

Fermented *Astragalus* in diet improved laying performance, egg quality, antioxidant and immunological status and intestinal microbiota in laying hens

Hongtao Shi

Henan University of Animal Husbandry and Economy

Baiyu Wang

Henan Agricultural University

Chuanzhou Bian

Henan University of Animal Husbandry and Economy

Yingqian Han (✉ twgjl@163.com)

Henan Agricultural University

Hongxing Qiao

Henan University of Animal Husbandry and Economy

Original article

Keywords: fermented *Astragalus*, laying hens, egg quality, antioxidant and immunological status, 16S rRNA, intestinal microbiota

Posted Date: July 30th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-30575/v2>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License. [Read Full License](#)

Version of Record: A version of this preprint was published at AMB Express on August 31st, 2020. See the published version at <https://doi.org/10.1186/s13568-020-01092-6>.

Abstract

In the era of increased antibiotic resistance and ever-stricter control on antibiotic use, it is urgent to develop green, safe, and non-residue alternatives to antibiotics applied to the poultry industry. To this end, we supplied the potential *Lactobacillus Plantarum* (*L. Plantarum*) fermented *Astragalus* in the diet of laying hens, with a final addition of 3‰. Its effects have been assessed on laying performance, egg quality, antioxidant and immunological status, and intestinal microbiota, and are compared to the control group, to the *Astragalus* group containing 3‰ unfermented *Astragalus*, and to the *L. Plantarum* group containing 2% *L. Plantarum* (5×10^8 colony-forming unit (CFU) per milliliter (mL)). During the second half of the experimental period (15 to 28 days), the egg production rate was considerably higher in the fermented *Astragalus* group than that in the other groups, with the fermented *Astragalus* group having the lowest feed conversion ratio. No significant difference ($P > 0.05$) was noted among treatments on egg quality. Fermented *Astragalus*-treated hens exhibited significantly increased catalase (CAT), glutathione peroxidase (GSH-Px), superoxide dismutase (SOD) and total antioxidant capacity (T-AOC) in serum, and reduced malondialdehyde (MDA) in serum. Furthermore, fermented *Astragalus* supplementation resulted in a significant increase in ileal microbiota abundance relative to control. In conclusion, feeding laying hens with *L. Plantarum* fermented *Astragalus* has beneficial effects on production, antioxidant potential, immunity, and ileal microbiota. *L. Plantarum* fermented *Astragalus* is expected to be a novel feed additive used in poultry production.

Introduction

Eggs are one of the most crucial sources of animal protein and nutritional content in human diets. Due to the widespread use of antibiotics in poultry, drug residues in eggs have been gaining worldwide concern in the past few years (Vandemaele et al., 2002). In addition, antibiotic abuse has led to intestinal dysbacteriosis, diarrhea, immunocompromised state (BP et al., 2011). Thus, it is urgent to develop green, safe and non-residue alternatives to antibiotics applied to the poultry industry. Traditional Chinese herbal medicines are the gem of China with characteristics of safety, efficiency, and low residue and are widely used in preventive or therapeutic strategies for animal diseases (Xu et al., 2017). Traditional Chinese herbal medicines have been used as feed additives for growth promotion and improvement of immunity and various effects, including anti-bacterial, anti-viral and antioxidative activities (Patra et al., 2015; Wang et al., 2015). Since ancient times, traditional Chinese herbal medicines can be processed by microbial fermentation for improving its quality (Zhu et al., 2014). For example, fermentation of Chinese herbal medicine mediated by microbes can degrade macromolecule-materials into small ones and reduce their side effects (Ai et al., 2019). Because microorganisms and their metabolic products can regulate the bioactive products of traditional Chinese herbal medicines, there is a close relationship between microorganisms and traditional Chinese herbal medicines.

Astragalus is a universal traditional Chinese herbal medicine and its main active pharmaceutical ingredients include polysaccharides, saponins, flavonoids, anthraquinones, alkaloids, amino acids, β -sitosterol and metallic elements (Li et al., 2014). *Astragalus* has been reported to possess anti-inflammatory (Kim et al., 2013), anti-viral (Kallon et al., 2013) and antioxidant (Shahzad et al., 2016) activities and to enhance

immunity (Qin et al., 2012), and it has been widely used in livestock. Nevertheless, challenges to the extraction yield of *Astragalus* functional ingredients are raised due to the recalcitrance of plant cell walls, and novel strategies for the improvement of *Astragalus* utilization efficiency need to be focused. The trend of microbial fermentation offers the possibility for addressing the above problem. In recent years, a research revealed that utilizing the fungus *Aspergillus* to ferment the *Astragalus* can significantly increase its phenolic contents and antioxidant activity, and the solid-state bioprocessing strategy could be an innovative approach to enhance the antioxidant activity of *Astragalus* (Sheih et al., 2011). Our previous studies have confirmed that the solid fermentation of *Astragalus* by *L. Plantarum* promotes the extraction yield of *Astragalus* active components and the production yield of organic acids (Qiao et al., 2018c). Further investigation showed that fermented *Astragalus* improves broiler growth performance, enhances serum antioxidant status, and reduces fecal pathogenic microbiota of broiler chickens (Qiao et al., 2018b).

Over the last few years, there has meant considerable research on the application of *Astragalus* polysaccharide as feed additive in livestock including laying hens. However, there has not been a systematic appraisal of the application of *Astragalus* fermented by *L. Plantarum* as feed additive in laying hens. In this study, we investigated the possible effects of *Astragalus* fermented by *L. Plantarum* on egg production, egg quality, antioxidant status, immune factors expression and gut microbiome of laying hens, combining the classical culture and detection methods with high throughput sequencing.

Materials And Methods

Fermentation of *Astragalus*

L. plantarum (CGMCC 1.557) was purchased from the China General Microbiological Culture Collection Center (CGMCC) (Beijing, China). The dried root of *Astragalus membranaceus* (Fisch.) Bge. var. *mongholicus* was obtained from Gansu Huisen Pharmaceutical Development Co., Ltd. (Minxian, Gansu, China) and verified by Dr. JingYu Zhang (Henan University of Traditional Chinese Medicine, Zhengzhou, Henan, China). The purchased *Astragalus* was crushed into powder and filtered with a 100-mesh filter for further studies. The fermentation of *Astragalus* was performed following the method reported in our previous publications with slight modification (Qiao et al 2018b). Briefly, dried *Astragalus* powder (7,500 g) was inoculated with *L. plantarum* (1×10^6 colony forming unit (CFU) per gram) with a water content of 45%, and *Astragalus-L. plantarum* mixtures were aliquot into 35 × 45-mm plastic film bags. The bags were sealed for fermentation at 37°C for 30 days, and then dried out at room temperature for future use.

