

THE FORAGE AND RANGE RESEARCH LABORATORY

Plants for the West

**Genetic Resources, Genomic
Diversity, and Functional Trait
Variation in the Perennial
Triticeae**

Steve Larson, Ivan Mott, Shaun
Bushman, and Richard Wang





Functional working groups at FRRL

Biomass and Biofuels



Rangeland Ecology and Restoration

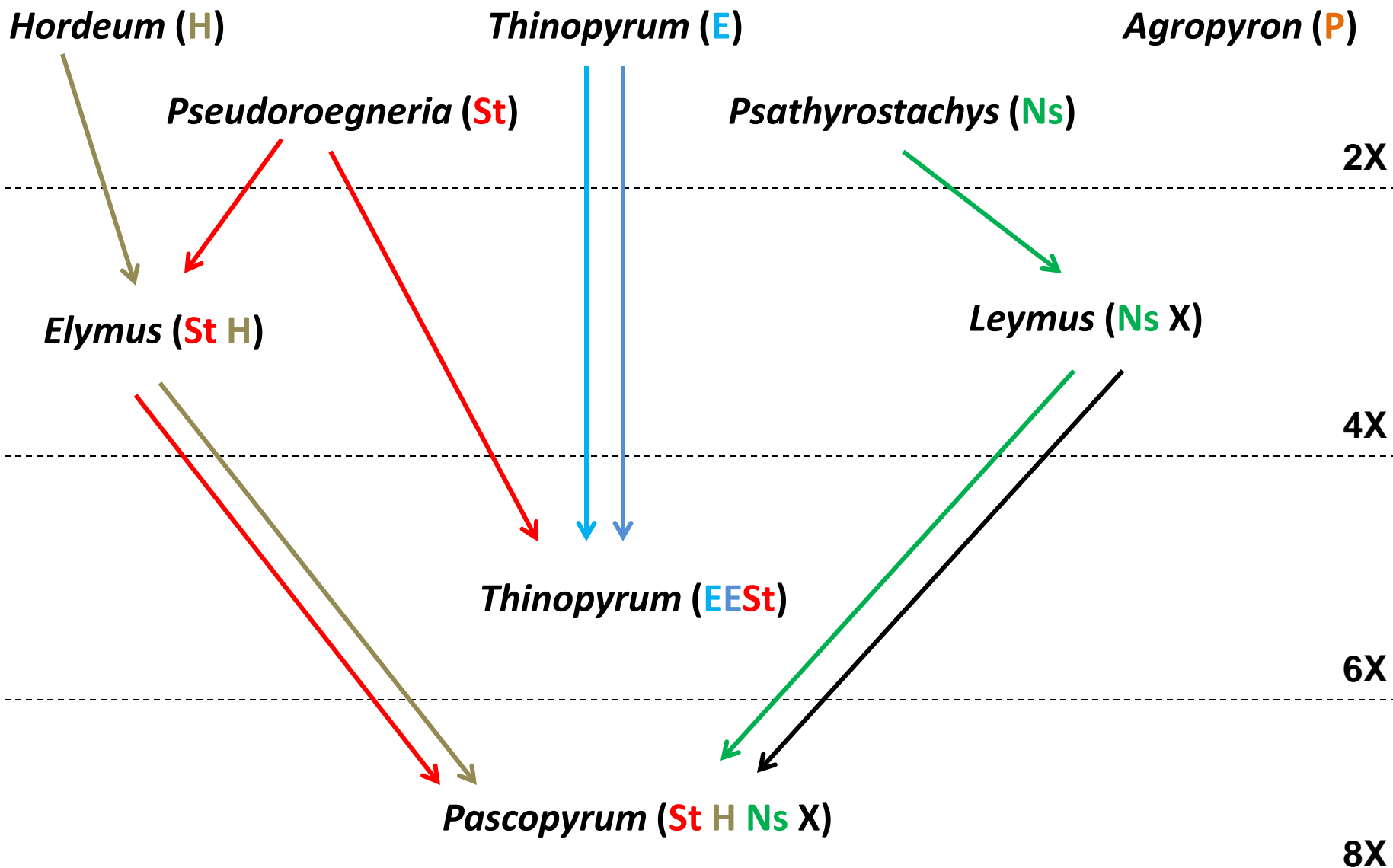
Low-Maintenance Turfgrasses



Irrigated Pasture Plants



Perennial Triticeae grasses are classified into nine genera comprised of six distinct genomes





***Psathyrostachys* and *Leymus* “wildryes” share the same Ns genome**

Psathyrostachys

- Eight diploid or autopolyploid species, which define **Ns** genome
- Native to arid regions of central Asia
 - Russian wildrye (*P. juncea*) is valuable forage in its native range and western North America

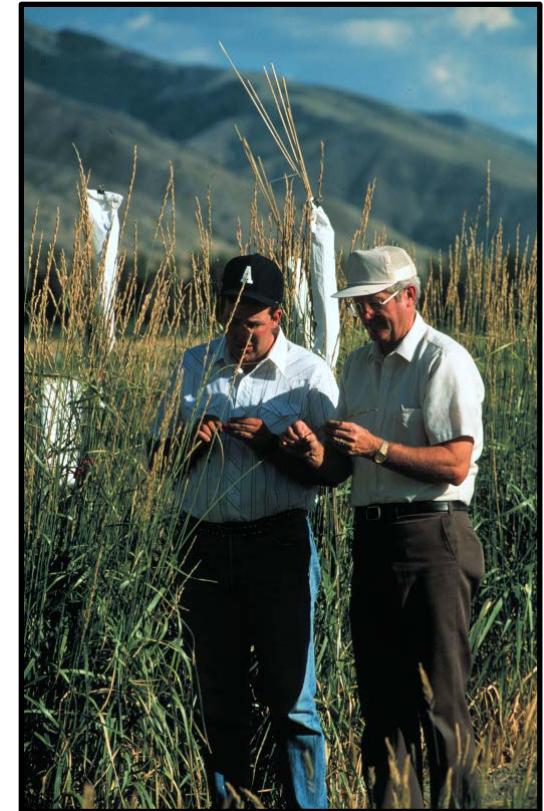
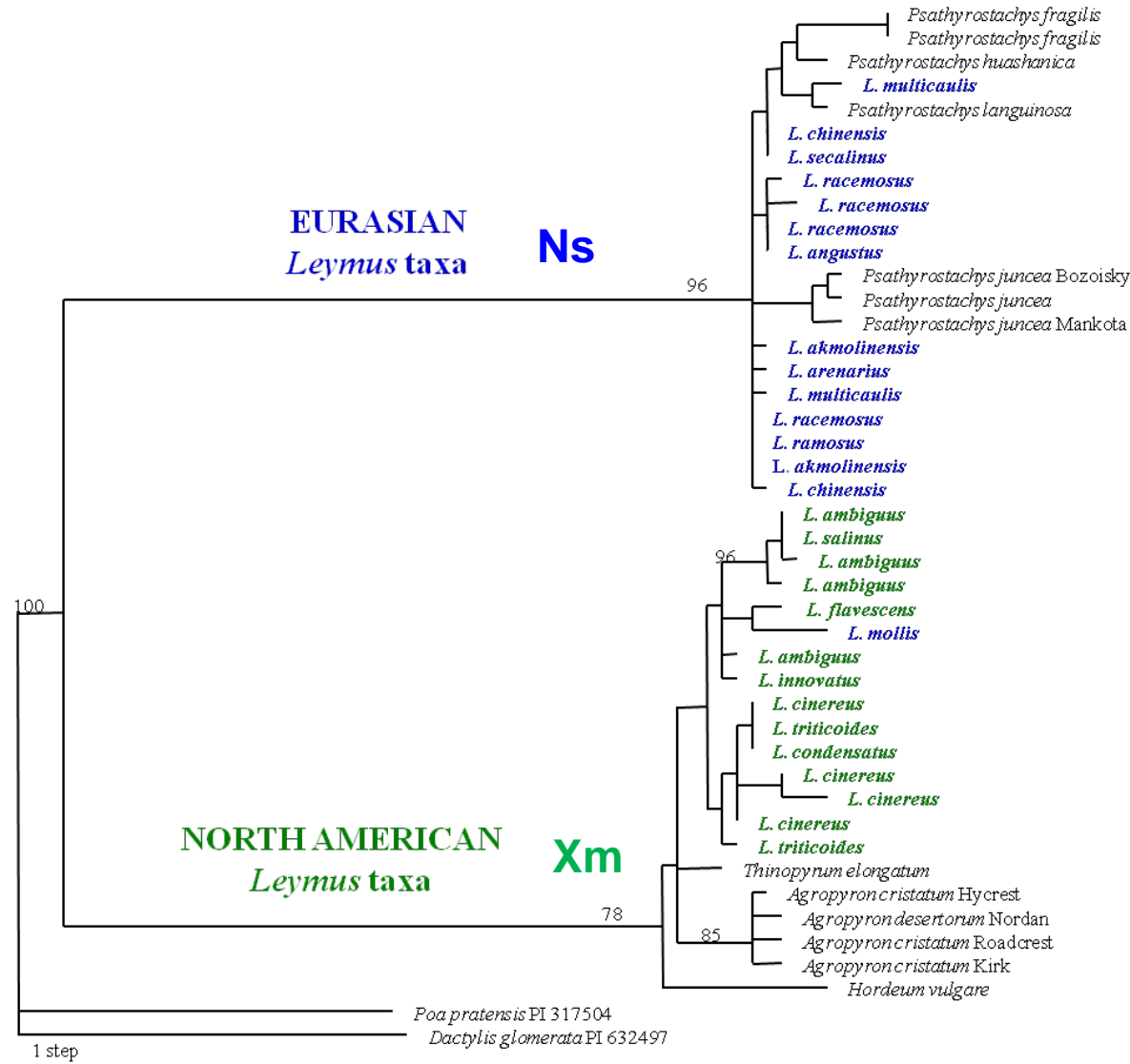
Leymus

