

Medusahead (*Taeniatherum caput-medusae*) Distribution and Genetics: Morphological and Genetic Differentiation Among Subspecies

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**TAXONOMIC COMPLEXITY:
RECOGNIZING DIFFERENT SUBSPECIES**

Taxonomic Complexity: Identification of Multiple, Morphologically Similar Subspecies

- Recognize invasive and non-invasive subspecies in their native range (e.g., *Acacia nilotica*, Kriticos et al. 2003)
- Identify native and non-native subspecies in the invasive range (e.g., *Phragmites australis* in N.A., Saltonstall et al. 2004)
- Identify different invasive subspecies of the same species (e.g., *Lepidium draba*, Gaskin et al. 2005)
- Detection of a cryptic invasion through the identification of a previously unrecognized invasive subspecies (Bickford et al. 2006)
- Aids in the search for the most specific and effective biological control agents in the native range (Wardill et al. 2005, Palmer et al. 2010)

Medusahead

Taeniatherum caput-medusae (L.) Nevski

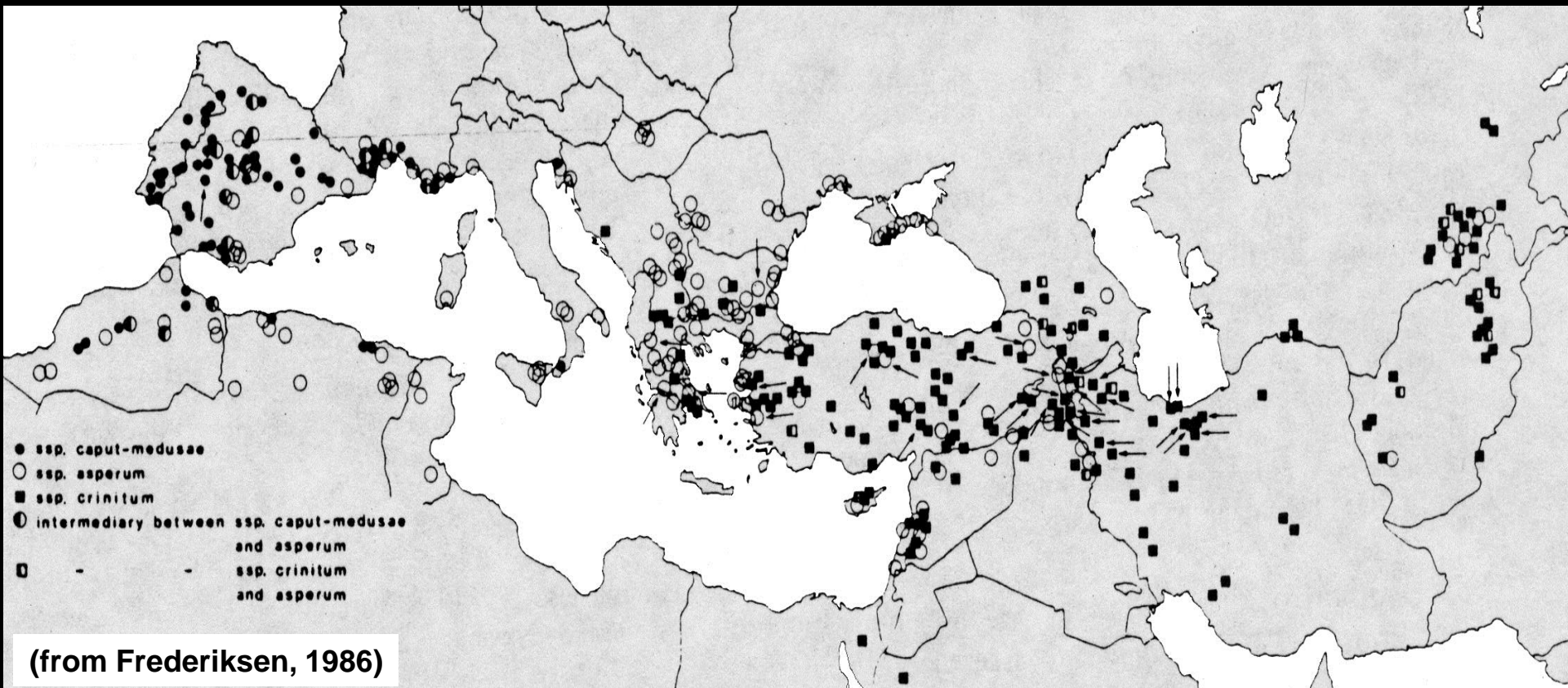


Medusahead



- Annual grass
- Triticeae “wheat tribe”
- Diploid ($2n = 14$)
- Primarily self-pollinating
- Occupies semi-arid habitats
- Found on disturbed sites
- Widely distributed in Eurasia
- Three subspecies
- Invasive in western USA
- Detailed collection history

Medusahead Native Range Distribution



Three Subspecies in Eurasia



ssp. crinitum



ssp. caput-medusae



ssp. asperum

“Apparently, the correct taxon for the medusahead of western North America is *Taeniatherum caput-medusae* ssp. *asperum*”

Young 1992 SRM

Objectives of the Study



- 1) Determine the utility of morphological characters to distinguish the three subspecies of medusahead
- 2) Assess morphological differentiation among native populations of the three subspecies
- 3) Determine genetic differentiation among native populations of the three subspecies

