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Gastric microbiome and ovine microhabitat variations in response to early and late stages of *haemonchus contortus* infection

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The interactions between gastric microbiota, ovine host, and *Haemonchus contortus* portray the ovine stomach environment as a complex ecosystem, where all factors play a pertinent role in fine-tuning each other and in the homeostatic maintenance. We delineated the impact of early and late *Haemonchus* infection on abomasal and ruminal microbial community, and ovine host. Twelve parasite-naive lambs were divided into four treatments, uninfected-control groups and 7- and 50- day post-infected groups, in triplicate. Six sheep were inoculated with 5,000 of *H. contortus* infective larvae and followed for 7 and 50 days with their corresponding uninfected-control ones. Ovine stomach tissues were collected for histological and anatomical analyses and gastric fluids collected to measure PH values, microbial community isolated and subjected to the Illumina MiSeq platform and bioinformatic analysis. Our results showed that *Haemonchus* infection increased the abomasal gastric pH ($P=0.04953$) and caused a substantial augmentation in anterior blind sac papillae numbers ($P=0.0463$), as well as resulted in necrotizing and inflammatory changes that were more severe during acute infection. Furthermore, infection increased the abomasal bacterial load and decreased the ruminal microbiome, but abrogated Archea in both gastric compartments. A 7-day infection of sheep with *H. contortus* significantly altered approximately 98% and 94% of genera in the abomasal and ruminal bacterial profile, respectively ($P=0.0369-0.0495$). However, the approximate altered genera 50 days after infection in the ovine abomasal and ruminal microbiome were about 62% and 69%, correspondingly ($P=0.0369-0.0495$) with increase in some bacteria and decrease in others. Overall, these results indicate that *Haemonchus* infection plays a crucial role for shaping stomach microbial community composition, and diversity.

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