- 50 allopolyploid species containing the **Ns** and **Xm** genomes
- Most abundant in eastern Asia
 - Important native forages such as *L. chinensis*
- 15 North American taxa
 - 10 native
 - 1 circumboreal (*L. mollis*)
 - 4 introduced, including cultivated Altai wildrye (*L. angustus*)

Psathyrostachys and *Leymus* species used for gene introgression in wheat



Phylogeny of *Leymus* chloroplast genomes



L. racemosus

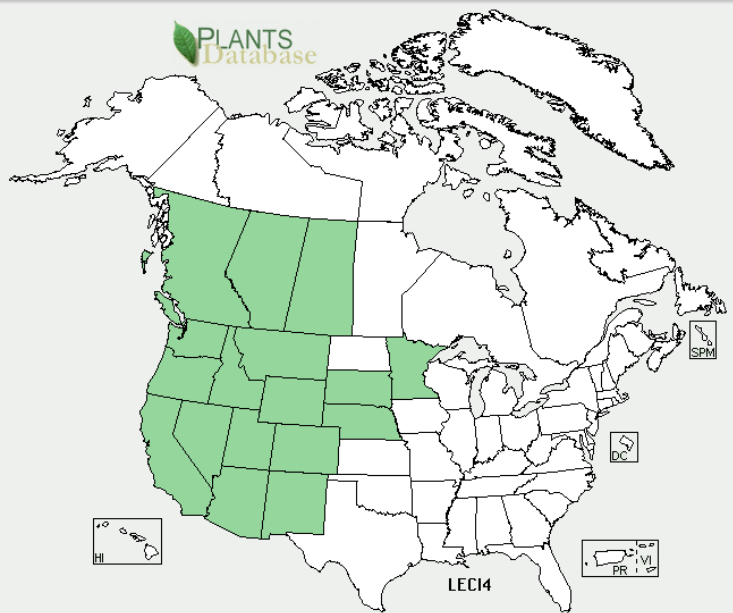
X

L. cinereus* / *L. triticoides



Basin wildrye

(*Leymus cinereus*)

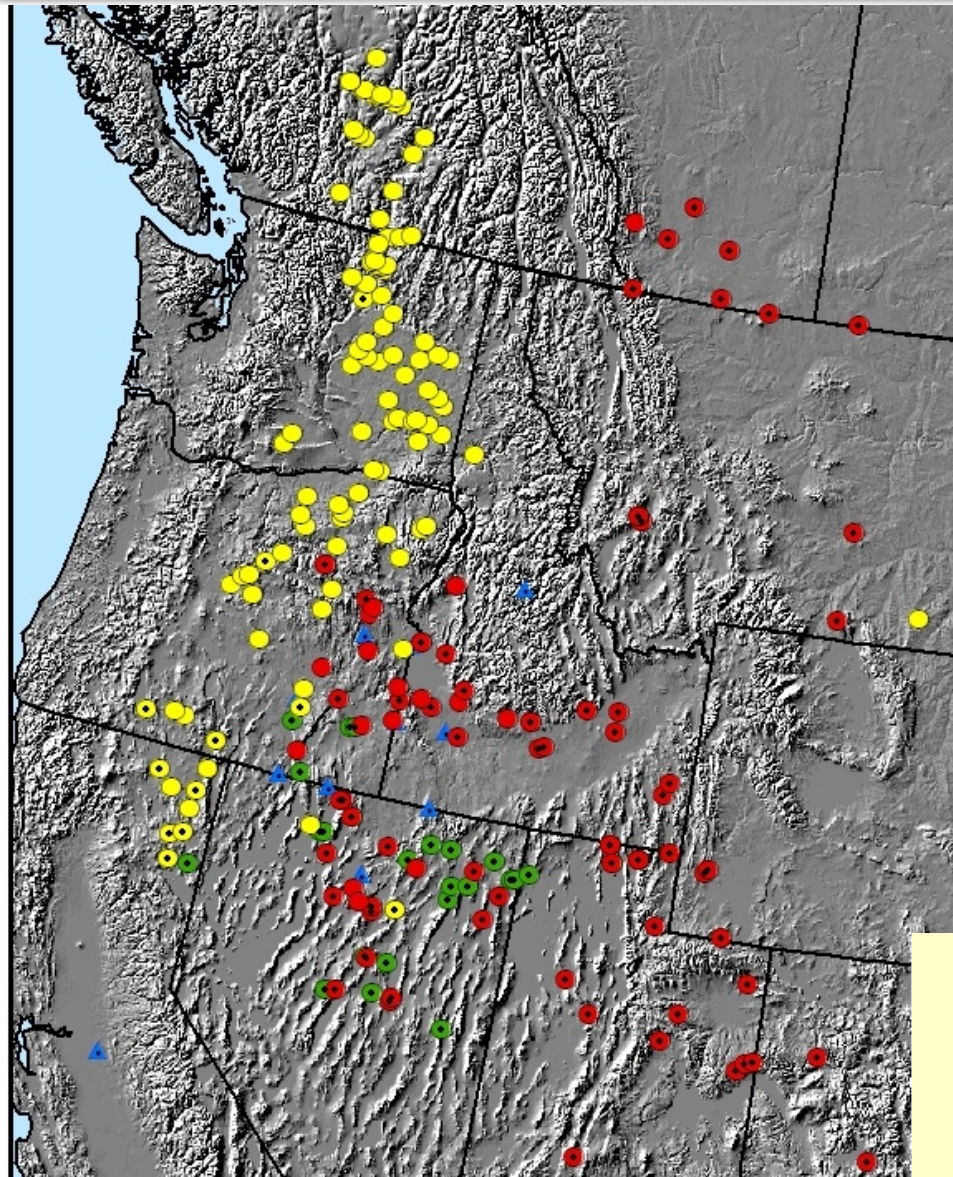


- Largest native grass of western North America
- Where water and soil accumulate, croplands
- Good early spring forage, grows coarse in summer
- Elevated growing point susceptible to clipping
- Large prolific spikes, seed shattering explosive
- Poor seedling establishment
- Five U.S. & Can. cultivars / 231 USDA accessions





DNA fingerprinting and flow cytometry analysis



basin wildrye ecotype

4x 8x



Western



Rocky Mountain



Great Basin

basin wildrye cultivars



Magnar



Trailhead, Tetra,
and Washoe

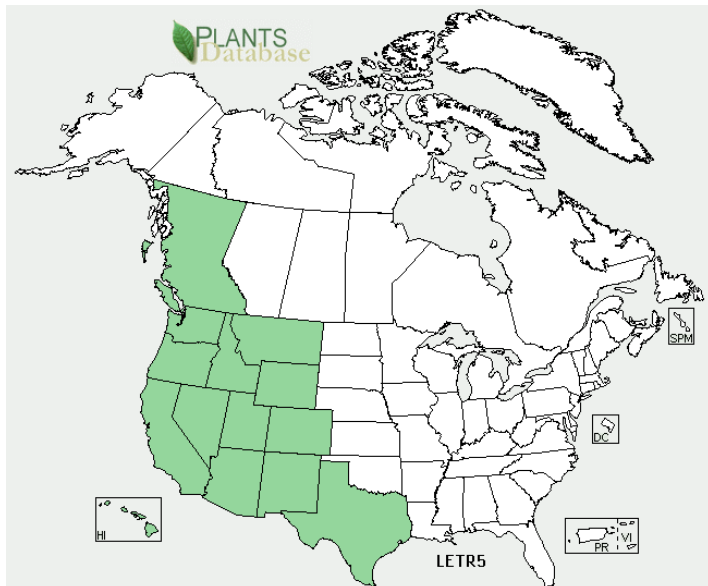


Continental
(Magnar x Trailhead)



