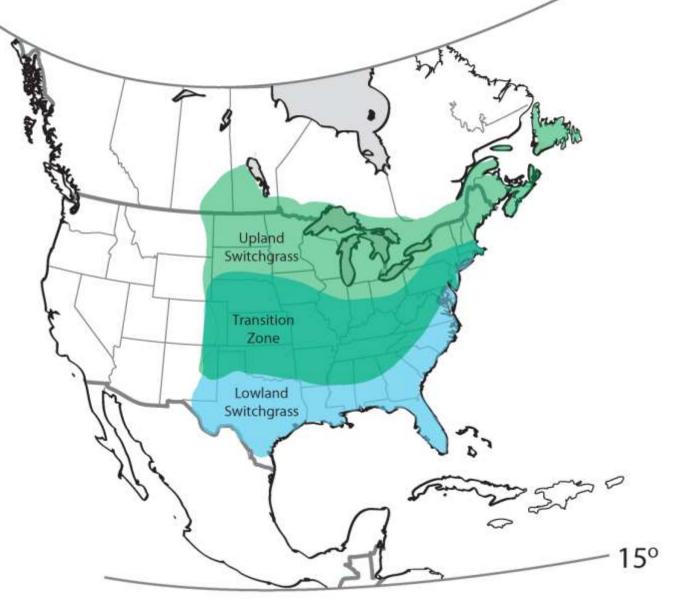
Origins, Adaptive Radiation, and Evolution of Switchgrass

Michael Casler U.S. Dairy Forage Research Center USDA-ARS, Madison, WI & University of Wisconsin



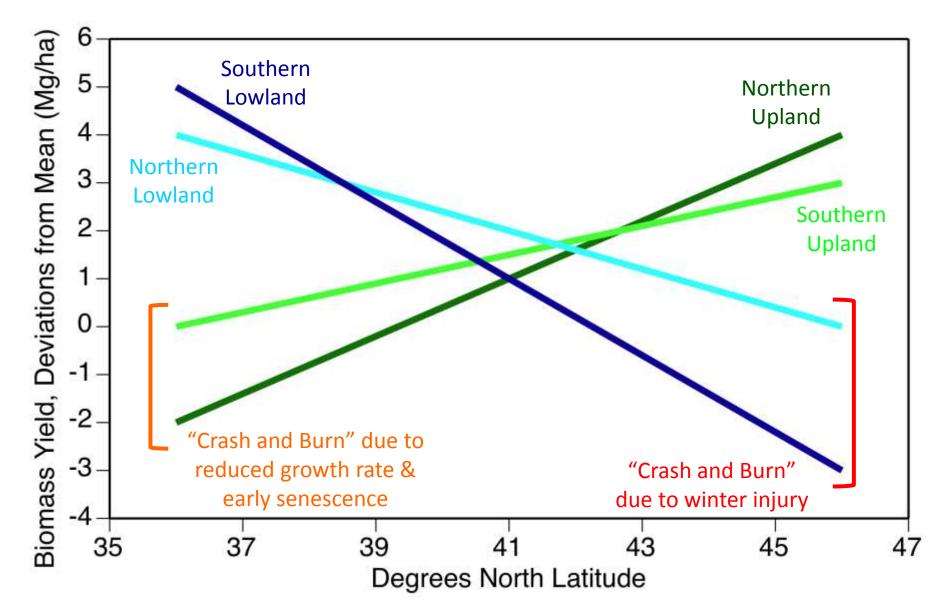
Geographic Distribution of Upland and Lowland Switchgrass Cytotypes



