Molecular Genetic Variation in Cogongrass Near the Point of Initial Introduction into the Southeastern United States

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Botanical Characteristics of I. cylindrica

Inflorescences of I. cylindrica

Morphological differences

Infestation with I. cylindrica

Year	Infested (ha)	Location	Reference
1954	200	Mobile Cty	Tabor (1952)
1974	4,000	Mobile Cty	Dickens (1974)
2003	200,000	SW Alabama	Faircloth et al. (2003)

- 20-fold increase from 1954 to 1974
- 50-fold increase from 1974 to 2003
  - Most likely an underestimate of the total area currently infested
    - Survey concentrated on highway right-of-ways

Sampling Cogongrass in Mobile Cty

Amplified Fragment Length Polymorphism (AFLP)

- A PCR-based molecular technique that can provide
  - An estimate of genetic diversity in introduced species,
  - Evidence of multiple introductions,
  - Evidence of zones of hybridization, and
  - Identify compatible relationships between biocontrol agent and weed host

AFLP protocol

- Extract total genomic DNA (CTAB protocol)
- Quantify and standardize DNA concentrations
- Standard AFLP protocol
  - Pre-amplification
  - Selective amplification
- Banding patterns visualized with IR dyes
- Manual scoring

Statistical Analysis

- Cluster analysis
  - Relationship based on the banding profile of individuals
  - Assigns these individuals to artificial clusters
- Canonical discriminant analysis
  - Analysis based on preexisting groups (sampling sites)
  - Maximizes among group differences based on the common profile of members of a group

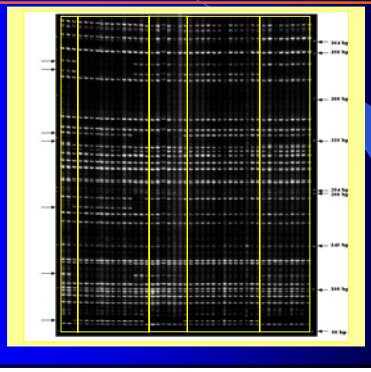
Statistical Analysis (cont.)

- Gene diversity estimates
  - A measure of genetic variance of a population equal to the probability of identity of randomly chosen genes
- Gene flow (Nm) estimates
  - Refers to all mechanisms resulting in the movement of genes from one population to another

Polymorphism and Gene Diversity

	Polymorhic markers		Gene
Population	n	%	diversity H_T
P1	59	43	0.10
P2	55	40	0.14
P3	68	50	0.16
P4	58	42	0.13
P5	48	35	0.09
P6	59	43	0.10
P7	44	32	0.11
P8	45	33	0.09
Pi	27	20	0.07

AFLP Fingerprint - Grouping by Location



Analysis of Molecular Variance (AMOVA)

Source of variation	df	Variance components	percentage	Fixation Index Φ_{ST}
Among populations	8	5.8	44	0.44
Within populations	126	7.5	56	
Total	134	13.3	100	

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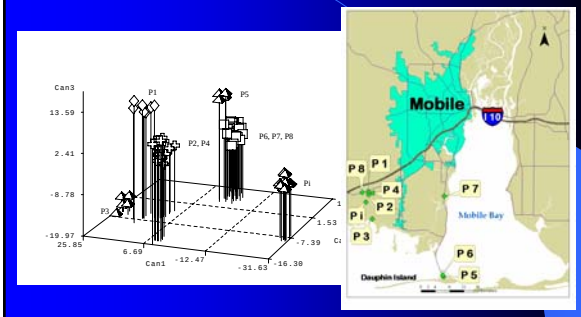
Canonical Discriminant Analysis



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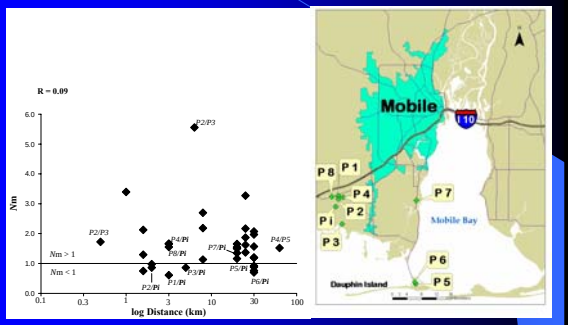
Gene Flow Estimates



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Why are Gene Flow Estimates N.S.

- Close geographic proximity
- Statistics are not very sensitive

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Summary

- AFLPs work well in weedy species
- Populations of I. cylindrica near the point of initial introduction contain quite a bit of genetic variation
- 74 % of all AFLP markers showed polymorphism

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Summary (cont.)

- Founder effect. The founder source contains the lowest gene diversity. Something that was not well-known
- 56 % of the molecular variance was contained within populations
- Evidence that populations are differentiated

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Summary (cont.)

- In both cases (molecular and historical) there is no evidence for private alleles
- Creation of genetic diversity
  - Genetic recombination
  - Variation created at vegetative level
- Anthropogenic dispersal is one of the powerful agents for local dispersal of I. cylindrica