Contents lists available at ScienceDirect

Biochemical Systematics and Ecology

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

Comparison of genetic variation between the seed bank and above ground vegetation of a wetland species



systematics

Fan Liu ^{a, b}, Tao Wan ^{d, 1}, Qing-xiang Han ^{a, b}, Bo Hu ^{a, b}, Yuan-yuan Chen ^{a, b}, Guang-xi Wang ^c, Wei Li ^{a, b, *}

^a Key Laboratory of Aquatic Botany and Watershed Ecology, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, Hubei, PR China

^b Hubei Key Laboratory of Wetland Evolution & Ecological Restoration, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, Hubei, PR China

^c Laboratory of Plant Conservation Science, Faculty of Agriculture, Meijo University, Aichi 468-8502, Japan

^d Key Laboratory of Southern Subtropical Plant Diversity, Fairylake Botanical Garden, Shenzhen 518004, China

ARTICLE INFO

Article history: Received 25 March 2013 Accepted 24 May 2014 Available online 19 June 2014

Keywords: Heleocharis valleculosa Seed bank Above ground vegetation Genetic variation Wetland

ABSTRACT

The seed bank is thought to be important for the conservation and restoration of the genetic diversity of the above ground plant population. It has been proposed that it may be no use to compare the genetic diversity between seed bank and above ground plants if there was no habitat fragmentation. Whether this prediction holds for aquatic plants is still unknown. Here, ISSR analysis of a common wetland species *Heleocharis valleculosa* (Cyperaceae) was conducted to evaluate if the seed bank has higher, equal or lower genetic variation than the above ground vegetation. Our results showed high genetic diversity in the seed bank, so the seedbank can act as a storehouse of genetic variation for the above ground vegetations. Thus, unlike terrestrial habitats where genetic diversity is often low, wetlands that are connected with water flow can accumulate many genotypes in the seed bank and the question of how genetic diversity varies above and below ground is still open.

© 2014 Elsevier Ltd. All rights reserved.

1. Introduction

When plants face stressful environments, many can survive temporally by producing seeds that are stored in the soil where they can await favorable conditions for germination (Cabin, 1996; Thompson et al., 1997). The persistent soil seed bank with different genotypes from multiple generations may establish a very diverse gene bank, potentially exceeding the genetic diversity of the above ground population (Templeton and Levin, 1979; Brown and Venable, 1986; Mandák et al., 2006). Thus, the seed bank is thought to be a way of conserving and restoring the genetic diversity of above ground plant populations (Templeton and Levin, 1979; Honnay et al., 2008).

The seed bank has the potential to influence the population genetics of the above ground vegetation, such as reducing genetic drift and bottleneck effects (Del Castillo, 1994). When the above ground plants are destroyed, the seed bank could

http://dx.doi.org/10.1016/j.bse.2014.05.009 0305-1978/© 2014 Elsevier Ltd. All rights reserved.

^{*} Corresponding author. Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, Hubei, PR China. Tel.: +86 27 87510140; fax: +86 27 87510251.

E-mail addresses: fanliu@wbgcas.cn (F. Liu), wantao1983@gmail.com (T. Wan), liwei@wbgcas.cn (W. Li).

¹ Co-first author. Tel.: +86 755 25735737; fax: +86 755 25722184.

provide enough "sleeping genes" and the subsequent regeneration from the seed bank of a population may be an important determinant of the success of a species at a given locality (Mandák et al., 2006). This is often the case for small fragmented habitats and rare plant populations. Fragmented plant populations are expected to be much more susceptible to extinction than large populations as they may suffer from genetic erosion and environmental and demographic stochasticity (Ellstrand, 1992; Young et al., 1996; Honnay et al., 2005). The soil seed bank may act as a gene buffer against the extinction of small and isolated plant populations, which are typical for our highly fragmented, urbanized and agricultural landscapes (Vitalis et al., 2004; Honnay et al., 2005).