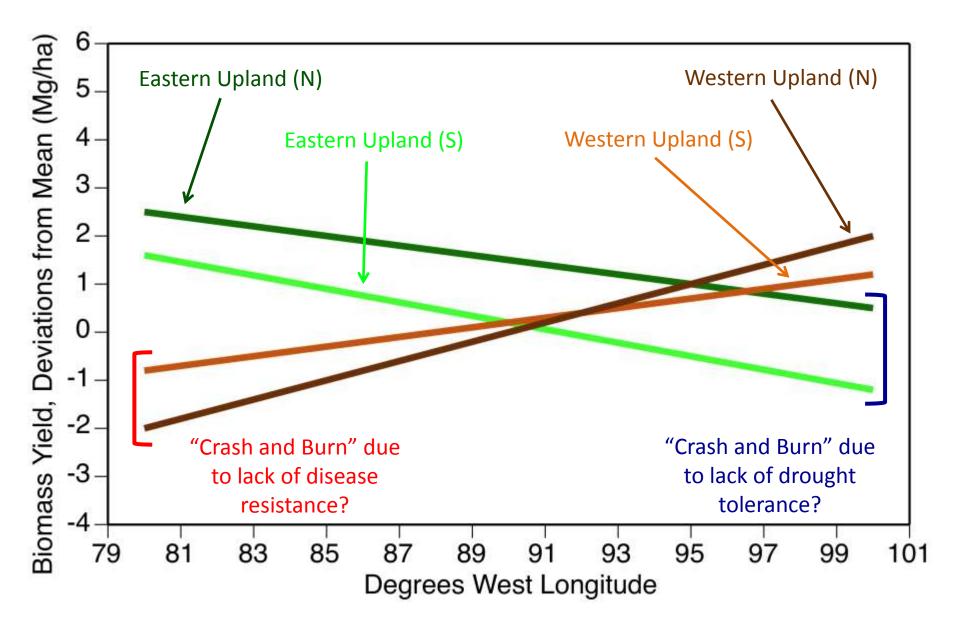
60°

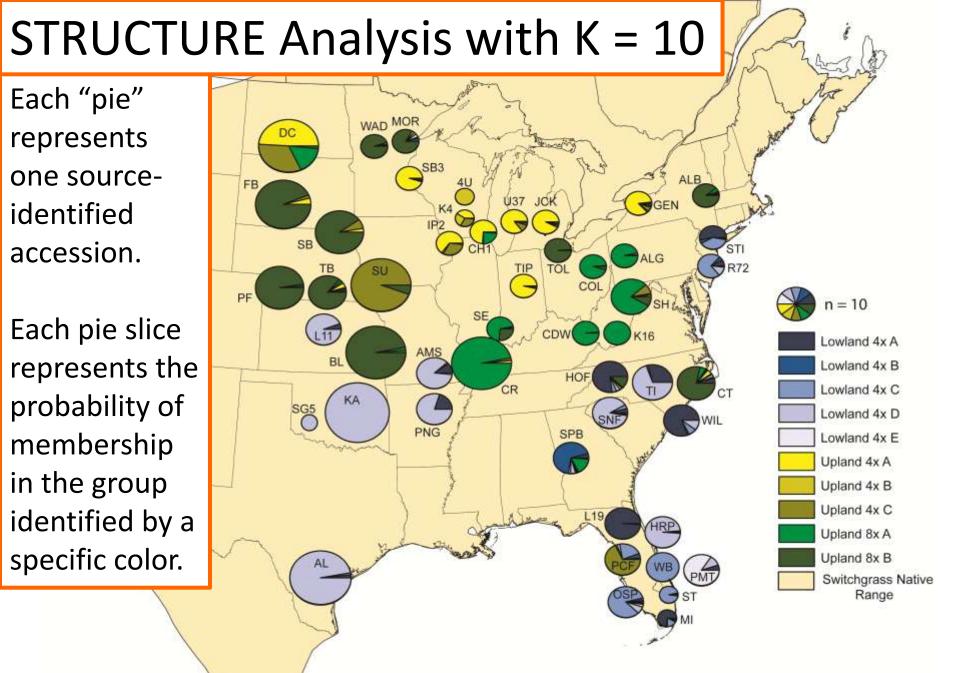


Biomass yield vs. Latitude

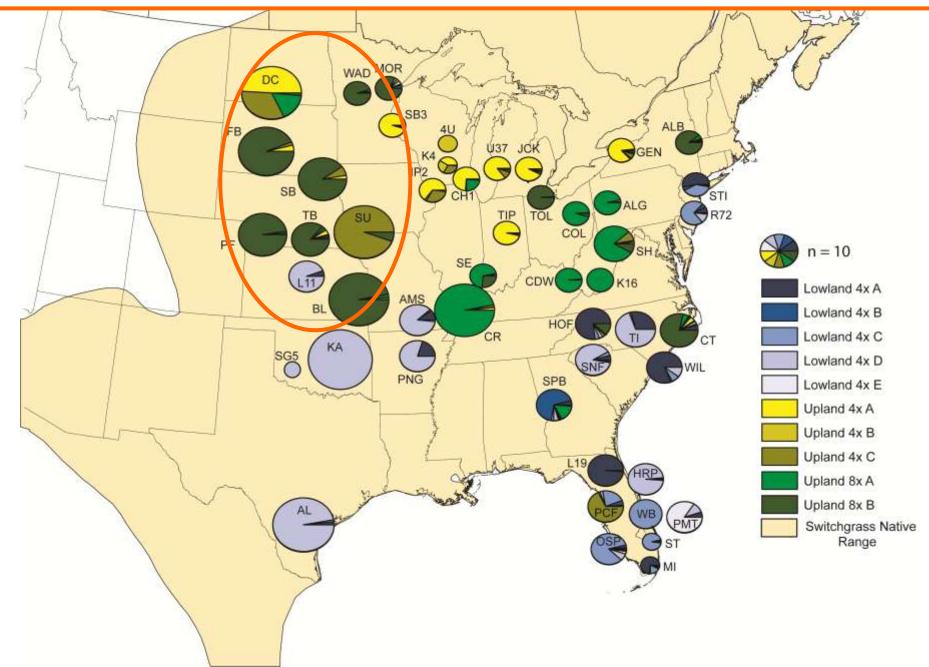


