The digestive/reproductive tract microbiota dominates over host genetics in regulating chicken egg production

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Diyan Li
Sichuan Agricultural University - Chengdu Campus

diyanli@sicau.edu.cn*Corresponding Author*
ORCiD: https://orcid.org/0000-0001-7490-3550

Shilin Tian
Wuhan University

Wei Zhu
Sichuan Agricultural University - Chengdu Campus

Yuan Su
Sichuan Agricultural University - Chengdu Campus

Tao Wang
Sichuan Agricultural University - Chengdu Campus

Tianyuan Ma
Sichuan Agricultural University - Chengdu Campus

Shailendra Kumar Mishra
Sichuan Agricultural University - Chengdu Campus

Lianzhe Shi
Sichuan Agricultural University - Chengdu Campus

Ranlei Wei
Sichuan University West China Hospital

Zhongxian Xu
Sichuan Agricultural University - Chengdu Campus

Chunyou Ning
Sichuan Agricultural University - Chengdu Campus

Dejing Zhang
Novogene Bioinformatics institute

Xuxu Lin
Sichuan Agricultural University - Chengdu Campus

Xiaoling Zhao
Sichuan Agricultural University - Chengdu Campus

Yan Wang
Sichuan Agricultural University - Chengdu Campus

Huadong Yin
Sichuan Agricultural University - Chengdu Campus

Yaodong Hu
Sichuan Agricultural University - Chengdu Campus

Xiaolan Fan
Sichuan Agricultural University - Chengdu Campus

Bo Zeng
Sichuan Agricultural University - Chengdu Campus

Mingyao Yang
Sichuan Agricultural University - Chengdu Campus

Deying Yang
Sichuan Agricultural University - Chengdu Campus

Qingyong Ni
Sichuan Agricultural University - Chengdu Campus

Yan Li
Sichuan Agricultural University - Chengdu Campus

Mingwang Zhang
Sichuan Agricultural University - Chengdu Campus

Yongfang Yao
Sichuan Agricultural University - Chengdu Campus

Huailiang Xu
Sichuan Agricultural University - Chengdu Campus

Mingzhou Li
Sichuan Agricultural University - Chengdu Campus

Qing Zhu
Sichuan Agricultural University - Chengdu Campus

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Abstract

Background: The microbiota of the digestive and reproductive systems has a prominent role in animal health and performance, but the extent of its contribution is difficult to determine. In chickens, the effect of host genetics on the reproductive and digestive tract microbiota is unclear, and the means by which digestive/reproductive microbiomes help improve egg production in chicken are unknown. Results: To gain insight into this, we examined genomes from 128 chickens reared under identical conditions and described their digestive (crop, gizzard and small intestine) and reproductive tract (vagina, uterus and isthmus) microbiota. Although the diversity, composition and predicted function of the digestive and reproductive tract microbiota exhibited notable microbiota variation substantially between different parts, host genetics had limited effects on the reproductive and digestive tract microbial community. The digestive and reproductive tract microbiota had a significant effect on egg production (accounting for 52.31% - 98.86% of the variance), after correcting for host genetic effects; in particular, the uterus and isthmus microbiota accounted for an average of 93.59% and 98.86%, respectively, of variance in egg production. We further identified four reproductive tract microbial species which were related to immune system, Bacteroides fragilis , Bacteroides salanitronis , Bacteroides barnesiae and Clostridium leptum , that were significantly positively correlated with egg production. Chickens with a lower abundance of these species had produced significantly fewer eggs at 300 days of age (37.13 vs. 113.75) than those with a higher abundance of these microorganisms. We speculated that these microorganisms regulate chicken reproductive activity by mediating its immune system. Conclusions: Host genetics has limited effect on digestive/reproductive microbiome composition. The distinct site-associated chicken microbiome may be determined by the differences of their physical function. These findings may help design strategies for controlling and altering the digestive/reproductive tract microbiota in chickens to improve egg production.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures

