Using ecological genetics and molecular tools to improve our understanding of invasive species

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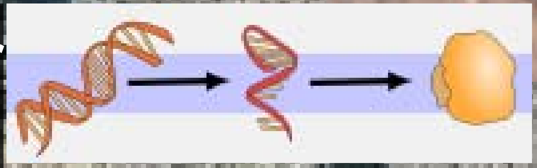
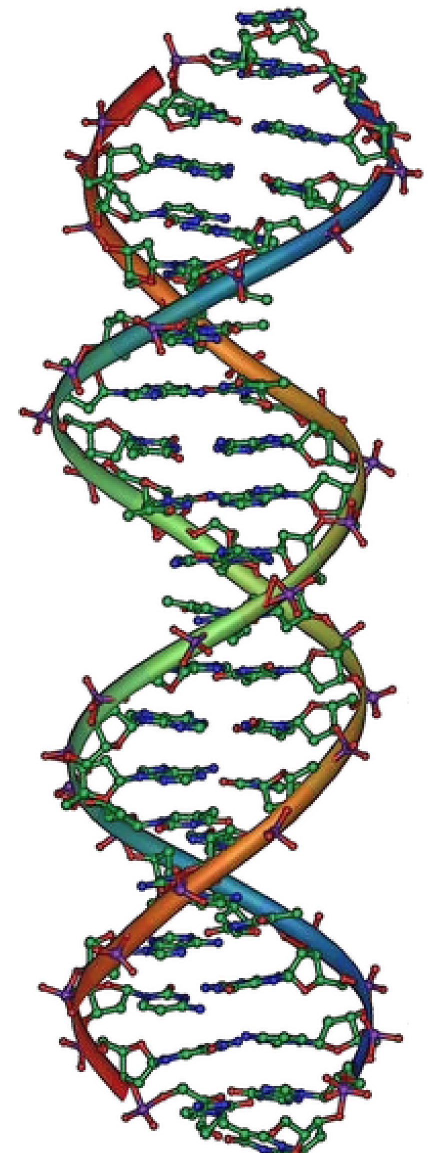




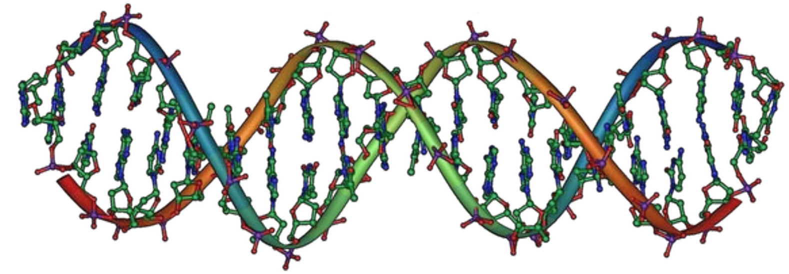


Molecular genetic techniques can help us to

- determine the origin of invasive species
- follow the main vectors of spread in the introduced range
- investigate rapid evolutionary adaptation
- detect hybridization within or between closely related species

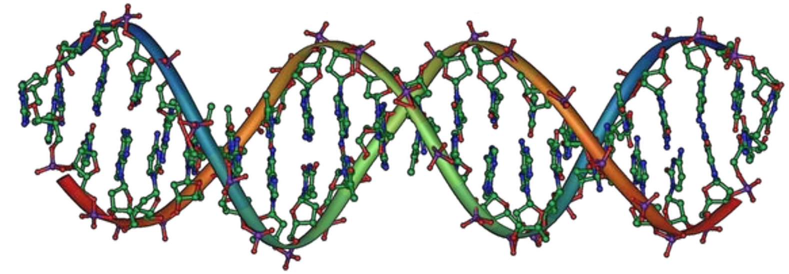


Genetic tools



	Allozymes	RFLPs (restriction fragment length polym.)	Microsatellites (SSRs)	AFLPs	DNA sequence analysis
Basics	non-denaturated proteins, enzyme specific histochemical stain	primary DNA structure, Southern blotting of digested DNA	short repeats of mono- to tetranucleotids	PCR amplification (preselective and and selective amplification)	specific DNA regions amplified
Data	mostly co-dominant inheritance	banding patterns, DNA length mutations, rarely inversions	variation in number of repeats	dialellic markers, dominant (codom. markers may be detected)	DNA sequence analysis, detect deletions and duplications
+	easy and cheap to detect, large numbers can be analyzed for many diff. enzymes	RFLPs are co-dominant, detect nDNA and organelle DNA differences, highly repeatable	SSRs abundant, uniform coverage, codom. markers detecting nDNA and org. DNA polymorphisms	highly polymophic, no prior sequence knowledge	easily scored, high-quality information, automated sequencing generates large amounts of data
-	detect low levels of polymorphisms	require large amounts of DNA, expensive, some enzymes have variable cutting (methylation)	identification expensive, large numbers of alleles (rather than loci) required	high technical skills, high quality DNA	expensive for diversity surveys (1 loci screened at a time)