Biomass yield vs. Longitude

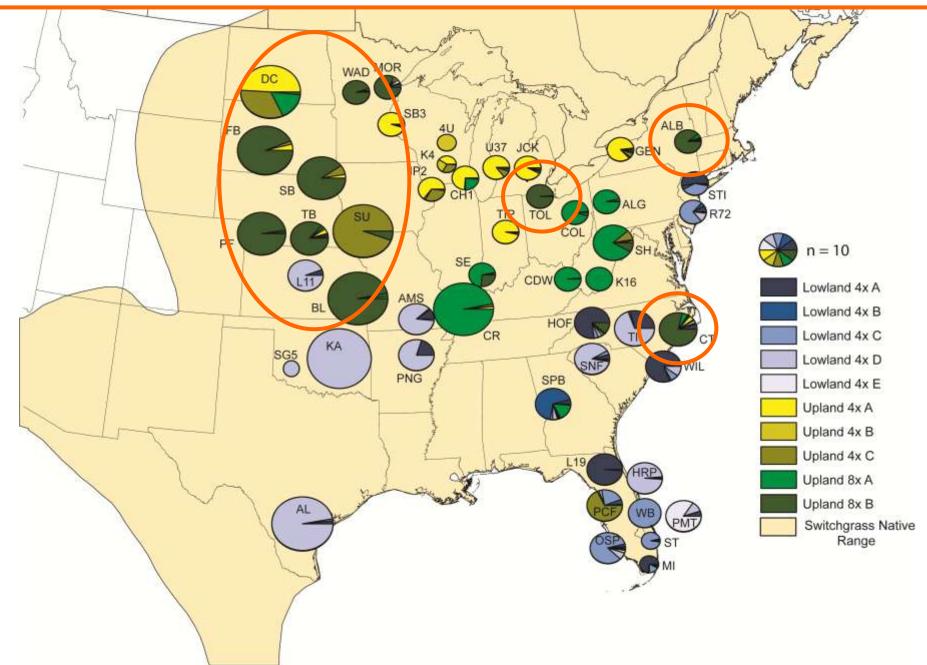




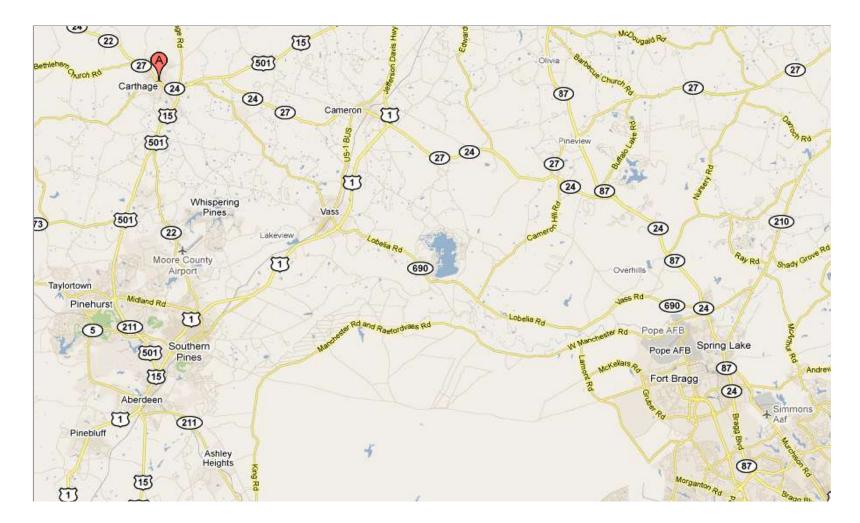
Central and Northern Great Plains 8x Upland Lineage



