Genetic, elevational and community structuring in the endangered vernal pool plant species Seastephol meadowfoam (Limnanthes vinculans)

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ABSTRACT

Just east of the Laguna de Santa Rosa lies the Santa Rosa Plain, a region that provides unique vernal pool habitat to many federally and state-listed endangered species. In this region and throughout California, vernal pool habitat has been dramatically reduced due to agricultural expansion and urban encroachment. Over the last 20 years, mitigation for impacts to vernal pools and their associated species has often involved the creation of new wetlands. As a result, the movement of soil inoctum has typically occurred without consideration for the spatial genetic structuring of the species or other local ecological processes that may affect species persistence in plant community composition (i.e., microtopographic position within pools). Utilizing spatial genetic data collected for an endangered vernal pool plant species (Ayres & Sloop 2008), Seastephol meadowfoam (Limnanthes vinculans), we recognize that genetic diversity may be structured within individual pools, instead of solely on a site by site or regional level. Additionally, data on topographic and community gradients have provided insight into the patterns of distribution for L. vinculans within and among created pools, natural pools, and natural swales. Through further genetic analyses we anticipate to assess patterns of infraspecific genetic variation, and the degree to which mitigation measures have modified such patterns within and among populations inhabiting both natural and created vernal pools.

RESULTS

Spatial Genetic Structure

The spatial autocorrelation analysis of the mean geographic coordinates of 34 pools provides evidence that genetic isolation by geographic distance is statistically significant (p<0.01), albeit slight (r =0.03, r<0.01). This indicates that even with extensive movement of seed throughout the species’ range from past mitigation events there is a subtle, but statistically significant decrease in the level of gene flow between pools at greater distances apart.

Since natural background levels of seed movement may occur on a more local scale, we looked at the relationship between spatial distance and genetic distance within an individual pool at the Shiloh Mitigation Bank. According to the Mantel test, approximately 14.42% of the genetic distance is explained by spatial distance (R=0.1442, p=0.01). This suggests that genetic spatial structure may develop on a local scale within individual pools compared to larger distances among different pools or sites.

METHODS

Spatial Genetic Structure in L. vinculans populations

Data collected in 2006 by Ayres and Sloop (2008) were used to identify the presence of spatial genetic structure within populations of L. vinculans occupying 34 vernal pools and swales. Individual genotypes were assigned using 10 neutral microsatellite loci as described by Ayres and Sloop (2008). Geographic data was collected using Geographic Positioning System (GPS) (NAD83) accuracy. All spatial autocorrelation and Mantel tests were conducted using GenAlex 6.2 (Peakall and Smouse 2006).

L. vinculans distribution, abundance and community structure

Field data were collected during the flowering season for L. vinculans from April through May 2009. The sampling design involved placing 0.25m x 0.25m quadrats at random positions off a transect that bisected the maximum length of a vernal pool. Within each quadrat, we estimated the percent cover of L. vinculans. Additionally, the most abundant species present in the quadrat also from individual pools were documented and categorized according to the vernal pool plant classifications listed in the California Vernal Pool Assessment Preliminary Report (Keeler-Wolf et al. 1998). The elevations at each quadrat position were measured using a CST/Berger 24x Automatic Level (Figure 2) and corrected due to spatial distance was also apparent at a local scale when analyzed within an individual pool (Figure 6). This indicates that spatial genetic structure in L. vinculans may be occurring at a local level within individual pools.

We compared the mean number of species across individual pools as well as across pool types. According to our model (R²=0.64, F=64.92, p<0.0001), the mean number of predominant species co-occurring with L. vinculans varied among pools (F=39.22, p<0.0001) and pool types (F=232.42, df=2, p<0.0001), with created pools having the greatest mean number of species, and natural swales having the least (Figure 9). The mean numbers of species within created pools, natural pools and natural swales are significantly different from each other (Tukey’s HSD test, α=0.05). Variation in the pooled number of vernal pool associates and vernal pool indicator species can also be explained by pool type (F=305.41, df=2, p<0.0001) and individual pool ID (F=34.63, df=12, p<0.0001). All pool types had significantly different mean percent cover from each other (Tukey’s HSD test, α=0.05). Overall, percent cover of L. vinculans was lowest in created pools and highest in natural swales (Figure 8). These results correspond to our spring 2008 field observations that individual L. vinculans plants in created pools were much smaller and produced fewer flowers than those found in natural swales.

DISCUSSION AND FUTURE RESEARCH

In order to expand our understanding of localized structuring in L. vinculans, we are currently working to quantify patterns of genetic variation in neutral markers within and among populations of L. vinculans, as well as patterns of spatial genetic structure within and among individual pools containing L. vinculans. Given our current results, we recommend that mitigation for impacts to L. vinculans other vernal pool species should be considered on a case by case basis with special attention paid to localized structure within individual pools and pool types.

Relative Elevations and Abundance

The mean elevations where L. vinculans was present, relative to the pool edge, were weighted by the percent cover (a proxy for abundance) of L. vinculans in the respective quadrant. Relative weighted means ranged from approximately 0.007 meters above the pool edge at the DSM001 site (which was the only natural convex feature) to -0.2203 meters below the pool edge at the FEMA002 site (Figure 7, Figure 3 – site locations). According to our model (R²=0.479, F=38.64, p<0.0001), patterns of species distributions and abundances vary among pools (F=36.35, df=13, p<0.0001) as well as among pool types (F=74.58, df=2, p<0.0001), with natural swales being significantly different than created and natural pools (Tukey’s HSD test, α=0.05). Since relative elevations in vernal pools and swales may be associated with the degree of inundation, these results imply that the geomorphology and hydrologic function of natural swales may be different than vernal pools, and perhaps should be considered as a unique case when mitigating impacts to endangered plant species found in this habitat type.

Additionally, we compared the mean percent cover of L. vinculans among pool types and individual pools. This model was also highly significant (R²=0.526, F=46.02, p<0.0001) for both pool type (F=75.36, df=2, p<0.0001) and individual pool ID (F=34.63, df=12, p<0.0001). All pool types had significantly different mean percent cover from each other (Tukey’s HSD test, α=0.05). Overall, percent cover of L. vinculans was lowest in created pools and highest in natural swales (Figure 8). These results correspond to our spring 2008 field observations that individual L. vinculans plants in created pools were much smaller and produced fewer flowers than those found in natural swales.

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REFERENCES

Ayres, J. P., and Sloop, C. A. 2008. Genetic structure of the endangered vernal pool plant Lasthenia vinculans (Asteraceae) from across the species’ range were sampled (6 created pools, 6 natural pools, and 4 natural swales having the least (Figure 9). The mean numbers of species within created pools, natural pools and natural swales are significantly different from each other (Tukey’s HSD test, α=0.05). In contrast, the number of generalist species was found to not be significantly different between pool types (Figure 9).

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