Experimental Design, Diets and Management

Two hundred and forty healthy Hy-Line Gray hens (351 days, Zhengzhou, China) were acclimated with the basal diets for 7 days. Then, hens were randomly divided into 4 groups (fermented *Astragalus* group, *Astragalus* group, *L. plantarum* group and control group), each containing five replicates, with 12 hens per replicate. The control group was fed with the basal diet; the *L. plantarum* group was fed with the basal diet supplemented with 2% *Lactobacillus* solution (5×10^8 CFU/mL) through uniform spraying; the *Astragalus*

group was fed with the basal diet supplemented with 3‰ *Astragalus*, and fermented *Astragalus* group was fed with the basal diet supplemented with 3‰ fermented *Astragalus* (pre-experimental results showed that supplementing at a rate of 3‰ of diet achieves optimal results). The trial lasted for 35 days (7-day adaptation period and 28-day experimental stage). The hens were housed in a clean environment with good ventilation and artificial lighting allowed 16 h of lighting per day, and with water and food ad libitum. The basal diet of all groups was the same and prepared according to the NRC (1994) laying hen nutrition requirement standard. The composition and nutrient levels of basal diet were showed in Table 1. All animal experiments were conducted according to the Guidelines for the Care and Use of Experimental Animals established and approved by the Laboratory Animal Management Committee of Henan University of Animal Husbandry and Economy (HNMY 1606).

Hen Productivity and Egg Quality

During the experimental period, egg production, broken egg production, egg weight and feed intake were recorded daily. The egg production rate and the feed conversion ratio (FCR) (feed intake/egg weight gain) during day 1 to day 14 and day 15 to day 28 were calculated to assess the laying performance. On day 14 and day 28, five eggs from each replicate were randomly sampled and measured egg quality parameters of egg shape index (ESI), eggshell strength (ESS), eggshell thickness (EST), albumen height (AH), haugh unit (HU), yolk color (YC) and yolk weight (YW).

Serum Antioxidant Indices

On day 14 and day 28, one hen from each replicate was randomly selected. Following blood collection from heart, the serum was isolated and stored at -20 °C until use. The CAT assay kit, GSH-Px assay kit, SOD assay kit, T-AOC assay kit and MDA assay kit were purchased from Shanghai yuanye Bio-Technology Co., Ltd (Shanghai, China).

Real-time qPCR

After blood samples collection, liver, spleen, ileum and cecum samples were harvested for interferon gamma (IFN- γ) and tumor necrosis factor-alpha (TNF- α) mRNA expression evaluation. Total RNA was extracted from these tissues using RNAiso Plus (Takara, Beijing, China) and reverse transcribed into cDNA with PrimeScript™ RT reagent Kit with gDNA Eraser (Perfect Real Time) (Takara, Beijing, China) according to the manufacturer's protocol. The primers used in the study were synthesized by Sangon Biotech (Shanghai) Co., Ltd. (Shanghai, China) and primer sequences are summarized in Table 2. The Real-time qPCR reactions were performed using a SYBR Premix EX Taq Kit (Takara, Beijing, China) in a 7500 Fast Real-Time PCR System (Thermo Fisher). b-actin was used as a housekeeping gene. The relative mRNA expression levels of the target genes compared to the housekeeping gene were calculated using the $2^{-\Delta\Delta Ct}$ method.

Sample Collection and DNA Extraction

On day 14 and day 28, a total of 48 hens were randomly selected (twelve hens per group) and euthanized to collect ileal and cecal contents. The samples were named as 14-d ileum control group (14IA), 14-d ileum *Astragalus* group (14IB), 14-d ileum *L. Plantarum* group (14IC), 14-d ileum fermented *Astragalus* group (14ID), 14-d cecum control group (14CA), 14-d cecum *Astragalus* group (14CB), 14-d cecum *L. Plantarum* group (14CC), 14-d cecum fermented *Astragalus* group (14CD), 28-d ileum control group (28IA), 28-d ileum *Astragalus* group (28IB), 28-d ileum *L. Plantarum* group (28IC), 28-d ileum fermented *Astragalus* group (28ID), 28-d cecum control group (28CA), 28-d cecum *Astragalus* group (28CB), 28-d cecum *L. Plantarum* group (28CC), and 28-d cecum fermented *Astragalus* group (28CD). All collected samples were immediately stored at -20°C until extraction. DNA extraction was performed with a commercial DNA extraction kit (Tiangen Biotech Corporation, Beijing, China) and quantified by a Qubit 2.0 fluorometer (Invitrogen Corporation, Carlsbad, CA, USA). The extracted DNA was qualitatively assessed by 0.8% agarose gel electrophoresis and spectrophotometry (optical density at 260/280 nm) and stored at -20°C until further analysis.

16S rRNA Gene Sequencing and Analysis

For amplicon library generation, the V4 region of the 16S rRNA gene of all DNA samples was amplified with gene-specific primers (F: 5'- AYTGGGYDTAAAGNG-3'; R: 5'-TACNVGGGTATCTAATCC-3'). PCR amplifications were performed using Q5 high-fidelity PCR DNA polymerase (NEB) and completed under the following conditions: a pre-denaturation at 98°C for 30 s; 27 cycles of 98°C for 15 s, 50°C for 30 s, and 72°C for 30 s; a final extension at 72°C for 5 min. Amplicons were purified using the Axygen AP-GX-250G AxyPrep™ DNA Gel Extraction Kit (Corning Life Sciences, Corning, NY, USA). DNA libraries were validated and quantified using the TruSeq Nano DNA LT Library Preparation Kit (Illumina, San Diego, CA, USA) and Quant-iT™ PicoGreen™ dsDNA Assay Kit (Invitrogen Corporation, Carlsbad, CA, USA). After quantification, the barcoded V4 amplicons were pooled to a final concentration of 2 nmol/L and sequenced using an Illumina MiSeq platform to generate 300 bp paired-end reads. Raw reads were quality-filtered to remove any reads less than 150 bp using Quantitative Insights into Microbial Ecology (QIIME) version 1.8 (Caporaso et al., 2010) and clustered into Operational Taxonomic Units (OTUs) based on a 97% similarity threshold. The representative sequence was chosen based on the abundance and was aligned under a given taxonomic classification using the Greengenes database, and low abundance OTUs of archaea and eukaryotes were removed (Bokulich et al., 2013). Alpha-diversity was calculated with Chao1 and ACE estimators, Shannon and Simpson indices. Partial least squares discriminant analysis (PLS-DA) was performed using QIIME software package v1.8 to discriminate between different groups (day 14 and day 28) and to establish β -diversity. The sequences generated in this study have been deposited in the National Center for Biotechnology Information sequence read archive (<https://www.ncbi.nlm.nih.gov/biosample>) under the accession number SRA: PRJNA533918.

Statistical Analysis

Only for genes mRNA expression assay, data were analyzed and graphed using GraphPad Prism 6.00 (GraphPad Software), and significance levels are indicated as: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. All other statistical analyses were performed by one-way analysis of variance using SPSS 24.0 software, and all data were expressed as means \pm SD, with $P < 0.05$ considered statistically significant.