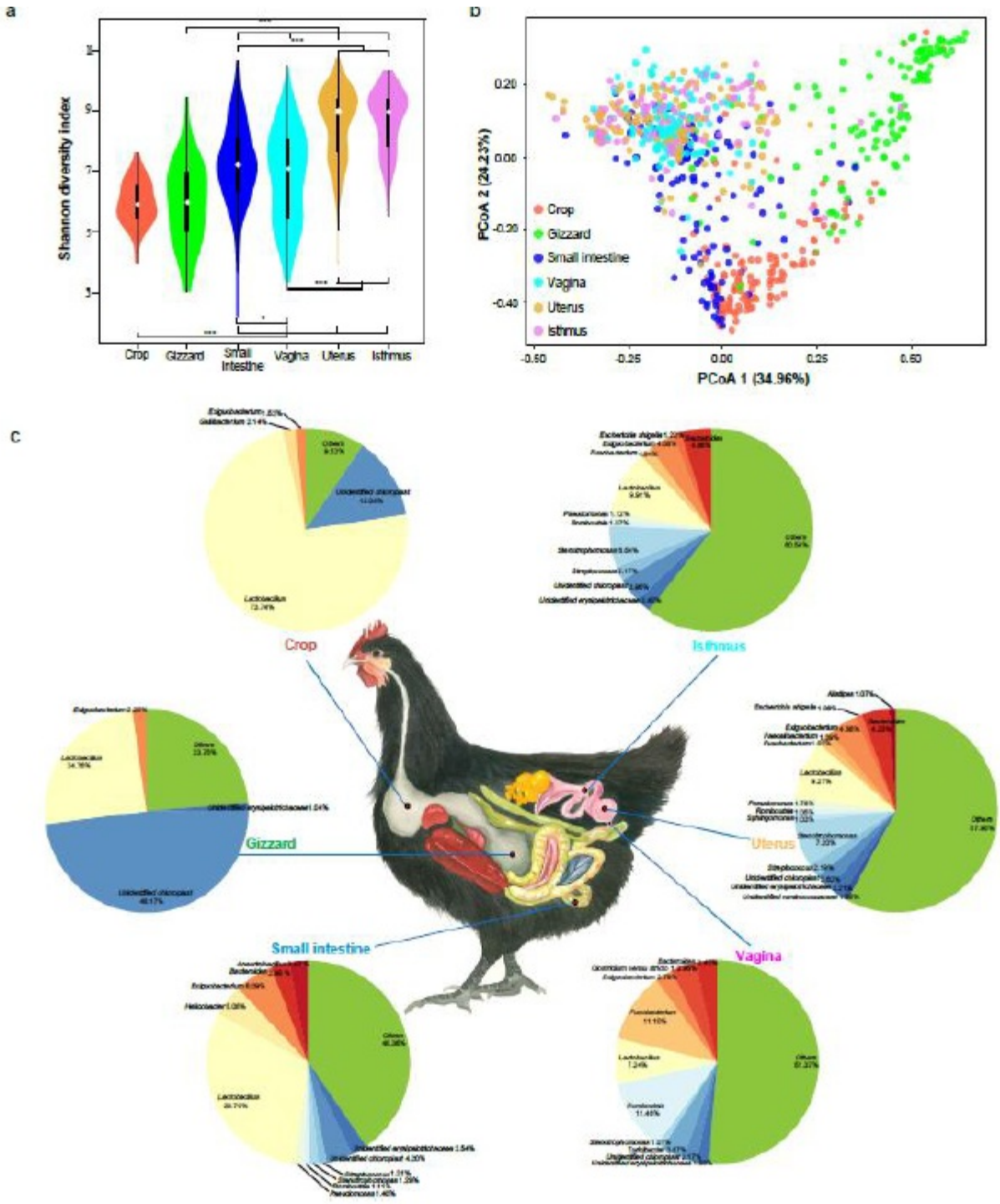

Figure 1

a An alpha diversity comparison based on the Shannon diversity index using the Wilcoxon rank-sum test to determine significant differences. b PCoA of the 768 samples based on weighted UniFrac distances. The first dimension and second dimension are shown. The fraction of the variance explained was 34.96% for component 1 ($P < 0.05$, Tracy-Widom test) and 24.23% for component 2 ($P < 0.05$, Tracy-Widom test). c Relative abundance of

the microbiota from the six sites at the genus level. Only genera with an abundance of >1.0% in any of the sites are described (Additional file 1: Table S3)