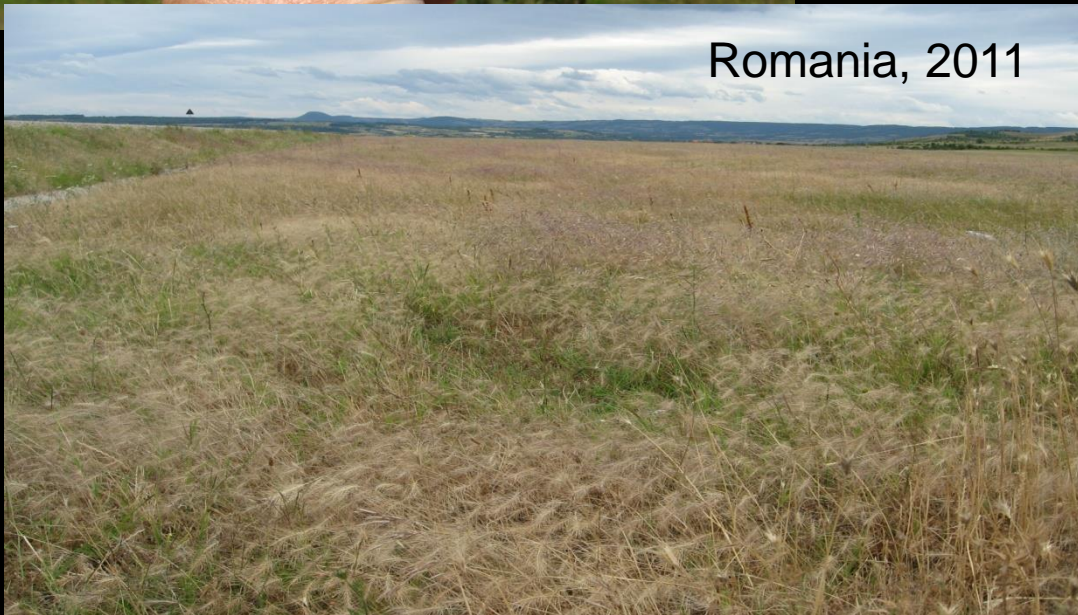
Medusahead Native Range

Macedonia, 2011



Spain, 2009

Romania, 2011



Portugal, 2009

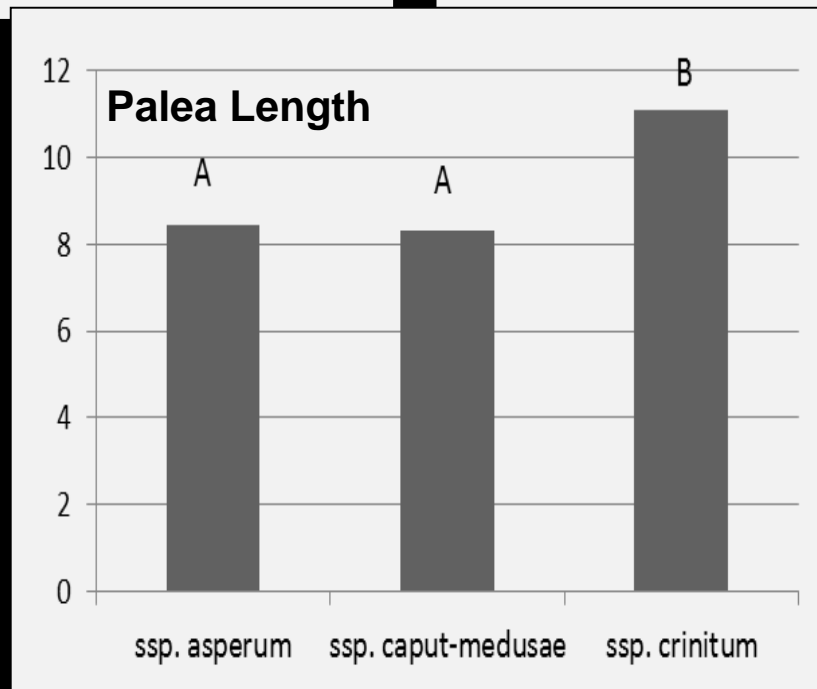
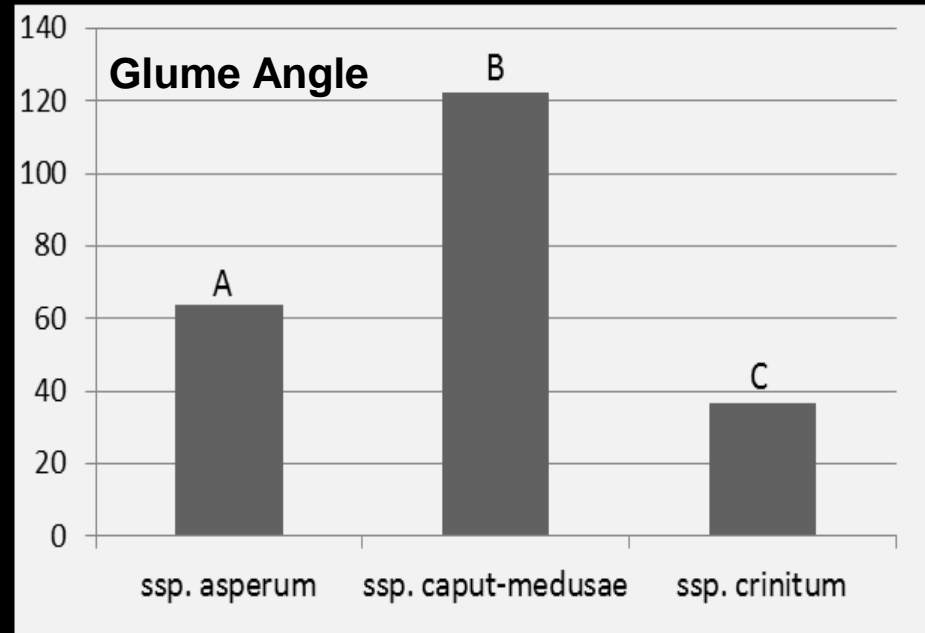
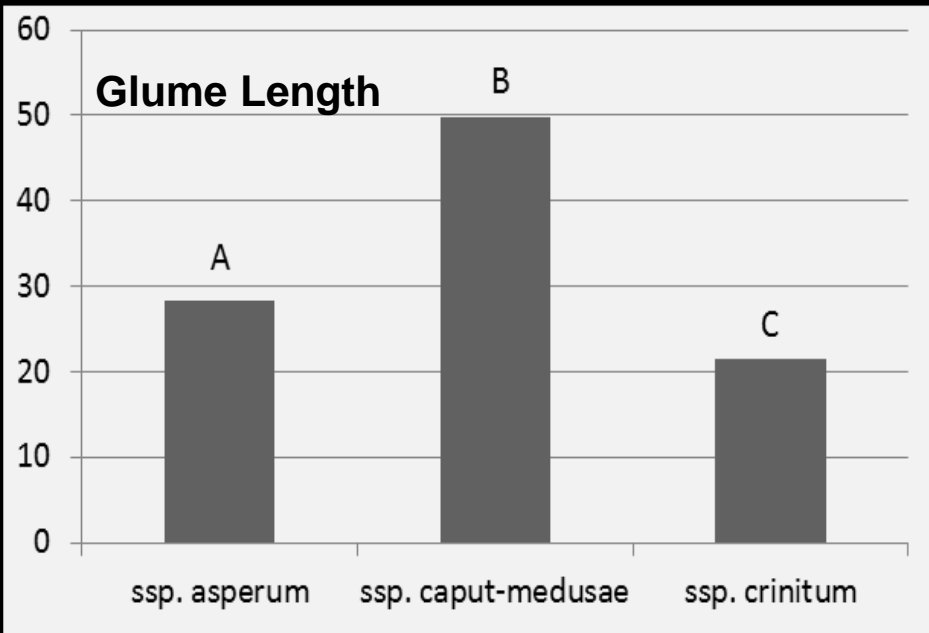
Dracula's Castle Bram, Romania