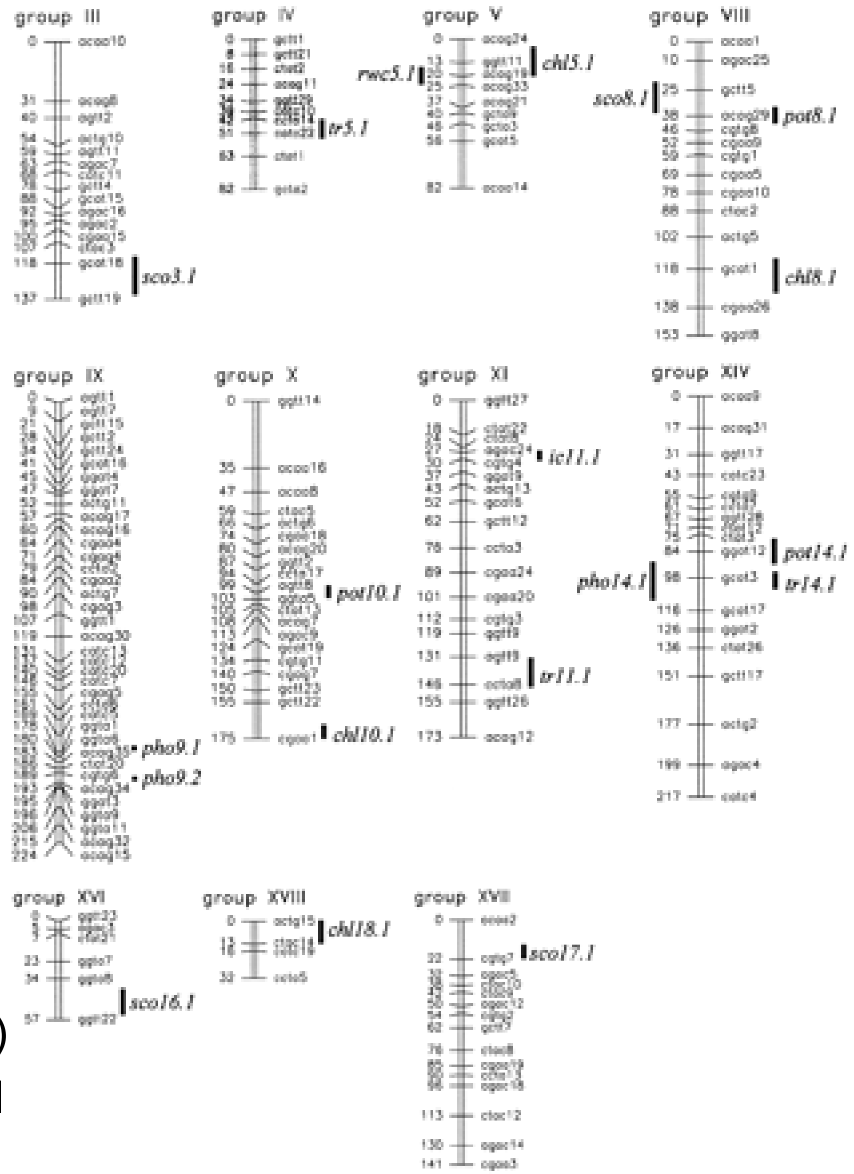
Genetic tools



	Allozymes	RFLPs	Microsatellites (SSRs)	AFLPs	DNA sequence analysis
Applica-tions	estimates of gene diversity and population structure, hybidization, introgression, gene flow, polyploidy	estimates of gene diversity and population structure, hybidization, introgression, gene flow, polyploidy	estimates of gene diversity and population structure, limited phylogenetic value (homoplasy)	genome mapping and breeding studies, gene diversity, population structure and clonality; use for phylogenetic studies controversial	estimation of gene diversity, hybridization, introgression, and gene flow; phylogenetic and phylogeogaphic analyses
similar tech-niques		CAPs (cleaved amplified polymophic sequences)	ISSRs		PCR-RFLPs, single-nucleotide polymorphism (SNP) analysis

Genetic tools - quantitative trait locus

- QTLs and QTL mapping (genetic architecture of a trait)
- example of QTL map for chlorophyll contents and PS activity in sunflowers (Helianthus annuus)
- CIM (composite interval mapping) - more sensitive analysis in a certain target region, marker loci used as covariates

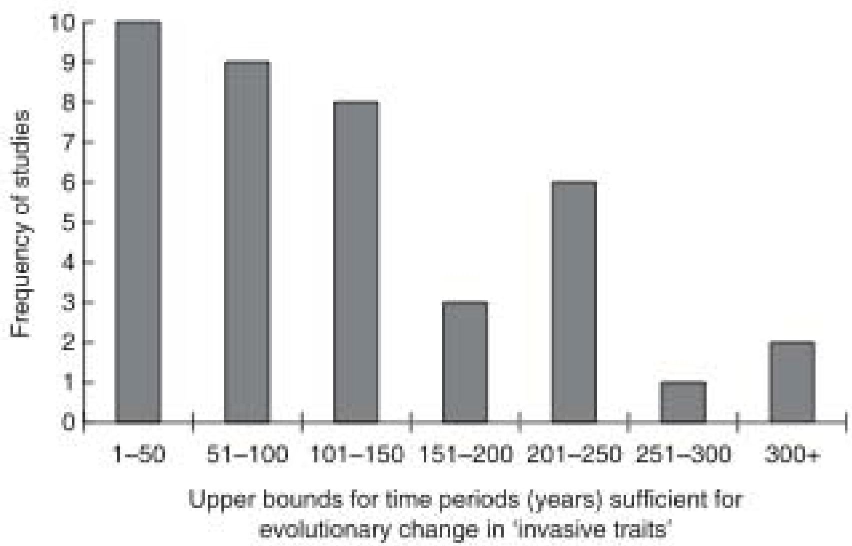


Herve & al 2001: QTL analysis of photosynthesis and water status traits in sunflower (Helianthus annuus L.) under greenhouse conditions Journal of Experimental Botany, Vol. 52: 1857-1864.

Contemporary evolution in invasive species

- ecological changes promote the development of genetic differences
- they reinforce reproductive isolation
- thus adaptive evolution is driving speciation
- speciation acts mostly at local scales or meta-population level

Evolutionary changes



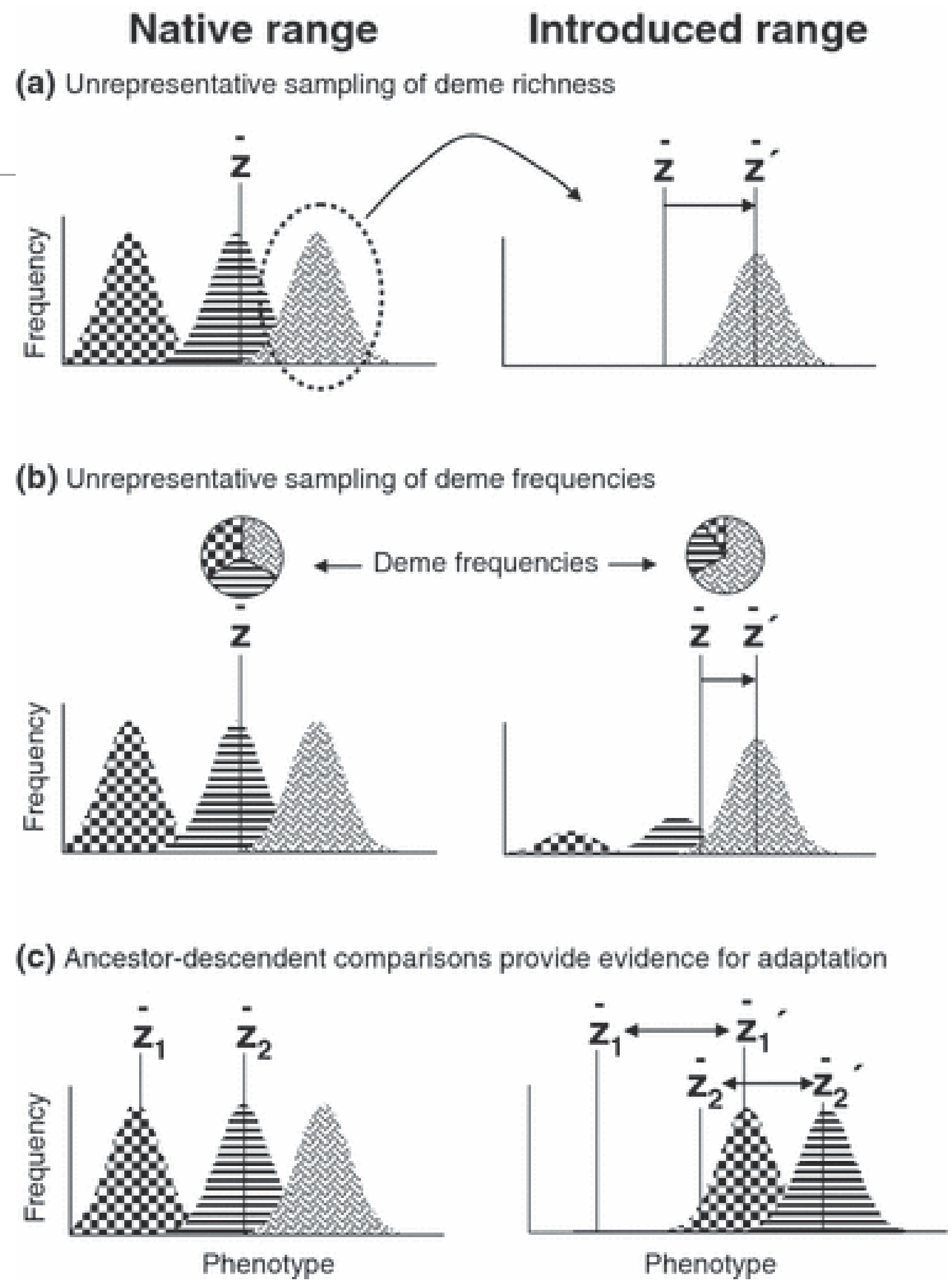
Whitney & Gabler 2008: Rapid evolution in introduced species... Diversity and Distributions,14:569–580

