GENETIC DIVERSITY AND MOLECULAR POLYMORPHISM OF SOME OKRA GERMPLASM

By

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ABSTRACT

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Twenty nine okra accessions (*Abelmoschus esculentus L.*) were morphologically characterized using the UPOV descriptor for quantitative and qualitative characters. Data were recorded on 20 individual plants per accessions in two consecutive summer seasons (2009-2010). Significant differences were obtained between some accessions for all quantitative characters studied while variations were detected and described for the qualitative characters. Morphological characterization did not fully discriminate between all the accessions.

Forty two ISSR primers, five AFLP combinations and three SSR primer pairs were used to determine the level of polymorphism, molecular fingerprinting, identification of unique markers, and the estimation of genetic distances among the 29 okra accessions. The ISSR primers amplified 508 fragments of which 415 were polymorphic, representing 82% level of polymorphism with an average of 12.1 fragments per primer. The number of positive and negative unique markers was 103 and was useful in identifying 24 genotypes out of the 29 accessions. The total number of amplicons generated by the 5 AFLP combinations was 422 with 376 polymorphic amplicons revealing 89% polymorphism and an average of 84.4 amplicon per primer combination. A total of 61 unique markers discriminated 26 accessions. In this study, 3 SSR primer pairs were selected based on the robust amplification of fragments with okra DNA. A total of 11 amplicons were obtained, 5 were polymorphic resulting in 45% polymorphism. Only one unique negative marker clearly identified one accession.

Genetic similarity matrices estimated from ISSR, AFLP and SSR data, showed similarity coefficients to range from 0.68 – 0.90, 0.57 – 0.91, and 0.70 – 0.10, respectively. In all three molecular markers systems (ISSR, AFLP, and SSR), the highest similarity coefficient was between accessions collected from the same governorate, while the lowest similarity coefficient was obtained between accessions from different governorates. Generally, the constructed dendrograms based on the two types of markers, ISSR and AFLP, exhibited a tendency to cluster accessions in groups according to their geographical locations. The level of genetic diversity estimated within each groups was: Sohag 30%, Qena 28%, North Sinai 23%, and El Behira 20%. In conclusion, additional okra germplasm needs to be collected from other locations and characterized to ensure the representation of most of the genetic diversity is conserved *ex situ*.

Key words: Okra *Abelmoscus esculantus*, ISSR, SSR, AFLP, genetic variation, genetic polymorphism, genetic distance, similarity coefficient.

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I- INTRODUCTION

The cultivated okra (*Abelmoschus esculentus L*.) which is commonly known as ‘Lady’s fingers’, ‘Gumbo’, ’Bamia ’, belongs to the *Malvaceae* family. The crop is a native of Africa and is still found growing wild around the River Nile as well as Ethiopia, in tropical and sub-tropical areas (Kochhar, 1986). It was taken to other parts of the world by the Portuguese (Sinnadurai, 1992). It can grow all the year round, but in Egypt its production is mainly concentrated during the summer season. India, Costa Rica, Nigeria and Ghana are among the major producers of okra (NARP, 1993).

The world okra production, as of 2007, was estimated at 4.8 million tons with India leading the production by 70% followed by Nigeria (15%), Pakistan (2%), Ghana (2%), Egypt (1.7%) and Iraq (1.7%) according to Gulsen *et al*., 2007.

Okra was previously included in the genus *Hibiscus*. Later, it was designated to *Abelmoschus* (Kundu and Biswas, 1973; Terrell and Winters 1974). Although about 50 species have been described, eight of them are most widely accepted (Borssum, 1966; IBPGR, 1990). There is significant variation in the chromosome numbers and ploidy levels in *Abelmoschus*. The lowest chromosome number known is $2n = 56$ for *A. angulosus* (Ford, 1938) and the highest are close to 200 for *A. caillei* (Siemonsma, 1982). Even within *A. esculentus*, chromosome numbers vary from $2n = 72$, 108, 120, 132 and 144 which are in regular series of polyploids with $n = 12$ (Dutta and Naug, 1968).

Contradicting evidence exists on the geographical origin of *A. esculentus*. One putative ancestor (*A. tuberculatus*) is native to Uttar Pradesh in North India, suggesting that *A. esculentus* originated in India. The other evidence is based on the plants cultivation in ancient times, and the presence of another putative ancestor (*A. ficulneus*) in East Africa, suggesting northern Egypt and Ethiopia as the geographical origin of *A.esculentus*. So far *A. caillei* ($2n = 196$ to 200) has been located only in