Results

Hen Productivity and Egg Quality

The effects of different dietary supplements on the laying hen production performance and egg quality are listed in Table 3 and 4. During day 1 to day 14, there were no differences in the laying rate and FCR among four groups ($P > 0.05$), with hens fed with fermented *Astragalus* had the highest laying rate. During day 15 to day 28, hens fed with fermented *Astragalus* had the highest laying rate, 7.14% higher than that of the control group ($P < 0.05$). Although the differences were not statistically significant ($P > 0.05$), laying rate of the *Astragalus* group and *L. Plantarum* group were also increased by 3.25% and 2.99%, respectively in comparison with the control group. Furthermore, the FCR of the fermented *Astragalus* group was reduced by 6.6% compared with that of the control group ($P < 0.05$), while the FCR of the *Astragalus* group and *L. Plantarum* group displayed no significant differences as compared with the controls ($P > 0.05$). In addition, no significant differences in the phenotype of the egg quality including ESI, ESS, EST, AH, YC, HU and YW were observed among dietary treatments, suggesting that dietary supplements have no significant effects on egg quality in this study. Therefore, we identified that dietary supplementation of fermented *Astragalus* can markedly improve egg production and decrease FCR, and the effect is substantially superior to that of *Astragalus* and *L. Plantarum*.

Serum Antioxidant Indices

The effects of different dietary supplements on the laying hen antioxidant status are listed in Table 5. The data indicated that all dietary supplementation did not have an effect on the biomarkers of antioxidative stress at day 14 ($P > 0.05$). However, serum CAT, GSH-Px, SOD and T-AOC concentrations were increased by 61.5%, 62.4%, 68.0% and 52.6% ($P < 0.05$) at the end of experimentation in the fermented *Astragalus* group as compared with the controls. No statistically significant differences were observed for CAT, GSH-Px and SOD among the control, *Astragalus* and *L. plantarum* groups ($P > 0.05$). Among the effects of different dietary supplements on MDA activity in serum of laying hens, hens fed with fermented *Astragalus*, *Astragalus* diet were significantly decreased by 54.7% and 43.0% than that of the control treatment ($P < 0.05$); treatment with *L. plantarum* diet did not dramatically differ from the control treatment ($P > 0.05$). The results presented above show that dietary supplementation of fermented *Astragalus* can markedly improve laying hen antioxidant status, and the effect is significantly superior to that of *Astragalus* and *L. Plantarum*.

IFN- γ and TNF- α mRNA expression

The expression levels of IFN- γ and TNF- α mRNA in the liver, spleen, ileum and cecum were assessed at 14 and 28 day. As shown in Figure 1 and 2, the addition of fermented *Astragalus* to the diets respectively increased the mRNA content on day 14 of IFN- γ and TNF- α in the ileum by 1.7-fold ($P<0.01$) and 3.1-fold ($P<0.001$), and the mRNA content on day 14 of IFN- γ in the cecum by 2.1-fold ($P<0.01$). Interestingly, we found that the highest amount of IFN- γ and TNF- α mRNA in the liver, spleen, ileum and cecum were present in the fermented *Astragalus* group at 28 day.

Sequencing Output

A total of 48 intestinal content samples were analysed by 16S rRNA gene sequencing and produced a total of 2,006,223 high-quality sequences with an average of 41,796 reads. After OUT clustering at 97% sequence identity, a total of 216,116 OTUs were classified into 49,235 phyla, 48,677 classes, 48,634 orders, 40,101 families, 24,072 genera and 4,995 species (Figure 3).

Diversity of Intestinal Microflora

The α -diversity of ileal and cecal microbiota of four groups at different days are shown in Table 6. For bacteria on day 14, fermented *Astragalus* treatment reduced the Chao1 and ACE index in the cecum in comparison to the control treatment suggesting that fermented *Astragalus* decreased the richness of the bacterial communities. On day 28, the fermented *Astragalus* treatment increased the diversity estimators (Shannon and Simpson) of the bacterial community in the ileum. PLS-DA was performed to evaluate the similarity (b-diversity) of microbial community structure among groups (Figure 4). PLS-DA plot defined groups where the samples from different groups occupied distinct positions.

Composition of Intestinal Microflora

A total of 20 phyla were identified within the intestinal microbiota among 48 samples as shown in Figure 5. There were 3 major groups of the intestinal microbiota, including *Firmicutes*, *Bacteroidetes* and *Proteobacteria*. The relative abundance (%) of cecal bacterial phyla of hens fed with different dietary supplements was presented in approximately the same amount on days 14 and 28. On day 28, fermented *Astragalus* led to a reduced abundance of ileal *Firmicutes*, with an increased abundance of ileal *Bacteroidetes* and *Proteobacteri*. Genus level analysis showed that the *Lactobacillus* and *Bacteroides* accounted for the largest proportion of the intestinal microbiota as shown in Figure 6. *Lactobacillus* showed high abundance in the ileum, and extremely low abundance in the cecum. In contrast, *Bacteroides* showed high abundance in the cecum, and extremely low abundance in the ileum. On day 14, fermented *Astragalus* addition increased the abundance of cecal *Bacteroides* by 5.06% as compared with the control, with no significant influence on the abundance of ileal *Lactobacillus*. On day 28, fermented *Astragalus* addition significantly decreased the abundance of ileal *Lactobacillus* by 48.51% as compared with the control, with no significant influence on the abundance of cecal *Bacteroides*.

Discussion

The present study was undertaken to investigate the effects of *L. Plantarum* fermented *Astragalus* supplementation on the performance, egg quality, antioxidant status of serum and gut microbiota in laying hens. When taking out the feeding trial, we observed that diets supplemented with fermented *Astragalus* increased egg production rate ($P < 0.05$) and decreased feed conversion rate ($P < 0.05$), which may likely be attributed to the improvement of laying hen health status. In vivo, free radicals are harmful by-products generated during normal cellular metabolism, and are prone to attack unsaturated fatty acid on the biological membrane, triggering lipid oxidation and lipid peroxides accumulation that result in impairment of organism health (Fang et al., 2002). The antioxidant enzymes CAT, GSH-Px and SOD are associated with free radical scavenging to protect cells from oxidative damage (Zhang et al., 2014). In the present study, supplementation with fermented *Astragalus* resulted in a significantly highest levels of CAT, GSH-Px, SOD and T-AOC and lowest level of MDA in the serum ($P < 0.05$) on day 28. Our findings are consistent with our previous studies on broilers (Qiao et al., 2018a), indicating that *Astragalus* fermented by *L. plantarum* can enhance the antioxidant ability of both broilers and laying hens.