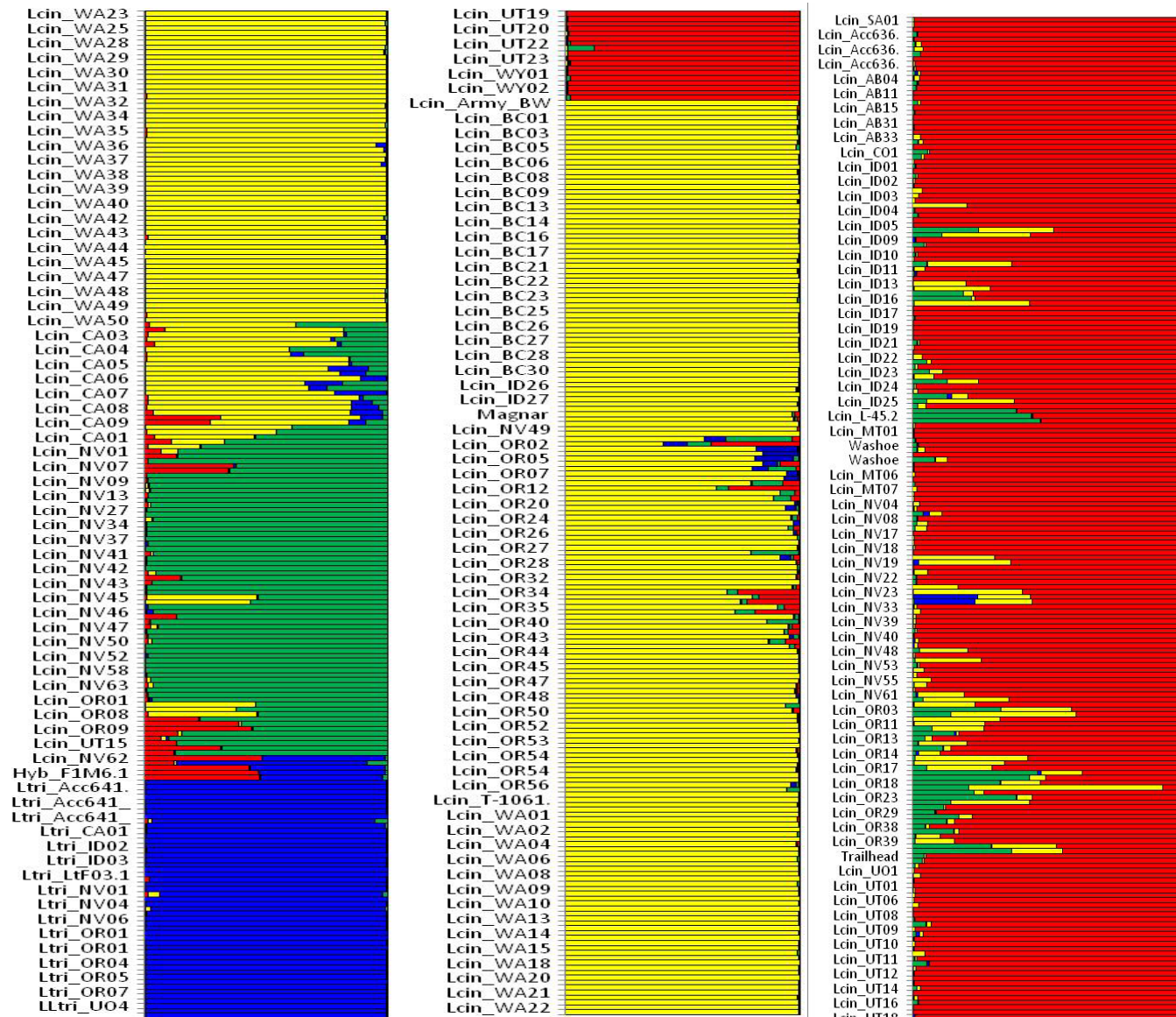
Creeping wildrye (*Leymus triticoides*)

- Relatively short (up to 1.3 m) but strongly rhizomatous grass
- Once dominant species in Central Valley, where it is still cultivated as saline biomass crop
- Good clipping and grazing tolerance
- Non-shattering, but recalcitrant seed dormancy
- One cultivar, Rio / 19 USDA accessions





Bayesian cluster analysis of 600 genotypes reveals some hybridization between species and ecotypes



basin wildrye races

Rocky Mountain

Western

Great Basin

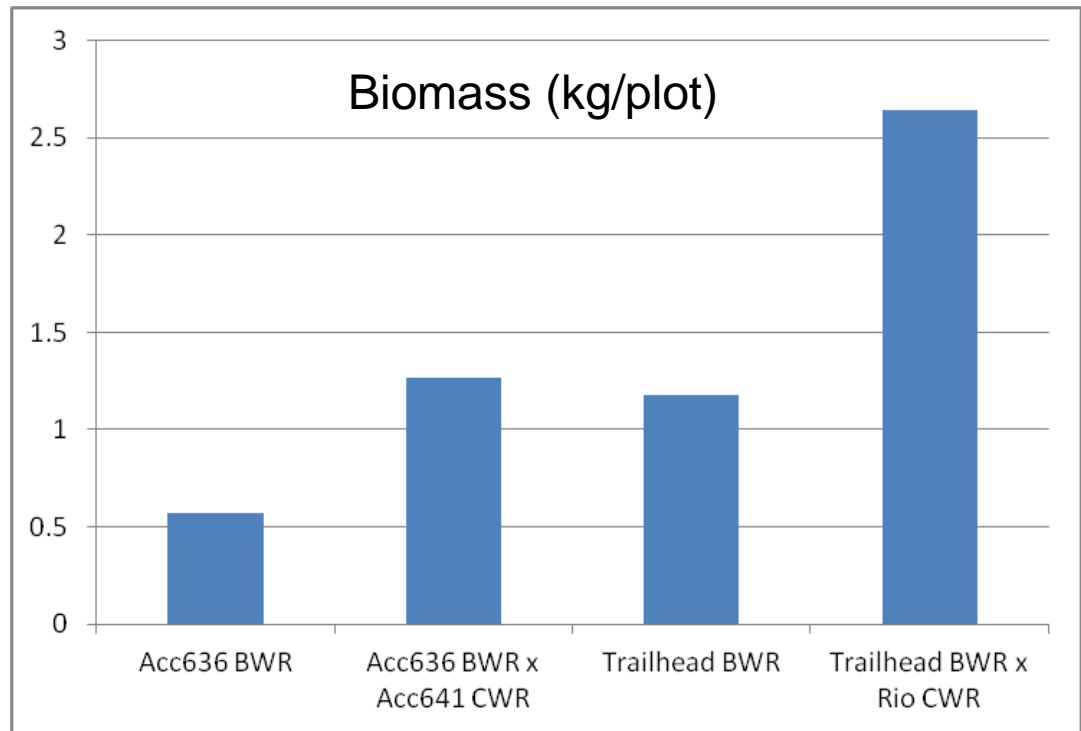
creeping wildrye



Experimental creeping x basin wildrye hybrids

Functionally important traits: rhizomes, seed dormancy, salt-tolerance, seed-shattering, and biomass heterosis.

Hypothesis: The tall plant height, large stems, and large leaves from basin wildrye combined with the prolific rhizomes and tillers of creeping wildrye produce biomass heterosis.





EST library from perennial rhizome/tiller buds creeping x basin wildrye hybrids



12,281 Sanger EST
unigene contigs
(average 973 bp)

69 STS primer pairs
for nine of then
known lignin
biosynthesis genes

1,798 SSR
primer pairs

91% amplify *Leymus* (**Ns**Xm)
74% *Psathrostachys juncea* (**Ns**)



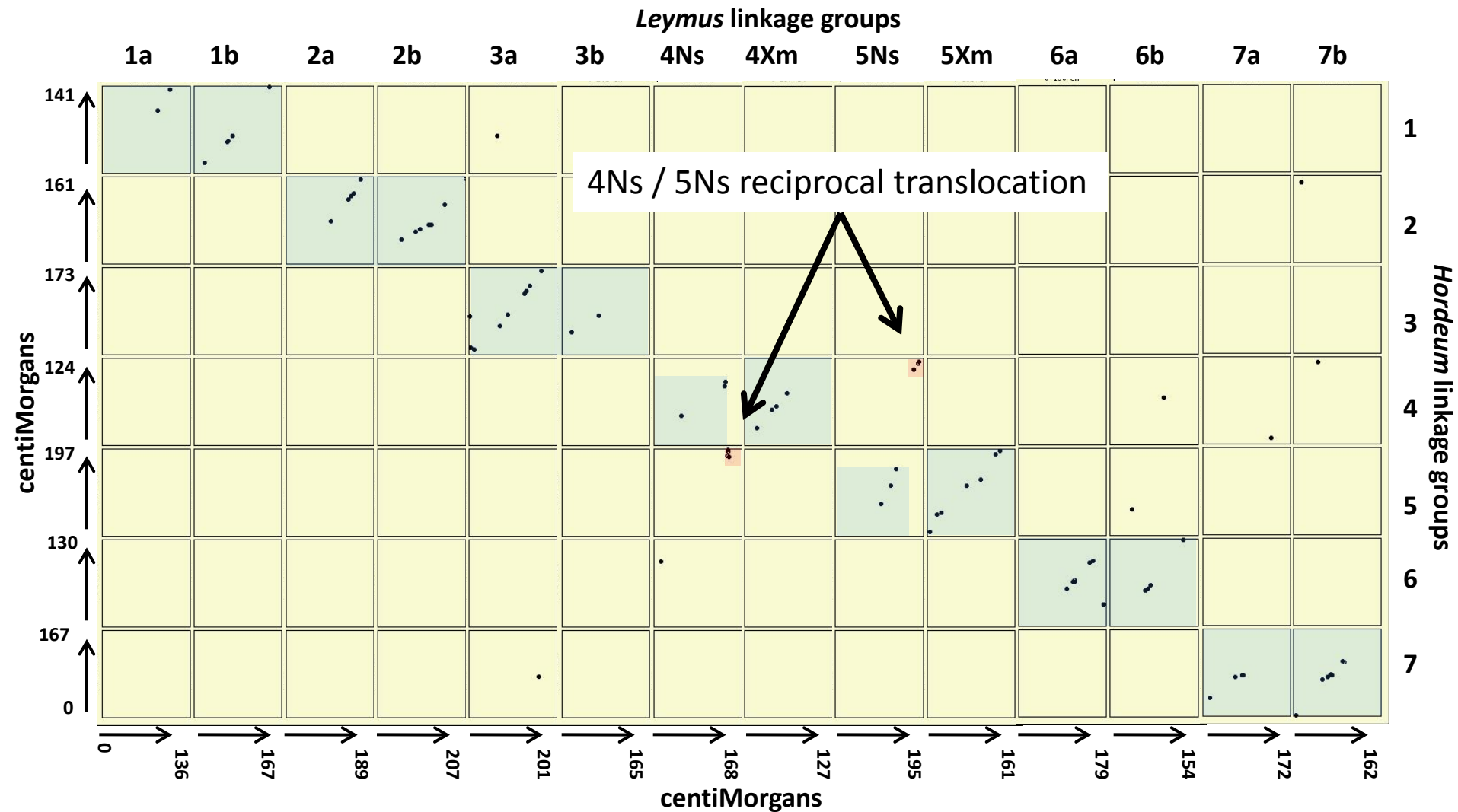
Genetic maps for creeping x basin wildrye hybrids