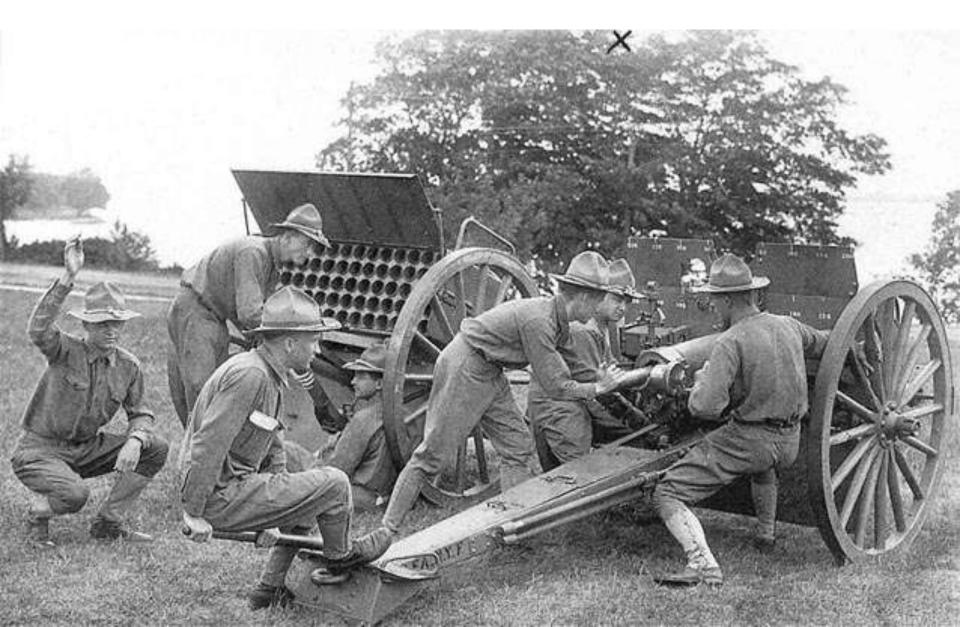
Central and Northern Great Plains 8x Upland Lineage



