

Assessment of genetic diversity in some *Chenopodiaceae* plants

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ABSTRACT

Chenopodiaceae, one of the largest plant families, which varies morphologically, is diverse in number and ecogeographically distributed mainly in Mediterranean and Egyptian Sahara, extending far into adjacent regions. In Egypt, previous studies on *Chenopodiaceae* had focused mainly on anatomy, taxonomy, physiology, morphology, genome description and medicinal values, which are insufficient for genetic affinities and very little for genetic diversity studies. Biochemical variability was studied by protein and isozymes electrophoretic patterns among *Chenopodiaceae* eight genotypes from different habitats. The molecular markers RAPD and ISSR were used to estimate the polymorphism among these genotypes. Somatic chromosome numbers were examined for karyotype analysis among the *Chenopodiaceae* eight studied genotypes. Sixteen protein bands generated 15 polymorphic bands with 94% polymorphism. Eight isozyme systems including ACPH, ADH, α -EST, β -EST, AO, MDH, SOD and POD revealed 34 total bands (94% polymorphism). RAPD revealed a total of 125 (93% of polymorphism) and nine ISSR primers revealed the highest total of 201 bands with the highest polymorphism (95%). Based on similarity matrix of overall analysis (protein, isozymes, RAPD and ISSR) the dendrogram was constructed and separated the eight *Chenopodiaceae* genotypes into two main clusters. The first included the genotypes *Chenopodium album*, *Spinacia oleraceae* and *Anabasis setifera*, while the second included *Salicornia fruticosa* genotypes. ISSR was better than RAPD to detect genetic diversity among *Chenopodiaceae* genera and species. The RAPD's and ISSR's have confirmed each other. Somatic chromosome number was $2n=18$, $n=9$ for all species except *Spinacia oleraceae* was $2n=12$, $n=6$. The outcome of this investigation can help strengthen the exiting pool of information on *Chenopodiaceae* species that may help assess national conservation programs in Egypt and may help in assessing breeding programs to get benefit from valuable stress tolerance genes for the improvement of crops.

Key words: *Chenopodiaceae*, Isozymes, SDS-PAGE, RAPD, ISSR and Karyotype.

INTRODUCTION

The family *Chenopodiaceae* comprises about 103 genera and 1300 species (Boulos, 1999). It comprises many species with pharmaceutical and economical values such as: *Chenopodium murale*, *Anabasis setifera*, *Salicornia fruticosa* and *Spinacia oleraceae*.

Chenopodium murale is a wild leafy vegetable that belongs to the goosefoot family with various pharmacological activities such as, laxative, diuretic, tonic, antioceptive, anti-oxidant, anti-proliferative, anti-inflammatory, antihistaminic and hepatoprotective. Various secondary metabolites, e.g., flavonoids, carotinoids, phenolic compounds have been reported from this plant (Neerja *et al.*, 2007). *Anabasis setifera* has analgesics, laxative and