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# Glutamate Supplementation Regulates Nitrogen Metabolism in the Colon and Liver of Weaned Rats Fed a Low-Protein Diet

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**Table S1.** Dietary amino acid composition (Dry matter basis, %).

| Items | Calculated Nutrient Level (%) | | | Analyzed Nutrient Level (%) | | |
|---|---|---|---|---|---|---|
| | NCP | LCP + Ala | LCP + Glu | NCP | LCP + Ala | LCP + Glu |
| Essential amino acids | | | | | | |
| Arginine | 0.68 | 0.68 | 0.68 | 0.69 | 0.69 | 0.68 |
| Histidine | 0.56 | 0.56 | 0.56 | 0.55 | 0.55 | 0.56 |
| Isoleucine | 0.98 | 0.98 | 0.98 | 1.03 | 1.04 | 0.99 |
| Leucine | 1.76 | 1.76 | 1.76 | 1.74 | 1.76 | 1.77 |
| Lysine | 1.50 | 1.50 | 1.50 | 1.46 | 1.45 | 1.46 |
| Methionine | 0.53 | 0.53 | 0.53 | 0.54 | 0.55 | 0.55 |
| Phenylalanine | 0.97 | 0.97 | 0.97 | 0.93 | 0.94 | 0.90 |
| Threonine | 0.82 | 0.82 | 0.82 | 0.77 | 0.81 | 0.80 |
| Tryptophan | 0.24 | 0.24 | 0.24 | 0.27 | 0.28 | 0.27 |
| Valine | 1.21 | 1.21 | 1.21 | 1.19 | 1.19 | 1.19 |
| Nonessential amino acids | | | | | | |
| Alanine | 0.55 | 1.52 | 0.28 | 0.53 | 1.55 | 0.29 |
| Aspartic acid | 1.29 | 0.64 | 0.64 | 1.31 | 0.67 | 0.68 |
| Cystine | 0.38 | 0.04 | 0.04 | 0.36 | 0.03 | 0.03 |
| Glutamate | 4.12 | 2.06 | 4.12 | 4.14 | 2.08 | 4.12 |
| Glycine | 0.37 | 0.19 | 0.19 | 0.39 | 0.16 | 0.17 |
| Proline | 2.16 | 1.08 | 1.08 | 2.20 | 1.11 | 1.02 |
| Serine | 1.02 | 0.51 | 0.51 | 1.04 | 0.51 | 0.53 |
| Tyrosine | 1.01 | 0.51 | 0.51 | 1.05 | 0.54 | 0.53 |
| EAA + NEAA | 20.15 | 15.80 | 16.62 | 20.18 | 15.91 | 16.54 |

**Table S2.** Sequences of primers used for quantitative real-time PCR.

| Genes | Primer Sequences (5′–3′) | GenBank Accession No. | Product (bp) |
|---|---|---|---|
| *ATP1A1* | F: TCTTGGCTTATGGCATCC<br>R: GGATGCCATAAGCCAAGA | NM_012504.1 | 288 |
| *ATP1A2* | F: TTTAGCAATCTCCCTTTAGA<br>R: TCTAAAGGGAGATTGCTAAA | NM_012505.2 | 198 |
| *ATP1A4* | F: CTTATTGGCATCATTGTGG<br>R: CCACAATGATGCCAATAAG | NM_022848.3 | 287 |
| *EAAT1* | F: GGTATGCACCTCTGGGCA<br>R: TGCCCAGAGGTGCATACC | NM_019225.2 | 125 |
| *EAAT3* | F: TATCTTCTGCCTCGTCTTTG<br>R: CAAAGACGAGGCAGAAGATA | NM_013032.3 | 137 |
| *EAAT4* | F: CGAGTGGTAACAAGGACGAT<br>R: ATCGTCCTTGTTACCACTCG | NM_032065.2 | 109 |
| *xCT* | F: TATCTTCTGCCTCGTCTTTG<br>R: CAAAGACGAGGCAGAAGATA | NM_013032.3 | 137 |
| *4F2hc* | F: GGGTGTCTACTGGCAACA<br>R: TGTTGCCAGTAGACACCC | NM_053442.1 | 210 |
| *$y^+$LAT2* | F: TCCATAAGAGTGACGCAG<br>R: CTGCGTCACTCTTATGGA | NM_001107424.1 | 200 |
| *$ATB^{0,+}$* | F: TCCCTTACCTGACCTACA<br>R: TGTAGGTCAGGTAAGGGA | NM_001037544.2 | 255 |
| *Cat-1* | F: AGTGAGTCCCAGACAGGC<br>R: GCCTGTCTGGGACTCACT | NM_001399982.1 | 255 |
| *SNAT9* | F: ACCACCATTATCCAAAGA<br>R: TCTTGGATAATGGTGGT | NM_001258286.1 | 105 |
| *$B^0AT1$* | F: TCCCTTACCTGACCTACA<br>R: TGTAGGTCAGGTAAGGGA | NM_001037544.2 | 255 |
| *SNAT2* | F: ACTTCACCCGATGCTTTC<br>R: GAAAGCATCGGGTGAAGT | NM_181090.3 | 165 |
| *ASCT2* | F: GCTCATCCGATTCTTCAAC<br>R: GTTGAAGAATCGGATGAGC | NM_175758.3 | 255 |
| *mGluR1* | F: CACATCCTGCTACCTCCA<br>R: TGGAGGTAGCAGGATGTG | NM_017011.2 | 235 |
| *T1R1* | F: GGAAACAGAAGAATGGGCA<br>R: TGCCCATTCTTCTGTTCC | NM_053305.1 | 236 |
| *CaSR* | F: TGTGCGGCGTAACATCAC<br>R: GTGATGTTACGCCGCACA | NM_001309638.1 | 211 |
| *GAPDH* | F: ATGTCGTGGAGTCTACTGGC<br>R: GCCAGTAGACTCCACGACAT | NM_017008.4 | 140 |

