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Adaptation of perennial triticeae to the eastern Central Great Plains

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Abstract

The tribe Triticeae contains over 250 perennial species that are components of grasslands in the temperate and sub-arctic regions of the world and includes some of the world's most valuable forage and rangeland species. Many of these species had not been evaluated previously in the Central Great Plains, USA. A subset of the germplasm of the tribe Triticeae which included over 100 accessions of 55 different species was evaluated in a replicated, space-planted trial in eastern Nebraska during 1994–1996 to determine the survival and forage productivity of the accessions. The evaluated accessions were representative of perennial Triticeae genera and genomes. Perennial grasses of the Triticeae are based on the P, St, H, Ns, E, W, Y genomes and an unknown Xm genome(s). Triticeae that survived and had acceptable forage yields during the period of the trial were the *Agropyron's* - crested wheatgrasses (PP and PPPP genomes), *Psathyrostachys*- Russian wildryes (NsNs genomes), *Thinopyron's*-intermediate and tall wheatgrasses (EEEEStSt and EEEEEEStSt genomes), some *Elymus* (StStHH genomes), several *Leymus* (NsNsXmXm genomes), and *Pascopyrum*-western wheatgrass (StStHHNsNsXmXm genomes). Several Leymus species had not been evaluated previously in this region but showed considerable potential and merit additional evaluation, including *L. chinensis, L. akmolinensi, L. racemosus, L. sabulosus,* and *L. secalinus*. Species with only the H genome (*Hordeum*) and St genome (*Pseudoroegneria*) were not adapted to the region because of poor survival or low productivity. The study provides an example of how the rapidly emerging field of genomics can have practical applications to grasslands and rangelands.

Key Words: Triticeae, *Agropyron*, *Thinopyrum*, *Elymus*, *Leymus*, *Pascopyrum*, survival, forage yield

Resumen

La tribu Triticeae contiene más de 250 especies perennes que son componentes de los pastizales de las regiones templadas y subárticas del mundo e incluyen algunas de las especies forrajeras más valiosas del mundo. Muchas de estas especies no se han evaluadas previamente en las Grandes Planicies Centrales de Estados Unidos. Un subgrupo de germoplasma de la tribu Triticeae, el cual incluyó mas de 100 entradas de 55 especies diferentes, se evaluó en un ensayo repetido en espacio en el este de Nebraska durante 1994 a 1996 para determinar la sobrevivencia y productividad de las entradas evaluadas. Las entradas evaluadas fueron representativas de generos perennes Triticeae y genomas. Los zacates perennes de la tribu Triticeae están basados en los genomas P, St, H, Ns, E, W, Y y en un genoma(s) desconocido Xm. Los Triticeae que sobrevivieron y tuvieron rendimientos de forraje aceptables durante el período del ensayo fueron: los *Agropyron's* – "Crested wheatgrasses" (genomas PP y PPPP), *Psathyrostachys* – "Russian wildryes" (genomas NsNs), *Thinopyron's*– "Intermediate" and "Tall wheatgrasses" (genomas EEEEStSt y EEEEEEStSt), algunos *Elymus* (genomas StStHH), varios *Leymus* (genomas NsNsXmXm) y *Pascopyrum* – "Western wheatgrass" (genomas StStHHNsNsXmXm). Varias especies de Leymus no habían sido previamente evaluadas en esta región, pero mostraron un considerable potencial y merecen una evaluación adicional, incluyendo *L. chinensis, L. akmolinensi, L. racemosus, L. sabulosus* y *L. secalinus*. Especies con solo el genoma H (*Hordeum*) y el genoma St (*Pseudoroegneria*) no se adaptaron a la región debido a su pobre sobrevivencia y baja productividad. Este estudio provee un ejemplo de cómo el emergente campo de genómicos puede tener aplicaciones prácticas en los zacatales y pastizales.

The tribe Triticeae contains over 250 cool-season, perennial species that are components of grasslands in the temperate and sub-arctic regions of the world. Some Triticeae species such as the crested (*Agropyron* species) and intermediate wheatgrasses (*Thinopyrum* sp.) are important species for revegetating grasslands and retired cropland in the Central Great Plains. There is an increasing demand for improved cool-season or C_3 grasses to provide high quality forage to livestock during spring, fall, and early winter in integrated livestock production systems in the central Great Plains. In this region rangelands, which are composed primarily of warm-season (C_4) grasses or seeded warm-season pastures, are used for summer grazing.

