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Clonal structure and reduced diversity of the invasive alien plant *Erigeron annuus* in Lithuania

Research Article

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Abstract: The alien species *Erigeron annuus* (L.) Pers. is in an intensive spreading phase in Lithuania. Random amplified polymorphic DNA (RAPDs) and inter-simple sequence repeats (ISSRs) assays were used to study the genetic structure of old and new invasive populations and to determine the most spread genotypes of this species in Lithuania. Pairwise genetic distances between populations established using RAPD and ISSR markers significantly correlated ($r=0.91$, $P<0.05$). Our study indicates that there are two genetically different types of *E. annuus* populations. The first type is represented by a widely spread main clone and related monomorphic populations. The second type is represented by polymorphic populations, some of them present at sites where *E. annuus* has not been previously observed. Main clone predominates in nine populations and is from the region where this species was first described in natural ecosystems of Lithuania. UPGMA cluster analysis revealed genetic relationships between the main clone and accessions from old cemeteries where *E. annuus* has been grown as an ornamental plant. We found high genetic differentiation among populations ($G_{ST}=0.58$ for RAPDs, $G_{ST}=0.64$ for ISSRs). Taken together, our results will contribute to the monitoring of *E. annuus* spread in Lithuania.

Keywords: *Bological invasions • Clonal distribution • Genetic diversity • Population structure • Molecular markers*

1. Introduction

Biological invasions are a major ecological and socio-economic problem in many parts of the world. Despite the current threat posed by this issue, the mechanisms contributing to the invasive success of certain exotic plant species are still only partly understood [1,2]. According to Baker [3,4], the long-distance dispersion of alien plant species can be achieved by one general-purpose genotype, and colonization of areas, characterized by a wide range of environmental conditions, occurs through phenotypic plasticity. A general-purpose genotype allows the success of populations, founded by small number of individuals, through reproductive systems that restrict outcrossing. Clonal reproduction is widely spread among invasive plant species. Mechanisms of clonal reproduction include vegetative spread, production of bulbils and apomictic seeds [5,6]. Reduced genetic variability is typically found in such populations of invasive species, due to marked founder effects and reproductive systems limiting the diversity of genotype [7]. The lower genetic diversity of some invasive plant populations has been shown with molecular markers such as ITS [8], RAPD [9-11] and ISSR [11-14]. In contrast, rather high genetic diversity has been shown in populations of the apomictic invaders *Taraxacum*, as revealed with AFLP markers [15], and *Erigeron annuus,* as revealed using RAPD and AFLP [16,17] markers. Five different clones were revealed in Chinese populations of *Eichhornia crassipes* with RAPD, and each population consisted of at least three clones [18]. Microsatellite markers revealed polymorphism among samples of *Salix alba-Salix fragilis* complex collected along selected river floodplains in Northern Patagonia (Argentina) [19]. Among the thirteen different genotypes detected, one dominant genotype formed monoclonal stands along river stretches approximately 790 km in length that were characterized by different ecological conditions. Such an observation can only be explained by the high phenotypic plasticity of that clone. Thus, the information on diversity and spatial spreading of genotypes of an alien clonal plant is crucial for the understanding of its invasive history and clonal structure.

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