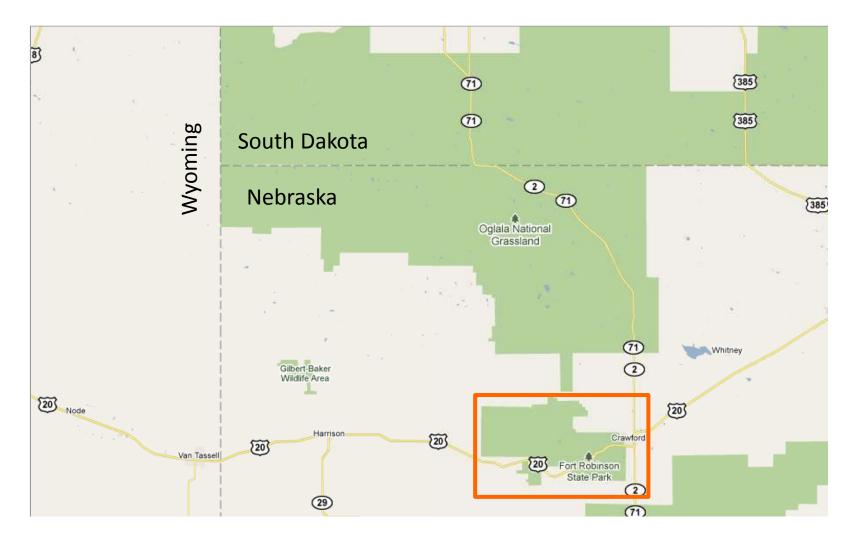
Origin of the 'Carthage' Accession



Fort Bragg: 1918 - 1939



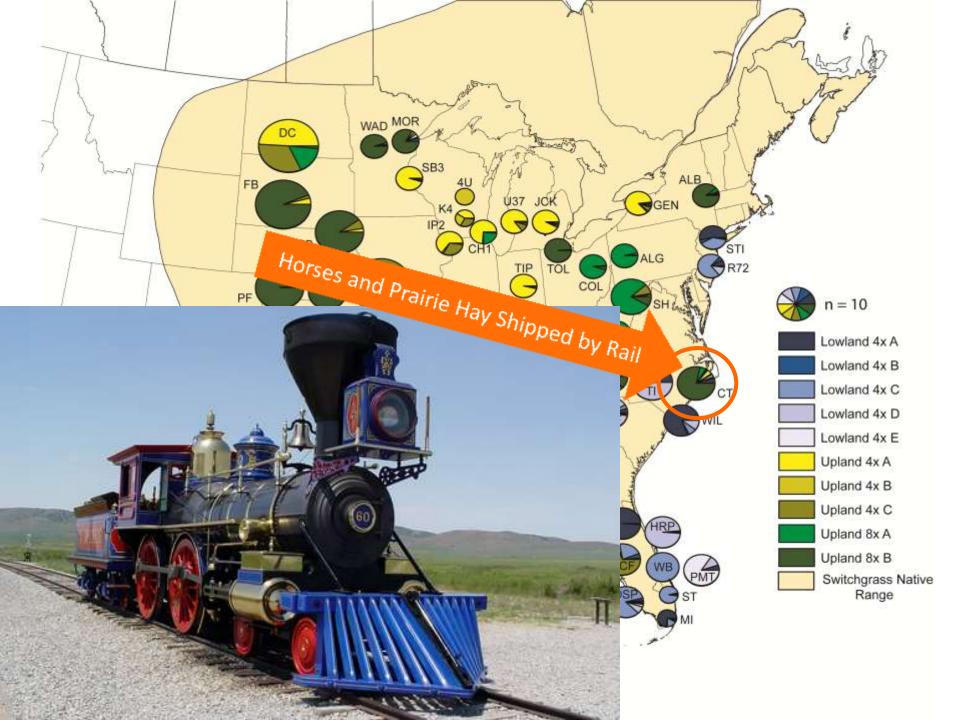
Fort Robinson Sand Hills Region of Nebraska

