Microbiota characterization of four autochthonous Italian chicken breeds

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The gastrointestinal tract (GIT) plays a vital role in animal productivity by performing key functions such as pathogen defence, nutrient breakdown and absorption, and the development of the host immune system. The microbiota is crucial for enhancing animal resilience, particularly in the face of climate change. Autochthonous animal genetic resources represent a valuable component of biodiversity and the characterization of their caecal microbiota could be an interesting tool for understanding host-microbe-environment interactions. The microbiota composition of four autochthonous Italian chicken breeds (Ancona, Ermellinata di Rovigo, Pepoi, Robusta Lionata) was characterized using a metagenomics approach to explore the potential influence of breed and environmental factors on microbial diversity. The chickens were reared in two distinct environments (both outdoor but with different climate influences), aiming to monitor the effects of genetic background and rearing conditions on the gut microbiota. Morpho-functional measurements were taken throughout the entire growth period (120 days) to integrate microbiota data with physiological development and performance traits. Using microbiome profiling techniques, the profile identified was similar among breeds, but we observed significant variations in microbial communities between the breeds in the same environmental settings. The most abundant genus was *Phocaeicola*, which exhibited great variability. But, other genera result more abundant in the Pepoi group than in other breed, *Escherichia/Shigella* and *Ligilactobacillus*. These findings highlight the interplay between breed and environmental factors in shaping the gut microbiome, offering valuable insights into sustainable poultry farming and breed-specific management practices.

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