Medusahead Native Range Sampling



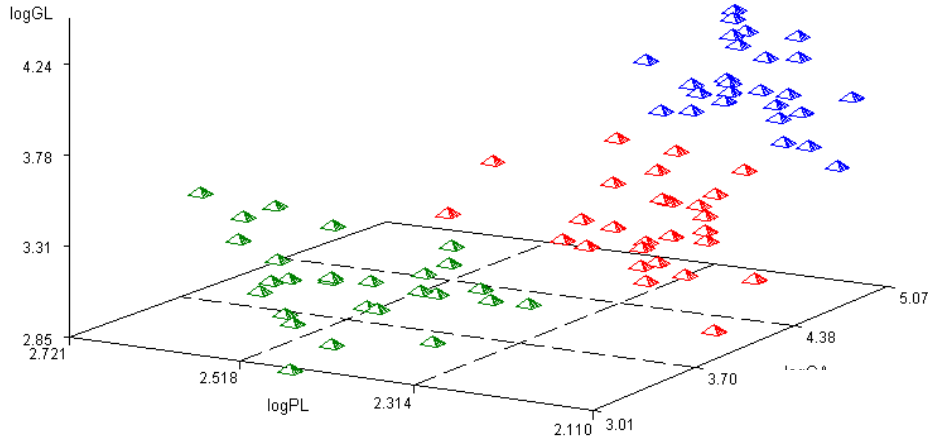
Results: Morphological Characters



Results: Morphological Differentiation

Taeniatherum caput-medusae Subspecies Assignment

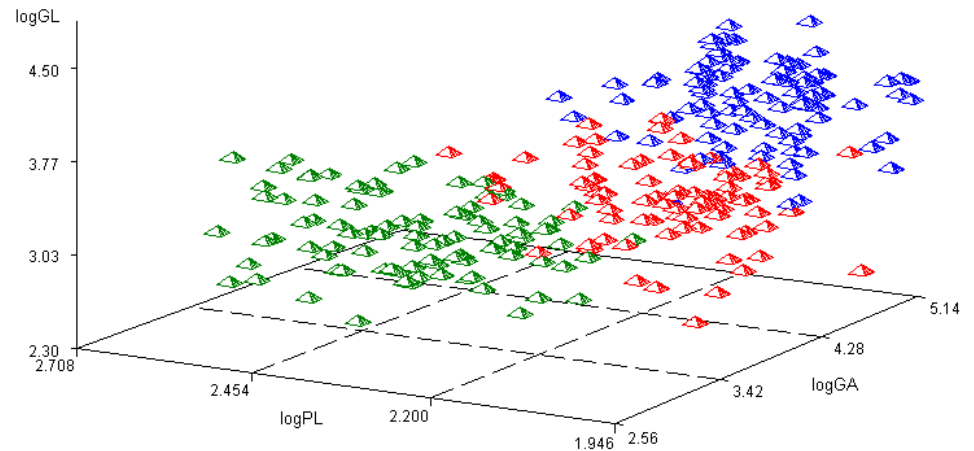
Morphological Measurements



Conical cell and surface hair data not shown

Taeniatherum caput-medusae Subspecies Assignment

Morphological Measurements



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Results: Genetic Diversity

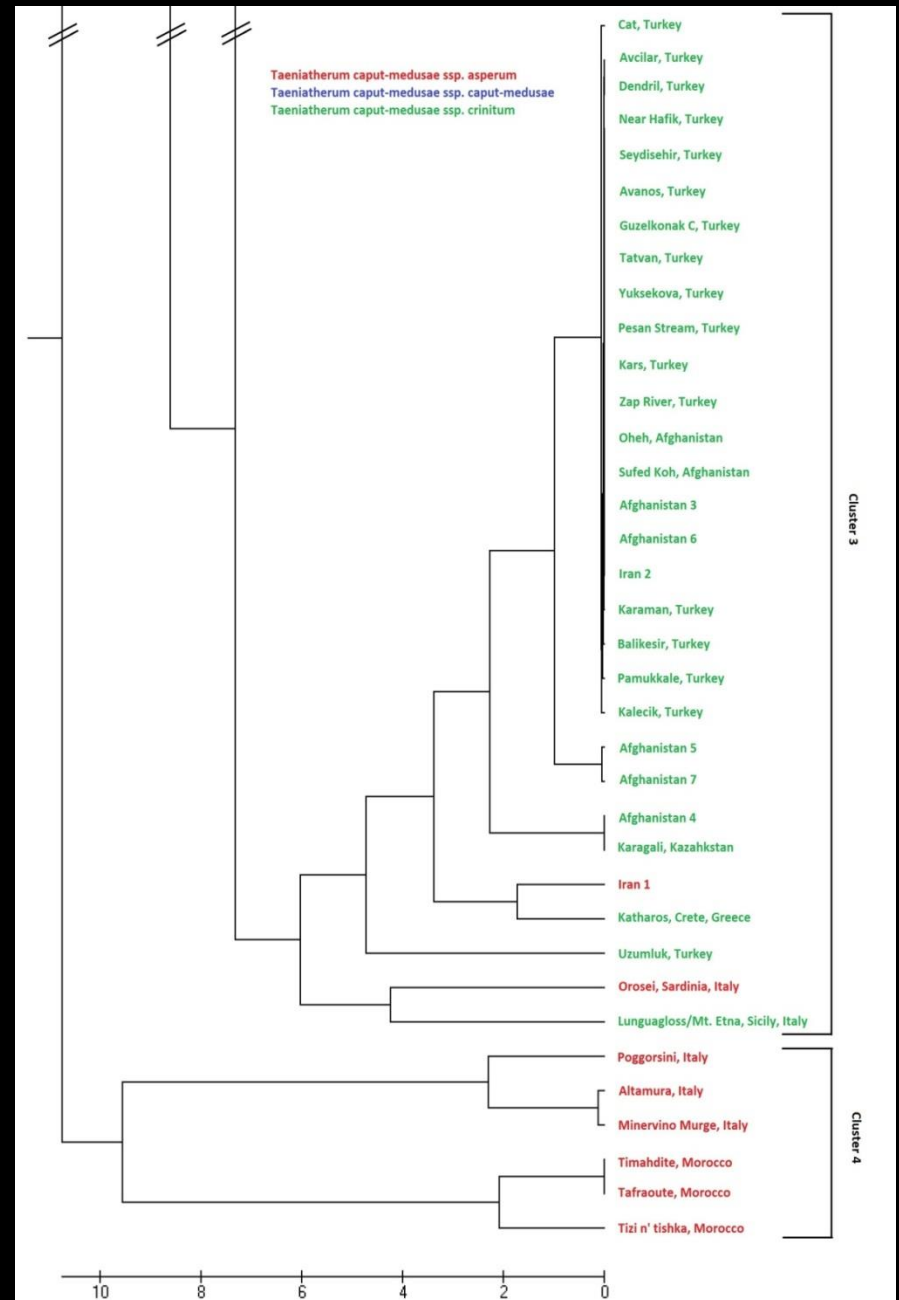
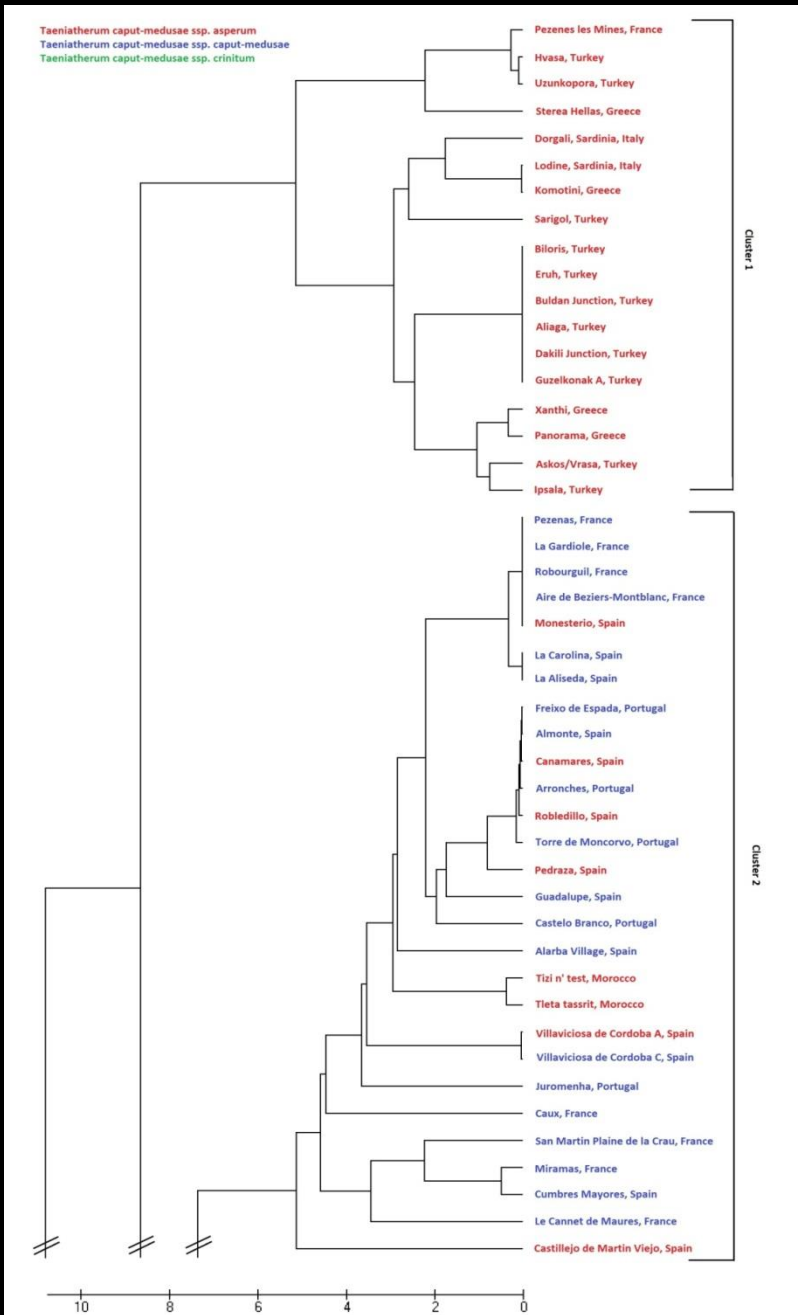
	<i>ssp. asperum</i> (n=34)	<i>ssp. caput-medusae</i> (n=20)	<i>ssp. crinitum</i> (n=28)	Overall
# Alleles	48	36	33	50
Alleles/Locus	2.09	1.57	1.43	2.17
# Polymorphic Loci	15	10	9	16
%Polymorphic Loci	65.22%	43.48%	39.13%	69.57%
%Polymorphic Populations	67.64%	50.00%	39.29%	53.66%
Nei's Expected mean Heterozygosity (H_{exp})	0.1408	0.0725	0.0258	0.1314
Mean observed Expected Heterozygosity (H_{obs})	0.0126	0.0126	0.0126	0.0126
Fst	0.8423	0.8663	0.8285	0.9081
Nm	0.0468	0.0386	0.0518	0.0253
# of Multilocus Genotypes	66	22	11	93

Genetic Structure of Native Populations of Medusahead

AMOVA:

	d.f.	Sum of Squares	Variance Components	Percentage Variation
Among subspecies	2	2651.552	0.86506	48.38
Among populations within subspecies	75	3455.088	0.79073	44.22
Among individuals within populations	2194	571.854	0.12845	7.18