- contemporary evolution is the rule rather than an exception
- time range for evolutionary adaptations of important traits in introduced species often rapid, in annual plants a few decades

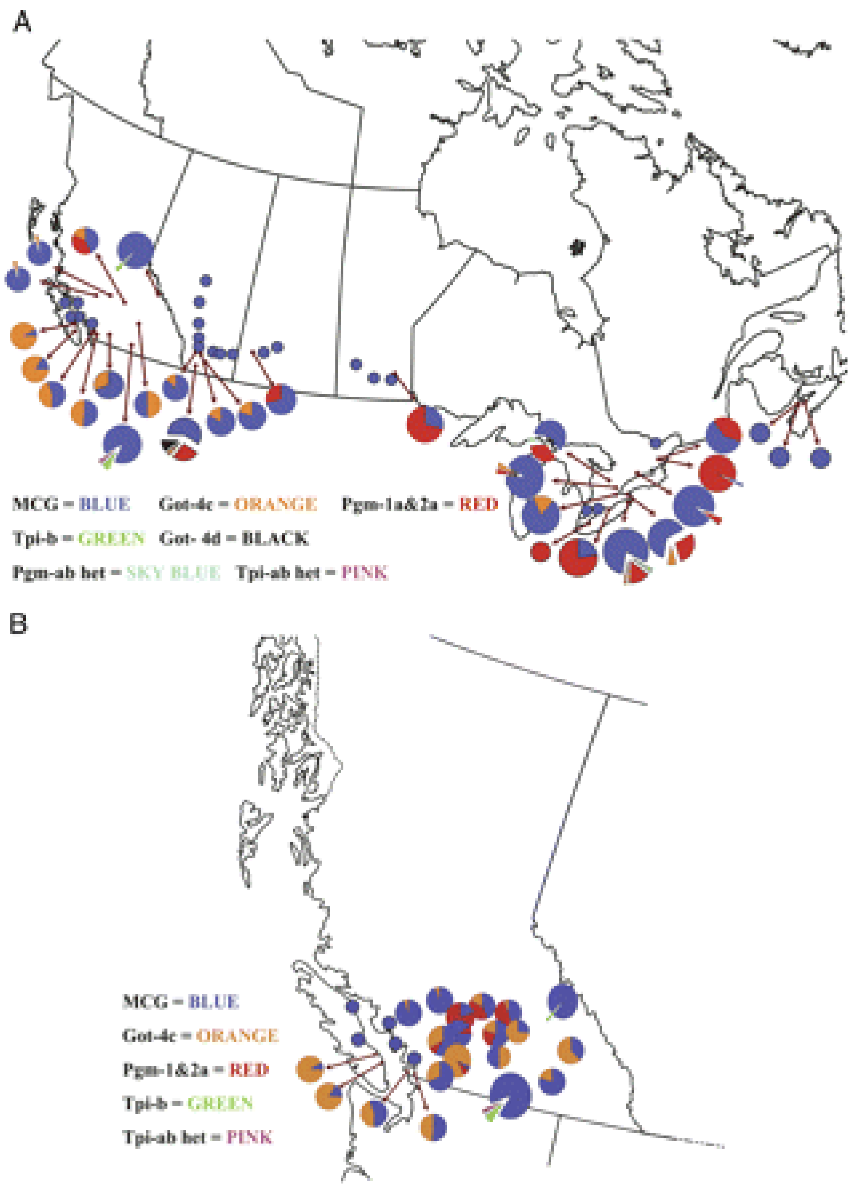
Adaptive evolution

- stochastic evolution vs. adaptation:
- phenotypic variation among putative invasion sources using phylogenetic methods
- estimates of differentiation within and among ranges for both traits and neutral markers

Stephen R. Keller, Douglas R. Taylor, 2008: History, chance and adaptation during biological invasion: separating stochastic phenotypic evolution from response to selection. Ecological Letters11(8): 852-866



