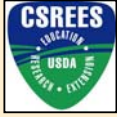


Hybridization, differentiation and invasion of the Pacific Northwest by *Brachypodium sylvaticum* (Huds.) Beauv.

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Introduction

Brachypodium sylvaticum, or slender false brome, is a Eurasian perennial bunchgrass brought into Oregon for forage research around the 1920s (Fig. 1).

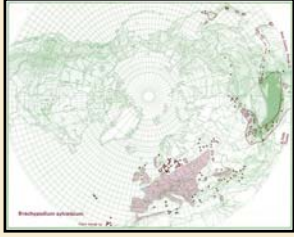


Figure 1. Native distribution of *B. sylvaticum*. Image courtesy of the Swedish Museum of Natural History (2005).

Early records suggest that it escaped near Eugene or Corvallis, OR, sometime before 1939, and did not appear problematic for half a century. Within the last few decades it has become widespread in Northwestern Oregon and has become an aggressively invasive weed. Its recent range expansion presents a unique opportunity to study the spread and evolution of an invasive species. **In this study we are attempting 1) to identify the origins of this noxious weed, 2) to test the hypothesis that its success may have been facilitated by intraspecific hybridization between previously allopatric populations and 3) to determine the degree of quantitative genetic differentiation within and among populations.** We used plastid (cpDNA) and nuclear (microsatellite) data to elucidate the possible origins of U. S. populations of *B. sylvaticum*.

Methods



We have sequenced a single 810 bp chloroplast DNA region (*trnS(gcu) – psbD*; Saltonstall 2001) for 196 individuals from 26 European (EUR), and 18 U.S. populations. The network was constructed

with TCS (Clement et al 2000) using 95% parsimony. 597 individuals from the populations sampled above were also scored at 6 nuclear microsatellite loci. We used assignment tests to elucidate the probable origin of U.S. individuals and to determine the degree of admixture within U.S. and EUR populations. We used a nested half sib design to identify genetic variation among families nested within U.S. populations.

Results

Figure 2. cpDNA haplotypes of reference populations (all U.S. accessions have haplotype A). Symbol size indicates the number of individuals sampled, pie color denotes proportion of a given type. Note: some symbols represent several populations. TCS resolved two unrooted haplotype networks (inset). One with 12 haplotypes (A - L) and one with two haplotypes (M - N). Haplotypes M-N can be linked by increasing the maximum number of inferred steps to 22.

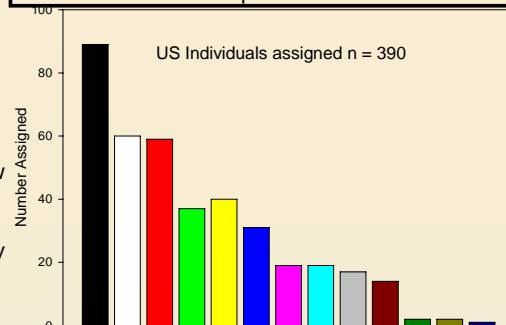
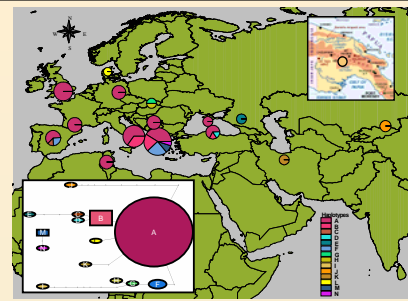


Figure 3. Assignment of U.S. individuals to most probable reference populations for nuclear microsatellite data using GeneClass2 (Piry et al. 2004). Note that U.S. individuals were only assigned to a subset of reference populations. It is highly likely that U.S. populations were introduced from Spain, England, Italy and France.