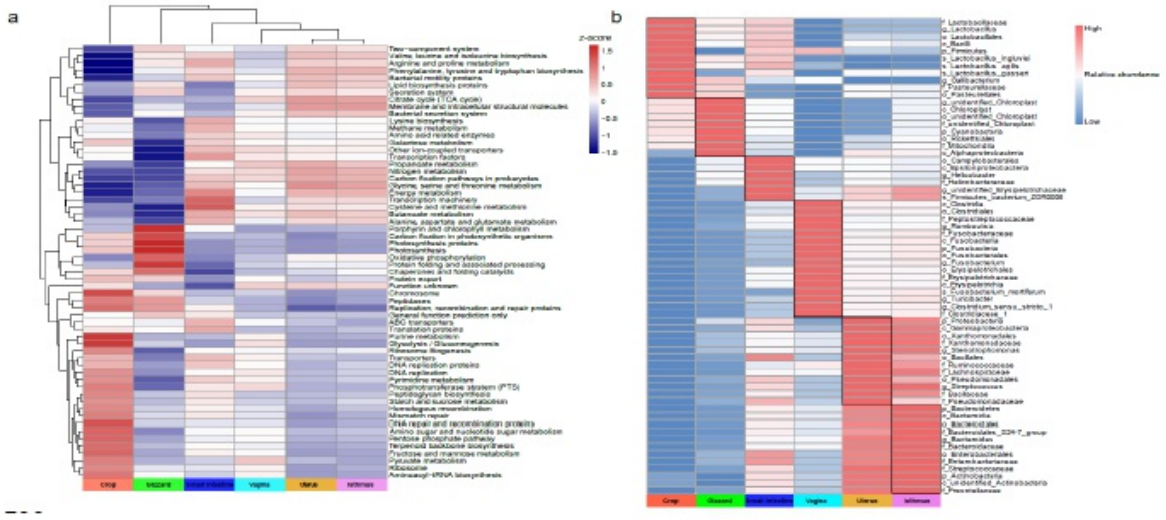

Figure 2

Comparison of the predicted functional capacities and site-associated taxa of the six microbial communities at diverse anatomical sites. a Heatmap showing the predicted KEGG pathways and their different abundances at different reproductive and digestive tract locations (see also Additional file 1: Table S4). The heatmap is color coded based on row z-scores of means of KEGG pathway abundances. b Heat map showing the 65 site-associated bacterial taxa identified by LEfSe (LDA > 4) and taxa whose abundances differed significantly among the six sites. p, phylum; c, class; o, order; f, family; g, genus.

