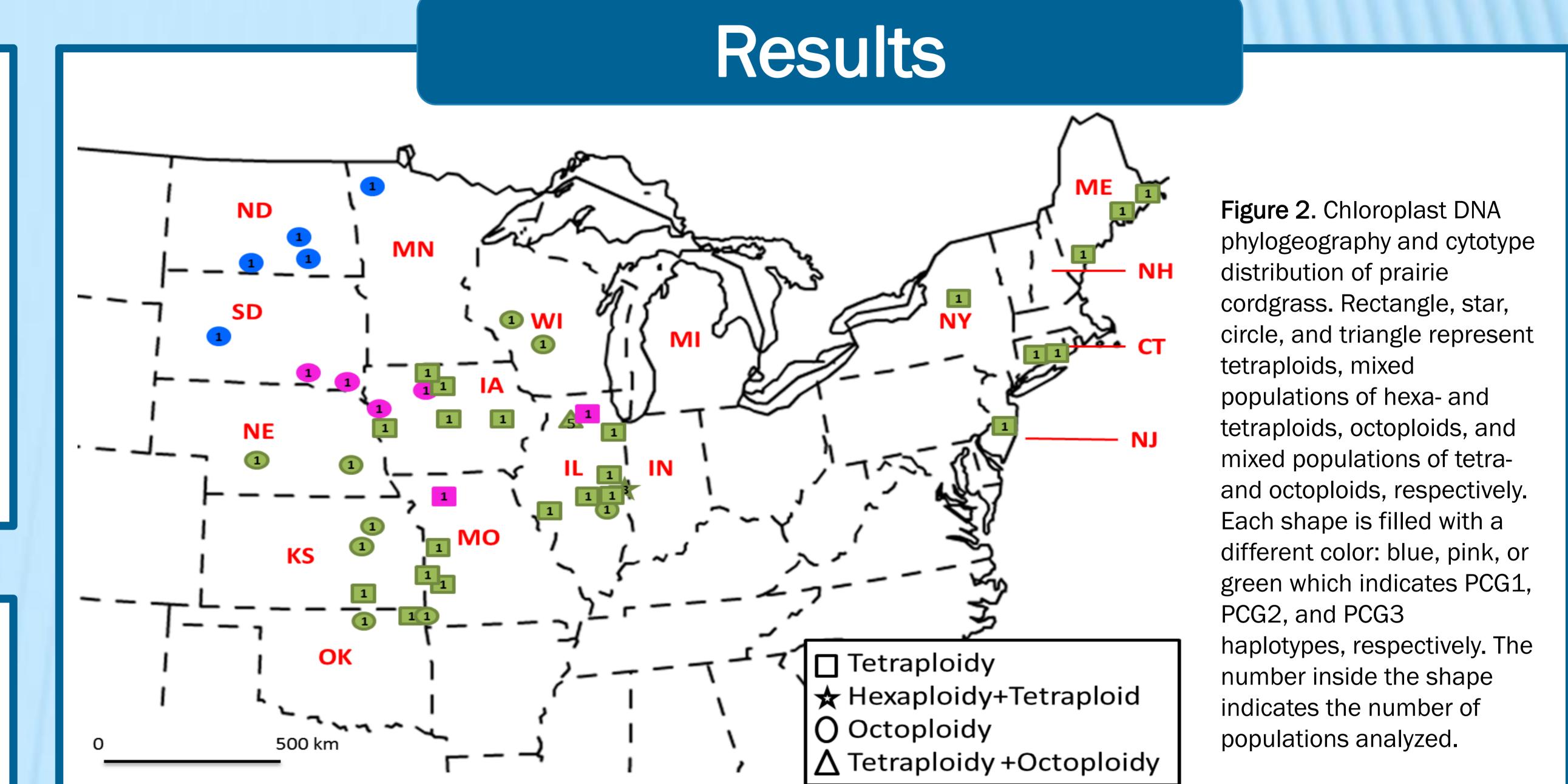
Chloroplast DNA Intraspecific Phylogeography of Prairie Cordgrass (Spartina Pectinata Link) in the U.S.