	AFLP	EST SSR	Lignin EST STS	Heterologous RFLP / STS	Total no. markers	Map Distance (cM)	Markers cM ⁻¹	<i>Oryza</i> alignments	<i>Brachypodium</i> alignments	<i>Hordeum</i> alignments
LG1a	28	18	1	4	51	135.9	2.7	16	21	2
LG1b*(6b)	43	20	0	1	64	166.9	2.6	18	19	5
LG2a	39	18	2	4	63	188.5	3	14	18	5
LG2b	23	34	1	4	62	207.2	3.3	25	32	8
LG3a	31	28	2	6	67	200.8	3	28	30	11
LG3b	28	19	0	5	52	164.7	3.2	17	20	2
LG4Ns	16	29	0	5	50	168.1	3.4	24	30	8
LG4Xm	18	25	0	7	50	127.3	2.5	24	26	4
LG5Ns	27	27	3	3	60	194.8	3.2	28	27	6
LG5Xm	25	27	3	4	59	160.5	2.7	28	29	7
LG6a	26	22	1	1	50	179.2	3.6	19	23	7
LG6b*(1b)	26	18	2	1	47	153.6	3.3	16	20	6
LG7a	24	33	4	1	61	171.7	2.8	28	32	6
LG7b	23	31	7	0	60	161.8	2.7	35	34	11
Overall	377	349	26	46	799	2381	3	320	360	88

Larson, S.R., Kishii, M., Tsujimoto, H., Qi, L., Chen, P., Lazo, G., Jensen, K.B., Wang, R.-R.C. (2011) *Leymus* EST linkage maps identify 4NsL-5NsL reciprocal translocation, wheat-*Leymus* chromosome introgressions, and functionally important gene loci. Theor Appl Genet (DOI)



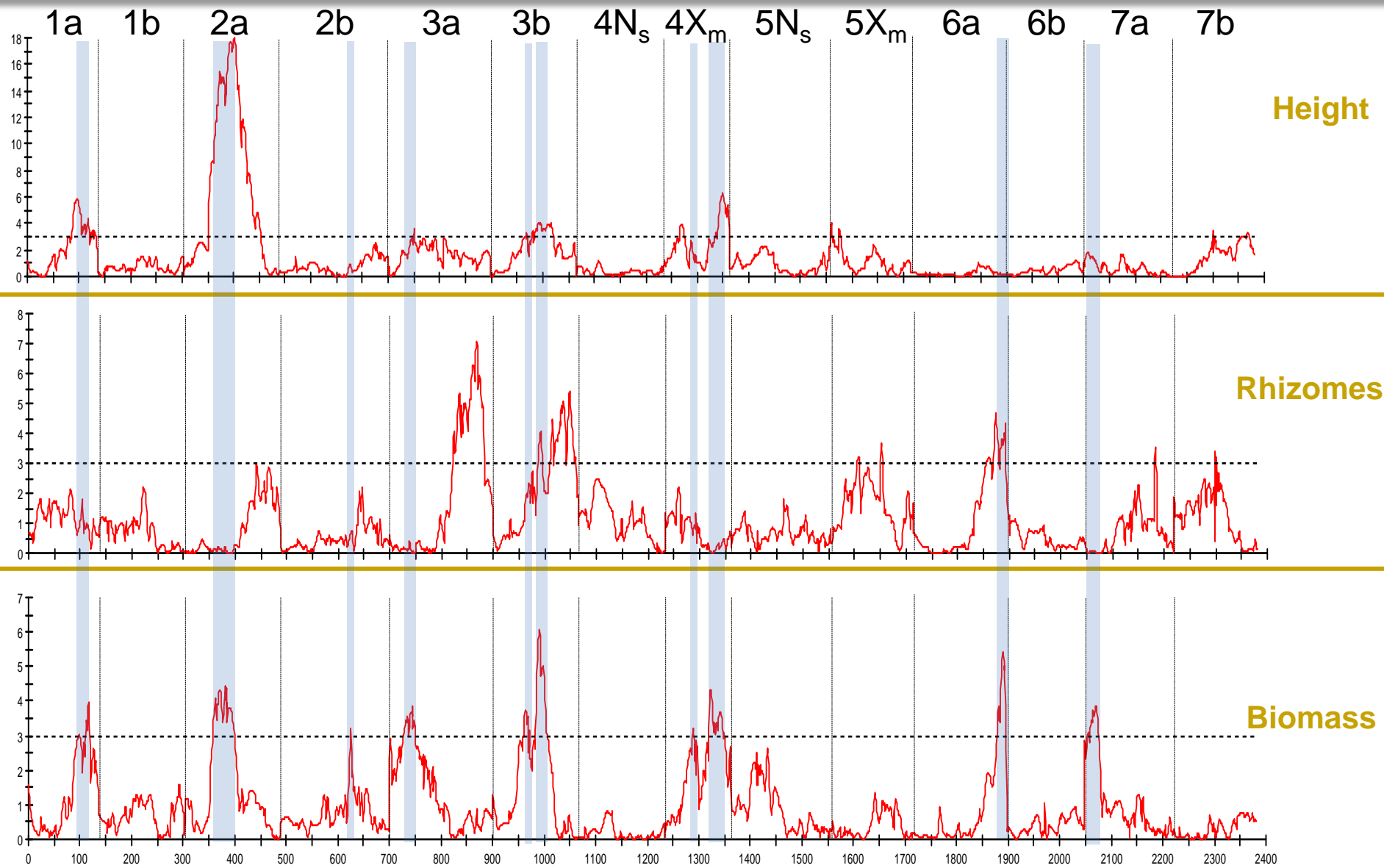
Alignment of 88 mapped *Leymus* ESTs to a high-density *Hordeum* EST map

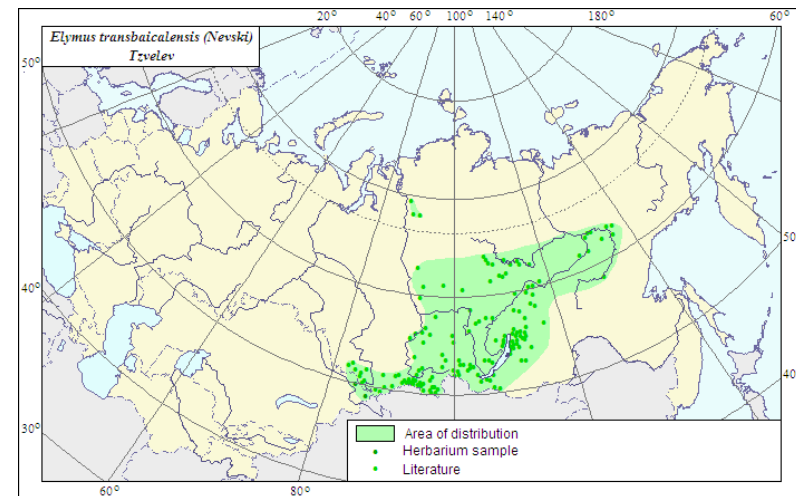




PLANTS FOR THE WEST

Comparison of QTLs that controlling plant height, rhizomes, biomass heterosis, and other traits







Transcriptome library of Russian wildrye



Russian wildrye

Psathyrostachys juncea (Ns)

270,000 reads (429 bp)

17,200 contigs (690 bp)

22,700 unmatched (369 bp)