Within individuals	2272	8.5	0.00374	0.21
Total	4543	6686.994	1.78799	--

Results: Genetic Differentiation



Conclusions: Morphological Differentiation

- 1) Means for glume length and glume angle are significantly different among all three subspecies; whereas ssp. *crinitum* has significantly longer palea length
- 2) In combination, these three morphological characters clearly differentiate populations of the three subspecies
- 3) Overlap occurs among individuals of ssp. *crinitum* and ssp. *asperum*, and ssp. *caput-medusae* and ssp. *asperum*. No overlap was detected for ssp. *crinitum* and ssp. *caput-medusae*
- 4) Morphological overlap among some subspecies is not surprising because intermediate forms have been reported

Conclusions: Genetic Differentiation

- 1) Subspecies *asperum* possesses the highest amount of genetic diversity; *ssp. caput-medusae* has intermediate values, and *ssp. crinitum* has the lowest values
- 2) Four distinct clusters of populations were observed; with populations of *ssp. asperum* occurring in several clusters
- 3) Subspecies *crinitum* is genetically differentiated from the other two (Cluster 3); some populations of *ssp. asperum* and *ssp. caput-medusae* co-occur within Cluster 2
- 4) Co-occurrence of some individuals of these two subspecies within the same cluster may reflect past hybridization events

