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Commentory Note

Correlation of the Microbial Composition of Food Sources Utilizing Amplicon Sequencing

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COMMENTORY

Conventional matured food varieties assume a significant part in the eating regimen of various networks around the world. Africa is maybe the mainland with the most extravagant assortment of aged food varieties, where aging actually assumes a significant part in fighting food deterioration, foodborne infections and addresses a critical postharvest esteem expansion. Truth be told, aging is as yet a generally locally established interaction utilized all through the continent. A wide assortment of crude materials is customarily aged in various locales of Africa. Accordingly, matured food sources with various qualities are created and they have been characterized in gatherings like aged non-alcoholic oats (predominantly delivered from sorghum, millet and maize), boring root crops (principally created from cassava), creature proteins (basically dairy items), vegetable proteins (created from vegetables and oilseeds) and cocktails (delivered from grains, sap, nectar or organic products, among other materials). Matured items have been depicted to give medical advantages, like security against gastrointestinal problems, avoidance of hypertension and coronary illness or assurance from diabetes and osteoporosis. Moreover, conventional African aged food sources contain live microorganisms that can create wellbeing advancing mixtures, like antimicrobials, fundamental supplements or particles with cell reinforcement action, and can go about as probiotic strains

Information about the microbial environment of regular food maturations can be utilized to recognize biomarkers to survey the nature of aged food varieties and would help in the plan of ideal starter cultures4. Dominating bacterial gatherings present in African matured food varieties have been generally investigated utilizing society dependant methods, yet these strategies present a few limits, for example, not having the option to recognize non-cultural populaces or being not able to identify microorganisms in low numbers in complex environments with prevailing populations6. As another option, culture-free techniques, especially amplicon sequencing, are progressively being utilized to examine the bacterial populaces of matured food varieties, in spite of the fact that to date, not many examinations have zeroed in on African food varieties.

CONCLUSION

Culture-independent methods present several biases, some of which are associated with the DNA extraction procedures used. The extraction of DNA from foods can be challenging due to the structure and chemical composition of the matrices. Therefore, due to the vast variety of raw materials that are fermented, diverse DNA extraction procedures can be found in the literature10. In fact, some food matrices require pre-processing steps before DNA extraction. In order to analyse the microbial population of different fermented samples, the application of a standardized method would be beneficial. Commercial extraction kits partially solve the bias problems, but usually they have been tested for common food matrices and cannot be applied to complex foods. In addition, commercial kits use small amounts of sample. This can be an advantage as less material is required, but for some types of food it may not yield enough microbial DNA, as we have experienced in previous experiments in our laboratory. Here, the use of a single method for the analysis of a wide range of African fermented products was evaluated for its performance across diverse food matrices.

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