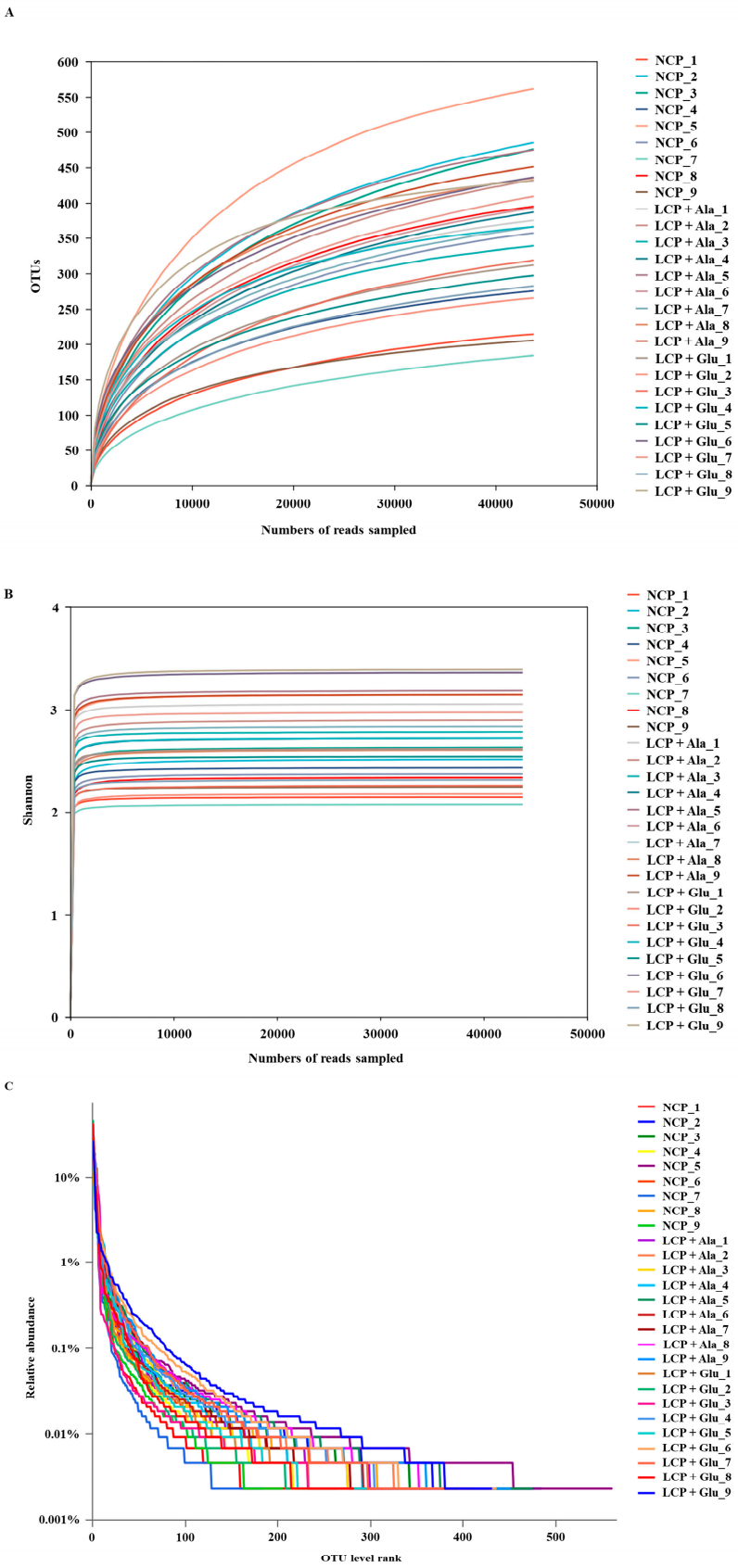



**Figure S1.** Evaluation of data from Illumina Miseq sequencing. Rarefaction (A), shannon (B), and rank-abundance (C) obtained from each sample.