Sumin Kim¹, A. Lane Rayburn¹, T.B. Voigt¹, M.L. Ainouche², A.K. Ainouche², and D.K. Lee^{*1} ¹Department of Crop Sciences, College of ACES, University of Illinois at Urbana-Champaign ²Genome Evolution and Speciation Laboratory. CNRS UMR 6553 University of Rennes 1 Campus Scientifique de Beaulieu, Bât





Prairie cordgrass (Spartina pectinata Link) is a warm-season (C_{4}) perennial grass native to North America. This species is adapted to a wide range of environmental conditions and is strongly recommended as a dedicated energy crop grown on marginal lands. Prairie cordgrass is a polyploid species comprised of three cytotypes, tetra- (2n = 4x = 40, hexa- (2n = 6x = 60), and octoploidy (2n = 8x = 80), with basic number of x=10 (Kim et al., 2010 and 2012). Polyploids have appeared to play a major role in prairie cordgrass evolution and genetic diversification. The comparative study between cpDNA phylogeny and different cytotypes will provide insight into the origin and establishment of polyploid species. Therefore, sufficient cpDNA variation in prairie cordgrass will elucidate the evolutionary processes and study intraspecific phylogeographical patterns, which are critical steps for effective breeding and germplasm conservation efforts.



Objective

- To address chloroplast diversity within and among prairie cordgrass population cytotypes
- To infer evolutionary migrations that might have shaped the observed population structure
- To determine the phylogeographic structure of prairie cordgrass across the U.S.