40,000 isotigs

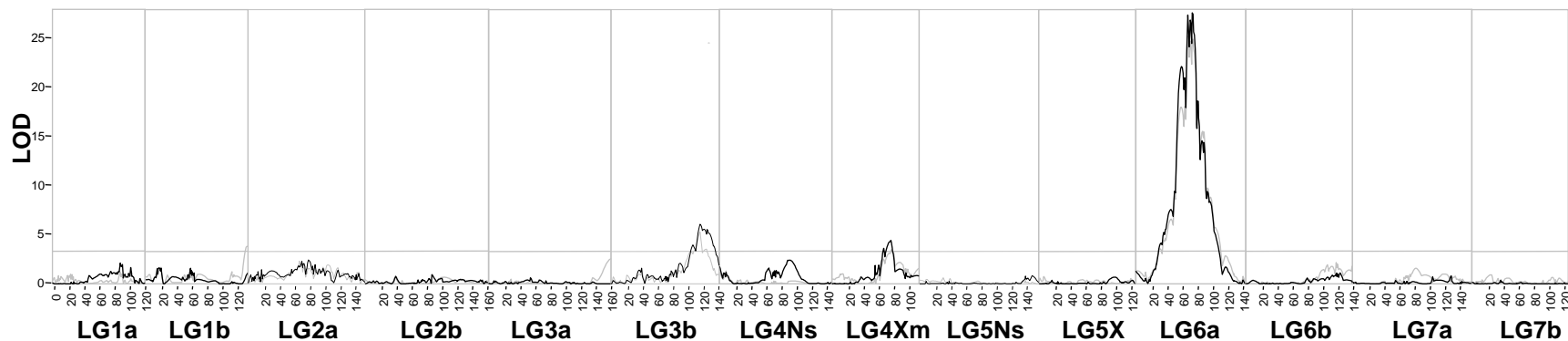
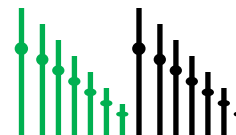
Unknown
ancestor (X)

creeping x basin wildrye

Leymus (Ns X)

11,281 Sanger EST unigenes (1017 bp)

375 mapped ESTs





Three perennial “wheatgrass” genera share the same *St* chloroplast and nuclear genome

Psuedoroegneria

- 15-20 Diploid or autopolyploid species, which define **St** genome
 - Mostly either Asian or Eurasian
 - One species, bluebunch, native but very widespread and abundant in western North America

Elymus

- 150 allopolyploid species containing **St** and **H** genomes
- 39 native or naturalized species in North America
 - *Elymus repens*

Pascopyrum

- One allooctoploid (**StHNsXm**) species, western wheatgrass, endemic to North America

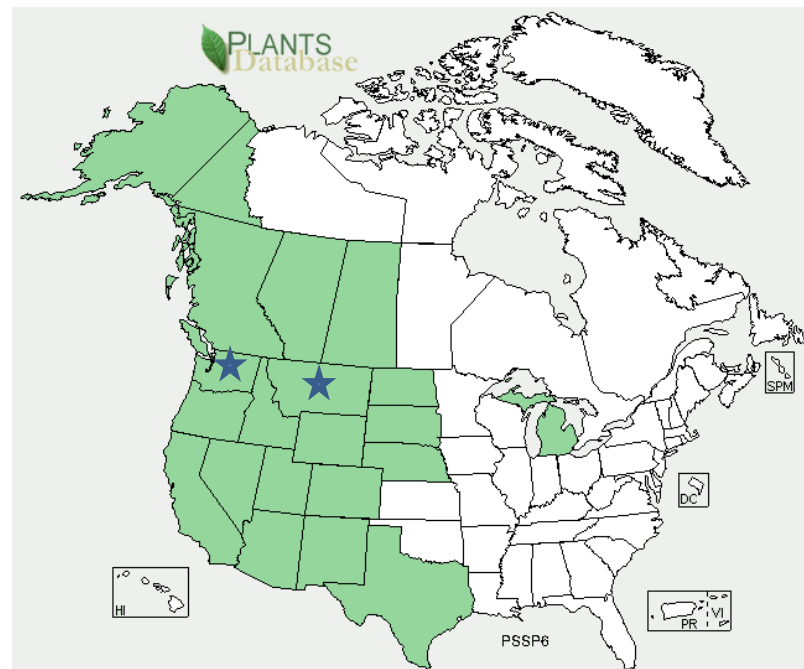


Bluebunch wheatgrass

(*Pseudoroegneria spicata*)

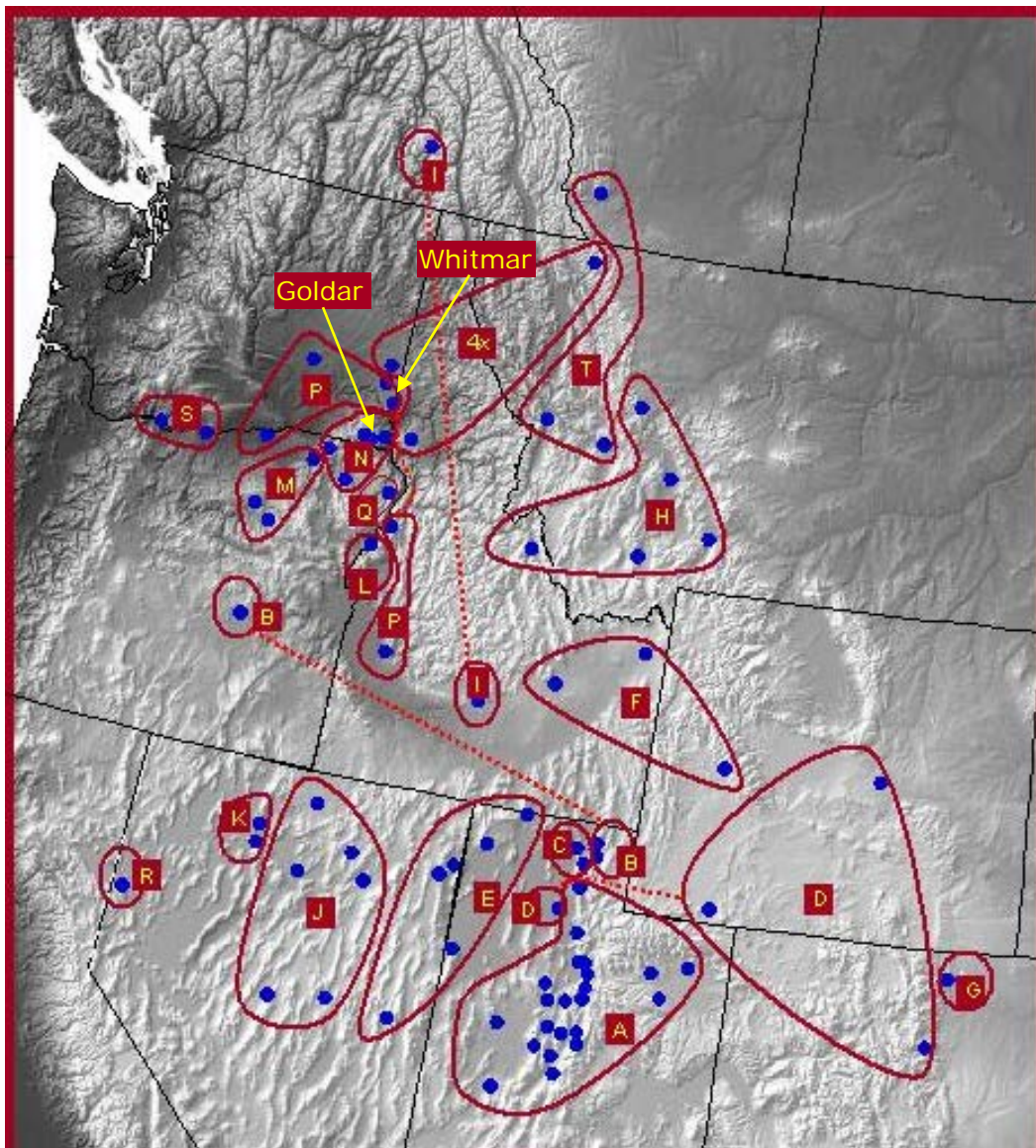


- Most widespread, abundant native bunchgrass western U.S.
- 30 – 50 cm precipitation
- Very palatable, nutritious forage
- Does not tolerate heavy grazing, easily overgrazed
- Four cultivars / 184 USDA accessions





Bayesian cluster analysis of 565 genotypes identify 20 metapopulations of bluebunch wheatgrass



	F (AFLP)	$\pi \pm SE$ (per 1000)
P-7 MOPX	0.563	38.7 ± 1.6
Goldar	0.597	34.2 ± 1.5
Whitmar	0.600	33.9 ± 1.5

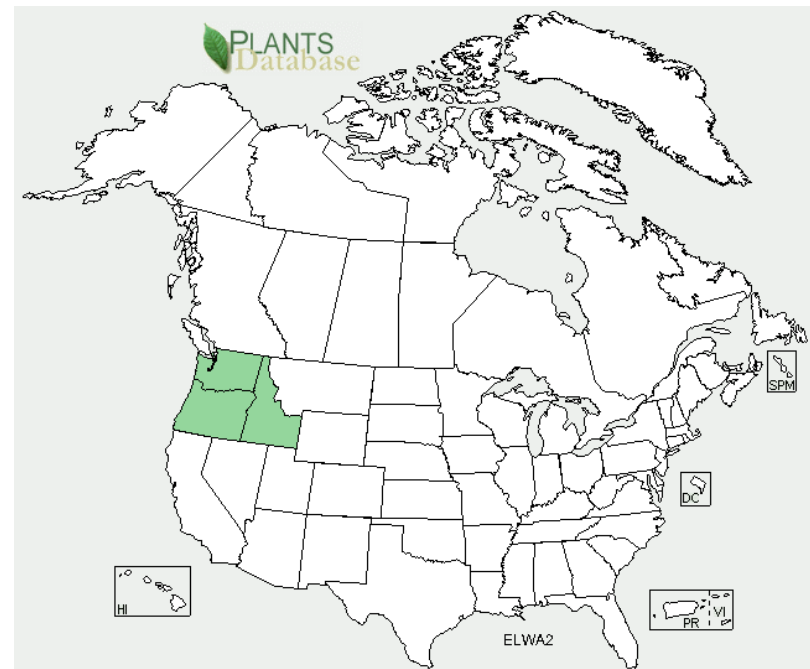


Allotetraploid Snake River wheatgrass

(*Elymus wawawaiensis*)