However, a recent report from a meta analysis of 13 published studies found that the genetic diversity in the seed bank was lower than in the above ground vegetation and there was little genetic variation between the seed bank and above ground vegetation (Honnay et al., 2008). Hence, it was proposed that there may be no use in comparing the genetic diversity between the seed bank and the above ground plants if there is no habitat fragmentation (Uchiyama et al., 2006; Honnay et al., 2008). However, the studies mostly focused on terrestrial systems and most plants chosen were endemic or species with low seed set and high seed germination. For these species, seeds hardly accumulate in the soil because they germinate soon, and simply because they lose their viability quickly; this can minimize genetic variation between the seed bank and the above ground vegetation (Liu et al., 2006; Honnay et al., 2008). Unlike terrestrial environments, in aquatic habitats such as wetlands, flow fluctuations and seasonal changes of water level tend to spread the seed uniformly, which decreases the accumulation of a seed bank (Keddy and Reznicek, 1982; Leck and Simpson, 1994). Furthermore, higher seed germination of aquatic plants might reduce seed accumulation in the soil. This may reduce the role of the seed bank for restoring genetic variation and species diversity in wetlands. However, aquatic species commonly set large numbers of seed and this will tend to increase seed accumulation. Thus, the aquatic plant seed bank may have higher, equal or lower genetic diversity and differentiation than the above ground vegetation.

Common aquatic plants, especially the emergent ones, also have the risk of extinction when facing environmental catastrophes such as flooding, long-term inundation, and eutrophication. Thus, the seed bank may also be crucial to preserve genotypes and ultimately to increase the rate of evolution in response to new selective pressures in these plants (Cabin, 1996). However, we know little of the above ground and below ground genetic diversity for common aquatic species. Here, we investigate the genetic variation between the seed bank and the above ground vegetation of a common emergent species *Heleocharis valleculosa* (Cyperaceae) in Poyang Lake wetlands to solve the two following questions: (1) Are there any differences in the genetic diversity between the seed bank and above ground vegetation of common aquatic plants? (2) Is it useful to compare the genetic diversity between the seed bank and above ground plants?

2. Materials and methods

2.1. Study sites

The Poyang Lake Wetland, covering an area of 3283 km², is the largest in China and one of the six global biodiversity hotspots in the large river eco-regions (Olson and Dinerstein, 1998; Wang et al., 2007). It places a crucial role in providing comprehensive eco-environment ecosystem services in terms of moderation of climate and storage of species (Brinson and Rheinhardt, 1996). However, over the course of many decades, due to the degradation of the lake wetland, biodiversity has declined and some endemic species have tended to decrease (Gibbs, 2000).

2.2. Study species

H. valleculosa is a perennial emergent plant, widespread on lakeshores and in swamps and marshes. The species reproduces sexually via seeds and the seed germination rate in the Poyang Lake wetland is high (Liu et al., 2005). It is also one of the dominant species in the wetland, which is crucial for the diversity of the aquatic community (Hu et al., 2009; Zhang et al., 2012).

2.3. Seed bank collection

Twenty five plots ($1 \times 1 \text{ m}^2$ in size) were established in four regions of Poyang Lake wetland; each plot was 50 m apart (Fig. 1, Table 1). At each plot, 5 soil samples in the form of cylindrical cores (diameter: 8 cm; depth: 10 cm) were randomly collected, following removal of the surface vegetation and loose layer. In total, 125 soil samples (5 soil samples * 25 plots) were collected from each region. The soil samples were placed in separate bags and brought to the laboratory.

Seed germination was performed using the modified procedure described by Van der Valk and Davis (1978). Soil samples from the same plot were mixed together for seed germination. After germination, 25 young seedlings were randomly sampled from the region of Xianghu, Da Huchi, and Shahu, with the exception of Banghu region where all germinated plants (n = 18) were sampled (Table 1).

Download English Version:

https://daneshyari.com/en/article/1354060

Download Persian Version:

https://daneshyari.com/article/1354060

Daneshyari.com