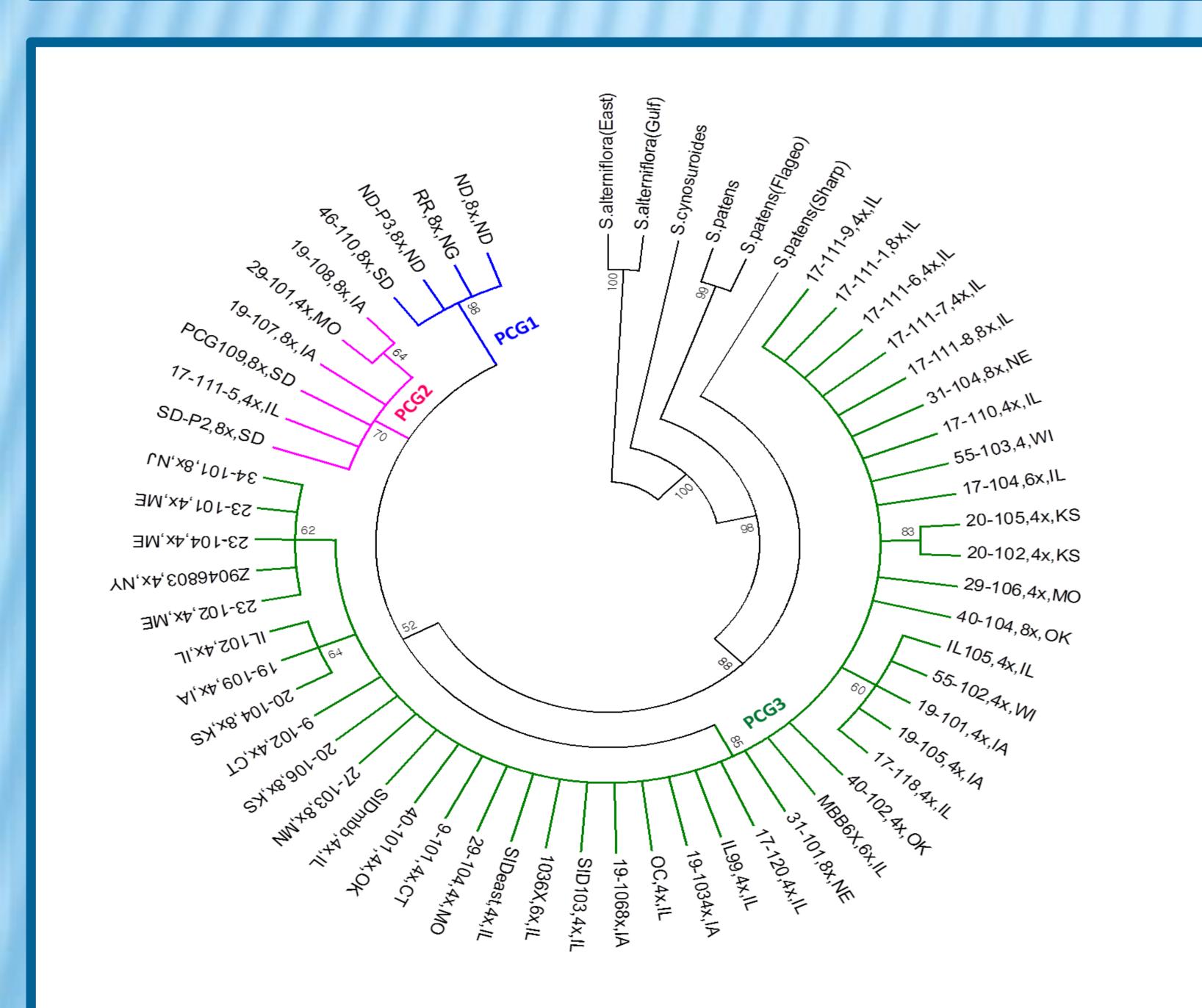


We analyzed the chloroplast haplotype variations in 54 populations of prairie

Table 1. Summary of sequences variations within prairie cordgrass populations and with outgroups. Numbers of populations analyzed are shown (N).

		Within prairie cordgrass (54)				With outgroups (60)			
Chloroplast	Alignment	Informative		Uninformative		Informative		Uninformative	
Regions	length (bp)	Variable sites	Indels	Variable sites	Indels	Variable sites	Indels	Variable sites	Indels
trnT-trnL	658-703	1	0	2	1	7	1	2	0

cordgrass using nine non-coding chloroplast regions (Fig. 1). All chloroplast regions are listed in table 1. In this study, these chloroplast analyses were combined with the previously published cytotype survey of prairie cordgrass.



trnL-trnF	914-919	1	4	0	0	12	5	0	0
petL-psbE	1154-1198	3	4	2	1	12	3	0	1
rpl32-trnL	648-663	0	2	1	0	8	2	0	0
rpL14-rpL36	1108	1	0	2	0	8	0	0	0
psbJ-petA	811-844	2	0	0	1	5	2	0	0
3'trnv-ndhC	294-298	0	1	0	0	3	2	0	1
atpL-atpH	416-420	0	1	0	1	5	3	1	1
3'rps16-5'trnK	595-598	2	3	1	0	6	1	1	0
Combined	6598-6750	9	15	7	7	66	16	9	2

In this study, three unique haplotypes, PCG1, PCG2 and PCG3, were identified (Fig. 1). In general, related haplotypes were strongly associated with geographic distribution (Fig. 2). cpDNA genome variations mainly corresponded to some useful indels found among prairie cordgrass populations. PCG1 haplotypes were distributed in octoploids in ND, SD, and MN, while PCG2 haplotypes were mostly identified in octoploids and a few tetraploids in SD, IA, IL, and MO. PCG3 haplotypes have been identified from the midwest to the New England regions of the U.S., where tetra-, hexa-, and octoploid prairie cordgrass populations were found.



This research reports the first widespread cpDNA-based phylogeographic study of prairie cordgrass across several U.S. regions.

Figure 1. Phylogenic tree of the cpDNA haplotypes in prairie cordgrass with bootstrapping confidences. Ploidy levels (4x, 6x, and 8x) and location are shown next to the population name. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap tests (1000 replicates) are shown next to the branches. Major clades were identified by PCG1(blue), PCG2 (pink), and PCG3 (green).

Comparison studies between phylogeography and different cytotypes provides insight into the origins and establishment of polyploids in natural populations of prairie cordgrass across the U.S. Moreover, this phylogeny study provides a useful springboard for further population genetic studies of Spartina spp.



□ Kim, S.; Rayburn, A.L.; Lee, D.K. (2010) Genome size and chromosome analyses in prairie cordgrass. Crop Sci 50:2277-2282. Kim, S.; Rayburn, A.L.; Parrish, A.; Lee, D.K. (2012) Cytogeographic distribution and genome size variation in prairie cordgrass (Spartina pectinata Bosc ex Link). Plant Mol Biol Rep 30:1073-1079.