

COMBINATION OF METABARCODING AND THE eDNA FROM FECAL SAMPLES IN THE SERVICE OF ANIMAL HUSBANDRY - APPLICATION AND DEVELOPMENT DIRECTIONS

Zoltán Bagi¹, Andrew Mbithi², Szilvia Kusza^{1*}

¹University of Debrecen Centre for Agricultural Genomics and Biotechnology, Faculty of Agricultural and Food Sciences and Environmental Management, 4032, Debrecen, Egyetem tér 1., Hungary

²University of Nairobi, Department of Animal Production, 00625-Nairobi, Kangemi 1, Kenya

*Corresponding author: kusza@agr.unideb.hu

Environmental DNA (eDNA) metabarcoding is an emerging and promising method for assessing biodiversity in which samples are taken from the environment, then DNA is extracted and amplified using general or universal primers in PCR for next-generation sequencing, which generates thousands or millions of reads. Based on this data, the presence of species can be determined, and the overall biodiversity can be assessed. The use of the eDNA faecal sample in farm animals is a commonly used method for examining the microbiome of intestinal tract. This sampling method, supplemented with metabarcoding, enables the identification and characterization of the bacterial, viral and parasitic communities in the animal gut, which can provide insight into the animal's health status and risks, as well as provide feedback on the effects of feeding, which has a direct impact on the animal's performance. The great advantage of the method is that – compared to previous methods – it enables a much more accurate diagnosis by identifying pathogens and parasites at the species level, and it can also significantly reduce the risk of sample contamination by applying appropriate protocols, especially compared to traditional methods, such as culture-based approaches. All this in a much shorter time and at a fraction of the cost compared to traditional methods. This is a unique method that is still under development and will change for some time as technology advances and protocols are standardized.



Environmental DNA (eDNA) metabarcoding presents an innovative and effective approach for assessing biodiversity and examining the microbiome of the intestinal tract of farm animals. This method, utilizing faecal samples, permits the identification and characterization of bacterial, viral, and parasitic communities within the animal gut. The resulting data provides valuable insights into the animal's health status, dietary impacts, and overall performance. eDNA metabarcoding represents a significant improvement over traditional methods, offering enhanced diagnostic accuracy at the species level, reduced risk of sample contamination, and considerable savings in terms of time and cost. Despite these promising advantages, it is critical to note that the methodology is still in its developmental stages and will continue to evolve with technological advancements and standardization of protocols. The anticipated future development and applications of this technique underscore its potential in revolutionizing our understanding and management of animal health and biodiversity.