Nowadays, *Astragalus* polysaccharide has attracted rising interests for its anti-cancer effects. Previous study has observed that *Astragalus* polysaccharide can significantly enhance the proliferation of spleen lymphocytes and increase phagocytosis of peritoneal macrophages in mice and is capable of up-regulating the expression of IL-2, TNF- α and IFN- γ in peripheral blood (Li et al., 2020). IFN- γ and TNF- α are cytokines possessing antitumor and immunomodulatory properties and are essential for host immune responses against infection or tissue injury (Li et al., 2019). At the end of our feeding trial (on day 28), *L. plantarum* merely increased the mRNA expression of ileal TNF- α , *Astragalus* increased the mRNA expression of splenic and cecal IFN- γ and that of hepatic, splenic and cecal TNF- α . Interestingly, fermented *Astragalus* significantly increased the mRNA expression of both IFN- γ and TNF- α in all the liver, spleen, ileum, and cecum. However, there are comparatively few findings to date regarding the impact of *L. Plantarum* fermented *Astragalus* on host immune responses. We speculate that components and metabolites of *Astragalus* are changed after fermentation and more effective components can enhance the body's immune function by increasing the expression of cytokines. Certainly, further investigations will be required to fully illustrate the intrinsic molecular mechanism.

Intestinal microbiota plays an major role in maintaining host health, immunity and production performance, it has become a research hotspot in recent years (Yeoman et al., 2012). In this study, we also evaluated the effect of fermented *Astragalus* on intestinal microbiota of laying hens. Our results showed that fermented *Astragalus* addition increases the diversity of ileal bacterial community with the increase of feeding time. Furthermore, at the phylum level, *Firmicutes*, *Bacteroidetes* and *Proteobacteria* were the most dominant phyla in the intestinal microbiota of hens, which is consistent with previous studies (Danzeisen et al., 2011; Yeoman et al., 2012). Interestingly, fermented *Astragalus* addition led to a reduced abundance of ileal *Firmicutes*, with an increased abundance of ileal *Bacteroidetes* and *Proteobacteria*. We speculate that increased diversity of ileal bacterial community might be explained by the fact that the abundance of ileal *Firmicutes* was reduced to enhance the abundance of other phyla. At the genus level, *Lactobacillus* as the largest proportion of ileal microbiota of hens is generally highly relevant to feed digestibility (Yan et al.,

2017). However, fermented *Astragalus* addition significantly decreased the abundance of ileal *Lactobacillus* by 48.51% as compared with the control at 28 days. These results were totally different from our previous report on the effect of fermented *Astragauls* on the broiler chicken fecal microbiota, which found that the count of *Lactobacillus* was increased in chickens fed fermented *Astragalus* as compared with those in the control group. Those factors responsible for the differences should be further studied.

In conclusion, this study suggested that *L. Plantarum* fermented *Astragalus* as an efficient dietary additive could significantly promote the production performance, antioxidant capacity and ileal microbiota diversity of laying hens during the late laying period. A higher expression level of IFN- γ and TNF- α in the liver, spleen, ileum and cecum of laying hens supplemented with fermented *Astragalus* indicates a particular role of fermented *Astragalus* on the innate immune system, and this needs a comprehensive investigation in the future to fully illustrate the exact mechanism.

Abbreviations

L. Plantarum: *Lactobacillus Plantarum*; CAT: catalase; GSH-Px: glutathione peroxidase; SOD: superoxide dismutase; T-AOC: total antioxidant capacity; MDA: malondialdehyde; CFU: colony forming unit; FCR: feed conversion ratio; ESI: egg shape index; ESS: eggshell strength; EST: eggshell thickness; AH: albumen height; HU: haugh unit; YC: yolk color; YW: yolk weight; IFN- γ : interferon gamma; TNF- α : tumor necrosis factor-alpha; OTUs: Operational Taxonomic Units; PLS-DA: Partial least squares discriminant analysis.

Declarations

Ethics approval and consent to participate

The animal experiments were conducted in accordance with the Guidelines for the Care and Use of Experimental Animals established and approved by the Laboratory Animal Management Committee of Henan University of Animal Husbandry and Economy.

Consent for publication

Not applicable.

Availability of data and materials

The datasets generated during this study have been deposited in the National Center for Biotechnology Information sequence read archive (<https://www.ncbi.nlm.nih.gov/biosample>) under the accession number SRA: PRJNA533918.

Competing interests

The authors declare that they have no competing interests.

Funding

This study was supported by the Key Discipline of Preventive Veterinary Medicine of Henan University of Animal Husbandry and Economy (mxk2016102), the Research and Innovation Team of Henan University of Animal Husbandry and Economy (2018KYTD13) and the Henan Science and Technology Research Project (192102110076).

Authors' Contributions

HXQ and HTS contributed to conception and design of the study. HTS, BYW and CZB performed the experiments. HXQ and BYW performed the statistical analysis. YQH and HXQ wrote the manuscript. All authors contributed to manuscript revision, read, and approved the submitted version.

Acknowledgements

Not applicable.

Author details

¹College of Veterinary Medicine, Henan University of Animal Husbandry and Economy, Zhengzhou, 450046, Henan Province, China. ²Key Lab of Freshwater Animal Breeding, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, College of Fishery, Huazhong Agricultural University, Wuhan, 430070, Hubei Province, China. ³College of Animal Sciences and Veterinary Medicine, Henan Agricultural University, Zhengzhou, 450046, Henan Province, China

Endnotes

[†]These authors have contributed equally to this work

* Correspondence: Yingqian Han (twgjl@163.com); Hongxing Qiao (zzmzqhx@163.com)

Reference

- Ai, S. et al. 2019. [Research progress on Chinese herbal medicine fermentation and profile of active substances derived]. *Zhongguo Zhong Yao Za Zhi* 44: 1110-1118.
- Bokulich, N. A. et al. 2013. Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. *Nat Methods* 10: 57-59.
- BP, W., R. SL, and F. BB. 2011. Shifting the balance: antibiotic effects on host-microbiota mutualism. *Nature reviews. Microbiology* 9: 233-243.
- Caporaso, J. G. et al. 2010. QIIME allows analysis of high-throughput community sequencing data. *Nat Methods* 7: 335-336.
- Danzeisen, J. L., H. B. Kim, R. E. Isaacson, Z. J. Tu, and T. J. Johnson. 2011. Modulations of the chicken cecal microbiome and metagenome in response to anticoccidial and growth promoter treatment. *PLoS One*

6: e27949.

