## ABSTRACT

Two filed trials were done in the summer seasons of the two years 1998 and 1999 to identify 6 Egyptian cowpea genotypes, which were Dokki 331,Cream 7, Fetriat, El-Menia, Aswan and Metrawy. The identification determinations included the vegetative (plant length, leaf area and leaf shape), flowering (earliness, number of flowers on peduncle and colour of flower), yield either the green pods (number and weight per plant) or the dry seed (number, weight per plant and shellout %), green pod specification (length, diameter, weight, volume and colour), dry seed (index, volume, density, germination%, germination rate and abnormal germination%, amino acids, total protein and total sugars). The 6 genotypes, however, differ in the majority of these morphological, physiological and chemical characteristics.

From another point of view, genetic identification by fingerprinting was performed on seed storage protein (SDS-PAGE) and leaf DNA (RAPD-PCR). On the first material, seed storage protein electrophoretic of SDS-PAGE indicated clear differences in protein bands among the tested genotypes. These bands were distributed through the high, medium and low molecular weight. The dissimilarity matrix of protein patterns revealed that the most closely related pair of cowpea genotypes were Dokki 331 - Cream 7 (0.54) where it was the lowest value. Meanwhile, the highest dissimilarity value (0.81) was observed between Cream 7 and Aswan. The other genotypes showed different levels of dissimilarity ranged between 0.60 (Fetriat and Cream 7) to 0.78 (El-Menia and Metrawy). The dendrogram of protein pattern for the tested cowpea genotypes showed two main clusters **A**

and **B**. Cluster **A** was subdivided into 2 sub-clusters **a** and **b**. The sub-cluster **a** included Dokki 331 and Cream 7 genotypes while the sub-cluster **b** included Fetriat and Metrawy genotypes. Meanwhile, Cluster **B** comprises 2 genotypes El- Menia and Aswan.

On the second material, leaf DNA, genomic DNAs extracted from cowpea genotypes were used as templates for RAPD-PCR amplifications. In this study, 13 random 10-mer primers were used. Only 2 primers resulted no PCR products in all the tested genotypes. The other 11 primers had amplified 510 scorable bands (392 present bands + 118 absent bands). The polymorphic fragments from the tested genotypes with the 11 primers ranged between 6 (OpB-11) to one (OpZ-12). The size of the amplified fragments ranged in different weights from 100 to 2072 base pair (bp). No polymorphism percentage (O%) was detected in primer OpZ-12. The dendrogram of the tested cowpea genotypes revealed two main clusters, **A** and **B**. The first cluster **A** was divided into two sub-clusters **a** and **b**. In sub-cluster **a**, there is only one genotype Dokki 331. The sub-cluster **b** was subdivided into two sub-sub-clusters **1** and **2**. The sub-sub-cluster **1** contained each of El-Menia and Metrawy genotypes while the sub-sub cluster **2** included each of Fetriat and Cream 7 genotypes. However, the main cluster **B** included only Aswan type. The dissimilarity from DNA matrix which attained 0.41 cleared that Aswan genotype was so-far from Cream 7 genotype and the opposite was true between Fetriat and Cream 7 genotypes, where the dissimilarity reached 0.22.

Both of protein and DNA fingerprinting techniques that have been applied in this study proved

to be very useful. The SDS-PAGE technique showed certain degrees of polymorphism among the tested cowpea genotypes except in two genotypes Cream 7 and Fetriat which, were so closed due to the segregation done in Fetriat genotype which led to the production of Cream 7. So, the application of SDS-PAGE technique facilitates the accurate separation in a short time between the seeds of different tested genotypes.On the other hand, the use of the rapid technique (RAPD-PCR) proved to be very efficient and sufficient to analyze and characterize all the tested genotypes. Thus, this technique (RAPD) can be recommended for the determination of genetic diversity among other genotypes or species. In the field of the use of primers in this investigation, it can be recommended that the high scorable bands in the identification of cowpea genotypes were OpB-20, OpG-06, OpB-11 and OpB-12. The first two of them are the most efficient in this identification.

# List of Abbreviations

DNA= Deoxyribonucleic Acid.
dsDNA= Double strand DNA.
ssDNA= Single strand DNA.
cDNA= Complementary DNA.
rDNA= Ribosomal DNA.
cpDNA= Chloroplast DNA.
A,C,T,G= Nucleotied.
DNAs= DNase= nuclases= Enzyme breaking the phosphodiester band.
dNTPs= dNTPbase= DNA polymerase= four deoxyribonuclotied triphosphates (dATP, dGTP, dCTP, dTTP)
ddNTPs= 2`, 3`. Dideoxynucleotied triphosphates. (ddATP, ddGTP, ddCTP, ddTTP.)
PCR= Polymerase Chain Reaction.
RAPD= Random Amplified Polymorphic DNA.
bp= Base pair
Kb= Kilo base pair.
KDa= Kilo dalton.
CTAB= hexa De Cyl Trimethyl Ammonium Bromid.
SDS-PAGE= Sodium dodecyl sulfate- Polyacrylamide Gel Electrophoresis.
TEMED= N, N, N, N Tetramethylethylendiamine.
EDTA= Ethylene Diamine Tetra-Acetic Acid.
TE= Tris EDTA buffer.
TAE=Tris Acetic Acid EDTA buffer.
TBE=Tris Borate EDTA buffer.
Ta= Annealing Temperature.
%T= Total monomer concentration.
%C= Crosslinking monomer concentration.
PVP= Polyvinylpyrrolidine
RFLP= Restriction fragment length polymorphism.
UPGMA= Unweighted Pair Grope Method with Arithmetical Averages.

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