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Diverse microbes inhabiting livestock feed resources

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The safety of animal feed resources is of global importance in livestock sector. Knowledge of the function and diversity of microorganisms dwelling in animal feed habitats is essentially required beforehand for the safe management of feed resources. Microorganisms are not only beneficial organisms in natural feed resources, but are also key players in spoilage processes changing feed quality. Depending on moisture and nutrient contents, diverse microbes are differentially inhabiting in various feed resources such as barley, soybean curd residue, brewer's grain, rice bran, spent mushroom substrates, pig feed, broiler feed, milking cow feed and corn silage etc. However, to date, microorganisms inhabiting naturally in feed resources were little reported. In this study, about 100 strains of both bacteria and fungi were isolated from various feed resources and then identified by 16S rDNA sequencing. Beneficial microorganisms include Bacillus amyloliquefaciens, Lactobacillus plantarum, Lactococcus lactis and Leuconostoc citreum, etc. Harmful microorganisms include Burkholderia vietnamiensis, Enterococcus casseliflavus, Staphylococcus saprophyticus, Enterococcus durans and Pantoea agglomerans, etc. Many other isolated strains were unclear for a safety as well as function. We will mention the strains of harmful microorganism involved in feed spoilage and pathogen by literature review. Enzyme activities related on nutrient digestion, drug resistance and antimicrobial activity were also investigated on the isolated strains.

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How far can we go with automation in metagenomic sequencing?

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Applying next-generation sequencing (NGS) to metagenomic research has revolutionized this field of genomics. Thanks to NGS, many technical bottlenecks, such as cloning and microbial culturing of environmental samples, became obsolete, which contributed to significant acceleration in microbial diversity exploration. Metagenomic studies usually require simultaneous analysis of a large number of environmental samples; however, they have a very limited amount of available starting material. To address these challenges, we developed a methodological approach that allows for a fully automated workflow process, which can accommodate up to 384 samples in a single MiSeq run. This improvement was developed based on the Eppendorf liquid handling system. Utilization of this increased processing capacity in our NGS facility at Western Sydney University resulted in a number of additional advantages as compared to the existing pipeline including: a 40% reduction of the sample processing cost, a hands-off approach, which guarantees highly reproducible results, a shortened sample turnaround, with 384 samples processed within only nine days, e.g. up to 8,000 samples can be processed annually and a significant reduction in the original sample input amount.

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