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Full Length Article

Biochemical and molecular genetic characterization of some species of family Malvaceae, Egypt

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ABSTRACT

The aim of the present study intended mainly to investigate the interrelationships between the six studied taxa namely *Abutilon theophrasti*, *Lavatera cretica*, *Hibiscus trionum*, *Hibiscus sabdariffa*, *Malva parviflora* and *Sida alba* collected from ten different accessions in Egypt belonging to family Malvaceae. Biochemical studies include protein profile using SDS-PAGE technique and three isozymes (esterase, peroxidase and acid phosphatase). The electrophoretic analysis revealed the presence of eighteen bands of molecular weight ranging from 11.3 to 115.3 KD. The highest number of bands 15 was observed in *H. sabdariffa* (Hs1) collected from Menia el-Kamh district and the two accessions of *M. parviflora* where as the lowest number 11 bands were recorded in *H. trionum* collected from Talkha district. Four loci of peroxidase isozyme distinguished, three loci of acid phosphatase isozyme and two loci of esterase isozyme. In regarding to random amplified polymorphic DNA technique (RAPD), ten primers were used to differentiate between these accessions. Primer OPA-4 gave the highest percentage of polymorphism (100%), while primer OP-B6 produced the lowest percentage (50%).

1. Introduction

Malvaceae or the mallow family is the family of flowering plants containing over 200 genera with close to 2300 species. The largest genera *Hibiscus* (300 species), *Streculia* (250 species), *Dombeya* (225 species), *Pavonia* (200 species) and *Sida* (200 species). The principle economic use of Malvaceae plants is as a source of natural fibers, the family providing perhaps the

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Table 1 – Names and localities of ten accessions of the six studied taxa collected from Egypt.

No.	Taxa	Codes	Locality
1	*Abutilon Theophrasti* Medik.	At	El-Behera governorate (Abo homos district)
2	*Hibiscus sabdariffa* L.	Hs1	El-sharkyia governorate (Menia el-kamh district)
3	*Hibiscus sabdariffa* L.	Hs2	El-Dakahlyia governorate (Talkha district)
4	*Hibiscus trionum* L.	Ht1	Kafr el-sheikh governorate (El-Riyad district)
5	*Hibiscus trionum* L.	Ht2	El-Dakahlyia governorate (Talkha district)
6	*Lavatera cretica* L.	Lc	El-Behera governorate (Rashid district)
7	*Malva parviflora* L.	Mp1	El-sharkyia governorate (Menia el-kamh district)
8	*Malva parviflora* L.	Mp2	El-Dakahlyia governorate (Nabrooh district)
9	*Sida alba* L.	Sa1	El-sharkyia governorate (Menia el-kamh district)
10	*Sida alba* L.	Sa2	El-Dakahlyia governorate (Nabrooh district)

worlds three most important fiber crops plants of the family are also used for food, beverages, timber, in traditional medicine and in horticulture [1].

Many researches have been published on the ecology, taxonomy, genetic, cytology, chemotaxonomy, physiology, seed germination and economic uses of family Malvaceae such as [2] in ecology; in taxonomy [3], in chemotaxonomy [4] and in genetic researches [5] studied the pollen.

Aerial parts of many species belong to family Malvaceae have Betaines, Glycine betaines were obtained in high yield (0.5–4.6% dry weight). Also, trigonelline was recorded, but the yield was low (0.005–0.07% dry weight) [4].

Isozymes have been widely used as a molecular markers for the identification the genetic relationships among genera, species and varieties. The phylogenetic relationships in many genera have been studied by isozymes electrophoresis [6] and [7].

Seed protein electrophoresis has been successfully used in define species relationships in various groups of plants [8].

The technology of the molecular biology has been developed over the 20 years and provided new methods for observing the genetic differences among species. These techniques offer and give many advantages over the conventional methods [9].

Therefore, the present study was designed to clarify the genetic relationships among six taxa belong to family Malvaceae collected from ten different accessions from Egypt. This work is very important to document in gene banks for sustainable conservation of plant genetic resources.

2. Materials and methods

2.1. Accessions selection

Ten accessions of the six studied taxa Table 1 subjected to analysis using available characterization methods. Viable seeds of the studied taxa were collected from 50 mature individuals. Identification and nomenclature of studied species were according to [10] and [11].

2.2. Protein analysis

Electrophoresis analysis of seed proteins followed the method for discontinuous SDS-PAGE technique of [12].

2.3. Native PAGE for isozymes

Isozymes variations identified using native polyacrylamide gel electrophoresis. Three isozymes (esterase, peroxidase and acid phosphatase) studied. These isozymes were separated on polyacrylamide gel according to [13].

2.4. DNA extraction

Genomic DNA of the ten accessions of six taxa was extracted from fresh young leaves according to [14].

2.5. Random amplified polymorphic DNA (RAPD-DNA)

Ten primers were used to generate RAPD markers according to [15] with some modifications. The sequence of these primers is given in Table 2. The percentage of polymorphism can be calculated according to this equation.

$$\%\ \text{of polymorphism} = \frac{\text{polymorphic bands}}{\text{total bands}} \times 100$$

2.6. Data analysis

All gels were photographed and analyzed using Bio-Rad video Documentation system Model Gel Doc 2000. The presence or absence of each band was treated as a binary character in a data matrix (coded 1 and 0 respectively). Data analyses were performed using SYSTAT version 7.0 program [16].

Table 2 – Primers and their composition used in RAPD analysis.

Primer names	Sequences
OP-AO1	CAGGCCCTTC
OP-AO4	AATCGGGCTG
OP-AO7	GAAACGGGTG
OP-A10	GTGATCGCAG
OP-A15	TTCCGAACCC
OP-BO1	GTTTCGCTCC
OP-BO4	GGACTGGAGT
OP-BO6	TGCTCTGCCC
OP-BO7	GGTGACGCAG
OP-B17	AGGGAACGAG