- Very similar to diploid bluebunch wheatgrass, but contains both **St** and **H** genomes
- Two cultivars / 47 USDA accessions
- Secar has been most widely used native grass cultivar, because it was mistaken as BBWG
- Sensitive to clipping / overgrazing

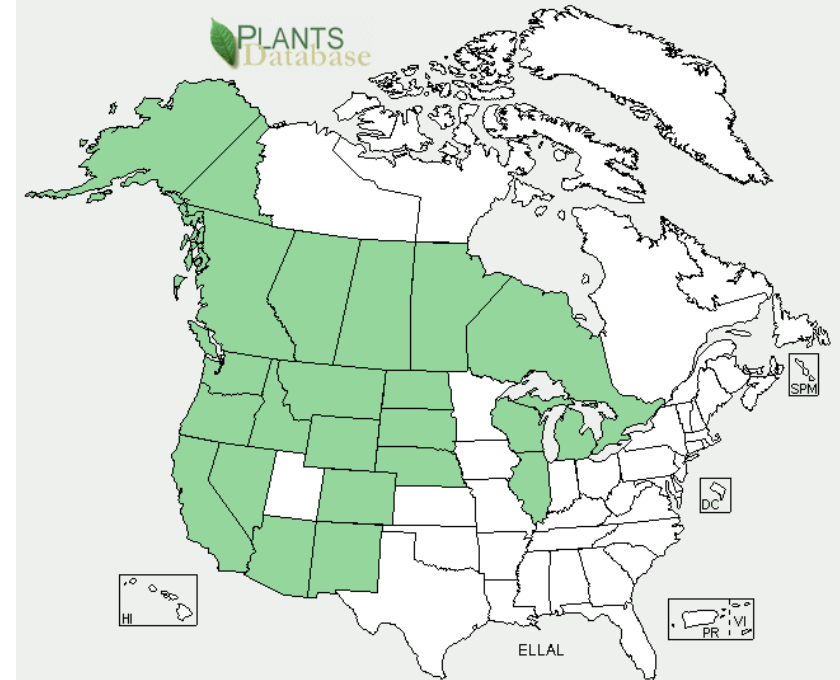




Streambank wheatgrasses (*Elymus lanceolatus*)



- Allotetraploid with **St** and **H** genomes
- Forage and low-maintenance turf types
- Better clipping and grazing tolerance
- Lower forage yield potential
- At least 4 cultivars
- 29 USDA accessions





Snake River x Streambank wheatgrass hybrids



- Rhizomes
- Turfiness
- Forage yield



EST libraries for the St and H genomes of *Pseudoroegneria* and *Elymus* "wheatgrasses"



Bluebunch wheatgrass

Pseudoroegneria (**St**)

8,780 Sanger EST

unigenes (1017 bp)

451 polymorphic SSR s

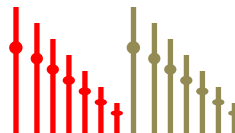


Snake River x Streambank

Elymus (**St H**)

7,212 Sanger EST unigenes

133 polymorphic SSRs





Genetic maps for Snake River x Streambank wheatgrass hybrids

<i>Elymus</i> linkage group	Subgenome	AFLP markers	<i>Elymus</i> (StH) markers	<i>Psuedoroegneria</i> (St) EST-SSRs	%St
1	H	32	6	0	0.0
2	H	33	6	0	0.0
3	H	34	11	1	8.3
4	H	23	4	0	0.0
5	H	27	5	1	16.7
6	H	24	7	0	0.0
7	H	31	5	1	16.7
1	St	17	5	4	44.4
2	St	33	10	1	9.1
3	St	28	4	6	60.0
4	St	19	5	9	64.3
5	St	38	4	3	42.9
6	St	26	2	4	66.7
7	St	35	5	7	58.3
		400	79	37	

Mott, I.W., Larson, S.R., Jones, T.A., Robins, J.G., Jensen, K.B., Peel, M.D. (2011) A molecular genetic linkage map identifying the St and H subgenomes of *Elymus* (Poaceae: Triticeae) wheatgrass. Genome 54:1-10



Synteny among rice, wheat, and *Elymus* wheatgrass identify homoeologous linkage groups

	Os 5 (Ta 1)	Os 10 (Ta 1)	Os 4 (Ta 2)	Os 7 (Ta 2)	Os 1 (Ta 3)	Os 11 (Ta 4)	Os 3 (Ta 4-5)	Os 9 (Ta 5)	Os 12 (Ta 5)	Os 2 (Ta 6)	Os 6 (Ta 7)	Os 8 (Ta 7)
<i>Elymus</i> 1H	3	2							1			
<i>Elymus</i> 1St	5	1			1			1				
<i>Elymus</i> 2H			2	3								
<i>Elymus</i> 2St	1		4	7			1					
<i>Elymus</i> 3H				2	5						1	
<i>Elymus</i> 3St	1				5							2
<i>Elymus</i> 4H		1				0	3					
<i>Elymus</i> 4St			1			1	2		2	1	1	
<i>Elymus</i> 5H				1			2	1	1		1	
<i>Elymus</i> 5St								0	3	3		
<i>Elymus</i> 6H	1	1					1			3		
<i>Elymus</i> 6St										2	1	
<i>Elymus</i> 7H					1					1	4	0
<i>Elymus</i> 7St			1		1					1	7	0

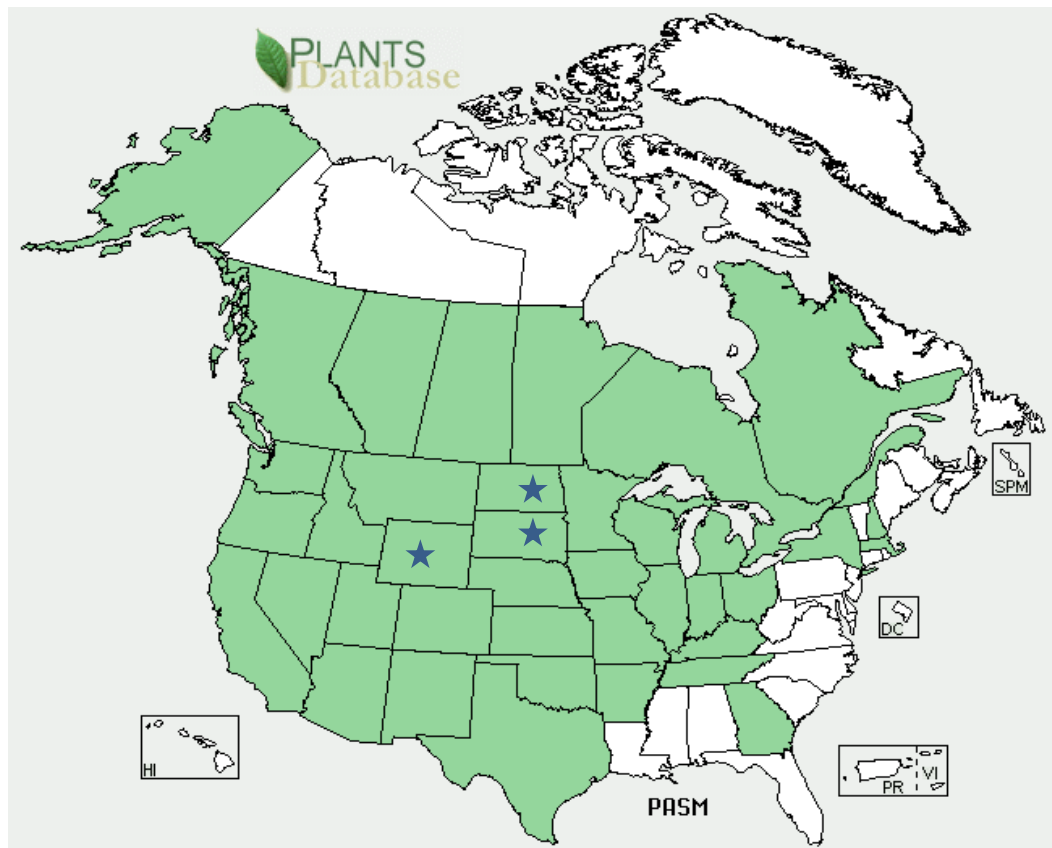
Mott, I.W., Larson, S.R., Jones, T.A., Robins, J.G., Jensen, K.B., Peel, M.D. (2011) A molecular genetic linkage map identifying the St and H subgenomes of *Elymus* (Poaceae: Triticeae) wheatgrass. Genome 54:1-10



Western wheatgrass (*Pascopyrum smithii*)

