Population Genetic Structure of Pampasgrass (*Cortaderia selloana*) and Jubatagrass (*C. jubata*) in California

Miki Okada, Riaz Ahmad, and Marie Jasieniuk
Department of Vegetable Crops and Weed Science, University of California, Davis

INTRODUCTION

Pampasgrass, *Cortaderia selloana*, and jubatagrass, *C. jubata*, are native to South America but have become highly aggressive invaders of wildlands in California. Pampasgrass was first introduced into the state by the horticultural trade in the mid 1800's, and continues to be sold as a landscape ornamental. It was also used in forage trials and for erosion control in the 1940's and 1950's. Jubatagrass was introduced in the late 1800's, probably as a horticultural contaminant. Since the 1950's, both pampasgrass and jubatagrass have expanded spatially, displacing native species and disrupting natural habitats.

Weed management strategies and prevention of future invasions benefit from understanding of population biology. Characterization of genetic structure in natural populations contributes to the understanding of breeding systems and gene flow.

QUESTIONS

How is genetic variation in naturalized pampasgrass and jubatagrass in California structured 1) among individuals within populations and 2) among populations over a wide geographical area?

MATERIALS AND METHODS

Microsatellite Markers

- We developed highly polymorphic and codominant microsatellite markers from a (CA)n and (CT)n enriched library constructed from a *Cortaderia selloana* plant collected in Red Bluff, CA.
- Leaf tissue was collected from 686 *C. selloana* plants over 28 naturalized populations, 227 *C. jubata* plants over 19 naturalized populations, and 15 *C. selloana* cultivars and plantings (figure 1).
- We screened these plants for five microsatellite loci.

Data Analysis

- Two similarity matrices using Jaccard's coefficient were constructed using NTSYS. One of the matrices contained all *C. selloana* individuals, and the other contained only cultivars and plantings of *C. selloana*. Principal coordinate analyses were performed using Eigen vectors extracted from the similarity matrices using NTSYS.
- Five cultivar groups ("A", "B", "C", "D", and "E") were assigned by eye from the plot of the principal coordinates (figure 2). Using these cultivar groups as *a priori* groupings, a discriminant analysis was performed to assign all naturalized *C. selloana* individuals to one of the five cultivar groups (Statistica).
- Nei's genetic distance was calculated among *C. selloana* populations (POPGEN) and used to construct a UPGMA tree (PHYLIP).

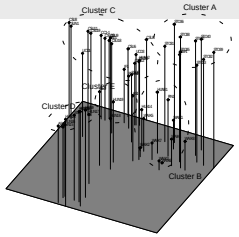

Figure 2. Cultivar Groupings in the 3-D Plot of Principal Coordinates

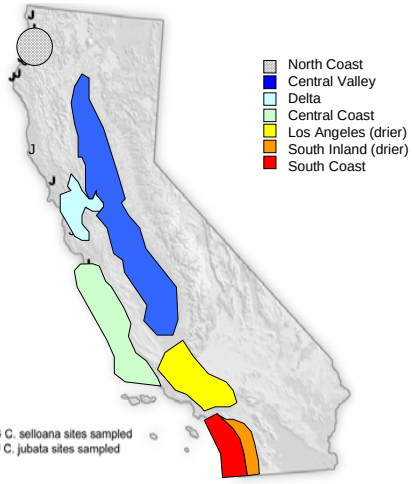

Figure 1. Pampasgrass and jubatagrass populations

RESULTS AND DISCUSSION

Jubatagrass

All but four out of 277 individuals investigated in this study had the identical genotype at all five loci. One out of those four distinct jubatagrass individuals was found to be missing an allele at one locus. The other three differ from the rest by carrying a novel allele, which is two nucleotides longer, at one locus. These two distinct genotypes are likely to be mutations that occurred in California. All jubatagrass in California are essentially of a single clone.

Pampasgrass

A cluster analysis using UPGMA on Nei's genetic distance revealed a general lack of correlation between geographical distance and genetic distance (figure 3). Fst, a measure of population differentiation, was 0.23 indicating high level of population differentiation, but the principal coordinate analysis also showed a lack of clustering of individuals into their respective populations (data not shown). Pie charts showing the composition of populations based on the cultivated groupings appear to correlate with population groupings in the phenogram (figure 3). Population structure and relatedness in pampasgrass appears largely to be a result of the genetic similarity to the cultivated source material and not due to post-introduction population differentiation. The data are consistent with expected patterns of genetic variation in naturalized populations that originated relatively recently from ornamentals.

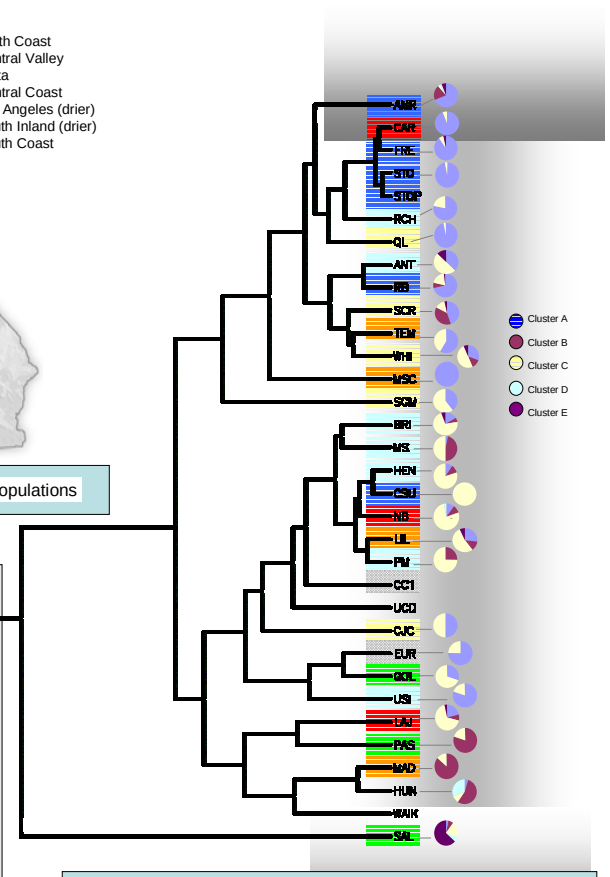

Figure 3. UPGMA Tree. Pie charts show distribution of cultivated genotypes among the naturalized populations.

CONCLUSIONS

1. Naturalized jubatagrass in California is comprised of a single genotype.
2. The pattern of genetic variation in naturalized pampasgrass in California is best explained by genetic differences/similarities of the cultivated material that gave rise to each individual within naturalized populations.

ACKNOWLEGEMENTS

Jeff Firestone
Chris Mallek
Cindy Yip