

Development of an Informative set of Simple Sequence Repeat (SSR) markers for Sweetpotato Fingerprinting and Diversity Assessment in the West African sub-region

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Abstract

The assessment of levels of genetic diversity in sweetpotato is important for conservation and utilization of genetic resources. Molecular markers can play an important role in determining genetic diversity. A number of informative markers have been developed for sweetpotato. Different research groups have identified different markers, and there is little overlap among the sets of markers. This study was conducted to validate polymorphic SSR markers for sweetpotato diversity studies in the West Africa sub-region. A collection of twenty one sweetpotato genotypes was assembled from Ghana and Nigeria. They were assessed with twenty five expressed sequence tag (EST) and twenty one simple sequence repeat (SSR) markers. Popgene software was used to assess results. A set of informative markers was identified for the rationalization of sweetpotato germplasm conservation and utilization in Ghana and West Africa.

Key words: Molecular marker, germplasm utilization, breeding