Bromus tectorum

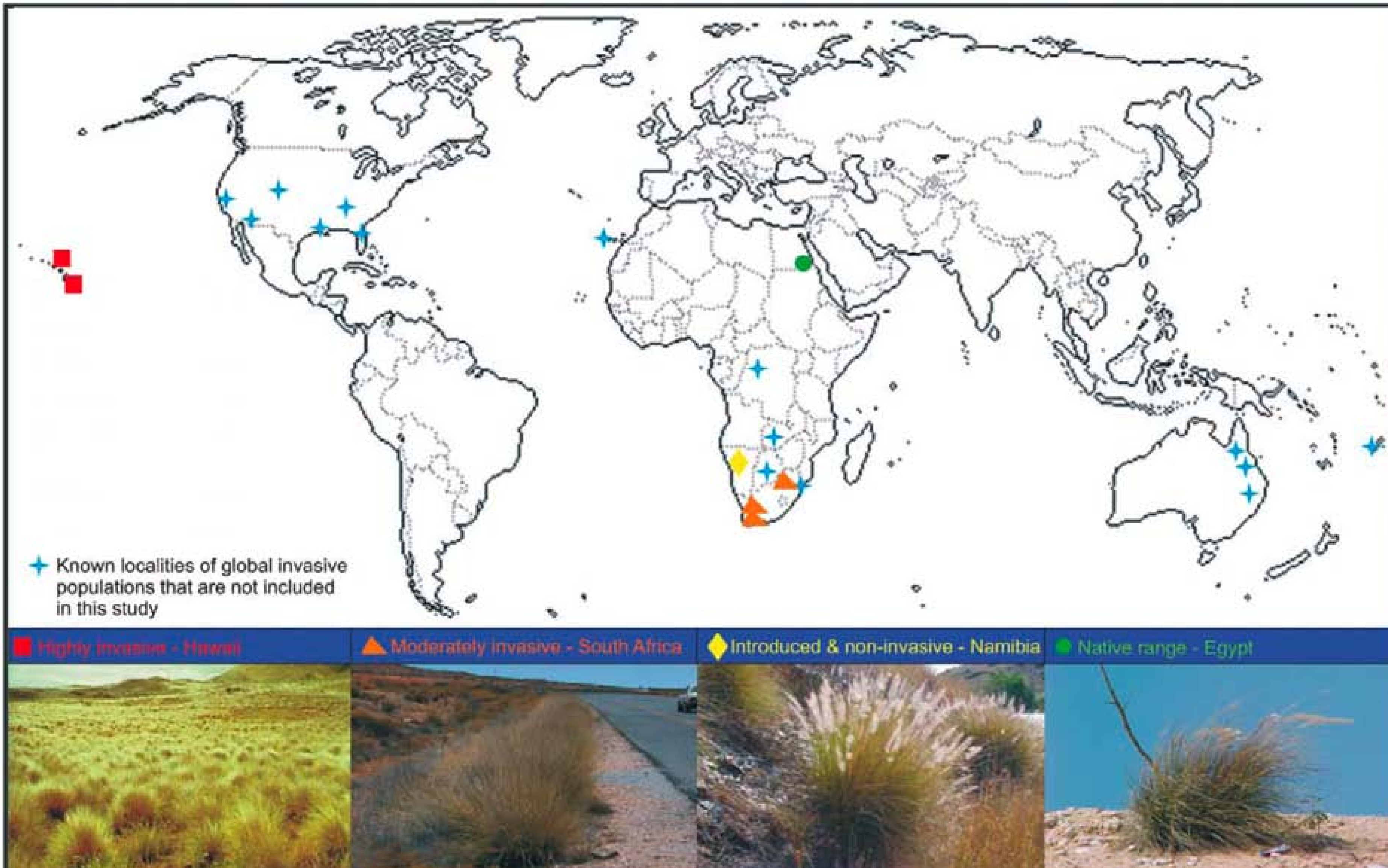


- East coast: genetic variation in Canada significantly higher
- West Coast: similar in the US
- more heterozygous individuals in Canada,
- outcrossing could create new genotypes, spark adaptive evolution and further range expansion

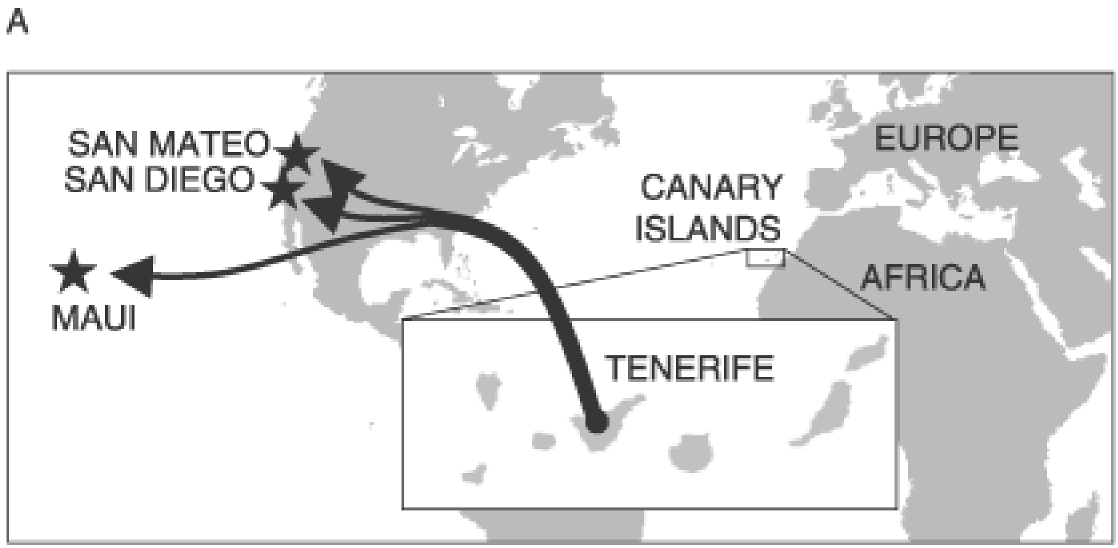
Valliant, Mack, & Novak: Introduction history and population genetics of the invasive grass Bromus tectorum (Poaceae) in Canada Am. J. Botany, Jul 2007; 94: 1156 - 1169.

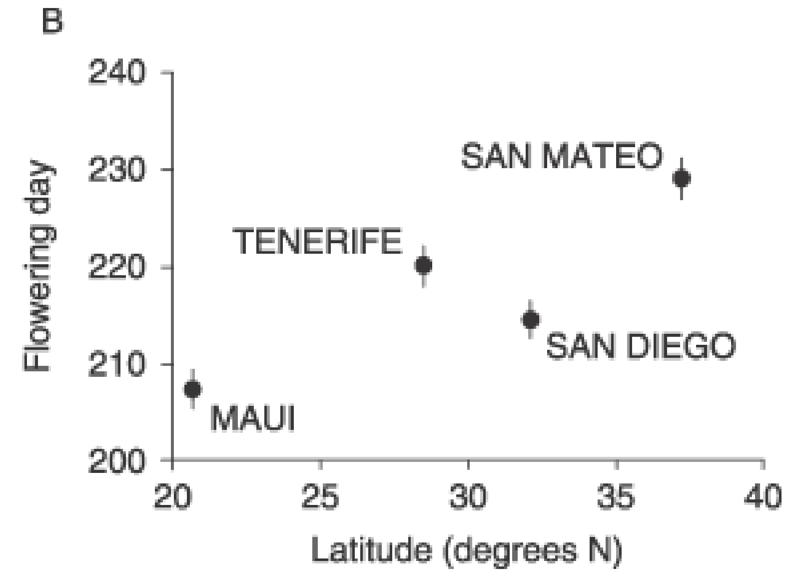
Pennisetum setaceum

Le Roux JJ, Wieczorek AM, Wright MG, Tran CT (2007) Super-Genotype: Global Monoclonality Defies the Odds of Nature. PLoS ONE 2(7):e590.



