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38. © Mating system analysis of *Alnus maritima* (Seaside alder), a rare riparian tree.
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Mating System Analysis of *Alnus maritima* (Seaside Alder), a Rare Riparian Tree

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ABSTRACT Effective conservation requires an understanding of the genetic interactions among populations and individuals of a species, particularly those with fragmented, isolated distributions. *Alnus maritima* (seaside alder) is a rare tree species with an extremely fragmented distribution of highly isolated populations in the Delmarva Peninsula, Georgia, and Oklahoma. We conducted a mating system study to estimate the outcrossing rate, inbreeding coefficient, biparental inbreeding rate, and correlation of paternity in progeny from a Georgia and an Oklahoma population to investigate the effects of isolation on the *A. maritima* mating system. Data from nine microsatellite loci showed similarly high multilocus outcrossing rates in both populations ($t_m = 0.94$). Individual tree outcrossing rates were also high ($t_m = 0.873$ – 1.047). There was no significant biparental inbreeding in either population, but there was significantly higher correlated paternity in the Oklahoma population. Results showed the high outcrossing expected for a wind-pollinated, monoecious species that can promote the maintenance of genetic variation detected in *A. maritima* seed pools and standing populations. Likewise, pollen flow among Oklahoma populations may promote maintenance of regional genetic variation. However, despite the genetic diversity in the seed pool generated by *A. maritima*'s highly outcrossed mating system, failure of new individuals to be recruited into populations from seed presents an obstacle that will need to be considered when developing conservation strategies for this rare species.

Key words: *Alnus*, fragmented populations, Georgia, mating system, Oklahoma, paternity analysis.

INTRODUCTION The mating system and ability for populations to genetically interact via gene flow are critical factors that must be considered in conservation and management planning for plant species with fragmented, isolated populations. Fragmentation is predicted to reduce gene flow, which can lead to loss of genetic variation, increased inbreeding and inbreeding depression, and significant genetic differentiation among populations as populations become smaller, more fragmented, and more isolated (Loveless and Hamrick 1984, Hamrick and Godt 1990). Consistent with many of these predictions, studies of plant species with natural or anthropogenically fragmented distributions have typically shown the

expected genetic differentiation among fragments (Gibson and Hamrick 1991, Gibson and Wheelwright 1995, Cardoso et al. 1998, Jones and Gibson 2011), reduced gene flow (Sork and Smouse 2006, Bittencourt and Sebbenn 2007), increased susceptibility to genetic drift (Barrett and Kohn 1991, Karron 1991), and higher levels of inbreeding (Barrett and Kohn 1991, Ellstrand and Elam 1993). These population genetic consequences of fragmentation are particularly important for species that are targets for conservation because the loss of genetic diversity and increase in frequency of deleterious alleles can potentially limit the ability of population fragments to respond and adapt to changing environments or shift their range in response to global climate change (Davis and Shaw 2001, Jump and Penuelas 2006, Sork and Smouse 2006, Coates et al. 2007, Kelly and Goulden 2008, Thuiller et al. 2008).

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