- Fang, Y. Z., S. Yang, and G. Wu. 2002. Free radicals, antioxidants, and nutrition. *Nutrition* 18: 872-879.
- Kallon, S. et al. 2013. Astragalus polysaccharide enhances immunity and inhibits H9N2 avian influenza virus in vitro and in vivo. *J Anim Sci Biotechnol* 4: 22.
- Kim, J. H. et al. 2013. Effects of topical application of *Astragalus membranaceus* on allergic dermatitis. *Immunopharmacol Immunotoxicol* 35: 151-156.
- Li, Q. et al. 2019. cGAS/STING/TBK1/IRF3 Signaling Pathway Activates BMDCs Maturation Following *Mycobacterium bovis* Infection. *Int J Mol Sci* 20.
- Li, W. et al. 2020. Characterization and anti-tumor bioactivity of astragalus polysaccharides by immunomodulation. *Int J Biol Macromol* 145: 985-997.
- Li, X. et al. 2014. A review of recent research progress on the astragalus genus. *Molecules* 19: 18850-18880.
- Patra, J. K., G. Das, and K. H. Baek. 2015. Chemical Composition and Antioxidant and Antibacterial Activities of an Essential Oil Extracted from an Edible Seaweed, *Laminaria japonica* L. *Molecules* 20: 12093-12113.
- Qiao, H., Y. Song, H. Shi, and C. Bian. 2018a. Fermented *Astragalus* in diet altered the composition of fecal microbiota in broiler chickens. *AMB Express* 8: 151.
- Qiao, H., L. Zhang, H. Shi, Y. Song, and C. Bian. 2018b. *Astragalus* affects fecal microbial composition of young hens as determined by 16S rRNA sequencing. *AMB Express* 8: 70.
- Qiao, H. et al. 2018c. Assessment of the physicochemical properties and bacterial composition of *Lactobacillus plantarum* and *Enterococcus faecium*-fermented *Astragalus membranaceus* using single molecule, real-time sequencing technology. *Sci Rep* 8: 11862.
- Qin, Q. et al. 2012. *Astragalus membranaceus* inhibits inflammation via phospho-P38 mitogen-activated protein kinase (MAPK) and nuclear factor (NF)- κ B pathways in advanced glycation end product-stimulated macrophages. *Int J Mol Sci* 13: 8379-8387.
- Shahzad, M., A. Shabbir, K. Wojcikowski, H. Wohlmuth, and G. C. Gobe. 2016. The Antioxidant Effects of *Radix Astragali* (*Astragalus membranaceus* and Related Species) in Protecting Tissues from Injury and Disease. *Curr Drug Targets* 17: 1331-1340.
- Sheih, I. C., T. J. Fang, T. K. Wu, C. H. Chang, and R. Y. Chen. 2011. Purification and properties of a novel phenolic antioxidant from *Radix astragali* fermented by *Aspergillus oryzae* M29. *J Agric Food Chem* 59: 6520-6525.
- Vandemaele, F., M. Vereecken, J. Derijcke, and B. M. Goddeeris. 2002. Incidence and antibiotic resistance of pathogenic *Escherichia coli* among poultry in Belgium. *Vet Rec* 151: 355-356.

- Wang, C. Z., W. J. Li, R. Tao, J. Z. Ye, and H. Y. Zhang. 2015. Antiviral activity of a nanoemulsion of polyphenols from ginkgo leaves against influenza A H3N2 and hepatitis B virus in vitro. *Molecules* 20: 5137-5151.
- Xu, J., H. B. Chen, and S. L. Li. 2017. Understanding the Molecular Mechanisms of the Interplay Between Herbal Medicines and Gut Microbiota. *Medicinal Research Reviews* 37.
- Yan, W., C. Sun, J. Yuan, and N. Yang. 2017. Gut metagenomic analysis reveals prominent roles of *Lactobacillus* and cecal microbiota in chicken feed efficiency. *Sci Rep* 7: 45308.
- Yeoman, C. J. et al. 2012. The microbiome of the chicken gastrointestinal tract. *Anim Health Res Rev* 13: 89-99.
- Zhang, Z. et al. 2014. Taurine supplementation reduces oxidative stress and protects the liver in an iron-overload murine model. *Mol Med Rep* 10: 2255-2262.
- Zhu, H., G. Cao, H. Cai, B. Cai, and J. Hu. 2014. Rapid and undamaged analysis of crude and processed *Radix Scrophulariae* by Fourier transform infrared spectroscopy coupled with soft independent modeling of class analogy. *Pharmacogn Mag* 10: 265-270.

Tables

Table 1 Composition and nutrient levels of the basal diet (air-dry basis %)

Ingredients	Content	Nutrient levels	Content
Corn	61.4	ME/(MJ/kg) ²	11.01
Soybean meal	23.8	CP	15.49
Wheat bran	2.0	Ca	3.50
Soybean oil	0.6	TP	0.56
CaHPO ₄	1.3	AP	0.35
Limestone	8.6	Lys	0.74
NaCl	0.3	Met+Cys	0.51
Premix ¹	2.0		
Total	100.0		

¹ The premix provided the following per kilogram of the diet: VA 11,000 IU, VD₃ 3,200 IU, VE 25 IU, VK₃ 2.2 mg, VB₁ 1.5 mg, VB₂ 3.5 mg, VB₁₂ 3 mg, nicotinic 28 mg, calcium pantothenate 8.5 mg, biotin 0.5 mg, choline 255 mg, Fe 55 mg, Zn 62 mg, Cu 6 mg, Se 0.20 mg.

² ME was a calculated value, while the others were measured values.

Table 2 Primers used for quantitative real-time PCR analysis

Primers	Sequences 5'~3'	Size
IFN- γ -F	AACAACCTTCCTGATGGCGT	107 bp
IFN- γ -R	TGAAGAGTTCATTCGCGGCT	
β -actin-F	TATGTGCAAGGCCGTTTCG	170 bp
β -actin-R	CAATGGGGTACTTCAGGGTCAG	
TNF- α -F	GCCCTTCCTGTAACCAGATG	71 bp
TNF- α -R	ACACGACAGCCAAGTCAACG	

Table 3 Effects of different dietary supplements on the production performance of laying hens

Parameters		Control	<i>Astragalus</i>	<i>L. plantarum</i>	Fermented <i>Astragalus</i>	<i>P</i> -value	SEM
Laying rate, %	1-14d	87.50±3.45	89.17±2.08	87.50±2.70	90.60±3.80	0.349	1.376
	15- 28d	88.96±3.76a	92.21±2.75ab	91.95±3.83ab	96.10±1.03b	0.017	1.368
FCR	1-14d	2.02±0.08	1.94±0.05	2.02±0.10	1.95±0.08	0.224	0.037
	15- 28d	1.81±0.08b	1.75±0.06ab	1.77±0.11ab	1.69±0.05a	0.172	0.035

Note: FCR, feed conversion ratio. Different lowercase letters in the same row indicate significant difference ($P < 0.05$), and the same letters or no letters indicate no significant difference ($P > 0.05$) (same as below).

