

Isolation-by-environment and its consequences for range shifts with global change: landscape genomics of the invasive plant common tansy

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Abstract

Invasive species are a growing global economic and ecological problem. However, it is not well understood how environmental factors mediate invasive range expansion. In this study, we investigated the recent and rapid range expansion of common tansy across environmental gradients in Minnesota, U.S.A. We densely sampled individuals across the expanding range and performed reduced representation sequencing to generate a dataset of 3071 polymorphic loci for 176 individuals. We used non-spatial and spatially-explicit analyses to determine the relative influences of geographic distance and environmental variation on patterns of genomic variation. We found no evidence for isolation-by-distance (IBD) but strong evidence for isolation-by-environment (IBE), indicating that environmental factors may have modulated patterns of range expansion. Land use classification and soils were particularly important variables related to population structure although they operated on different spatial scales; land-use classification was related to broad-scale patterns and soils were related to fine-scale patterns. All analyses indicated a distinctive genetic cluster in the most recently invaded portion of the range. Individuals from the far northwestern range margin were separated from the remainder of the range by reduced migration, which was associated with environmental resistance. This portion of the range was invaded primarily in the last 15 years. Ecological niche models also indicated that this cluster was associated with expansion of the niche. While invasion is often assumed to be primarily influenced by dispersal limitation, our results suggest that ongoing invasion and range shifts with climate change may be strongly affected by environmental heterogeneity.

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