Hypericum canariense - a single source population

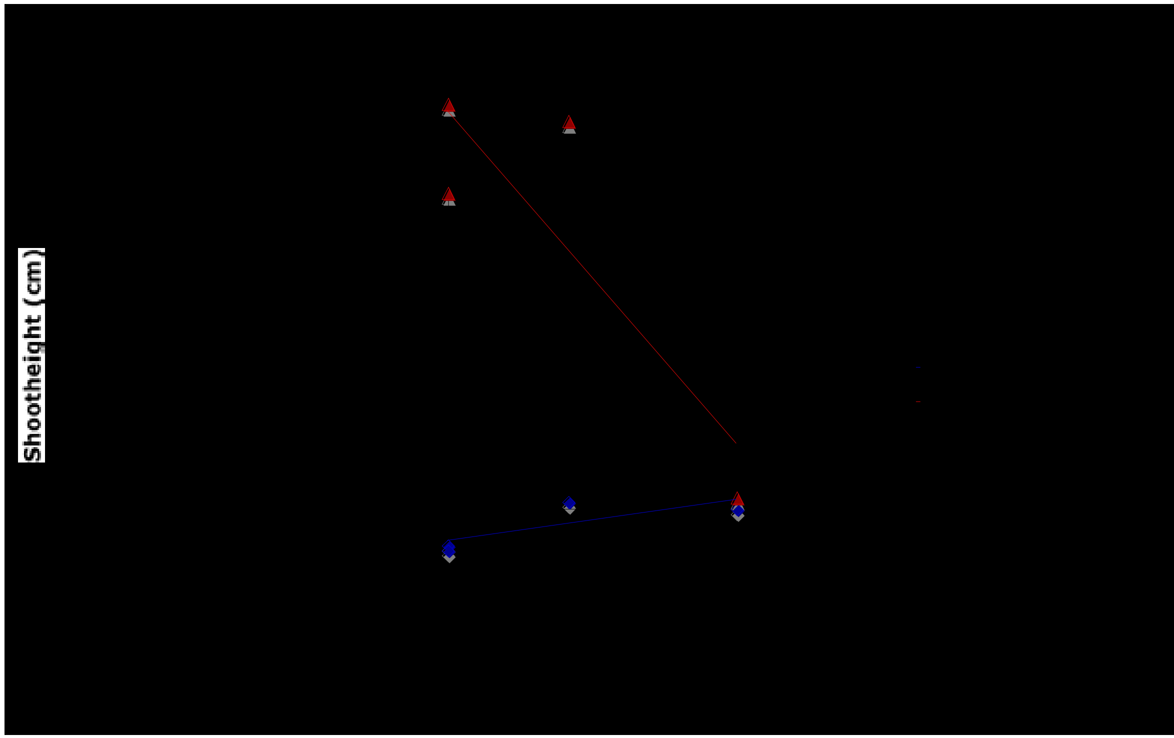




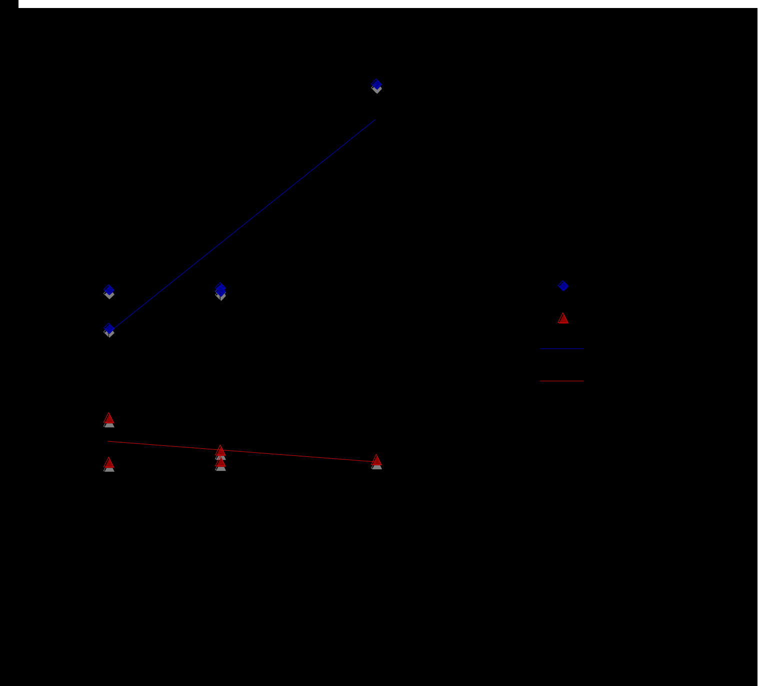
- reproductive isolation has been hypothesized as important first step in adaptive evolution of introduced populations

- may be essential along the altitudinal gradients of the Hawaiian volcanos

Plant performance (Garden experiment 1st year)