Table 4 Effects of different dietary supplements on the egg quality

Parameters	Control	<i>Astragalus</i>	<i>L. plantarum</i>	Fermented <i>Astragalus</i>	P-value	SEM
14 d						
ESI	1.29±0.02	1.29±0.03	1.29±0.03	1.29±0.03	0.961	0.012
ESS (kg/N)	3.59±0.41	4.04±0.33	3.87±0.32	3.90±0.40	0.302	0.164
EST (mm)	0.344±0.013	0.344±0.011	0.346±0.008	0.348±0.008	0.927	0.005
AH (mm)	8.74±0.43ab	8.74±0.63ab	8.47±0.51a	9.21±0.33b	0.162	0.219
YC	5.15±0.32	5.00±0.28	5.44±0.21	5.32±0.40	0.160	0.139
HU	92.84±1.90	92.16±3.42	92.10±2.82	94.75±1.61	0.183	1.138
YW	15.75±0.37	15.47±0.32	15.60±0.22	15.27±0.73	0.417	0.202
28 d						
ESI	1.28±0.02	1.28±0.01	1.29±0.01	1.29±0.03	0.452	0.008
ESS (kg/N)	4.31±0.37	4.34±0.60	4.20±0.16	4.54±0.41	0.625	0.185
EST (mm)	0.375±0.014	0.392±0.020	0.389±0.013	0.387±0.018	0.396	0.007
AH (mm)	8.80±0.40	8.92±0.43	8.85±0.24	9.08±0.44	0.676	0.173
YC	5.59±0.39	5.55±0.47	5.22±0.12	5.44±0.45	0.435	0.170
HU	92.57±2.19	92.80±2.42	92.74±1.03	93.80±2.07	0.763	0.895
YW	15.40±0.39	15.50±0.59	15.78±0.38	15.76±0.58	0.556	0.222

Note: ESI, egg shape index; ESS, eggshell strength; EST, eggshell thickness; AH, albumen height; HU, haugh unit; YC, yolk color; YW, yolk weight.

Table 5 Effects of different dietary supplements on the antioxidant status of laying hens

Parameters	Control	<i>Astragulas</i>	<i>L. plantarum</i>	Fermented <i>Astragulas</i>	<i>P</i> -value	SEM
14 d						
CAT (U/mL)	43.90±2.46	57.21±13.66	76.80±44.15	61.52±31.03	0.445	13.960
GSH-Px (U/L)	90.80±14.36	115.32±32.20	145.76±79.19	120.37±54.47	0.450	23.989
SOD (U/mL)	276.62±44.10	313.42±87.16	321.99±91.99	339.02±127.71	0.757	43.954
T-AOC (U/mL)	12.25±2.13	14.33±4.66	15.40±4.63	14.79±6.31	0.753	2.211
MDA (nmol/mL)	6.93±0.52	8.58±2.50	8.71±2.62	8.63±3.52	0.734	1.276
28 d						
CAT (U/mL)	47.93±2.41a	45.58±8.17a	86.63±17.73ab	124.58±66.85b	0.020	17.563
GSH-Px (U/L)	90.07±20.18a	108.12±31.99a	159.86±36.77ab	239.78±142.58b	0.043	35.992
SOD (U/mL)	230.98±29.88a	321.95±125.37a	473.54±125.13ab	722.33±418.70b	0.030	108.041
T-AOC (U/mL)	10.78±1.62a	12.81±2.82a	20.29±4.68b	22.72±7.16b	0.006	2.226
MDA (nmol/mL)	14.79±4.97c	8.43±3.28ab	12.47±2.69bc	6.70±1.04a	0.011	1.542

Figures

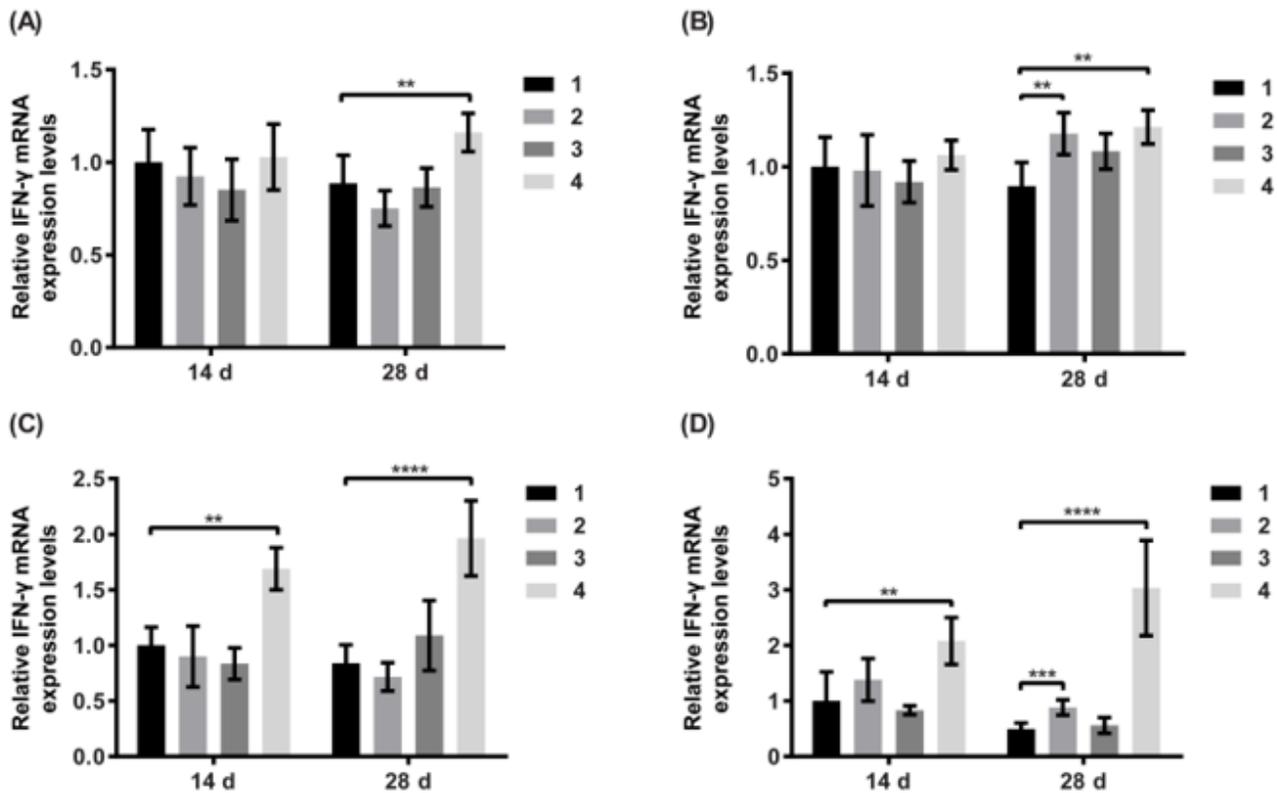


Figure 1

Effects of different dietary supplements on the relative mRNA expression of IFN- γ of laying hens. (A) Expression levels of IFN- γ mRNA in the liver at different time points; (B) Expression levels of IFN- γ mRNA in the spleen at different time points; (C) Expression level of IFN- γ mRNA in the ileum at different time points; (D) Expression level of IFN- γ mRNA in the cecum at different time points; 1: the control group; 2: The Astragalus group; 3: The L. Plantarum group; 4: The fermented Astragalus group.