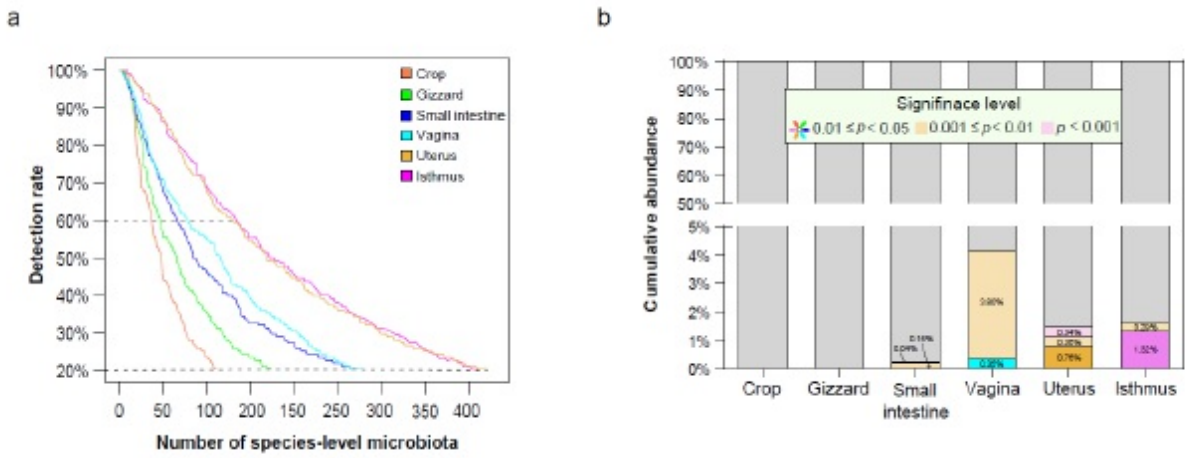

Figure 3

Host genetics have a limited effect on the reproductive/digestive tract microbiota. a Number of species identified in all chickens at the six different anatomical sites. b The cumulative relative abundance of heritable microbial species in each segment.

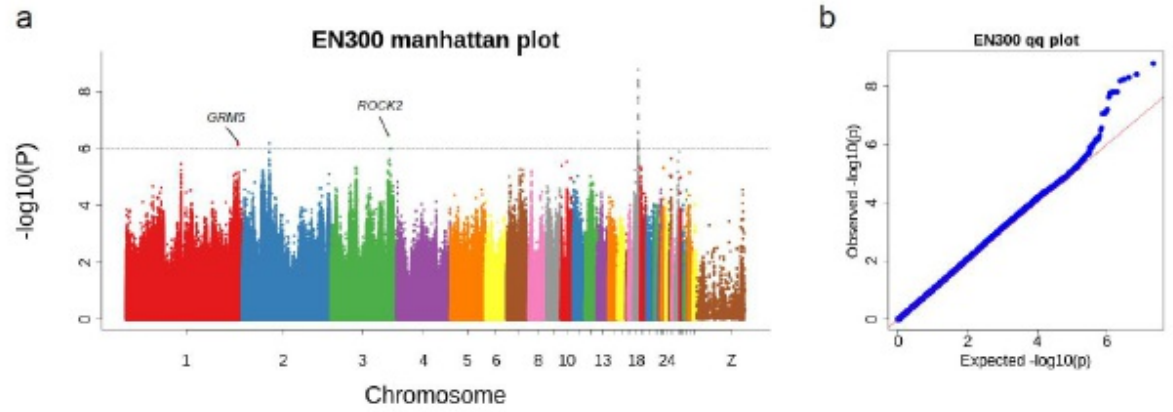

Figure 4

Genome-wide association study analysis of single-nucleotide polymorphisms associated with egg number at 300 days of age (EN300). a The horizontal dashed gray line indicates genome-wide significance thresholds (1.0 × 10-6). Each point represents a single-nucleotide polymorphism. The association analysis was conducted with the genome-wide efficient mixed-model association (GEMMA) software package. b Quantile-quantile plot of the genome-wide efficient mixed model for EN300. A 45-degree reference line is shown in red. The greater the departure from this reference line, the greater the likelihood that the two data sets came from populations with different distributions.

