Harnessing Nanopore Sequencing to Characterize the Composition of Commercial Probiotics

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ABSTRACT:

The use of probiotics as livestock health supplements has grown rapidly, yet most products are still evaluated with low-resolution methods and uncurated databases, leading to frequent misidentification and labeling errors. In this study, we applied and compared two Oxford Nanopore long-read workflows—full-length 16S rRNA gene sequencing and metagenomic sequencing—to assess the microbial composition of liquid and solid animal probiotic products. The 16S workflow enabled sensitive detection of bacterial taxa, even at low abundance, and provided species-level resolution for prokaryotes, though it was limited in characterizing yeast communities. By contrast, the metagenomic approach allowed recovery of high-quality genomes, offering deeper insights into bacterial and yeast populations, as well as antimicrobial resistance and functional genes. Together, these results highlight the potential of long-read sequencing workflows to ensure the quality and safety of commercial probiotics, supporting the sustainable development of the livestock probiotic industry.