GEOGRAPHIC ORIGINS, MULTIPLE INTRODUCTIONS AND FOUNDER EFFECTS

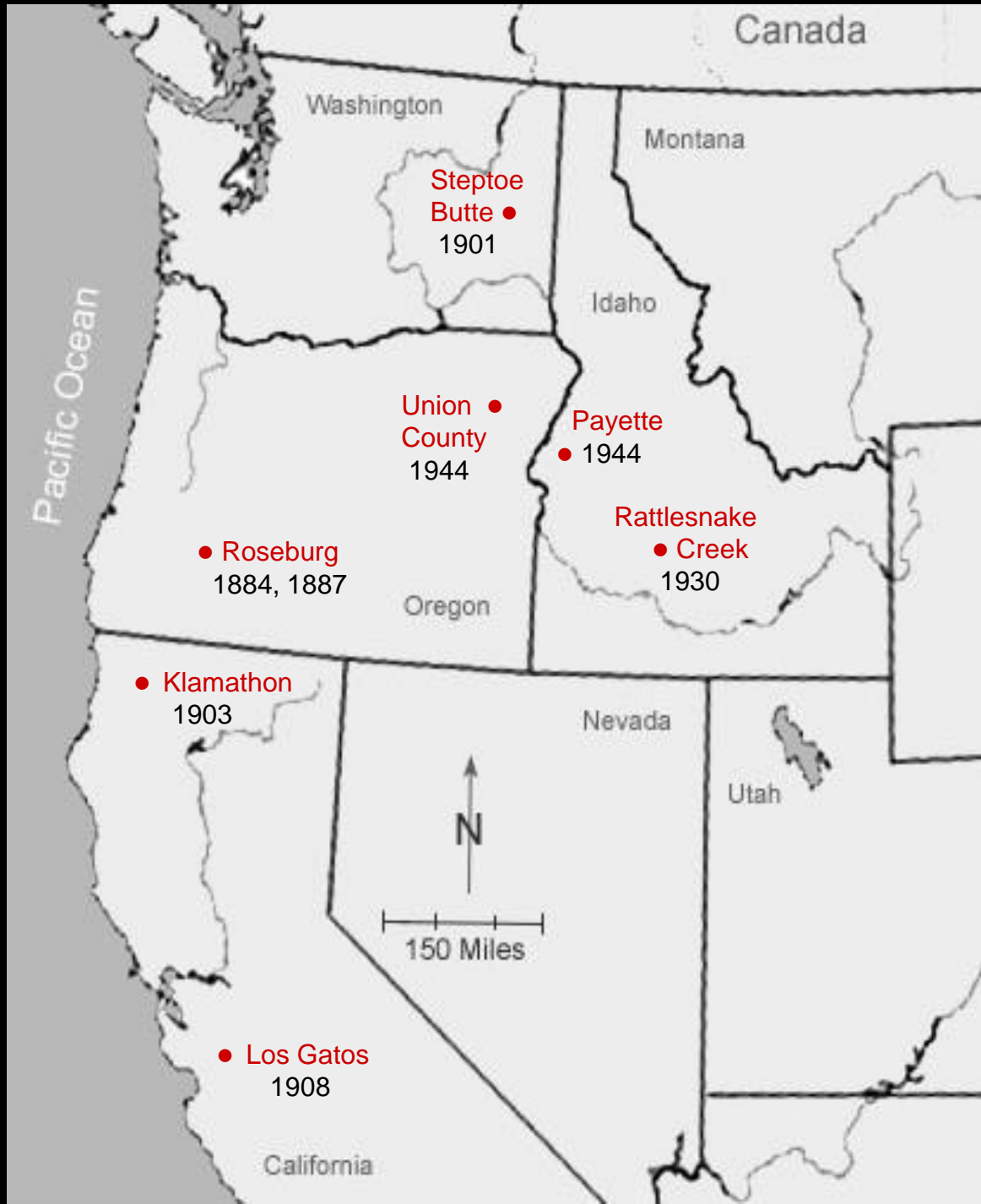
Insight from the Combined Analysis of Native and Invasive Populations

- Identify geographic origins (source populations)
- Assess introduction dynamics (multiple vs. single introductions) and mechanism of range expansion (local vs. widespread)
- Genetic consequences of introduction events (founder effects?)
- Role of post-immigration evolution vs. pre-adaptation in invasion
- Implemented in management of invasive species (biological control programs)

