Biochemical Systematics and Ecology 55 (2014) 164–169

Contents lists available at ScienceDirect

Biochemical Systematics and Ecology

journal homepage: www.elsevier.com/locate/biochemsyseco

Genetic variation of *Sherardia arvensis* L. – How land use and fragmentation affect an arable weed

Daniela Listl[*], Christoph Reisch

University of Regensburg, Institute of Botany, 93040 Regensburg, Germany

ARTICLE INFO

Article history:
Received 18 October 2013
Accepted 15 March 2014
Available online

Keywords:
AFLP
Agricultural fields
Germany
Southern France
Population genetics
Sherardia arvensis

ABSTRACT

The distribution of arable weeds extends over regions, where the species occur naturally in different kinds of habitats and regions, where they are mainly limited to arable fields.
Here, we present a comparative study on the genetic structure of the arable weed *Sherardia arvensis* L. comprising populations from Mediterranean grasslands in Southern France and populations from arable fields in Germany. Enhanced by intensified land use since the 1960th, overall population density in Germany is very low compared to the density of populations in Southern France. We tested whether genetic variation within and among populations differ between France and Germany due to different patterns of distribution and land use. Therefore, we analysed 231 individuals of *S. arvensis* from 24 populations using AFLPs. Based on fragment analysis data we compared spatial genetic structure and genetic variation of populations from the two regions.
Genetic variation within populations from the two regions (Shannon Index = 0.13 for both) and genetic variation among populations (26.8% and 30.0% in an analysis of molecular variance) were comparable. In both regions a drift-migration model supported the assumption of gene flow between populations. However, a clear correlation of geographical and genetic distances could only be reported for the indigenous populations from France ($r = 0.46$; $P = 0.02$), whereas in Germany a spatial genetic relationship between populations was missing ($r = 0.16$; $P = 0.21$).
Our study revealed that neither French nor German populations are genetically impoverished. For French populations further the spatial genetic structure suggests that there is current gene flow between populations through pollinators and seed dispersal by cattle. For German populations comparable levels of genetic diversity and gene flow were detected, but gene flow was random. This can be traced back in all likelihood to diffuse dispersal by agriculture and the mechanical reshuffling of the individuals from the soil seed bank.

© 2014 Elsevier Ltd. All rights reserved.

1. Introduction

About 6000 years ago agriculture spread all over Europe with migrating settlers starting from the Middle East. Many plants growing commonly in a Mediterranean climate were taken along with the crops and migrated to agricultural fields in Central Europe (Bonn and Poschlod, 1998).

---

[*] Corresponding author. Tel.: +49 941 943 3137.
E-mail address: daniela.listl@ur.de (D. Listl).

http://dx.doi.org/10.1016/j.bse.2014.03.013
0305-1978/© 2014 Elsevier Ltd. All rights reserved.

These regions differ concerning population history and population frequency in the landscape. In regions, where the species occur naturally, they are common and numerous populations can be found also in habitats other than arable fields, like grassland and ruderal habitats. However, in regions where they have immigrated to in antiquity, some weeds (e.g. *Agrostemma githago*, *Centaurea cyanus*, *Scandix pecten-veneris* or *Sherardia arvensis*) depend on regular artificial disturbances of the vegetation and so, are restricted to arable fields (Schneider et al., 1994). In those areas populations are rare and distant from each other. This effect has strongly been intensified by modern agricultural practices. Before industrialisation these weeds were dispersed with agricultural machinery and alongside seeds of crops. Since the 1960th the cleaning of crops is very efficient and the dispersal of "seed-debasers" is very rare this way. Moreover, intensive agricultural practices repress the plants accompanying crops to the field margins, restricting their habitat even more (Marshall, 2008).

In continuously populated habitats gene flow between populations maintains a certain level of genetic diversity, which is important for adaptive processes (Heywood, 1991). In contrast, due to isolation by distance effects, gene flow between populations in fragmented habitats can be restricted (Young et al., 1996). The effects of disrupted gene flow also depends on the species life history traits (Hamrick and Godt, 1996; Nybom and Bartish, 2000; Jacquemyn et al., 2003) and especially for common species drastic consequences have been demonstrated, as they have not the preconditions in their life-history traits to compensate the decreased gene flow (Bijlsma and Loeschcke, 2005). Since population frequency and distance strongly affect gene flow, differences in the genetic structure of arable weed populations can be assumed between regions where they are widespread and regions where they are limited to arable fields.

We selected the blue field madder (*S. arvensis* L., Rubiaceae) and analysed the genetic variation of populations with amplified fragment length polymorphisms (AFLPs). *S. arvensis* is an arable weed, which can be found both in German arable fields and in different habitats in the Mediterranean area. We compared populations in two areas of comparable dimension. The first area is located in Southern France (Mediterranean), where *S. arvensis* is a common plant in anthropogenic digged soil like arable fields, but also – due to the Mediterranean hot climate – in grasslands with partly open soils and ruderal habitats, where natural gaps to germinate and establish are given. The second area is situated in South-eastern Germany, where *S. arvensis* is relatively rare and almost solely associated with extensive arable fields (Schneider et al., 1994).

The aim of the study presented here, was to analyse how fragmentation and land use patterns affect the population genetic structure of *S. arvensis*. We assume a higher level of gene flow, for the French populations compared to German populations, due to land use and the actual distribution pattern of the species, which should result in higher levels of genetic variation within and a lower level of genetic variation between populations from France.

2. Materials and methods

2.1. Species description and sampling design

S. arvensis is an annual, herbaceous plant which is in temperate regions mainly restricted to arable fields, while it can be found in almost all grassland communities in its provenance in the Mediterranean (Schneider et al., 1994). To study differences in the genetic structure of the populations in two contrasting landscape areas, we selected 12 occurrences from Southern France (Luberon) and 12 populations from South-eastern Germany (Franken-Alb). The populations have a comparable arrangement within the areas (Fig. 1). Coordinates of each site were acquired with GPS (MDPNA 240, Medion, Germany) (Table 1).

2.2. Molecular analysis

For each population leaf material of 10 individuals was collected, placed into filter bags and dehydrated in silica gel. DNA was isolated from 3 mg of dry plant material of individual plants using the CTAB (cetyltriammonium bromide) method

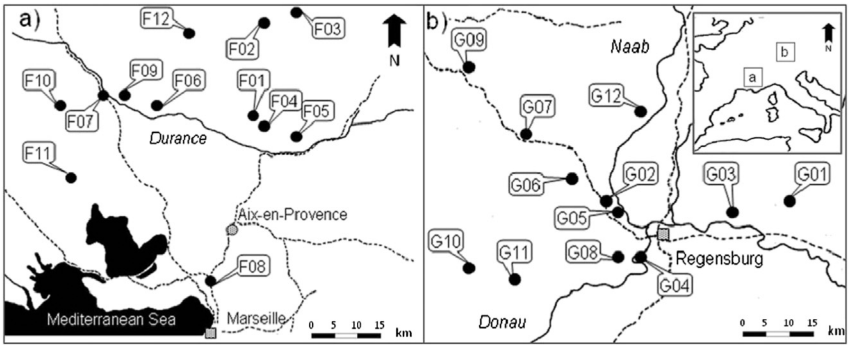

Fig. 1. Detailed maps of the collection sites for *S. arvensis* populations in Southern France (a) and South-eastern Germany (b) are shown; in the right corner the position of the study sites in Europe can be seen.

Download English Version:

https://daneshyari.com/en/article/7768740

Download Persian Version:

https://daneshyari.com/article/7768740

Daneshyari.com