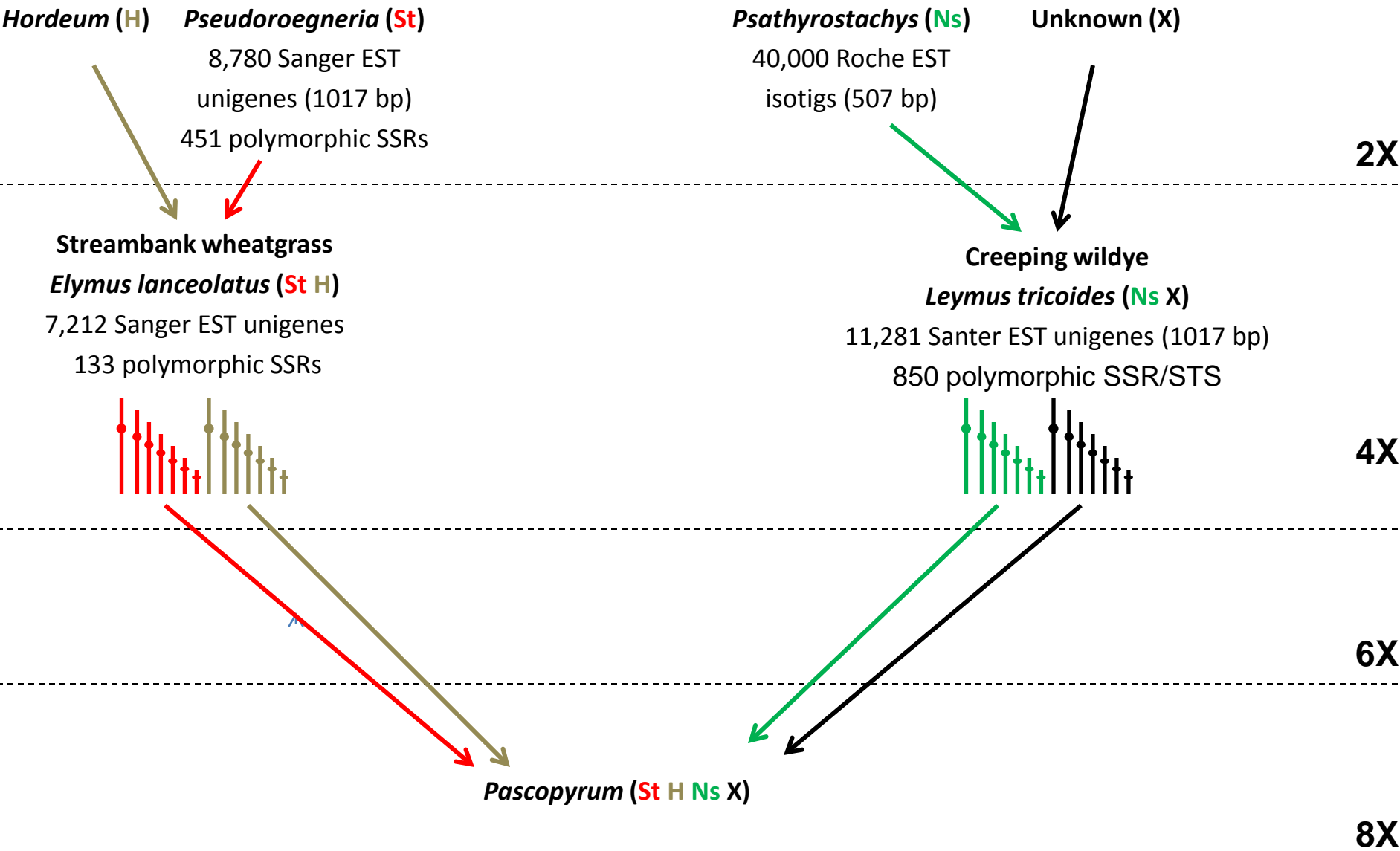


- Only known species of allooctoploid (StHnSX) genus
- Most widespread and abundant native sod grass of Northern Great Plains
- Seed dormancy problems





Genetic resources from *Elymus* and *Leymus* have strong potential in western wheatgrass



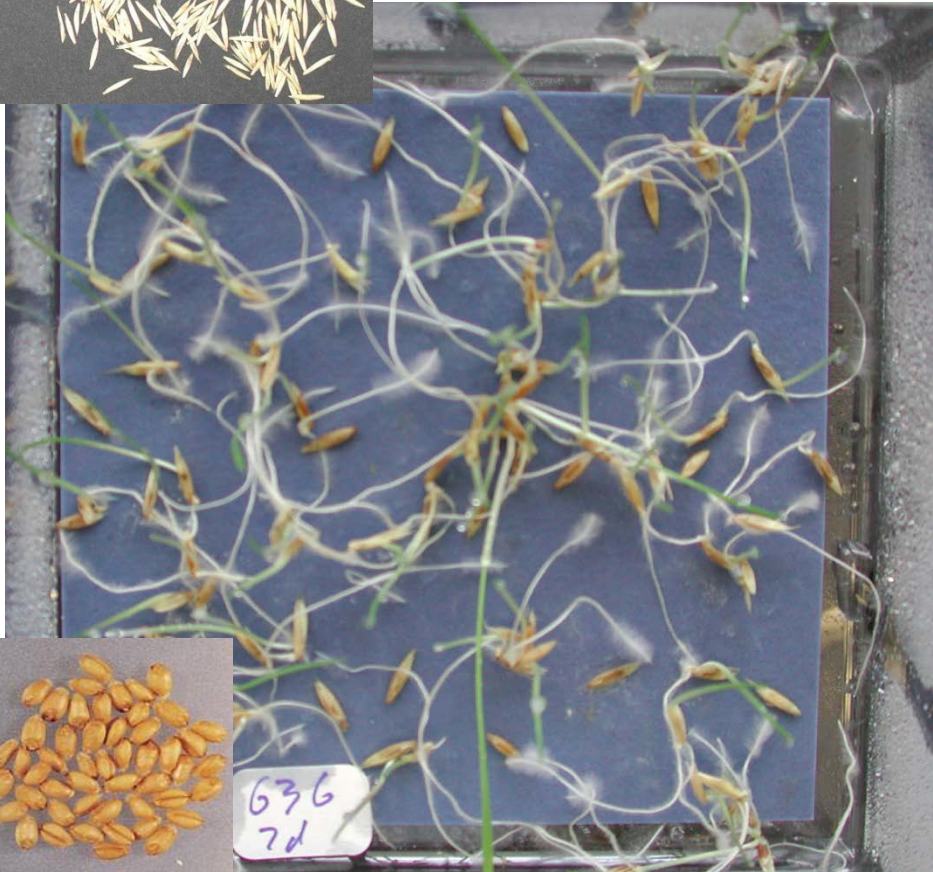


Genetic markers for seed dormancy in *Leymus* may have application in western wheatgrass

Creeping wildrye
(*Leymus triticoides*)



Basin wildrye
(*Leymus cinereus*)





Intermediate and tall wheatgrasses share the E genome of genus *Thinopyrum*

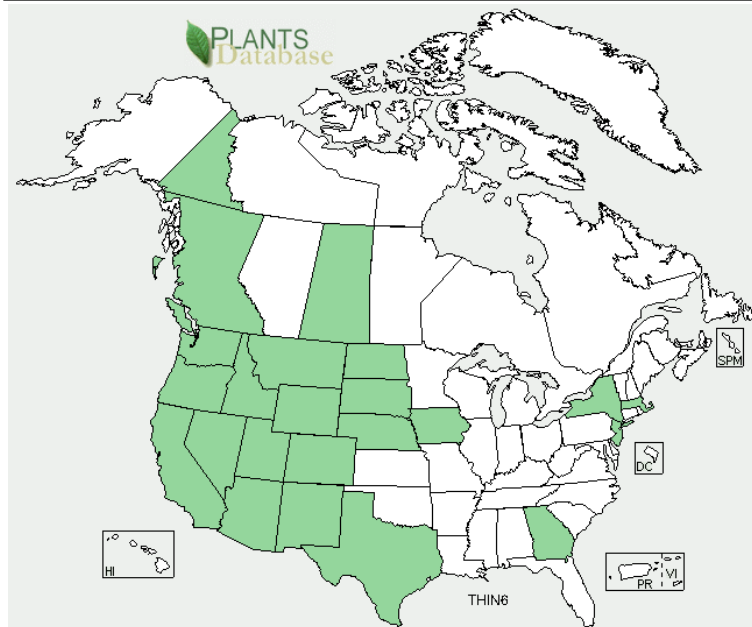
Thinopyrum

- Ten diploid, autopolyploid or allopolyploid species containing at least one **E** genome (set)
- Intermediate and tall wheatgrasses are cultivated and widely naturalized throughout North America
- Native to Mediterranean region and other parts of Eurasia



Intermediate wheatgrass (*Thinopyrum intermedium*)

- Relatively drought tolerant hay and pasture grass, very good single-crop hay
- Many chromosome introgressions in wheat
- Perennial cereal breeding in U.S.
- At least 12 “active” cultivars released in U.S. / Can.
- 252 USDA accessions

