

Selection of a Diversity Research Set to facilitate efficient genetic and breeding studies of Guinea yam (*Dioscorea rotundata*)

Yam, the common name for crop species belonging to the genus *Dioscorea*, is widely cultivated as a staple crop in tropical and sub-tropical regions. West Africa, which accounts for 95% of the world's annual yam production (approximately 54 million tons) recognizes the important role of yam in regional food security and income generation. Guinea yam (*D. rotundata*, Fig. 1) is the most cultivated species in this region, representing majority of the total yam production. While *D. rotundata* is one of most important crops in West Africa due to its long growth cycle, large plant size, dioecy, inconsistent flowering habit, polyploidy, and a high level of heterozygosity, activities related to genetic research and breeding have been limited. To facilitate efficient utilization of plant genetic resources and promote genetic research and breeding of this crop, the *Dioscorea rotundata* Diversity Research Set (DrDRS) was developed. The DrDRS is a subset with a small number of accessions representing the genetic diversity of a core collection of *D. rotundata* accessions, the largest collection of this species worldwide.

In general, the so-called “non-redundant collection” such as Diversity Research Sets representing the genetic diversity of the original collection plays a vital role in facilitating efficient utilization of plant genetic resources. This is particularly relevant for vegetatively propagated large plant size tuber crops with a long growing period such as *D. rotundata*, to enable researchers to conduct detailed research more efficiently. In this study, a total 102 accessions were selected as DrDRS from the available 447 accessions, which serve as the base collection and are maintained at the International Institute of Tropical Agriculture (IITA), using the simple sequence repeat (SSR) markers we developed (JIRCAS Research Highlights 2015, B05). DrDRS retains the same level of genetic diversity as the base collection (Fig. 2 and Table 1). The average Shannon's diversity index with respect to 21 morphological traits of DrDRS and base collection (1.138 and 1.114, respectively) suggested that a similar level of morphological diversity was also captured within the DrDRS. The accessions of DrDRS showed a wide range of variation in basic agronomic traits such as growth period, number of tubers per plant, and average tuber weight. This variation was considerable when compared with the variation observed among the 10 lines/genotypes conventionally used in the breeding program at IITA (Fig. 3).

The DrDRS accessions could serve as a working collection to broaden the genetic variation for use in practical breeding programs as well as in future genomic analyses using the genome information of *D. rotundata* (JIRCAS Research Highlights 2017, B02) aimed at the genetic improvement of *D. rotundata* in West Africa. The DrDRS is expected to facilitate the development of excellent varieties that make effective use of the wide range of genetic diversity of this crop.

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Fig. 1. Cultivation of Guinea yam in West Africa (left) and harvested tubers (right)

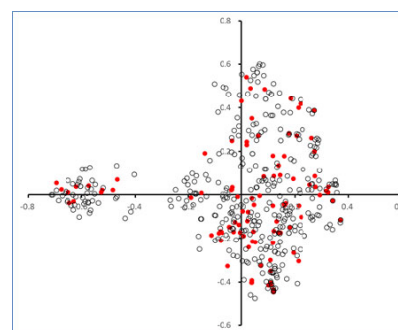


Fig. 2. Distribution of base collection (open) and DrDRS (red) on the principal coordinate analysis plot based on SSR variation

Table 1. Genetic diversity indices in base collection and DrDRS through analysis of 16 SSR markers

	<i>Na</i>	<i>Ho</i>	<i>He</i>	PIC
Base (n=447)	96	0.373	0.583	0.549
DrDRS (n=102)	94	0.383	0.563	0.529

Na: number of alleles, *Ho*: observed heterozygosity, *He*: expected heterozygosity, PIC: polymorphic information

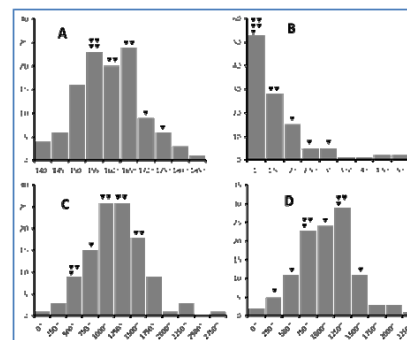


Fig. 3. Variation of basic agronomic traits in DrDRS

A: Growth period (days to harvest), B: Number of tubers per plant, C: Yield per plant (g), D: Average tuber weight (g) Arrowhead: distribution of ten IITA breeding materials.