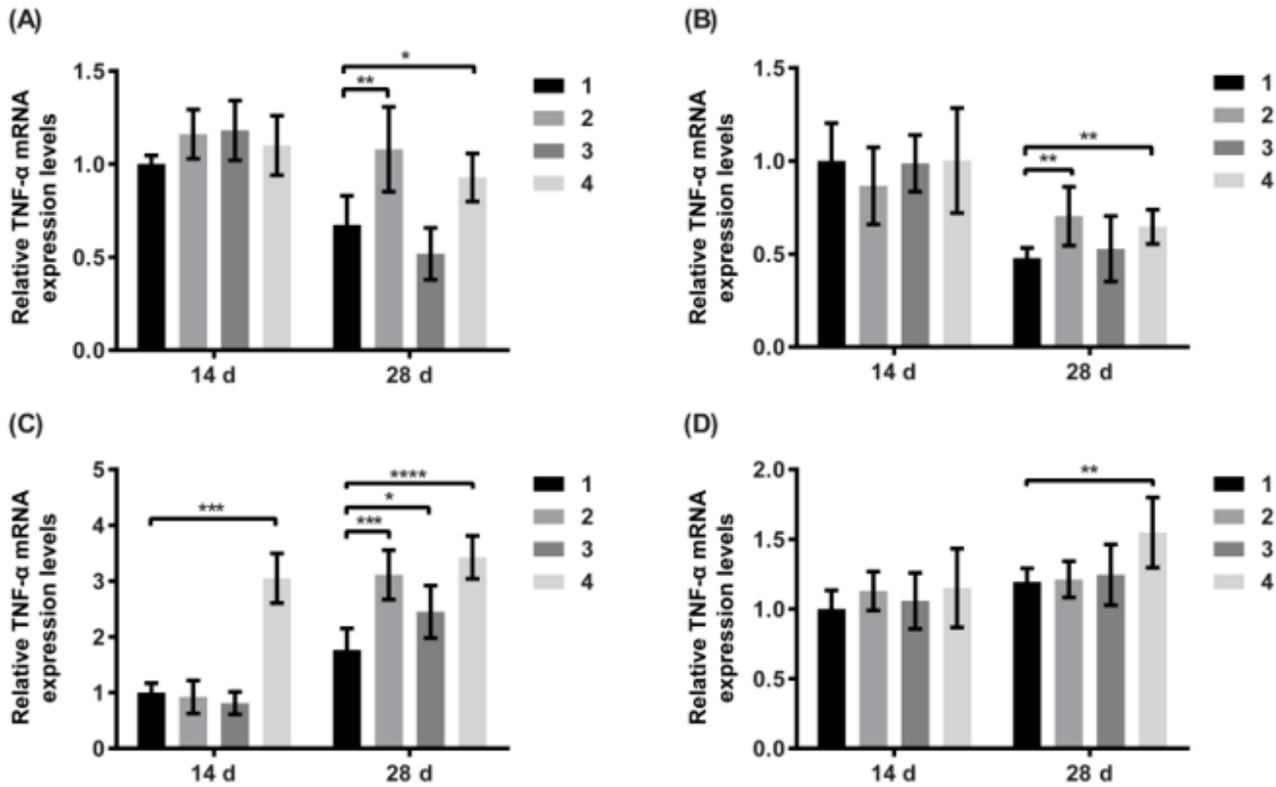


Figure 2

Effects of different dietary supplements on the relative mRNA expression of TNF-α of laying hens. (A) Expression levels of TNF-α mRNA in the liver at different time points; (B) Expression levels of TNF-α mRNA in the spleen at different time points; (C) Expression level of TNF-α mRNA in the ileum at different time points; (D) Expression level of TNF-α mRNA in the cecum at different time points; 1: the control group; 2: The Astragalus group; 3: The L. Plantarum group; 4: The fermented Astragalus group.

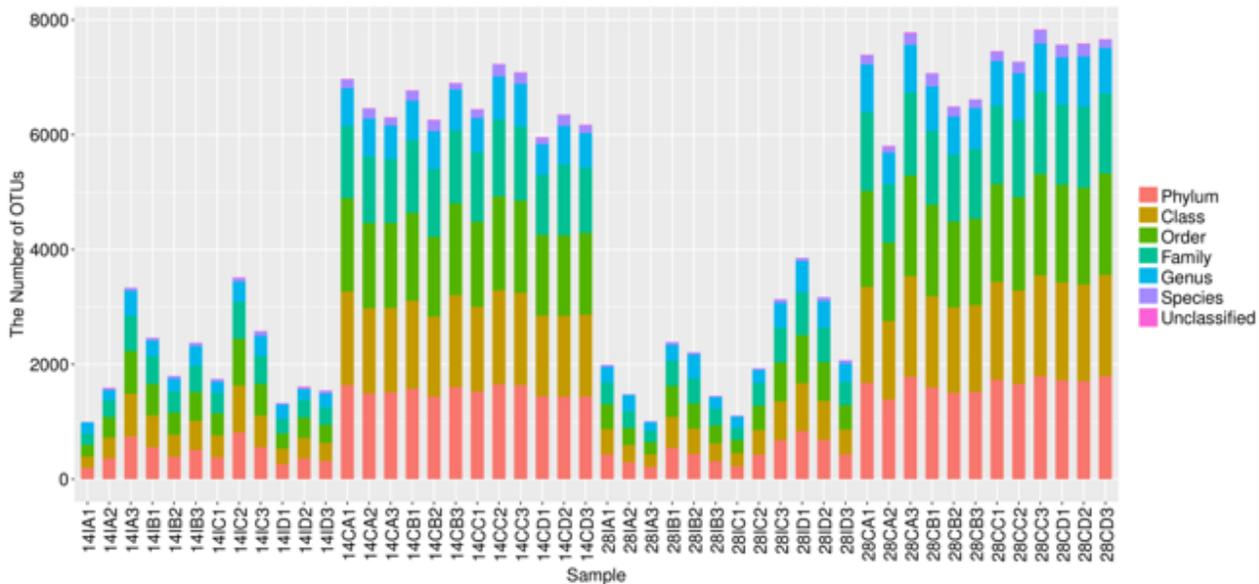


Figure 3

Number of identified taxa (from phyla to species) among the diverse groups.