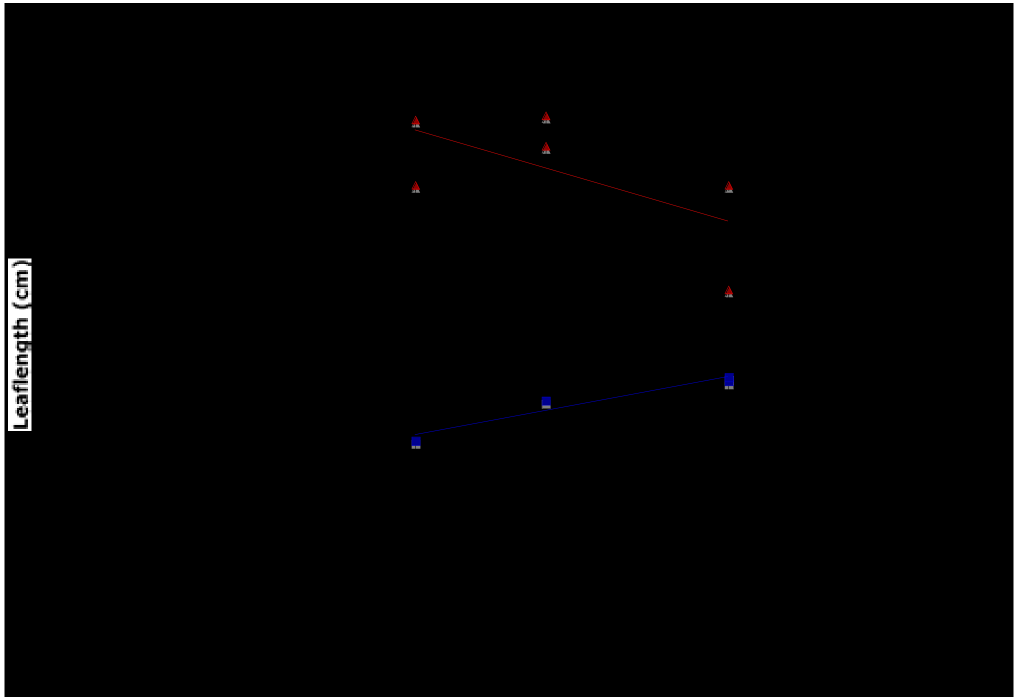


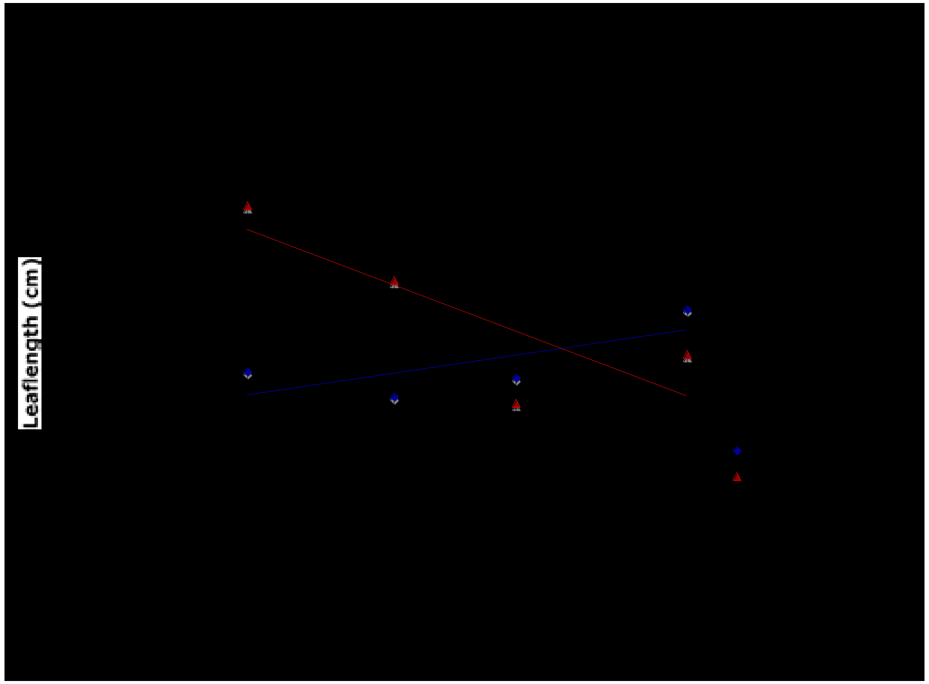
Sonchus oleraceus



Rumex acetosella

Plant performance(Garden experiment 1st year)