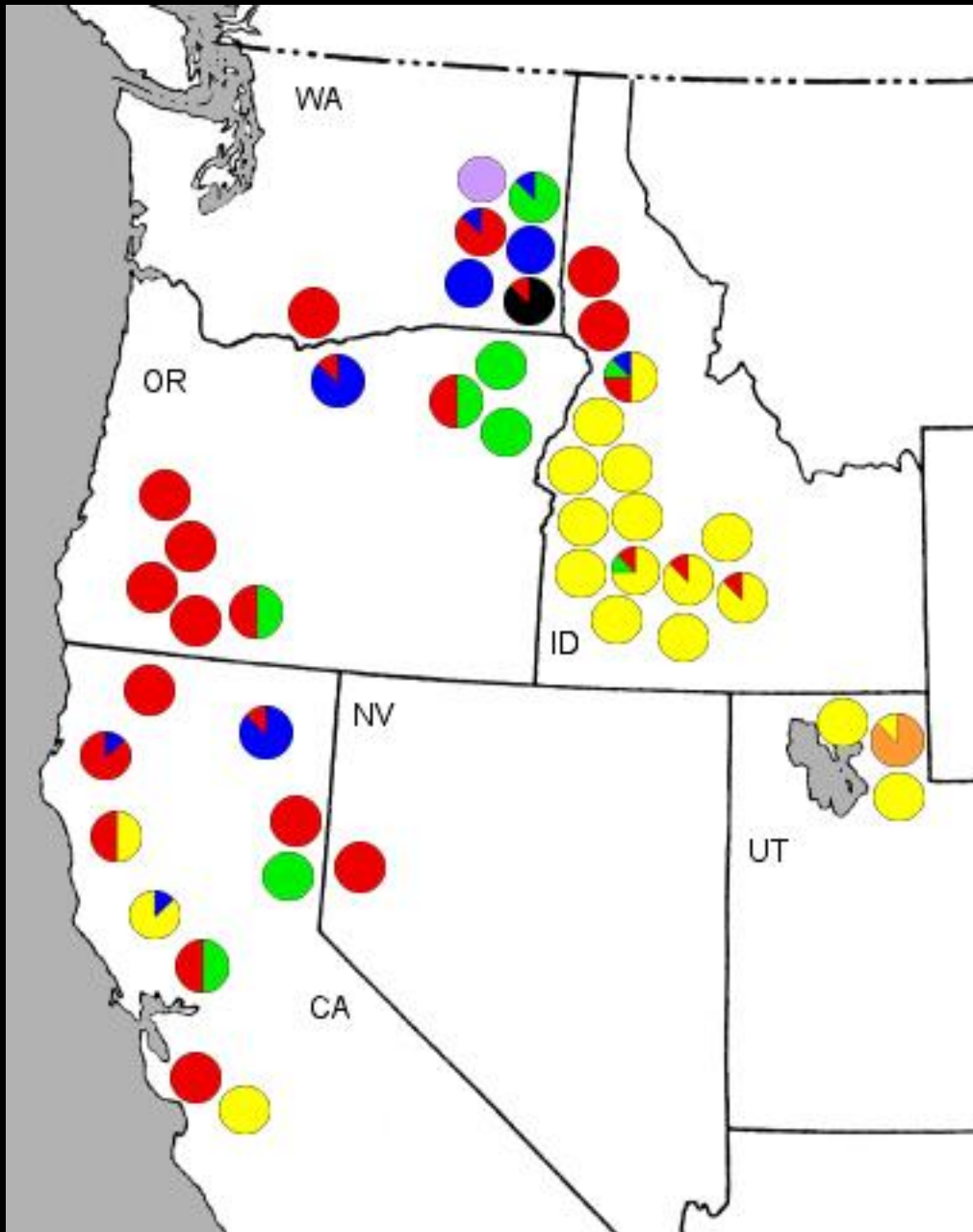
Medusahead



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Results



- 45 populations (1663 indivs.)
- 15 enzyme systems (29 loci)
- 5 variable loci (*Pgi-2*, *Mdh-2*, *Adh*, *6Pgd-2*, *Pgm-2*)
- 7 homozygous multilocus genotypes (MLG)
- 4 MLG associated with early collection sites



Multiple Introductions

Objectives of the Study

Spain, 2009



- 1) Determine the geographic origins for the invasion of medusahead in western US
- 2) Assess the introduction dynamics (single vs. multiple) of medusahead
- 3) Determine whether medusahead has experienced founder effects during its invasion in western USA

Medusahead Native Range

Italy, 2009

Romania, 2011



Spain, 2009

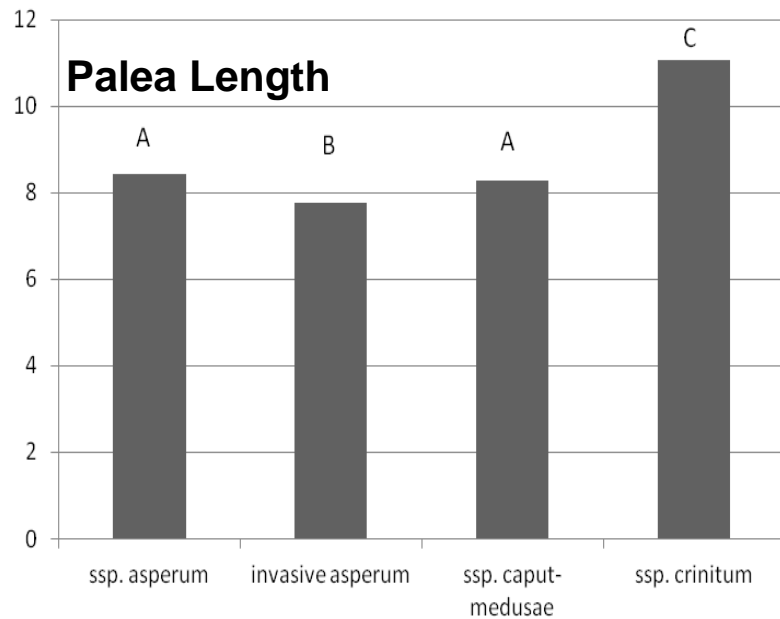
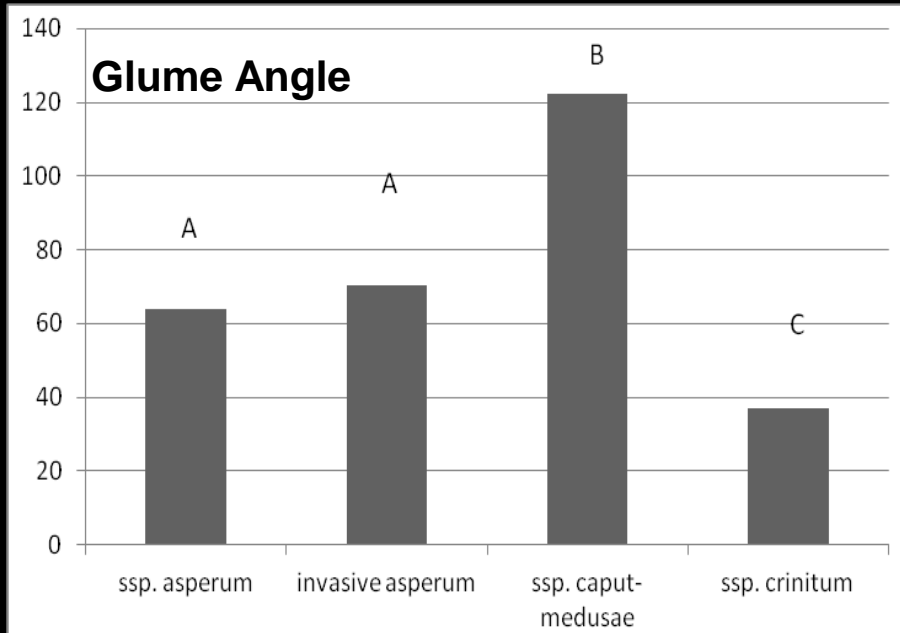
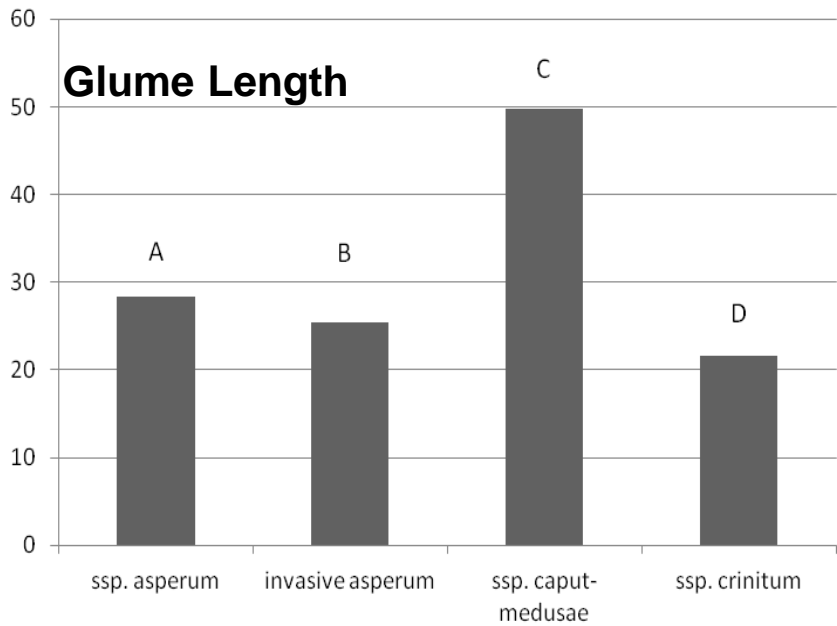