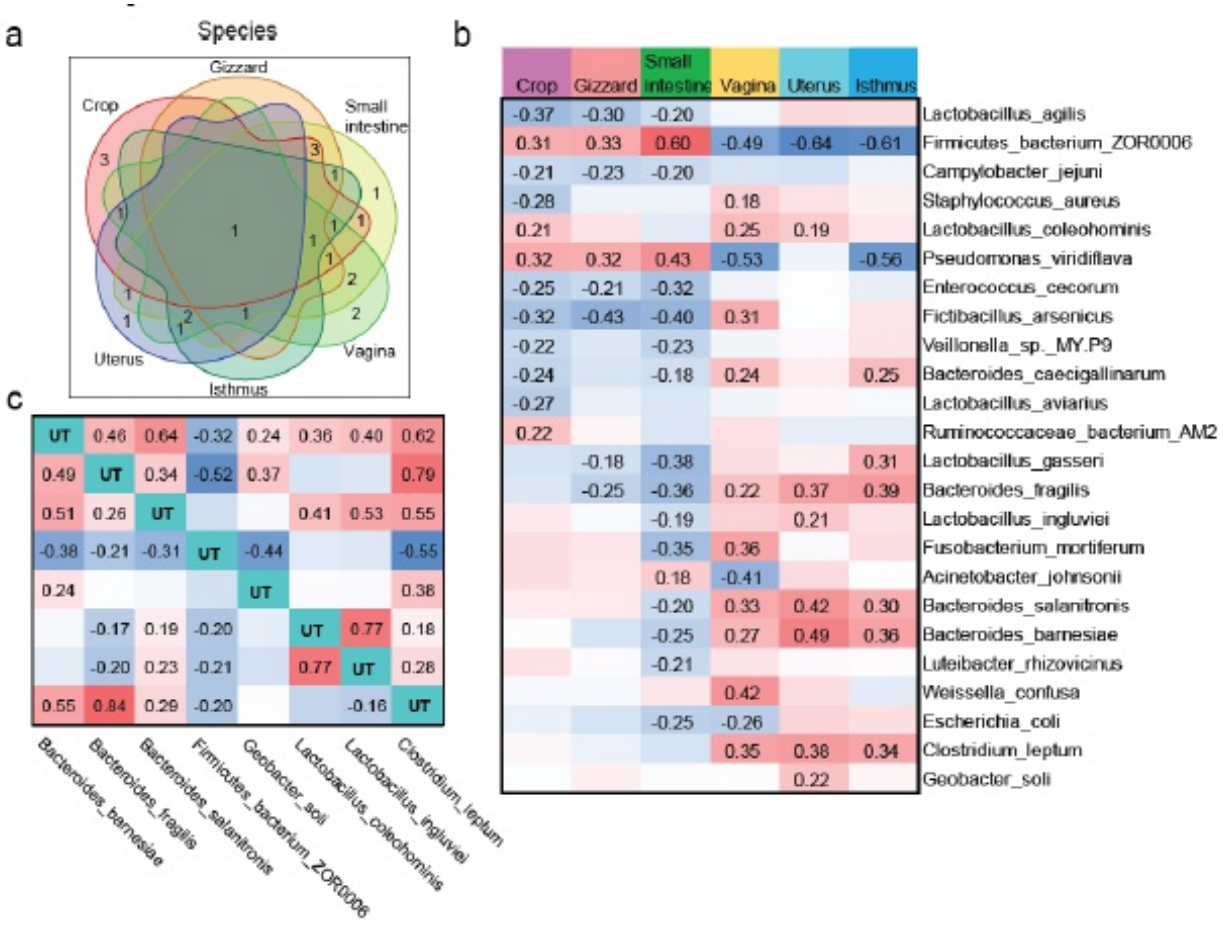

Figure 5

EN300-associated microorganisms. a The number of microbial species at the six anatomical sites associated with EN300 based on a significance threshold of $P < 0.05$, and the overlap between sites. b Pearson correlations between EN300 and the 24 EN300-associated microbial species; significant R-values are filled numerically ($P < 0.05$). Red and blue tiles indicate positive and negative correlations, respectively. c Pearson correlations among microbial species in the uterus (UT).