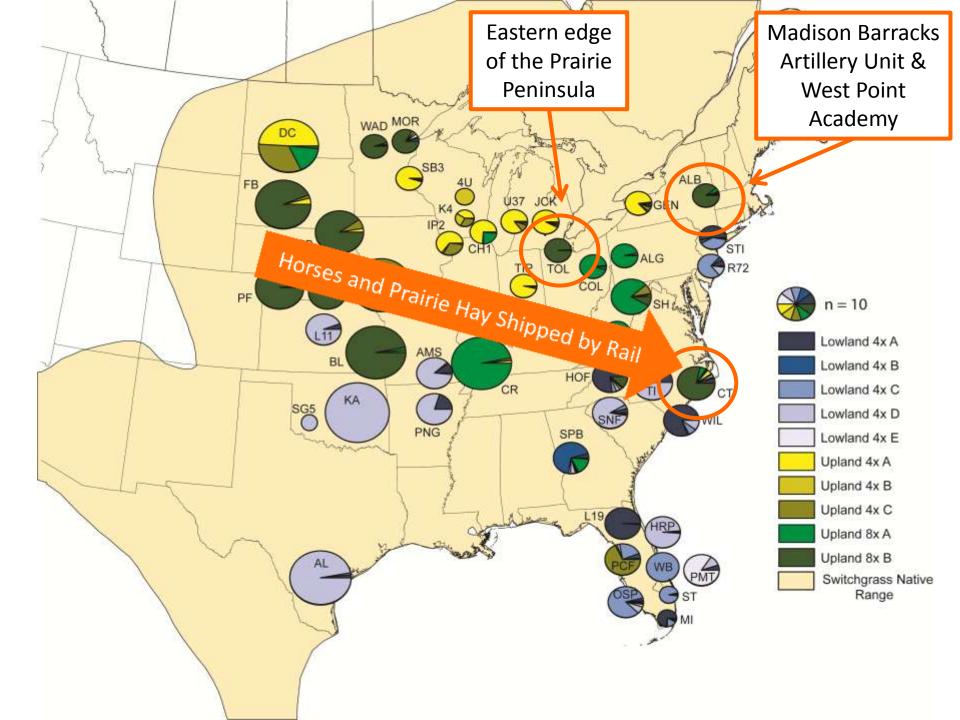


Fort Robinson U.S. Army Remount Station, 1919-1943

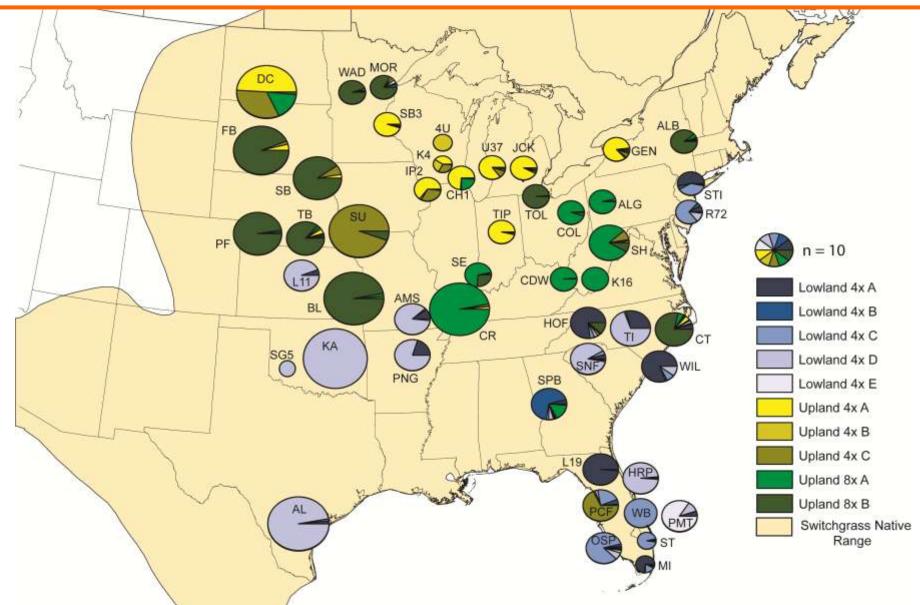






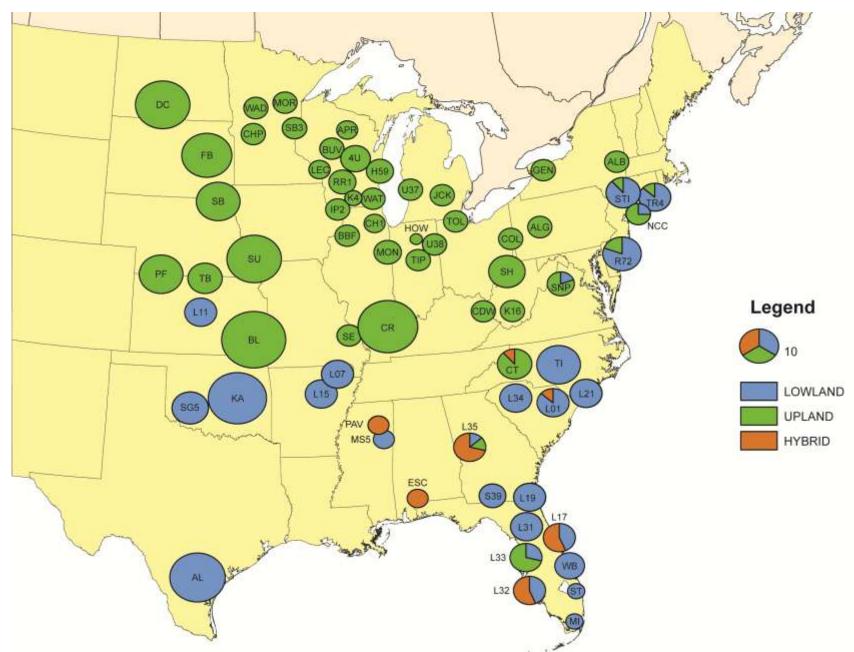


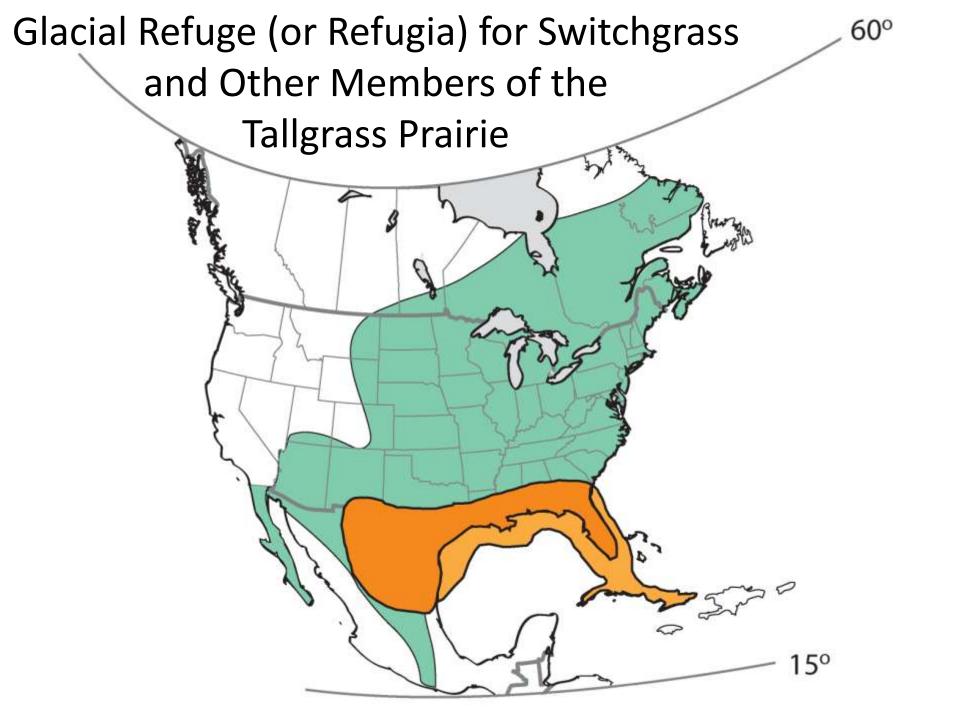
Strong patterning in the Upland Accessions (North).



