Original Article

Monosodium L-Glutamate and/or Dietary Fat Differently Modifies the Composition of the Intestinal Microbiota in Growing Pigs

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Supplemental Material
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Supplementary table 1. Composition of experimental diets

| Item                                      | Basal diet (BD) | High fat diet (HF) | Basal diet + 3% MSG (BDM) | High fat diet + 3% MSG (HFM) |
|-------------------------------------------|-----------------|-------------------|---------------------------|-------------------------------|
| **Ingredient composition (%)**           |                 |                   |                           |                               |
| Corn                                      | 71.37           | 59.80             | 70.30                     | 59.58                         |
| Soybean meal                              | 19.20           | 21.27             | 16.80                     | 21.50                         |
| Corn starch                               | 0.00            | 7.00              | 0.00                      | 5.00                          |
| Corn gluten meal                          | 5.00            | 2.50              | 7.00                      | 3.10                          |
| MSG                                       | 0.00            | 0.00              | 3.00                      | 3.00                          |
| Alanine                                   | 1.58            | 1.58              | 0.00                      | 0.00                          |
| L-lysine monohydrochloride                | 0.15            | 0.15              | 0.20                      | 0.12                          |
| Soybean oil                               | 0.00            | 5.00              | 0.00                      | 5.00                          |
| Premixa                                   | 2.70            | 2.70              | 2.70                      | 2.70                          |
| **Calculated analysis**                   |                 |                   |                           |                               |
| DE, Mj/kg                                 | 13.98           | 13.92             | 13.87                     | 13.98                         |
| CP, %                                     | 17.93           | 17.88             | 17.95                     | 17.91                         |
| Fat, %                                    | 4.35            | 9.39              | 4.51                      | 9.45                          |
| Ca, %                                     | 0.60            | 0.59              | 0.58                      | 0.59                          |
| P, %                                      | 0.45            | 0.48              | 0.44                      | 0.46                          |

*Composition (%): CaHPO₄, 27.78; Mountain flour, 24.07; NaCl, 11.11; Medical stone, 12.33; Powdered rice hulls, 18.81; FeSO₄, 0.74; ZnSO₄, 0.74; Selenium powder (1%), 0.15; Iodine powder (1%), 0.15; CuSO₄, 0.37; MnSO₄, 0.30; Choline chloride, 2.22; Growth pig multidimensional, 1.11; Antioxidants (Ethoxyquin 66%), 0.11.*
Supplementary table 2. Group and species-specific 16S rDNA gene-targeted primers used in this study

| Name                          | Sequence                                      | Length | Reference                                |
|-------------------------------|-----------------------------------------------|--------|------------------------------------------|
| **All bacteria**              | UniF 5’ TCCTACGGGAGGGCAGCATG 3’              | 466 bp | In this study                            |
|                               | UniR 5’ GACCTACAGGG- TATCTAATTCTGTT 3’       |        |                                          |
| **Bacteroidetes**             | g-Bacte-F 5’ AGCAGCGCGGGTATATA 3’            | 184 bp | Armougom & Raoult, 2008                   |
|                               | g-Bacte-R 5’ CTAGGCTTCTGCTGCTA 3’            |        |                                          |
| **Bacteroides fragilis**      | g-Bfra-F 5’ ATAGCCTTTCCGAAAGRAAGAT 3’        | 495 bp | Matsuki et al., 2002                     |
|                               | g-Bfra-R 5’ CCAGTATCAACTGCAATTATTA 3’        |        |                                          |
| **Bacteroides thetaiotaomicron** | BT-F 5’ GGCAGCATTCTGTTGTGAA 3’             | 423 bp | Wang et al., 1996                        |
|                               | BT-R 5’ GGTATATACACAAATATTCCACAGT            |        |                                          |
| **Firmicutes**                | g-Firmi-F 5’ GTCAAGCTTCTGCTGTA 3’            | 179bp  | Armougom & Raoult, 2008                   |
|                               | g-Firmi-R 5’ CTAATGKACGGTGTTG 3’             |        |                                          |
| **Akkermansiamuniciniphila**  | AkmUC-F 5’ CAGCAGTGGAAGGTTGAGC 3’           | 329 bp | Collado et al., 2007                     |
|                               | AkmUC-R 5’ CCTGCGGTGTGCTTCAATG 3’           |        |                                          |
| **Clostridium cocoides group**| g-Ccoc-F 5’ AATTAGCGATCTGACTAA 3’           | 440 bp | Matsuki et al., 2002                     |
|                               | g-Ccoc-R 5’ CTTTGAGTTTCATTCTTGCA 3’          |        |                                          |
| **Clostridium leptum subgroup**| sg-Clept-F 5’ GCACAGCAGTGGAAGT 3’           | 239 bp | Matsuki et al., 2004                     |
|                               | sg-Clept-R 5’ CTCCTCTGTTTCACCCAA 3’          |        |                                          |
| **Clostridium difficile**     | Cdif-F 5’ TTGAGCGATTTACTTCGGTA 3’           | 157 bp | Rinttilä et al., 2004                    |
|                               | Cdif-R 5’ CCATCTCTCTTGTGCTATGC 3’           |        |                                          |
| **Clostridium clostridiiforme**| CC-F 5’ CGCAGTTCGCGGTTCTGAAA 3’             | 255 bp | Wang et al., 1996                        |
|                               | CC-R 5’ CTCTCTCAGTCAGGCTTTCATC 3’           |        |                                          |
| **Clostridium cocoides - eubacteria rectale group** | ClEub-F 5’ CGGTACCTGACTAAGAAGC 3’ | 429 bp | Bartosch et al., 2004                    |
|                               | ClEub-R 5’ AGTTTYATTCTCTGCAAGGC 3’          |        |                                          |
| **Prevotella**                | g-Prevo-F 5’ CACGTTAAACGAGGAGATG 3’         | 513 bp | Matsuki et al., 2002                     |
|                               | g-Prevo-R 5’ GTTCGCGGTGCAGACC 3’            |        |                                          |
| **Faecalibacterium prausnitzii** | FaPRA-F 5’ GGAGGAAAGAGGTCTTCGCG 3’       | 248 bp | Wang et al., 1996                        |
|                               | FaPra465R 5’ AATTCGCCGCACTCTCGACT 3’        |        | Ramirez-Farias et al., 2009              |
| **Fusobacterium prausnitzii** | FuPRA-F 5’ CCCTCGATGCAGCGAGCTG 3’           | 158 bp | Rinttilä et al., 2004                    |
|                               | FuPRA-R 5’ GTCCGAGGGATGTCAAGACG 3’          |        |                                          |
| **Peptostreptococcus productus** | PSP- F 5’ AACTCCCGGTTGATACATG 3’       | 268 bp | Wang et al., 1996                        |
|                               | PSP-R 5’ GGGGCTTCTGAGGTGAGT 3’              |        |                                          |
| **Methanobrevibacter smithii**| g-MeSMI-F 5’ CGGGTATCTAATCCGGTTC 3’         | 123 bp | Armougom et al., 2009                    |
|                               | g-MeSMI-R 5’ CTCCCGAGG-TAGAGGTGAAA 3’       |        |                                          |
| **Roseburia**                 | RosF 5’ TACCTGATTTGAAACTGTCG 3’             | 230 bp | Larsen et al., 2010                      |
|                               | RosR 5’ CGGCCACCAGAGCAAT 3’                  |        |                                          |
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