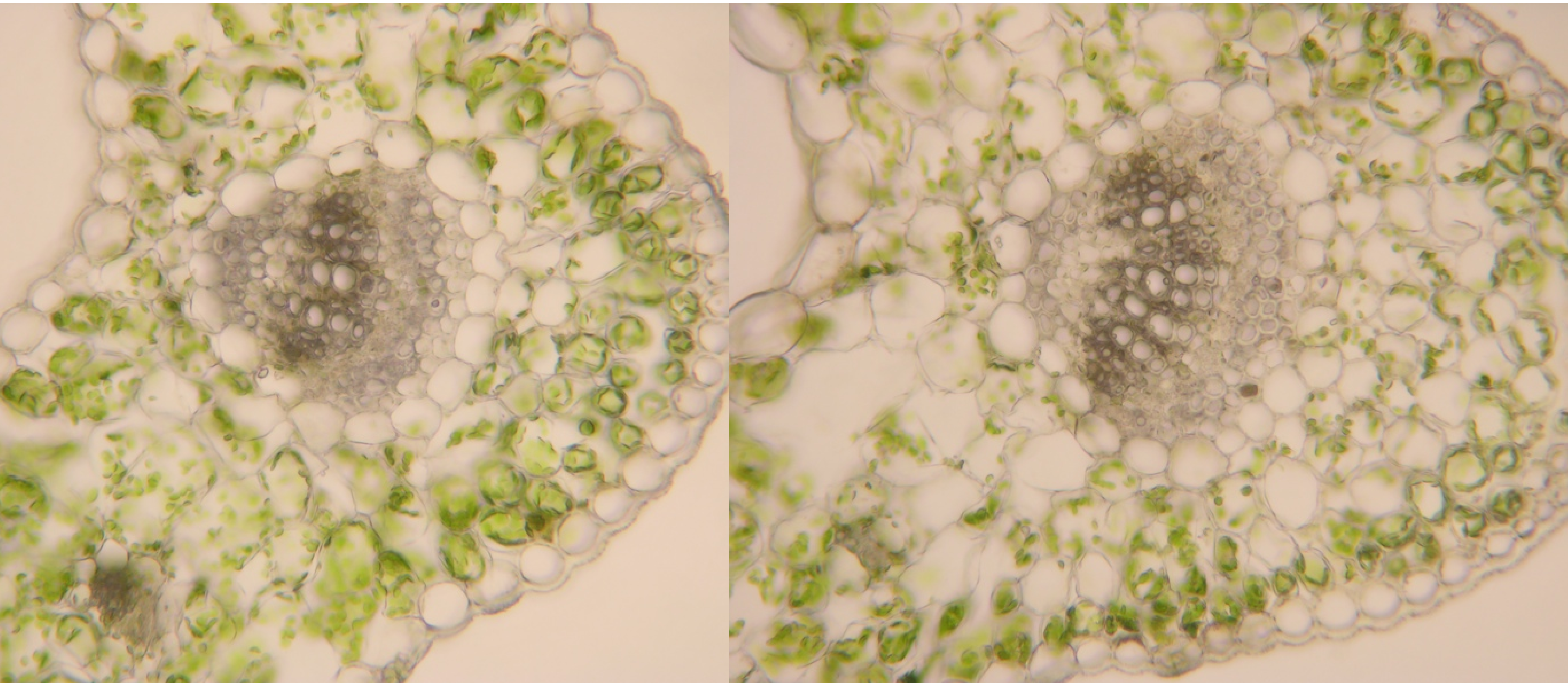




Holcus lanatus

Hypochaeris radicata

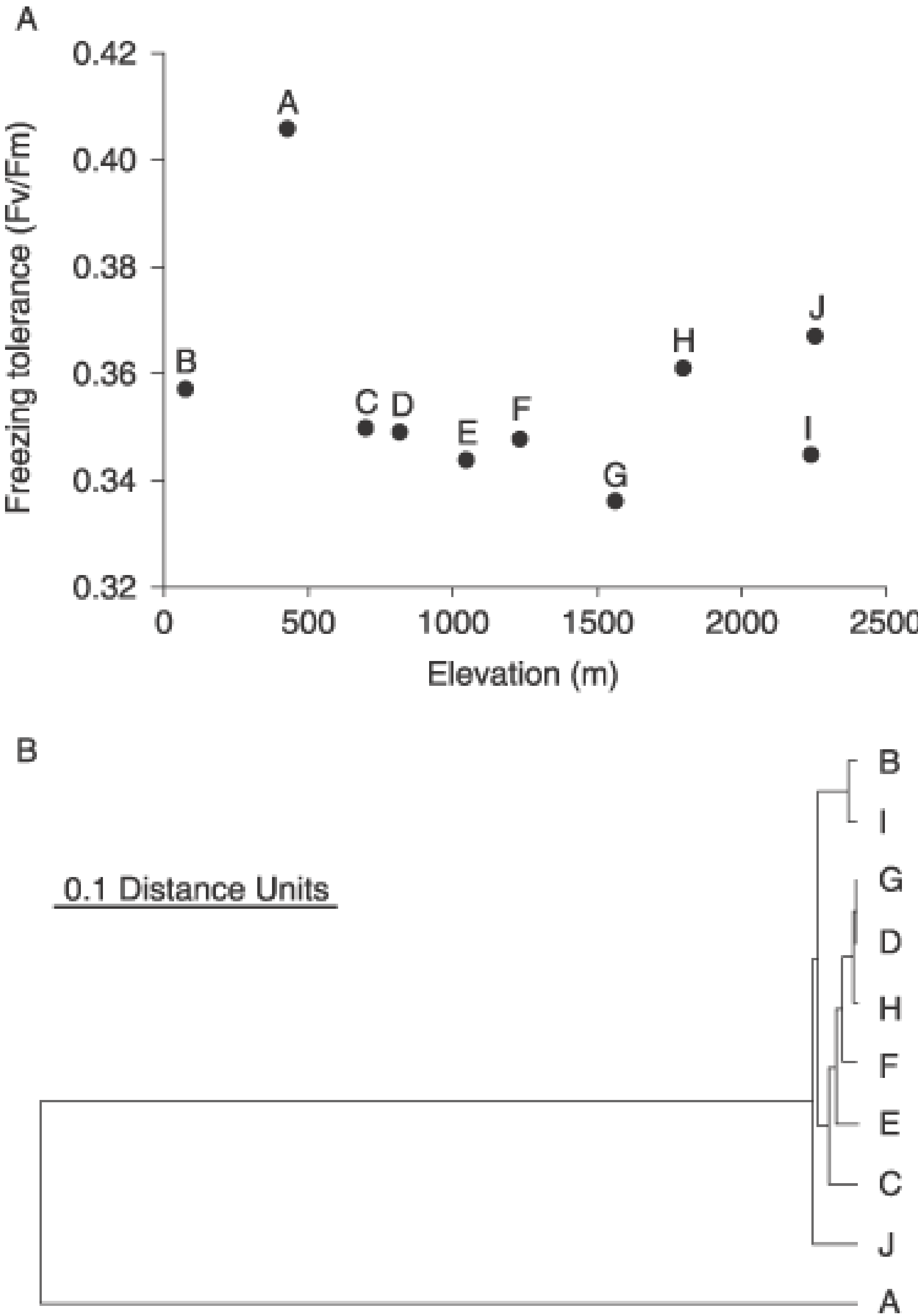
Rapid evolutionary adaptation



- Plantago lanceolata

Rapid evolutionary adaptation

- Plantago lanceolata at high elevations has
- thicker leaves,
- larger mesophyll and larger intercellular air volume,
- higher stomata density,
- thicker cuticles, more trichomes.



Verbascum thapsus

- introduced to California in 1800s
- mal-adapted to frost, even at high elevations,
- A is a separate introduction from the native Eurasian range, presumably from higher altitudes
- repeated introduction not required to explain invasion success of this species

Polyploidisation

- autopolyploidy
- allopolyploidy
- polyploid hybrids tend to have higher fitness than diploids, reduced inbreeding depression

examples: Senecio inaequidens, Follopia species, Caboprotus edulis

Solidago gigantea

Hybridization

- inter- and intraspecific hybrids generate novel genotypes

- examples:
    - Hawaiian duck Anas wyvilliana
    - Hypochaeris radicata and H. glabra, Sonchus oleraceus, and S. asper

Hybridization

- rust Puccinia psidii in myrtle family (Puccinia strains in Florida substantial genetic diversity)

Bright 1998: “An exotic may spend decades as an innocuous good citizen in its new home before some subtle adaptation or shift in the ecological dynamic triggers an explosive invasion.”