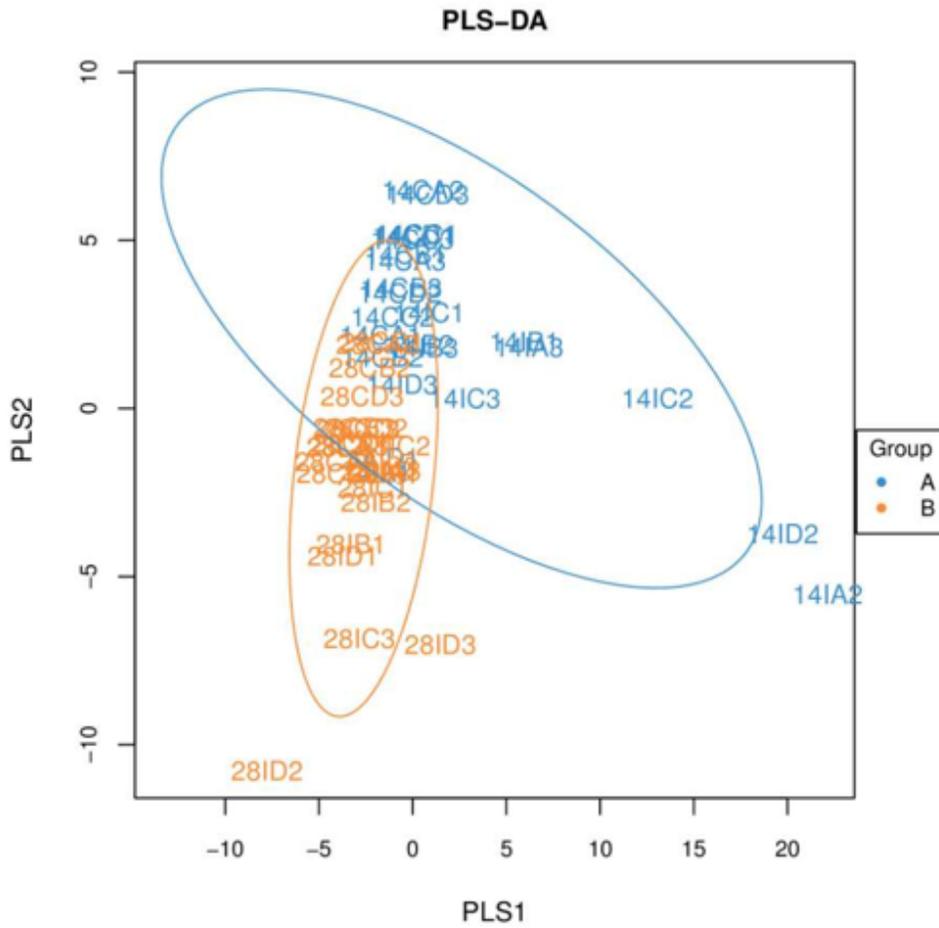


Figure 4

Partial least squares discriminant analysis (PLS-DA) of ileal and cecal microbiota among groups. A: 14-day sample groups; B: 28-day sample groups.

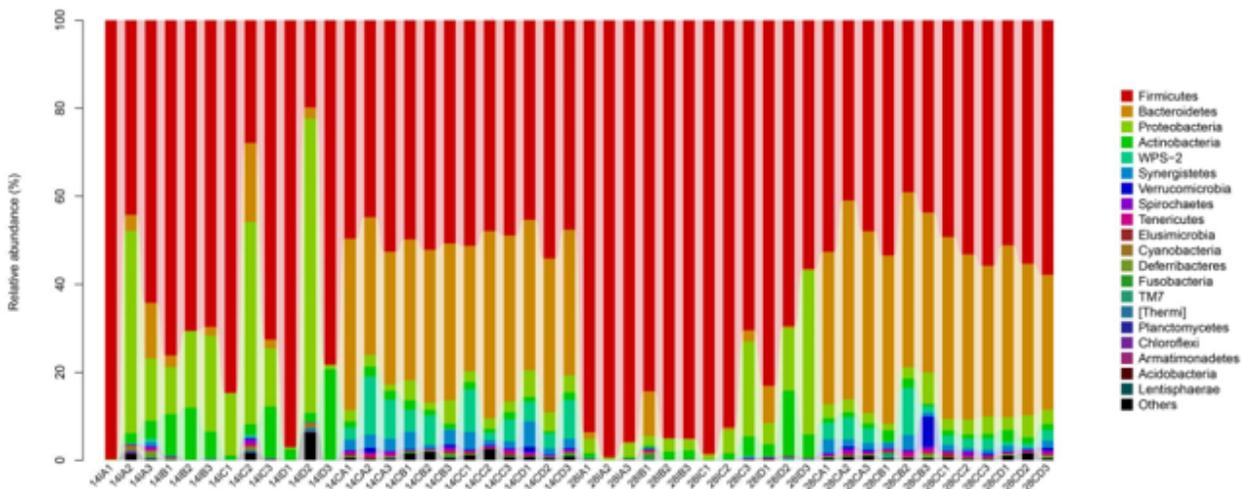


Figure 5

The phylum level distribution of ileal and cecal microbiota among groups. 14IA: 14-d ileum control group; 14IB: 14-d ileum Astragalus group; 14IC: 14-d ileum L. Plantarum group; 14ID: 14-d ileum fermented Astragalus group; 14CA: 14-d cecum control group; 14CB: 14-d cecum Astragalus group; 14CC: 14-d cecum L. Plantarum group; 14CD: 14-d cecum fermented Astragalus group; 28IA: 28-d ileum control group; 28IB: 28-d ileum Astragalus group; 28IC: 28-d ileum L. Plantarum group; 28ID: 28-d ileum fermented Astragalus group; 28CA: 28-d cecum control group; 28CB: 28-d cecum Astragalus group; 28CC: 28-d cecum L. Plantarum group; 28CD: 28-d cecum fermented Astragalus group.

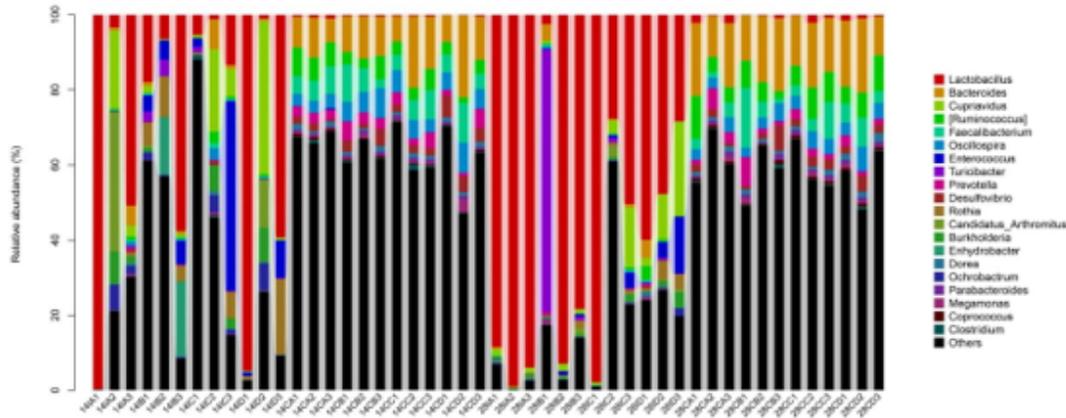


Figure 6

The genus level distribution of ileal and cecal microbiota among groups. 14IA: 14-d ileum control group; 14IB: 14-d ileum Astragalus group; 14IC: 14-d ileum L. Plantarum group; 14ID: 14-d ileum fermented Astragalus group; 14CA: 14-d cecum control group; 14CB: 14-d cecum Astragalus group; 14CC: 14-d cecum L. Plantarum group; 14CD: 14-d cecum fermented Astragalus group; 28IA: 28-d ileum control group; 28IB: 28-d ileum Astragalus group; 28IC: 28-d ileum L. Plantarum group; 28ID: 28-d ileum fermented Astragalus group; 28CA: 28-d cecum control group; 28CB: 28-d cecum Astragalus group; 28CC: 28-d cecum L. Plantarum group; 28CD: 28-d cecum fermented Astragalus group