Bulgaria, 2011

Medusahead Native Range Sampling



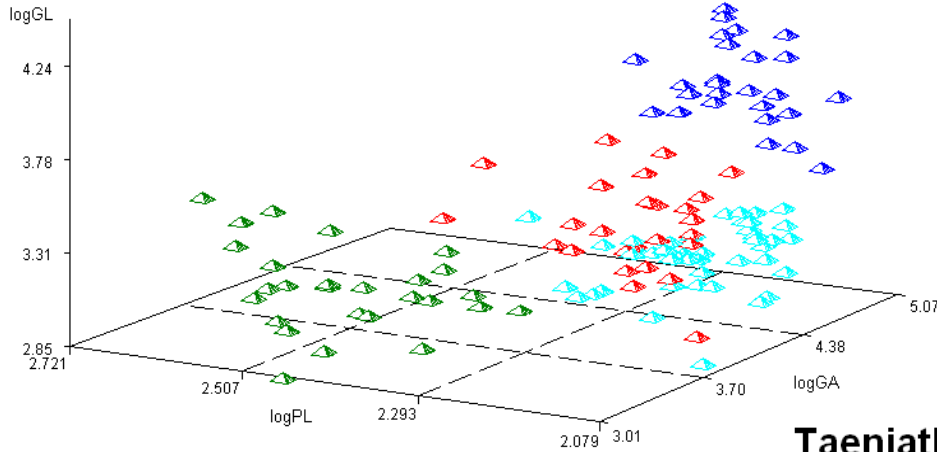
Results: Morphological Characters



Results: Morphological Differentiation

Taeniatherum caput-medusae Subspecies Assignment

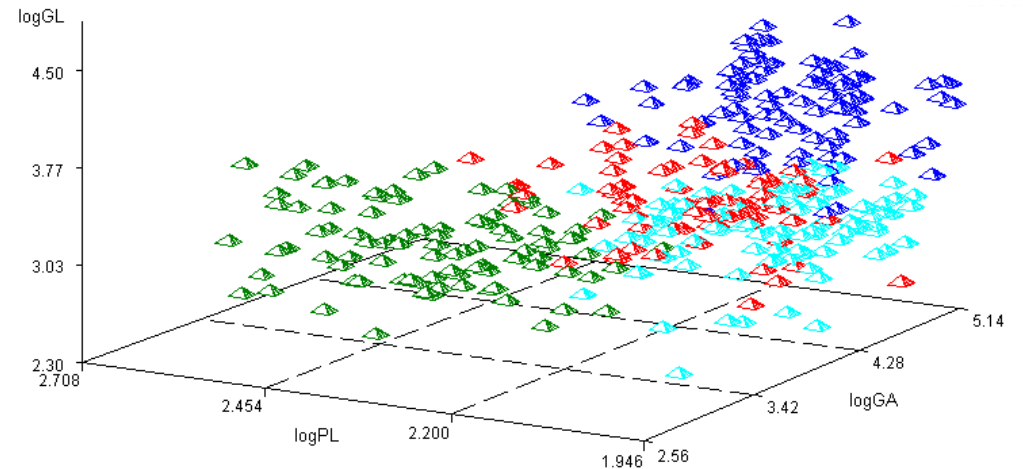
Morphological Measurements



Conical cell and surface hair data not shown

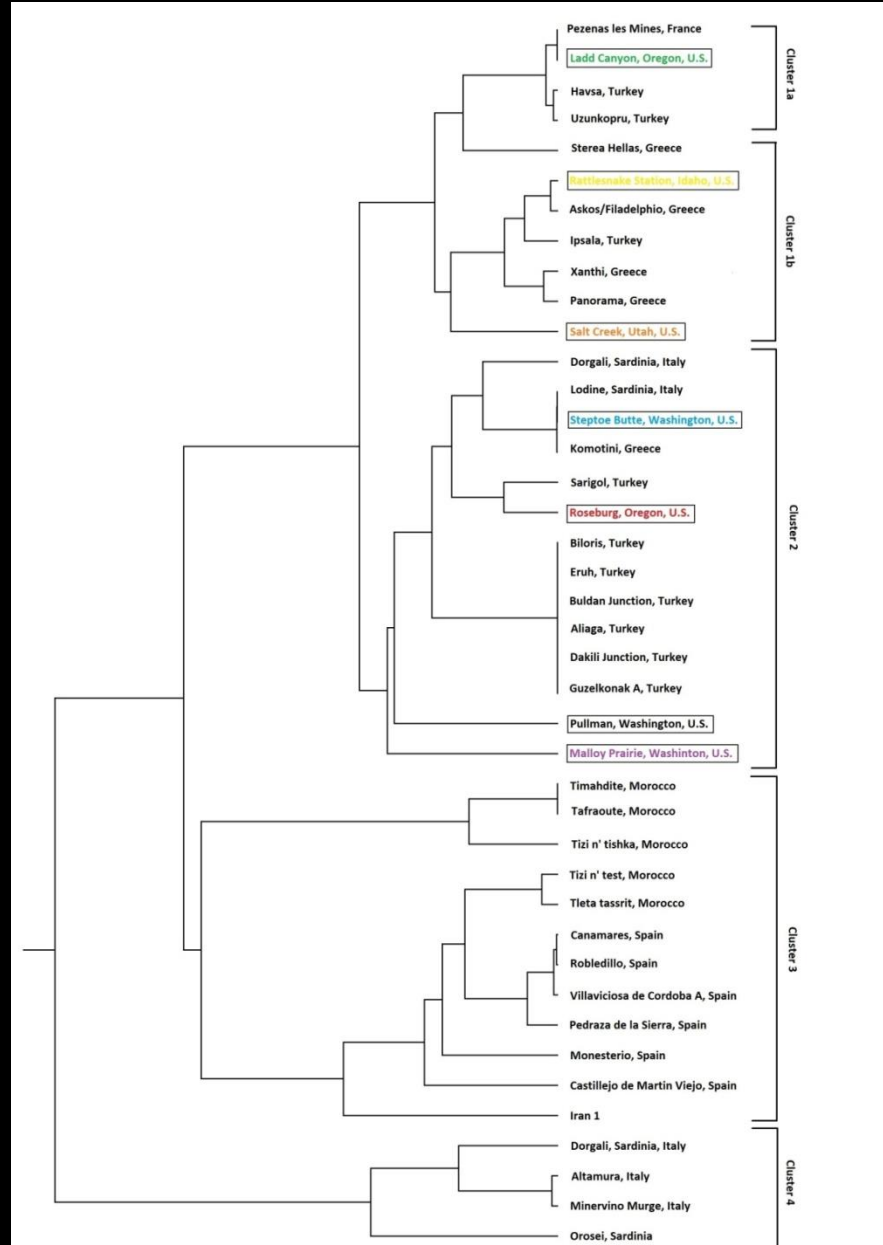
Taeniatherum caput-medusae Subspecies Assignment

