



KEY WORDS

- ✓ Microbiota
- √ Fecal Feces
- ✓ DNA İsolation
- ✓ PCR
- √ 16S rDNA

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DETERMINATION OF THE MICROBIOTA PROFILE OF ANADOLU-T BROILER BREEDER CHICKENS USING THE 16S METAGENOMIC SEQUENCING METHOD

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THESIS ABSTRACT

In this thesis study, 2000 purebred broiler chickens of 5 different characteristics (A1, A2, A3, B1, B2) were used at the Eskişehir Transition Zone Agricultural Research Institute. A total of 100 cecal fecal samples were collected from each purebred line, with 20 samples randomly selected at 3, 8, 15, 25, and 32 weeks of age. DNA was isolated from these samples, and the diversity of the bacterial flora in the cecum was examined through 16S rDNA gene sequence analysis. The most abundant genus in all samples was Bacteroides, with an average value of 9.125%, while the least abundant genus was Ruminococcus, with an average value of 0.005%. A total of 306 different bacterial species were identified. The most frequently detected taxon was Akkermansia muciniphila, with an average proportion of $(1.4 \pm 8.31)\%$. In conclusion, the findings obtained after metagenomic analyses are consistent with the literature.

APPLICATION AREAS OF THE THESIS RESULTS

The microbiota diversity of our Anatolian-T broiler breeder pure lines was determined. Differences in microbiota between the lines were identified. By understanding the normal microbiome composition of broiler breeders, it will be possible to prevent future health problems and shed light on the selection of microbiota that have a positive impact on host performance.

ACADEMIC ACTIVITIES

- 1. Tetik K., Özkan İ., Kahya Demirbilek, S. (2025). Determination of the cecal microbiota profile of Anadolu-T broiler breeder chickens using 16S metagenomic sequencing. *Turkish Journal of Veterinary & Animal Sciences* 49 (6): 249-258..
- 2. Sarıca, M., Erensoy, K., Özkan, İ., Oğuzhan, E., & Çağlak, S. (2021). Anadolu-T Etlik Piliç Saf Hatlarının Gelişme ve Karkas Özellikleri. *Turkish Journal of Agriculture-Food Science and Technology*, *9*(11), 1980-1987