NEW GEOGRAPHICAL INSIGHTS INTO LYTHRUM SALICARIA POPULATIONS



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INTRODUCTION

Lythrum salicaria is an annual herbaceous species belonging to *Lythraceae* family. It is an invasive wetland species in North America, naturally occurring in Europe, North Africa, and Asia. Molecular biology of this species has been studied within its invasive range, although an understanding of population genetics within native range remains limited to central and western parts of Europe. Information about *Lythrum salicaria* populations in Baltic countries is missing.

OBJECTIVES

The **aim** of our study was applying eight amplified fragment length

polymorphism (AFLP) markers to evaluate the genetic diversity of Lithuanian populations of *L. salicaria* in relation to river basins.

MATERIALS AND METHODS

Fifteen populations of *Lythrum salicaria* were chosen along several river basins of Lithuania. AFLP analysis was performed on a capillary electrophoresis. Statistical analysis were done by using PopGene v. 1.31 and GenAlEx v. 6.41 softwares.

RESULTS

Genetic diversity parameters of populations of *L. salicaria* were as followed: percentage of polymorphic loci per population was between 35.0 and 65.4, range of Nei's genetic diversity index per population were 0.172–0.329, and Shanon index per population 0.113–0.225. Mantel test results for populations of *L. salicaria* are shown in the Fig. 2.



Fig 1. Purple loosestrife (Lythrum salicaria) growing along the river

Table 1. AFLP loci based genetic diversity parameters of 15 Lithuanian populations of Lythrum salicaria

Source	df	SS	MS	Est. Var.	%	Φ	р
Among populations of Nemunas,							
Seaside and Lielupė river basins	2	1639	819	13.19	5	$\Phi_{\rm PT} = 0.054$	0.001
Among populations within river basins	12	5336	445	42.48	17	$\Phi_{\rm PR} = 0.183$	0.001
Within populations	75	14239	190	189.85	77	$\Phi_{\rm RT} = 0.227$	0.001
Total	89	21214		245.5	100		

Note. df = degrees of freedom, SS = sum of squares, MS = mean squares, Est. var. = estimated variability, % = percentage of variation, p = probability of differences, p < 0.01; Φ = pairwise population genetic distances: Φ_{PT} , Φ_{PR} , Φ_{RT} = proportion of variance among the river basins/land cover types/river fragments, among populations and within populations, respectively (p < 0.001)



CONCLUSIONS

1. Genetic diversity parameters (mean per population) were as followed: percentage of polymorphic loci (% P) was 57.2, expected heterozygosity (H_e) was 0.183, and Shannon's information index (/) was 0.280, and polymorphic information content 0.218.

- 2. Mantel test showed significant correlation between genetic and geographic distances of populations.
- 3. Significant genetic differentiation was found between populations

Fig 2. AFLP loci-based Mantel test of correlation between Nei's genetic and geographic distances for 15 Lithuanian populations of *L. salicaria*

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belonging to distinct river basins of Lithuania.

Such information might be useful for selection of new cultivars, recultivation practice and preparing effective strategies of eradication of the species within invasive range.