Weak patterning in the Lowland Accessions (South).

Distribution of Putative Hybrids

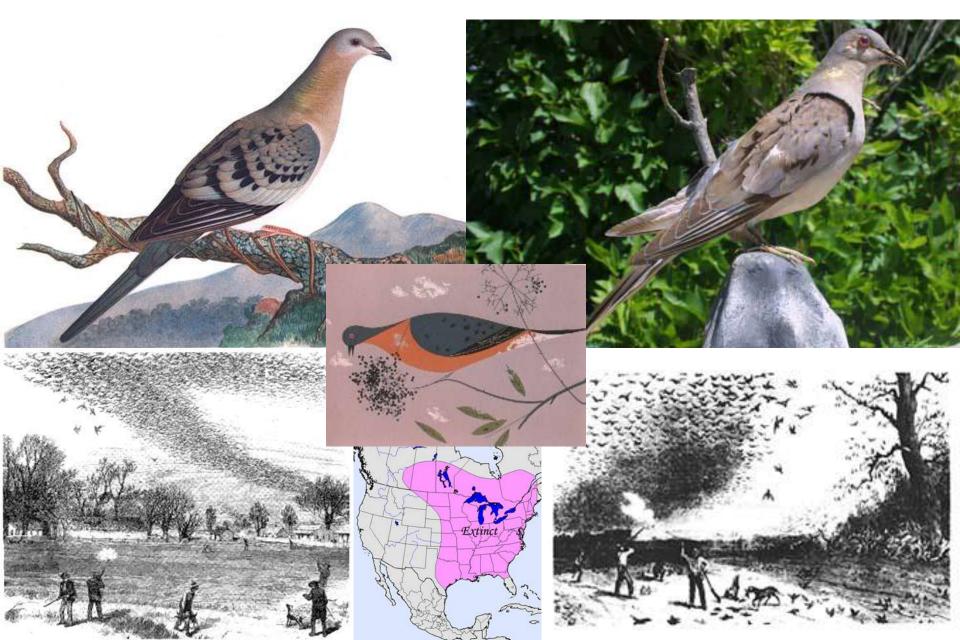




Post-Glacial Migration Routes



How Did Switchgrass Migrate Northward?

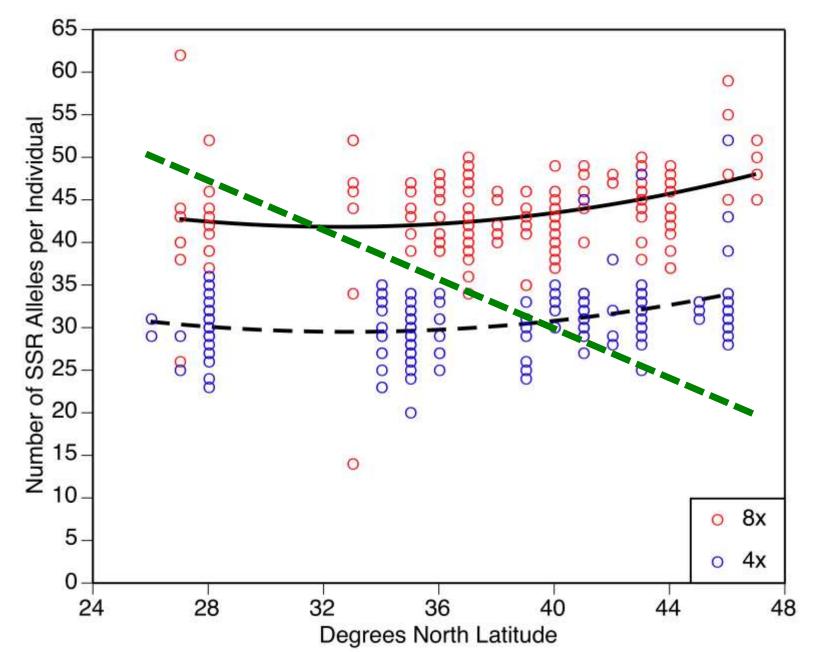


Migration, Mixing, and the Existence of Genetic Bottlenecks?

