Biological Conservation 220 (2018) 299–307

Contents lists available at ScienceDirect

Biological Conservation

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

Landscape genetics of a threatened maple, *Acer miyabei*: Implications for restoring riparian forest connectivity

Ikuyo Saeki[a,b,*], Akira S. Hirao[c], Tanaka Kenta[c], Teruyoshi Nagamitsu[d], Tsutom Hiura[e]

[a] Graduate School of Comprehensive Human Sciences, University of Tsukuba, 1-1-1 Tennodai, Tsukuba, Ibaraki 305-8571, Japan
[b] Makino Herbarium, Tokyo Metropolitan University, 1-1 Minami-Osawa, Hachioji, Tokyo 192-0397, Japan
[c] Sugadaira Research Station, Mountain Science Center, University of Tsukuba, 1278-294 Sugadaira-kogen, Ueda, Nagano 386-2204, Japan
[d] Forestry and Forest Products Research Institute, Hokkaido Research Center, 7 Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8516, Japan
[e] Tomakomai Experimental Forest, Hokkaido University, Takaoka, Tomakomai, Hokkaido 053-0035, Japan

ARTICLE INFO

Keywords:
Circuit theory
Corridor
Endangered species
Gene flow
Habitat fragmentation
Isolation by resistance

ABSTRACT

Because forest fragmentation affects ecological connectivity, establishing corridors is increasingly important in conserving biodiversity. Conserving the connectivity of riparian forests should be a priority because they often support rich and unique biota but are greatly modified by humans. *Acer miyabei* is a threatened maple which grows in floodplain ecosystems in northern Japan. We examined the effects of forest fragmentation on its genetic connectivity and identified candidate areas to be restored as riparian forest corridors. We collected leaf samples from 290 of *A. miyabei* individuals in 13 populations and determined pairwise genetic distances among the populations using 12 microsatellite loci. We also calculated geographic and resistance distances; the latter was quantified by least-cost path and circuit theory models by designating forested or riparian forested areas as having lower resistance than other types of land use. According to multiple regression analyses, genetic distance showed significant positive relationships with resistance distance but was not significantly related to geographic distance. The results indicate that forest fragmentation impedes gene flow of the species. Genetic differentiation among populations was greater in the smaller tree group than in larger one, suggesting that more recently established individuals are exposed to greater genetic isolation than the mature individuals owing to increasing forest fragmentation over time. Reduction of genetic connectivity was conspicuous in and around deforested areas. Such areas can be targeted for promoting connectivity of riparian habitats in future landscape planning.

1. Introduction

Forest fragmentation affects ecological connectivity (Radford and Bennett, 2007; Wilcove et al., 1998). Thus, establishing corridors and new habitats has increasing significance in conserving biological diversity (Beier and Noss, 1998). Although the number and coverage of natural areas are limited in urban and agricultural regions, effective networks in such regions facilitate movement, dispersal, and gene flow of organisms, contributing to long-term persistence of natural populations (Gilbert-Norton et al., 2010; Tewksbury et al., 2002). Yet few practical models are available for the implementation of habitat networking (Brodie et al., 2016; Lacher and Wilkerson, 2014). Such knowledge is particularly restricted for riparian forest ecosystems, although rivers intrinsically have a high potential to function as corridors owing to their linear characteristics, as well as their rich and unique biota (Lees and Peres, 2008; Rouquette et al., 2013).

Historically, the utility of rivers in transportation has induced intensive urbanization and development along them. In addition, large levees have been built, and river channels have been regulated for flood prevention (Nakamura et al., 2006; Washitani, 2001). This trend is becoming common in many places across the world, making the conservation of river floodplain ecosystems one of the great challenges of the 21st century (Gergel et al., 2002; Richardson et al., 2007; Tockner and Stanford, 2002). Japan has numerous rivers owing to its abundant precipitation under a monsoon climate and wide elevational gradients. But the flat land alongside these rivers has been heavily altered by development into agricultural and residential areas.

