析。提取瘤胃微生物基因组DNA,扩增细菌16S rRNA基因,构建16S rRNA基因克隆文库,分析梅花鹿瘤胃细菌区系组成。结果表明:1)试验共得到107个非嵌合体16S rRNA基因序列。按照97%序列相似性,划分为22个分类操作单元(OTUs)。其中91个序列(10个OTUs,85%总克隆序列)与已培养菌序列相似性 $\geq 97\%$,13个序列(10个OTUs,12.2%总克隆序列)与已培养菌序列相似性为90%~97%,其余序列相似性<90%。87.9%序列与普雷沃氏菌属(*Prevotella* spp.)相似。2)系统发育分析表明,梅花鹿瘤胃细菌由厚壁菌门和拟杆菌门组成。由结果可知,以富含单宁的柞树叶为主要粗饲料来源的梅花鹿的瘤胃中,普雷沃氏菌属是优势细菌,而牛、羊瘤胃中常见的纤维素降解菌未检测到,这可能与饲料中单宁含量高有关。

关键词: 梅花鹿 细菌区系 普雷沃氏菌属 单宁

Abstract: Bacterial diversity in the rumen of sika deer feeding tannin-rich plants (oak leaves) was investigated. The extracted genomic DNA was used to amplify bacteria 16S rRNA gene. Bacterial communities in the rumen of sika deer were determined based on the 16S rRNA gene library. The results showed as follows: 1) a total of 107 non-chimeric 16S rRNA gene sequences were obtained. These sequences were assigned to 22 operational taxonomic units (OTUs) based on 97% sequence similarity. Ninety-one sequences (10 OTUs, 85% of total clones) showed $\geq 97\%$ sequence similarity to known species, thirteen sequences (10 OTUs, 12.2% of total clones) had sequence similarity to known species in the range of 90% to 97%, and the remaining sequences displayed similarity less than 90%. Eighty-seven point nine percent sequences were similar to *Prevotella* spp.. 2) Phylogenetic analysis indicated that bacteria in the rumen of sika deer belonged to phyla *Bacteroidetes* and *Firmicutes*. It is concluded that *Prevotella* spp. is the dominant bacteria in rumen of sika deer feeding oak leaves containing high content of tannins. While, the lack of fibrolytic bacteria in the rumen of sika deer may be the result of high content of tannins in diets.

Keywords: [sika deer](#), [bacterial communities](#), [Prevotella spp.](#), [tannins](#)

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- [1] 李国华,秦荣前,梁凤锡.梅花鹿采食草原地区野生植物的调查[J].中药材,1986(1): 12-14,16.
- [2] 杨镒峰,魏海军,李光玉,等.不同单宁水平日粮对育成前期雄性梅花鹿生长和血液生化指标的影响[J].特产研究,2010(2): 25-29.
- [3] SHI P J,MENG K,ZHOU Z G,et al.The host species affects the microbial community in the goat rumen[J].Letters in Applied Microbiology,2008,46(1): 132-135.
- [4] LAMONTAGNE M G,MICHEL F C,HOLDEN P A,et al.Evaluation of extraction and purification methods for obtaining PCR-amplifiable DNA from compost for microbial community analysis[J].Journal of Microbiological Methods,2002,49(3): 255-264. 
- [5] 郑刚,陈己任,胡博文,等.基于DGGE分析的大鼠粪便及肠道细菌DNA提取方法研究[J].食品科学,2011,32(17): 215-218.
- [6] LANE D J.16S/23S rRNA sequencing[M].New York:Wiley,1991: 115-175.
- [7] COLE J R,WANG Q,CARDENAS E,et al.The ribosomal database project:improved alignments and new tools for rRNA analysis[J].Nucleic Acids Research,2009,37:D141-D145.
- [8] WRIGHT A D G,KLIEVE A V.Does the complexity of the rumen microbial ecology preclude methane mitigation?[J].Animal Feed Science and Technology,2011,23: 248-253.
- [9] WU S,BALDWIN R L,LI W,et al.The bacterial community composition of the bovine rumen detected using pyrosequencing of 16S rRNA genes [J].Metagenomics,2012,1: 1-11.
- [10] KRAUSE D O,DENMAN S E,MACKIE R I,et al.Opportunities to improve fiber degradation in the rumen:microbiology,ecology, and genomics[J].FEMS Microbiology Reviews,2003,27(5): 663-693. 
- [11] MCSWEENEY C S,PALMER B,KENNEDY P M.Effect of *Calliandra* tannins on rumen microbial function[J].Animal Production in Australia,1998,22: 289.
- [12] JONES G A,MCALLISTER T A,MUIR A D,et al.Effects of Sainfoin (*Onobrychis viciifolia* Scop.) condensed tannins on growth and proteolysis by four strains of ruminal bacteria[J].Applied and Environmental Microbiology,1994,60(4): 1374-1378.
- [13] MCSWEENEY C S,PALMER B,MCNEILL D M,et al.Microbial interactions with tannins:nutritional consequences for ruminants[J].Animal Feed Science and Technology,2001,91(1/2): 83-93. 
- [14] 王梦芝,王洪荣,徐爱秋,等.徐淮白山羊瘤胃细菌和原虫的类群结构研究[J].中国农业科学,2009,42(8): 2915-2922.
- [15] PATEL T R,JURE K G,JONES G A.Catabolism of phloroglucinol by the rumen anaerobe *Coprococcus*[J].Applied and Environmental Microbiology,1981,42(6): 1010-1017.
- [16] TAN H Y,SIEO C C,ABDULLAH N,et al.Effects of condensed tannins from *Leucaena* on methane production,rumen fermentation and populations of methanogens and protozoa *in vitro*[J].Animal Feed Science and Technology,2011,169(3/4): 185-193.
- [1] 鲍坤,徐超,宁浩然,王凯英,赵家平,李光玉.常用饲料原料蛋白质在梅花鹿瘤胃内降解率的测定[J].动物营养学报,2012,(11): 2257-2262
- [2] 徐晓锋,张力莉.单宁对反刍动物促营养作用的研究进展[J].动物营养学报,2011,23(12): 2084-2089
- [3] 鲍坤,李光玉*,崔学哲,王凯英,刘佰阳,刘晗璐.不同形式铜对雄性梅花鹿血清生化指标及营养物质消化率的影响(英文)[J].动物营养学报,2010,22(03): 717-722
- [4] 胡锐,黎立,韦旭斌,周道玮.VC和VE对应激梅花鹿血液中白细胞及糖皮质激素的影响[J].动物营养学报,2004,16(01): 53-56