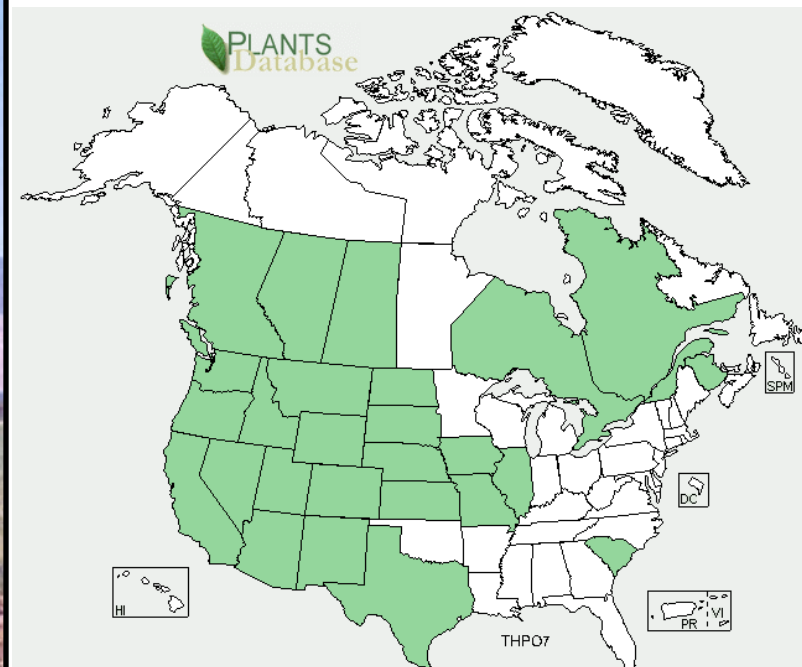




Tall wheatgrass

(*Thinopyrum ponticum*)

- Used for hay, pasture, and conservation
- Very salt tolerant with high biomass potential
- Poor forage quality
- $10n=70$ autopolyploid (genetically recalcitrant)
- Six cultivars released in U.S. and Canada
- 18 USDA accessions





Transcriptome libraries for allohexaploid intermediate wheatgrass and its diploid ancestors

***Pseudoroegneria* (St)**

8,780 Sanger EST
unigenes (1017 bp)
451 polymorphic SSRs

***Thinopyrum
elongatum* (E^e)**

448,000 reads (422 bp)
28,800 contigs (662 bp)
44,400 unmatched (373 bp)
73,200 isotigs

***Thinopyrum
bessarabicum* (J or E^b)**

364,000 reads (426 bp)
14,800 contigs (716 bp)
23,700 unmatched (348 bp)
38,500 isotigs

2X

4X

Intermediate wheatgrass
***Thinopyrum intermedium* (E^eE^bSt)**

567,000 reads (432 bp)
27,700 contigs (646 bp)
55,100 unmatched (384 bp)
27,700 isotigs

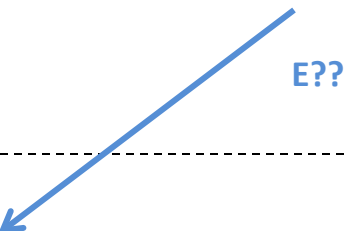
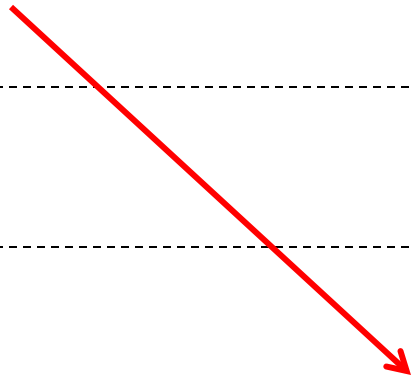
6X

8X

Tall wheatgrass

***Thinopyrum ponticum* (E^e E^e E^e E^e E^e)**

10X



E??



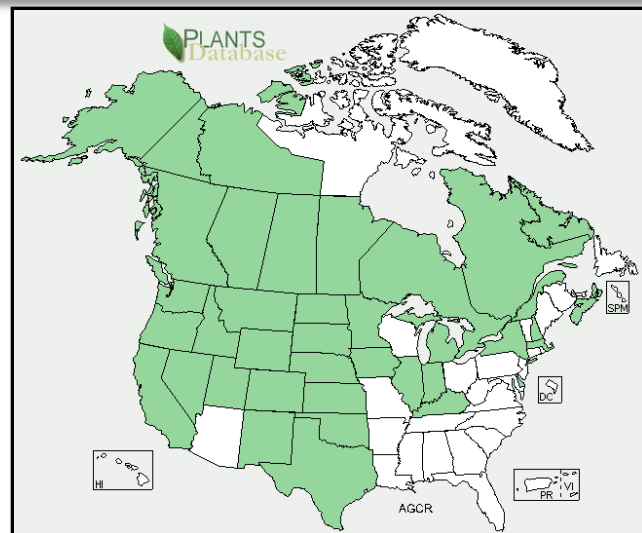
Development of genetic mapping families for intermediate wheatgrass forage varieties

		<u>High Quality</u>		<u>High Yield</u>	
		PI 383561 (Turkey)	PI 401020 (Turkey)	PI 098568 Oahe (Russian via SD)	PI 440002 (K-C, Russia)
<u>High Quality</u>	PI 383561 (Turkey)				
	PI 401020 (Turkey)				
<u>High Yield</u>	PI 098568 Oahe (Russia vi SD)	52 + 89	74 + 75		
	PI 440002 (Karachay-Cherkess)	58 + 11	15 + 21	110 + 5	



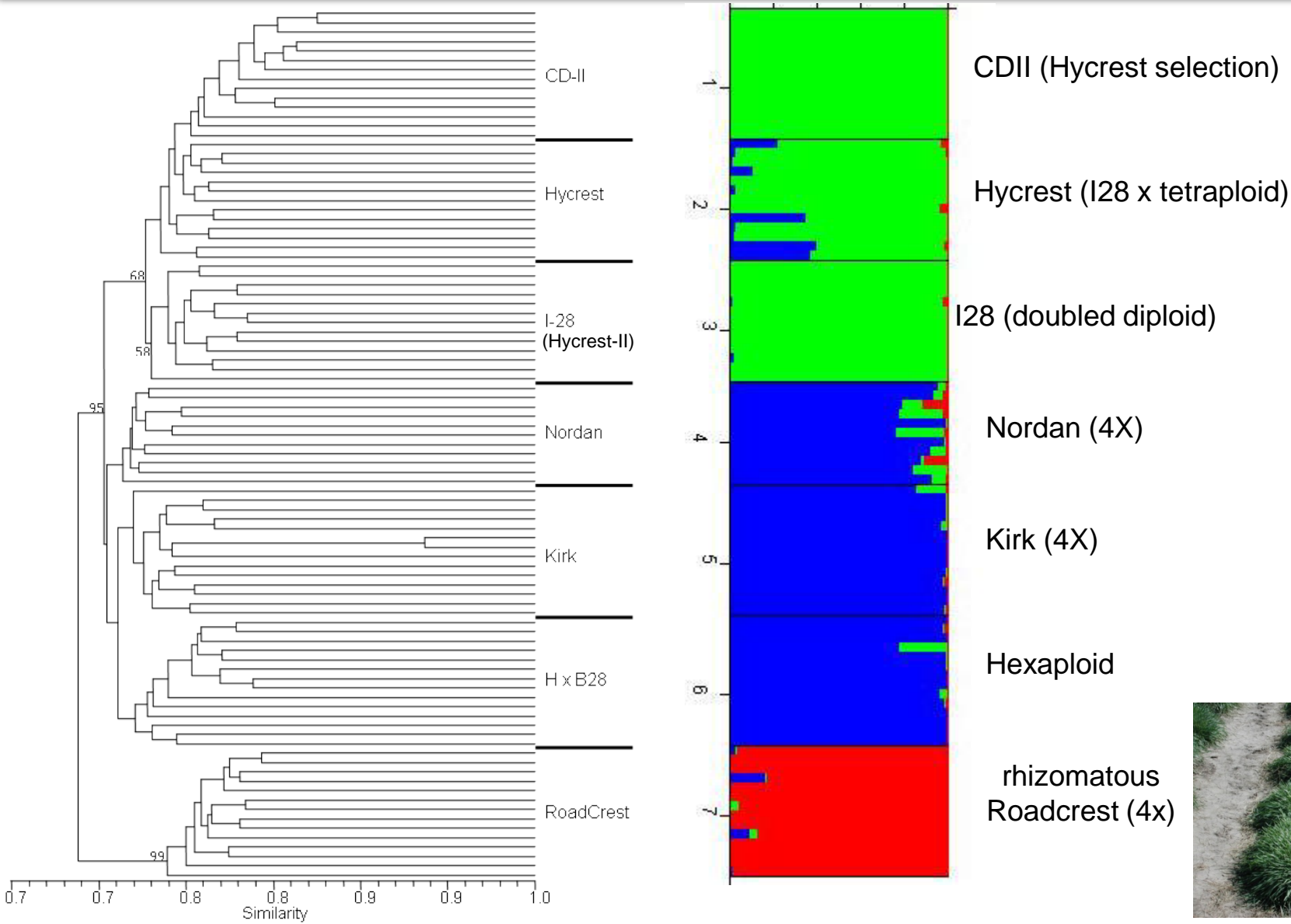
Crested wheatgrass (*Agropyron spp.*)

- Widely naturalized and recommended forage, withstands heavy grazing
- Two recognized taxa in U.S. (*A. cristatum* and *A. fragile*)
- Diploid or autopolyploid forms of **P** genome
- About 10 cultivars released in U.S. and Can.
- More than 700 USDA accessions





Crested wheatgrass (*Agropyron* spp.)





Summary of genetic resources representing genomic diversity among perennial Triticeae