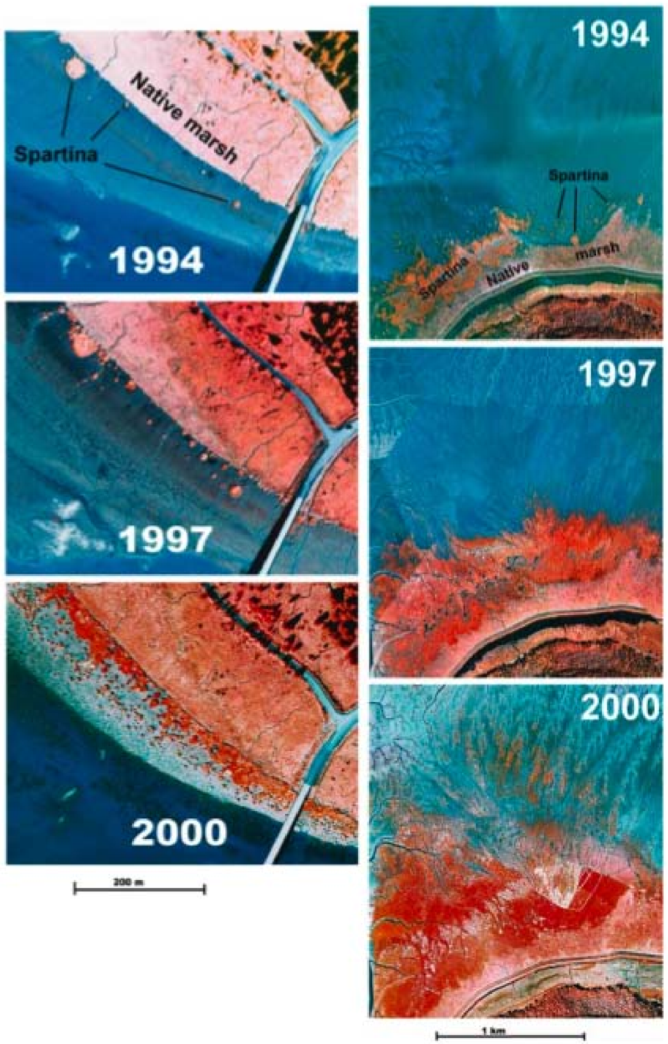
Secondary introductions, quarantine

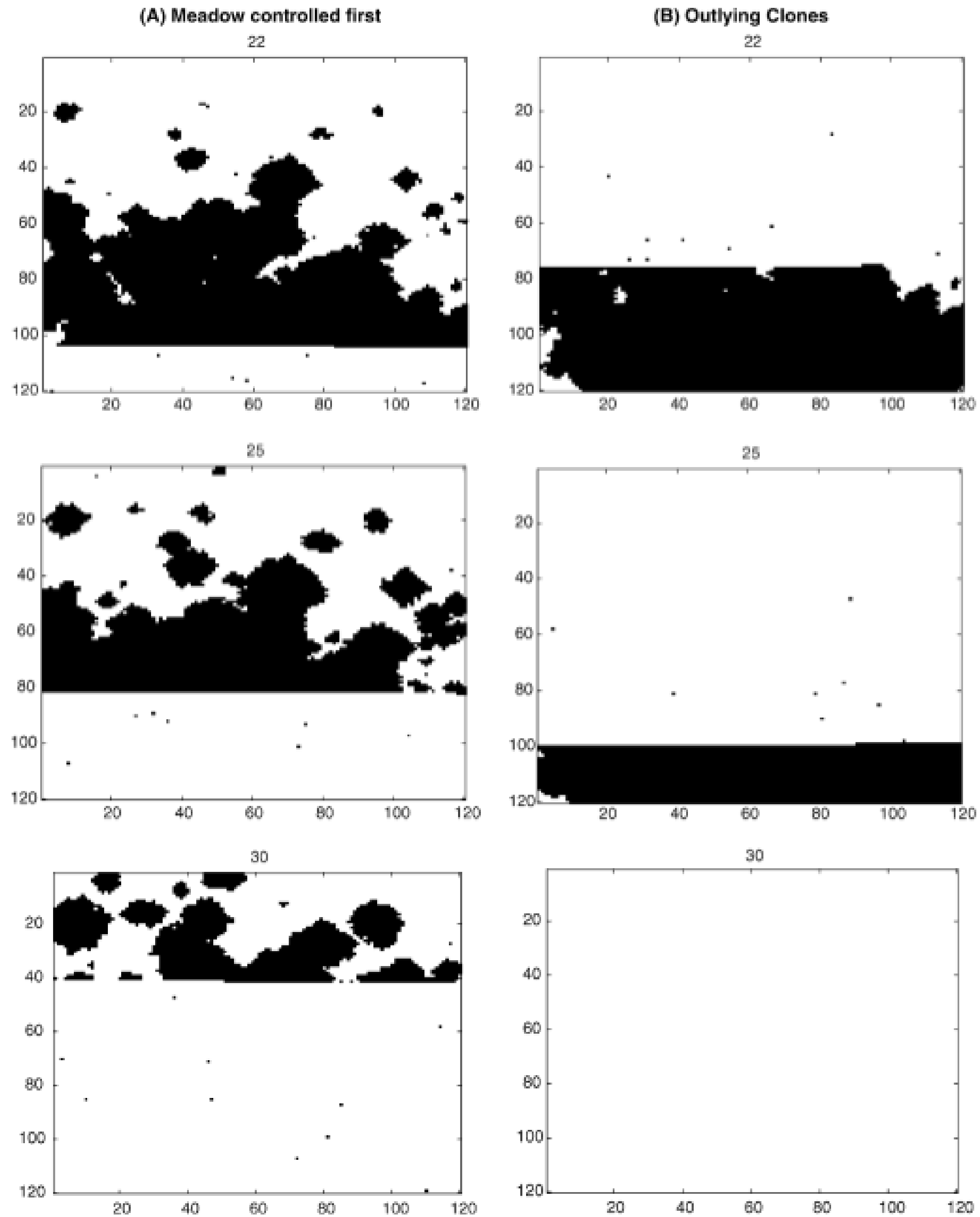
- single vs. multiple introductions
- multiple introductions may provide the genetic resources for better adapted ecotypes in the introduced range
- quarantine important also for species already introduced
- thus: substantial effort should also be directed to preventing secondary introductions and even movement of individuals among introduced populations
- e.g. Puccinia in Florida only became as invasive after several lineages were introduced, multiplying the genetic diversity within the species

Biocontrol agents

- Miconia calvescens
- advantage: no close relatives in Hawaii
- possible species for biocontrol: Ditylenchus drepanocercus
- capable of infecting the Brazilian form of Miconia, but not the Hawaiian one (Seixas & al 2004)
- control agents most successful if sampled in the native range of the target species (Costa Rica for the Hawaiian M. calvenscens)

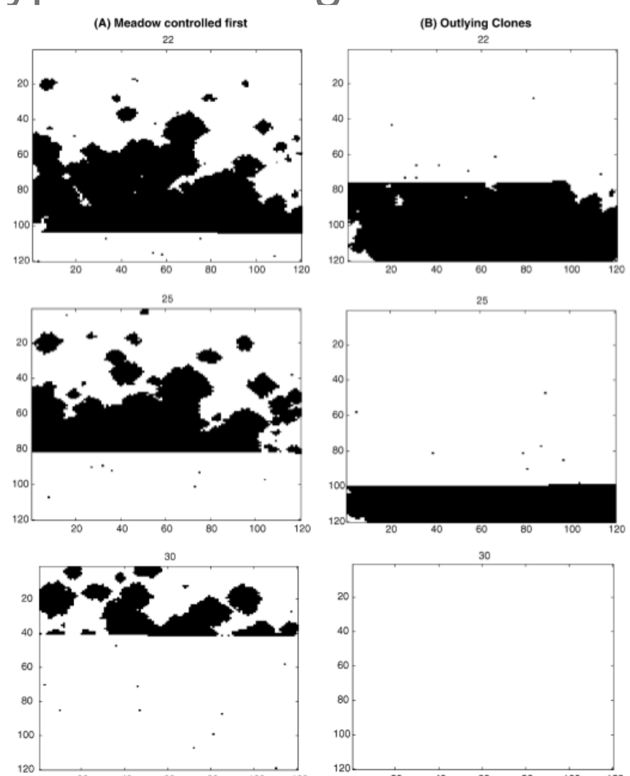
Spartina alternifolia





Strategies for control

- high evolutionary potential:
- population margins with more extreme environmental conditions to prevent the formation of new, better adapted genotypes and range increase



- low evolutionary potential:
- center of the population with higher population densities to limit propagule pressure from the source populations