FERMENTATION AND NUTRITIONAL ASSESSMENT OF DIFFERENT GENOTYPES OF FERMENTED SWEETPOTATO (IPOMOEA BATATAS (L) FLOUR

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Sweet potato (Ipomoea batatas(L)) has become increasingly important in many parts of the world but underutilized in developing countries with food security problems. Though the crops is processed into unfermented flour, chips or boiled before consumption, its fermentation before flour production invariably enhances the nutritional quality. Sweetpotato genotypes (TIS87/0087 and TIS5232.OP.1.13) were fermented for 24h. Microbiological and chemical properties of the fermenting medium as well as the proximate composition of the fermented and unfermented flour were assessed. The total viable counts (TVCs) of both fermenting genotypes were highest (3.95 x 10^6 and 4.35 x10^6 cfu/ml respectively) at 12h and decreased till the end of fermentation. While the lactic acid bacteria (LAB) counts followed similar trend, the fungal counts (3.45 x 10^3 and 3.02 x 10^3 cfu/ml respectively) were detected from the 12th hour of fermentation. Bacteria isolated from the medium were Lactobacillus plantarum, Streptococcus sp, Bacillus sp and Staphylococcus aureus while the fungal species include Penicillium sp, Rhizopus stolonifer, Aspergillus niger and Saccharomyces cerevisiae. The titratable acidity (TA) for both genotypes increased from 0.51 to 4.96 for TIS87/0087 and 0.40 to 4.04% for TIS2532.OP.1.13 while pH decreased. The proximate composition of the fermented flour from both genotypes showed significant (p=<0.05) difference in protein (5.16 – 5.09%), carbohydrate (81.25 – 81.0%), fibre (0.76 – 0.64%) and fat (0.68 – 0.47). While the fermented samples had significantly increased protein, fat, fibre and ash contents than the unfermented, the unfermented had higher carbohydrate content. Fermentation of the genotypes improved the nutritional quality of the products.