Nemabiome metabarcoding shows varying levels of genetic diversity in anthelmintic-resistant gastrointestinal nematodes

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Gastrointestinal nematodes (GINs) pose a significant threat to the livestock industry. Faecal egg count reduction tests (FECRTs) are commonly used to detect anthelmintic resistance of GINs. However, they do not provide information about the dynamics of resistant GIN species. In this study, we conducted a molecular analysis of GIN populations from pre- and post-treatment samples collected from 18 sheep farms in southeast England. We collected faecal samples from three groups (10 lambs each) at the time of treatment with recommended doses of ivermectin, levamisole, and a combination of both; and at 14 days post-treatment. Eggs from the samples were hatched for DNA extraction, followed by nemabiome metabarcoding and next-generation Illumina sequencing. The results showed that anthelmintic resistance was widespread, and different GIN species showed different levels of resistance to the tested drugs. The post-treatment results showed a dominance of *Teladorsagia circumcincta* and *Trichostrongylus colubriformis*, indicating the most anthelmintic resistance in these species. Our findings provide insights into the diversity of resistant GIN species and may aid in determining the most suitable drugs or combinations for individual farms. Moreover, the study provides a strong foundation for understanding the diversity present in resistant GIN species and the genomic basis for anthelmintic resistance.