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Advanced Technologies for Genetic Enhancement of Yam

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Abstract

Yam (*Dioscorea* spp.) is a multi-species clonally and sexually propagated edible tuber of the tropical and sub-tropical regions. The majority of yam production comes from West Africa which accounts for about 93 % of the world's production of 63 million tons from 5.3 million hectares. The crop makes major contributions to the livelihood of more than 60 million people in West Africa, providing about 300 dietary calories per person per day. Most of the yams are cultivated landraces using indigenous cropping methods, showing considerable lack of resistance to pests and diseases. Nematodes *(Scutellonema bradys*, *Melodoigyne* spp.), the yam mosaic virus (YMV), and anthracnose (*Colletotrichum gloeosporioides*) are most devastating, reducing yield by 30–90 %. Yam cultivation also faces the challenge of progressive declining soil fertility, increased exposure to irregular rainfall, extreme weather events and prolonged dry spells during the growing season, all contributing to tuber yield losses.

Dioscorea rotundata (white Guinea yam) and *D. alata* (water or greater yam) are the most important among the 10 cultivated *Dioscorea* spp. Genetic enhancement of these species is constrained by a number of challenges imposed by clonal nature of the crop, negligible knowledge on genetic diversity, long breeding cycle, low propagation ratio, and limited tools and technologies to aid breeding and selection. An integrated approach, combining advanced technologies to enhance yam breeding, is essential to improve efficiency and accuracy in improvement for disease resistance, food quality, and other desired traits. The International Institute of Tropical Agriculture (IITA) has been leading efforts for more than a decade to develop and apply advanced techniques for yam improvement. The introduction of vine propagation at the nursery and early clonal stages of the breeding programme enables early availability of planting materials for multi-site field evaluations and a shortening of the breeding cycle. Next-generation sequencing techniques such as genotyping-by-sequencing (GBS) and whole genome re-sequencing are being used to understand the genetic structure and relationships between different *Dioscorea* species. These will facilitate genomic studies such as linkage mapping, gene/QTL identification and association mapping for marker-assisted breeding.

Keywords: *Dioscorea alata, Dioscorea rotundata*, disease resistance, food quality, soil fertility, stable yields

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