Morphological Measurements



Conical cell and surface hair data not shown

Results: Genetic Differentiation



Results: Geographic Origins

- Five multilocus genotypes matched those in western USA
- Source populations: France, Sardinia, Greece and Turkey



Genetic Diversity Across Populations of Medusahead: Founder Effects

	# Pops.	Alleles	Alleles/ locus	# Poly. Loci	% Poly. Loci	% Poly. Pops.
All native pops.	34	48	2.09	15	65.2	67.6
Putative source pops.	10	38	1.65	10	43.5	80.0
Invasive pops.	45	28	1.22	5	21.7	37.8

Genetic Diversity Within Populations of Medusahead: Founder Effects

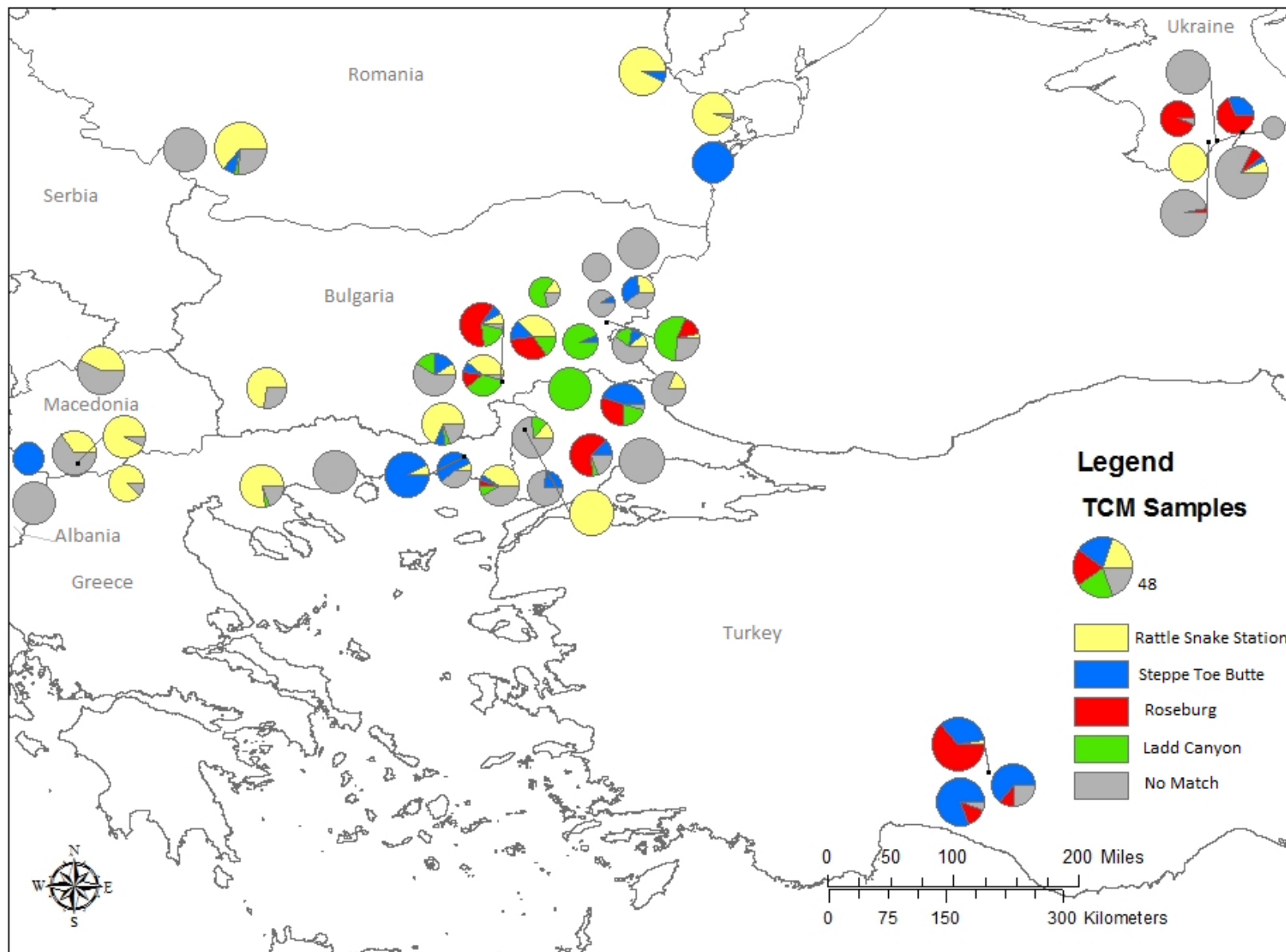
	Alleles/locus	% Poly. Loci	H _{obs}	H _{exp}
All native pops.	1.10	9.08	0.00003	0.0246
Putative source pops.	1.14	12.18	0.00000	0.0361
Invasive pops.	1.02	1.90	0.00010	0.0040

Conclusions: Geographic Origins, Introduction Dynamics and Founder Effects

- 1) Geographic origins of the invasion of medusahead in western US could have been drawn from across much of the native range = France, Sardinia, Greece and Turkey
- 2) Pattern of allozyme diversity in medusahead is consistent with the multiple introduction hypothesis = minimum of 7 introductions
- 3) Founder effects appear to have reduced genetic diversity both across and within invasive populations = genetically depauperate

Conclusions: Genetic Diversity and Management

- 1) Because invasive populations are genetically depauperate, highly adapted biocontrol agents are likely to be quite effective
- 2) Approximately 38% of invasive populations have two or more native genotypes = genetic admixtures
- 3) Thus, complex management strategies may be needed to control invasive populations of medusahead that are admixtures = multiple biological control agents
- 4) The search for biocontrol agents should occur broadly across the Mediterranean, where putative source populations have been identified



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Boise State University

Genetic Structure of Medusahead

AMOVA:

Source	d.f.	Sum of Squares	Variance Components	Percentage Variation
Among regions	3	172.366	0.010692	22.21
Among populations within regions	30	387.291	0.23378	48.57
Among individuals within populations	892	250.433	0.14011	29.11
Within individuals	926	0.5	0.00054	0.11
Total	1851	810.589	0.48135	--

Nei's Gene Diversity Statistics:

Range

\underline{H}_T

\underline{H}_S

\underline{G}_{ST}

Native

0.262

0.043

0.745

Invasive

0.224

0.028

0.906