60°

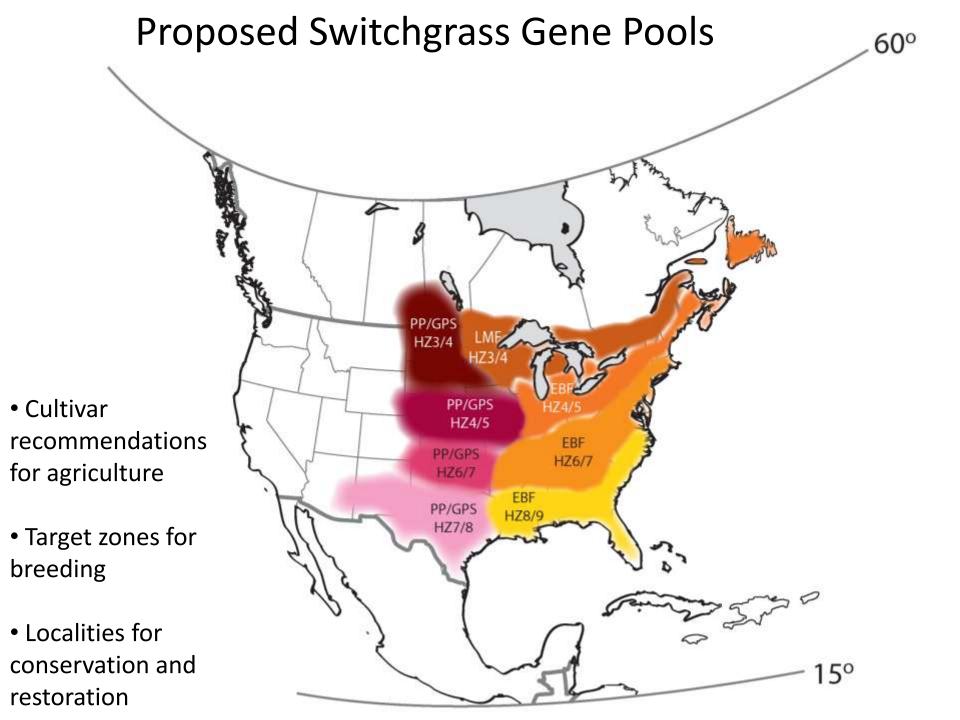
Prevailing Winds

No Genetic Bottleneck for Switchgrass



Ice Age Cycles

- Major Northern Hemisphere glaciations began ~2.7 Mya.
- Since the earliest estimated divergence between upland and lowland types, there have been about 15-20 major North American glaciation events.
- Tallgrass prairie species have undergone massive forward and reverse migrations within each cycle. Due to migration patterns and causes, most sites contain multiple haplotypes, some of widely divergent origins.



Conclusions

- We have identified one Center of Diversity in the SE USA and suspect that others exist all along the Gulf Coast and perhaps in West TX.
- Genetic diversity exists throughout the range of switchgrass; genetic bottlenecks associated with northward migration have been overcome by long-range east-west migration and hybridization.
- Phenotypic and genotypic studies have led to identification of a gene-pool concept to assist in a wide range of germplasm decisions.

Acknowledgements

- Casler lab (USDA-ARS, University of Wisconsin, & DOE Great Lakes Bioenergy Research Center)
 - Yunwei Zhang, Visiting Professor, CAU, Beijing
 - Juan Zalapa, Post-doc, GLBRC
 - Andy Jakubowski, Ph.D. graduate student
 - David Price, Ph.D. graduate student
 - Shawn Kaeppler, Professor, UW
- Brummer lab (UGA and Noble Foundation)
 - Ananta Acharya, Ph.D. graduate student
 - Yanling Wei, Post-doc, University of Georgia

Funding Sources

- USDA-ARS
- Department of Energy, Great Lakes Bioenergy Research Center (UW, MSU, ISU)
- University of Wisconsin, Agricultural Research Stations
- University of Georgia
- Department of Energy, BioEnergy Sciences Center (UGA, ORNL, Noble)
- The Samuel Roberts Noble Foundation, Ardmore, OK



QUESTIONS?