

Advances in yam (*Dioscorea* spp.) genetics and genomics

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Abstract. Yams (*Dioscorea* spp.) constitute a staple food crop for over 100 million people in the humid and subhumid tropics. They constitute a multi-species, polyploid crop that is vegetatively propagated. *Dioscorea rotundata* and *D. cayenensis* (known as white and yellow Guinea yams, respectively) are the most important yams in West and Central Africa where they are indigenous, while *D. alata* (referred to as water yam) is the most widely distributed species globally. The genetics of yams is least understood among the major staple food crops due to several biological constraints and research neglect. Research to unravel the apparent complexity of the yam genome will have far-reaching implications for genetic improvement of this important tuber crop. Some progress has been made in recent years in germplasm characterization and the development of molecular markers for genome analysis. Genetic linkage maps based on amplified fragment length polymorphism (AFLP) markers have been constructed for *D. rotundata* and *D. alata*. These linkage maps were used to scan the genome for quantitative trait loci (QTL) associated with genes conferring resistance to *Yam Mosaic Virus* (YMV) in *D. rotundata* and anthracnose (*Colletotrichum gloeosporioides*) in *D. alata*. In addition, candidate random amplified polymorphic DNA (RAPD) markers associated with major genes controlling resistance to YMV and anthracnose have been identified that could be used for selection and pyramiding of YMV and anthracnose resistance genes in yam improvement. Also, molecular markers such as RAPDs, AFLPs, and microsatellites or simple sequence repeats (SSRs) have been developed for yam genome analysis. An initial c-DNA library has been constructed in order to develop expressed sequence tags (ESTs) for gene discovery and sources of additional molecular markers. This paper will review the advances made, discuss the implications for yam genetic improvement and germplasm conservation, and outline the direction for future research.