To facilitate networking of habitats, examination of genetic connectivity among extant populations is important because it helps with identifying the spatial features impeding gene flow (Dyer and Nason, 2004; Mech and Hallett, 2001; Storfer et al., 2007). In this framework, landscape genetics, which integrates population genetics and landscape

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[*] Corresponding author at: 1-1-1 Tennodai, Tsukuba, Ibaraki 305-8571, Japan.
E-mail addresses: saeki.ikuyo.ge@u.tsukuba.ac.jp (I. Saeki), akihirao@gmail.com (A.S. Hirao), kenta@sugadaira.tsukuba.ac.jp (T. Kenta), nagamit@affrc.go.jp (T. Nagamitsu), hiura@fsc.hokudai.ac.jp (T. Hiura).

https://doi.org/10.1016/j.biocon.2018.01.018
Received 18 July 2017; Received in revised form 22 December 2017; Accepted 21 January 2018

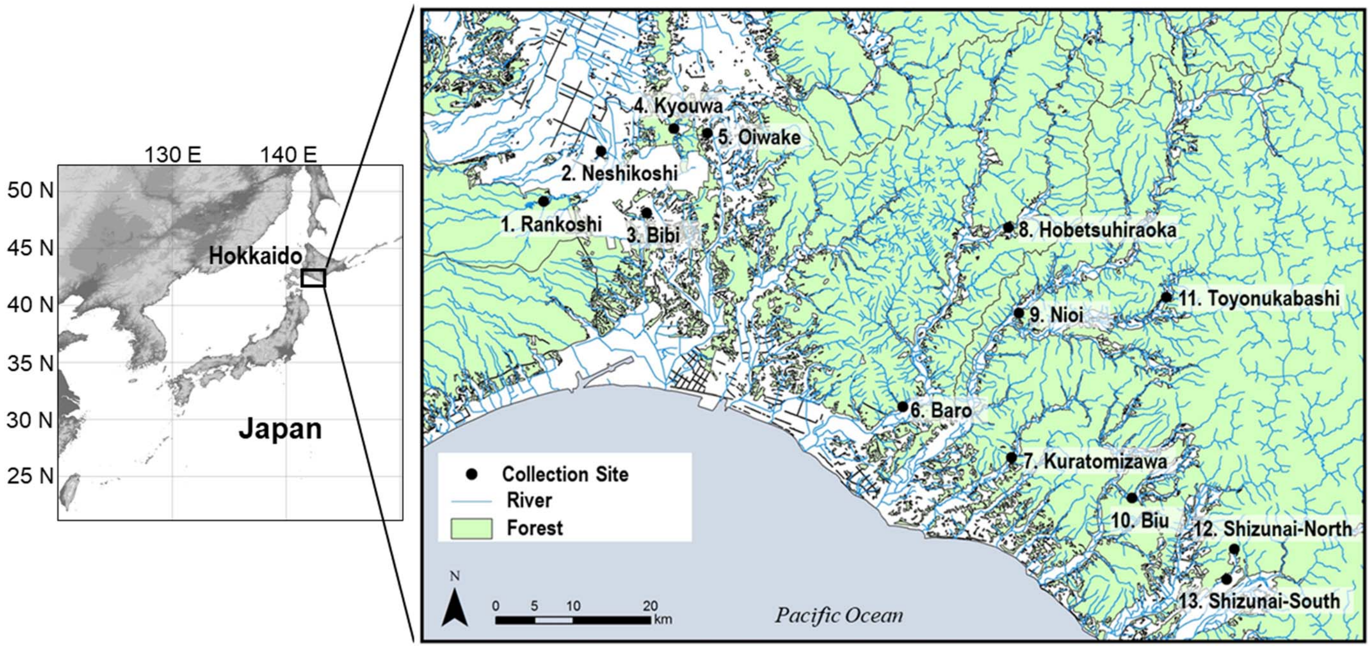

Fig. 1. Map of Japan (left) and inset of southern Hokkaido showing the 13 *Acer miyabei* populations sampled.

ecology (Manel et al., 2003), is a powerful tool and is increasingly being applied to a wide range of conservation projects (Holderegger and Wagner, 2008; Manel and Holderegger, 2013). Since the research field emerged, animals have been a major target of study (Storfer et al., 2010); in particular, large mammals and birds are well studied because information on their movement is often essential in landscape-level conservation planning (e.g., Epps et al., 2013; Pavlova et al., 2012). In contrast, plants have drawn less attention. Yet their gene exchange occurs via pollen and seeds, which is difficult to measure by direct observation in the field. Thus, genetic data are useful in evaluating ecological connectivity of their natural populations (e.g., Dyer et al., 2012; McRae and Beier, 2007; Sork et al., 2010). Furthermore, many plant species are strictly associated with specific ecosystem types, making them excellent, easily observable indicators of threatened ecosystems.