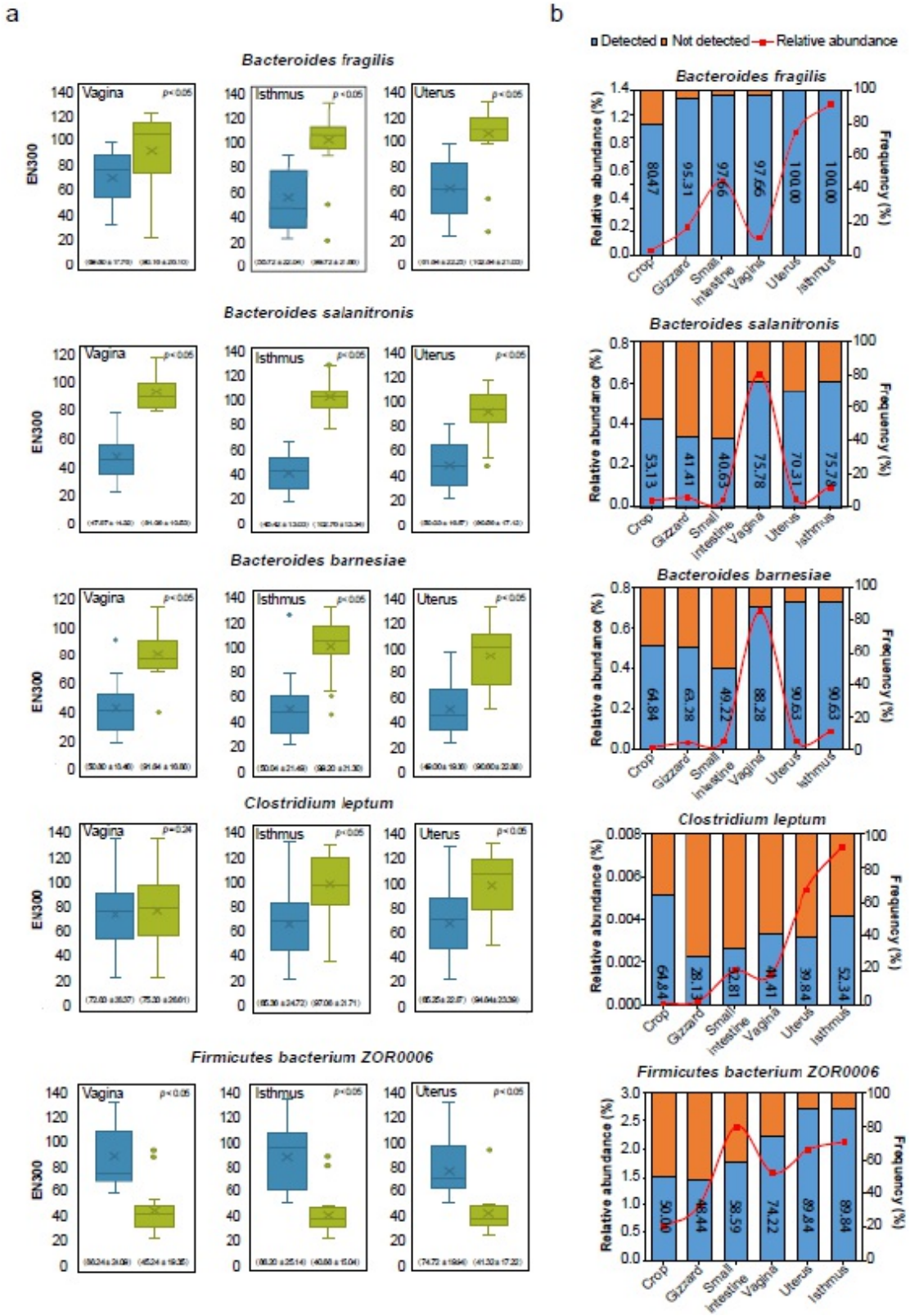

Figure 6

Effect of microbial species associated with egg number at 300 days of age (EN300) on egg production. a EN300 for the 20% of birds with the highest and lowest abundances of

Bacteroides fragilis, Bacteroides salanitronis, Bacteroides barnesiae, Clostridium leptum and Firmicutes bacterium ZOR0006 at the three reproductive sites. The box plots show the median and the 25% and 75% quantiles. The cross and horizontal line indicate the mean and median values in the corresponding group, respectively. Significance levels were calculated using a permutation test with 10,000 replicates. Significance was established at $P < 0.05$. b Relative abundance and detection rate of 5 species (Bacteroides fragilis, Bacteroides salanitronis, Bacteroides barnesiae, Clostridium leptum and Firmicutes bacterium ZOR0006) in the 6 segments. The values shown in the blue bars indicate the detection frequency of each species at each site.

Supplementary Files

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