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Genetic diversity analysis reveals weak population structure in invasive *Triantheme portulacastrum* L. at Fayoum depression, Egypt

Abstract

Trianthema portulacastrum L. (Aizoaceae) is a common weed associated with cultivated crops. It is an exotic weed that originated in South Africa and is spreading all over the world. Thirty-five accessions were collected from six populations at Fayoum depression (FD), Egypt. Molecular analyses of start codon targeted (SCoT) markers were performed to identify genotypic variation among collected populations. The effectiveness of employing SCoT markers was demonstrated by the high percentage of polymorphisms. These markers revealed high genetic diversity, as well as high levels of genetic differentiation (GST), elevated gene flow (Nm) (0.195 and 2.052, respectively), high variation among a population and lower variation within populations. Linkage disequilibrium analysis supported the presence of sexual and clonal reproduction of *T. portulacastrum* in different populations. The data confirmed the weak population structure of *T. portulacastrum* demonstrated in this study via different tools such as STRUCTURE, Minimum spanning network (MSN), and discriminant analysis of principal components (DAPC) and confirmed gene flow between populations. Based on our results, we hypothesize that FD was invaded multiple times by *T. portulacastrum* facilitated by both local adaptation and phenotypic plasticity.