Here, we analyzed the effects of forest fragmentation on gene flow of an endangered plant, *Acer miyabei* Maxim. (Sapindaceae), a riparian maple inhabiting lowland floodplain ecosystems in northern Japan (Ogata, 1965; van Gelderen et al., 1994). The species is designated as Vulnerable (VU) in the national Red List due to recent population declines resulting from habitat loss and fragmentation (Ministry of Environment, Japan, 2012). We focused on this species because of its conservation concern and strict indication of rare and undisturbed riparian forest ecosystems. Its long lifespan allows us to compare the degree of genetic differentiation in young (small) and mature (large) individuals and thus examine how recent landscape changes have affected the genetic diversity of the species.

Our general objective was to characterize the effects of habitat fragmentation on patterns of genetic variation in *A. miyabei* as a basis for landscape connectivity planning of riparian forest ecosystems. The specific objectives were (i) to examine fragmentation effects in recent years by comparing genetic differentiation between small and large individuals; (ii) to test the hypothesis that forest fragmentation interferes with gene flow by using the isolation by resistance model (Adriaensen et al., 2003; McRae, 2006); and (iii) to identify candidate areas to be prioritized for future restoration projects to promote riparian forest connectivity in the landscape.

2. Materials and methods

2.1. Study species

Acer miyabei is a deciduous tree species that grows in temperate forests in East Asia (Ogata, 1965; van Gelderen et al., 1994). Mature trees often grow > 15 m tall with a diameter at breast height (DBH) of 40 cm. Its occurrence is strongly associated with river floodplain ecosystems, occurring on both first and second terraces and on the slopes along river valleys. *Acer miyabei* consists of three intraspecific taxa: (i) ssp. *miyabei* f. *miyabei* in central to northern Japan; (ii) ssp. *miyabei* f. *shibatae* (Nakai) K. Ogata in a small area of Honshu; and (iii) ssp. *miaotaiense* (Tsoong) A. E. Murray in China. All of these taxa are listed in national or IUCN Red Lists because of their limited range and habitat decline caused by agricultural and residential development (Ministry of Environment, Japan, 2012; IUCN, 2016). This study focused on natural populations of *A. miyabei* ssp. *miyabei* f. *miyabei* (hereafter, *A. miyabei*). This taxon covers a relatively wide area of southwestern Hokkaido, enabling us to assess genetic connectivity at the landscape level. Sexual expression is polygamo-dioecious, characterized by dichogamous hermaphrodite, female, and male flowers (Hotta, 2004). Flowers are yellow, and the pollinators are Diptera (Bibionidae) (Hotta, 2004; Nagamitsu et al., 2014), Coleoptera (Cerambycidae), and Hymenoptera (Tenthredinidae) (pers. obs.), which are generally known to be more abundant in natural forests than in urbanized areas. Samaras are dispersed by wind and occasionally by water when trees grow beside rivers and streams.

2.2. Field collection

Leaf tissues of *A. miyabei* were collected from 290 individuals at 13 sites (i.e., populations) in southwestern Hokkaido (42.42°–42.80°N, 141.59°–142.48°E; Fig. 1, Table 1). The sampled populations lay within an area of approximately 80 km × 100 km including seven major river basins. The average elevation of collection sites was 83.8 m a.s.l. (range, 7–204 m).

For population genetic analyses, we collected foliage from 18 to 45 individuals per population and recorded their DBH (ranging, 0.7–54.1 cm; Table 1). We noted that individuals with DBH ≥ 15 cm tended to be of reproductive age and consisted of 33% of our samples.