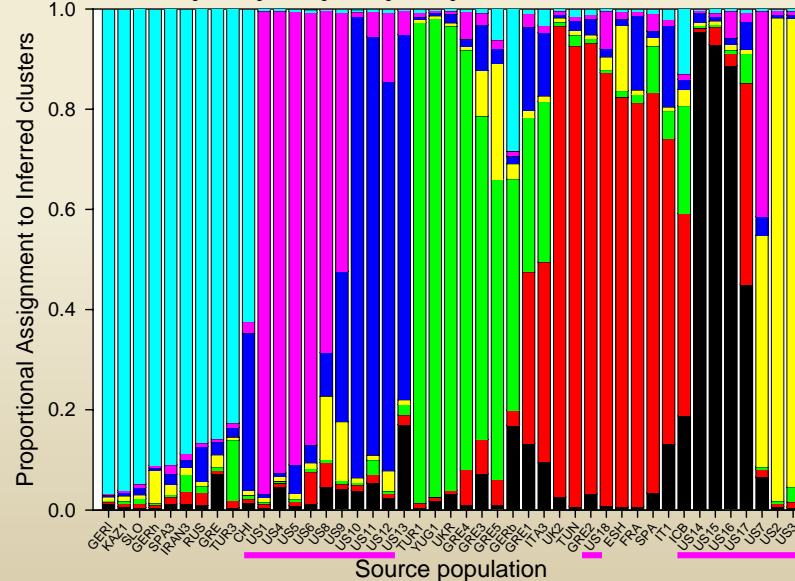
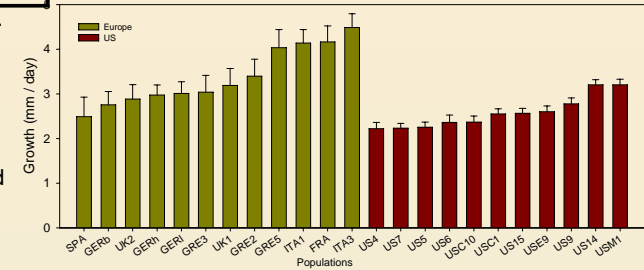


Figure 4. Proportion of a given population assigned to inferred clusters using Structure (Pritchard et al. 2000). Inference is for K=7 populations using the admixture model with a 50,000 step burn-in period followed by 20,000 reps.

Figure 5. Tillers were taken from greenhouse grown maternal plants that were initially raised from field collected seeds. European and U.S. populations differ significantly ($F_{1,31.4} P = >0.0002$). Moreover, populations within regions also differ ($F_{21,946} P = >0.0001$) for growth and other traits (data not shown). Within the U.S., significant family within population effects for growth ($F_{121,702} P = <.05$) and other traits (data not shown) indicate **these differences are heritable.**



Conclusions

Chloroplast DNA variation in one gene region indicates that U.S. populations sampled to date have the same haplotype (Fig.2). Nuclear microsatellite variation clusters U.S. populations with a distinct subset of European accessions (Fig.3).

These data indicate that *B. sylvaticum* populations in the U.S. arose from individuals that came from possibly four founding populations in Europe (Figs. 3 and 4). Moreover, the genotypes in certain U.S. populations (e.g., US7, US8, US9, Fig. 4) are an admixture of several U.S. clusters. It appears that intraspecific hybridization between previously allopatric populations may have played a role in the formation of aggressively invasive genotypes in Oregon (e.g., pop. US9 compare Fig. 4 and Fig. 5).

Significantly slower growth rates in U.S. than European populations (Fig. 5) may be due to founder effects. Nonetheless, U.S. populations are vigorous and invasive. We found significant genetic variation for growth rate among U.S. populations. If heritable differences among these populations are adaptive selection may facilitate the invasion of *B. sylvaticum* in newly colonized habitats.

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 Piry, S., A. Alapetite, J. M. Cornuet, D. Paetkau, L. Baudouin and A. Estoup (2004). GENECLASS2: A software for genetic assignment and first-generation migrant detection. Journal of Heredity 95: 536-539
 Pritchard, J. K., M. Stephens and P. Donnelly (2000). Inference of population structure using multilocus genotype data. Genetics 155: 945-959.