In the last 25 years, several germplasm collection expeditions have been made in eastern Europe and Asia to collect grass germplasm, particularly of the Tribe Triticeae. Many of the collections were made in areas which were previously not open for collection. Extensive germplasm collections of Triticeae species currently are available for evaluation. Except for many of the *Thinopyrum* accessions (primarily intermediate wheatgrasses, *T. intermedium,* and tall wheatgrasses, *T. ponticum*) and some crested wheatgrasses (*Agropyron* spp) most of these accessions have not been previously evaluated in the Central Great Plains.

The objective of this study was to evaluate species of the perennial Triticeae that may have potential for use in grassland agriculture in the central Great Plains of the USA and to identify specif-

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ic genomes within the Triticeae grasses that are critical for survival and forage productivity in the eastern part of the Central Great Plains.

Previous research summarized by Dewey (1984), Wang et al. (1994), and Asay and Jensen (1996a, 1996b) and others has demonstrated that perennial grasses of the tribe Triticeae are comprised of the genomes P, St, H, Ns, E, W, Y and an Xm genome of unknown orgin. The cytogenetic definition of genome, i.e, the haploid set of chromosomes of a diploid species (Shultz-Shaffer 1980) will be used in this report. The classification of the Triticeae has been and remains a matter of controversy (Barkworth 1992, Kellogg 1994). For this paper, the genomic classification, which groups species according to genome content (Dewey 1984, Barkworth and Dewey 1985) will be used with the following exceptions. Under the current GRIN classification system, Tzvelev's (1984) treatment of the Triticeae that lumps the genus *Thinopyrum* and *Pseudoroegneria* into the enlarged *Elytrigia* is used. We will follow Dewey's (1984) treatment that recognizes both *Thinopyrum* and *Pseudoroegneria* as separate genera. Dewey (1984) indicated that *Leymus* species and *Pascopyrum* contain the J (=E) genome. Subsequent reports (Zhang and Dvorak 1991, Wang and Jensen, 1994) based on molecular genetic and cytogenetic analysis indicate that the J genome does not occur in *Leymus* or *Pascopyrum*. Asay and Jensen (1996a, 1996b) have designated the unknown genome in *Leymus* and *Pascopyrum* the Xm or unknown genome following the genome nomenclature system for the Triticeae proposed by Wang et al. (1994). Species classified as *Critesion* by Barkworth and Dewey (1985) are listed as *Hordeum* in this report. To simplify reporting, genus and species names with associated authorities of the plant material used in this study are listed in Table 1 along with common names of some of the more widely used grasses.

Materials and Methods

Grasses used in this study (Table 1) were primarily plant introductions obtained from the U.S. Department of Agriculture's National Plant Germplasm System via the USDA-ARS Forage and Range Research Laboratory at Utah State University, Logan, Ut. where they were identified. These accessions have a PI (for plant introduction) numerical designation and can be obtained from the USDA Plant Germplasm System. The other accessions used in this study are experimental breeding lines maintained by USDA-ARS Laboratory at Logan, Ut. or were released cultivars (designated cv.) obtained by the USDA-ARS grass breeding program at Lincoln, Neb. The accessions used in the study (Table 1) were chosen to represent the autoploid and alloploid combinations that exist within the perennial Triticeae. Many of the species were represented by 2 accessions originating from different areas. Seeds of the genus *Australopyrum* which are comprised of the W genome were not available for use in this study. Chromosome numbers of these accessions were determined by the USDA-ARS Forage and Range Laboratory at Logan, Ut. using conventional chromosome counts or at Lincoln, Neb. where they were estimated by flow cytometry estimates of cellular DNA content (Vogel et al. 1999). The genomic constituents of the species are based on previously summarized or reported research by Dewey (1984), Barkworth and Dewey (1985), Zhang and Dvorak (1991), Liu and Wang (1993), Wang and Jensen (1994), Wang et al. (1994), Asay and Jensen (1996a, 1996b), Zhang and Wang (1996), and Zhang et al. (1996).

Seed of these grasses was planted on 23 March 1994 in a greenhouse at Lincoln, Neb. Prior to seeding, seed was wet-chilled for 2 weeks at 4.5°C to break dormancy. The seeds were planted in super-cell cone-tainers or mini-pots (22 cm deep, 4 cm diam.) which contained a mixture of 2:1:1 soil/peat/vermiculite and were thinned to 1 per cone-tainer after emergence. Natural light was used and the greenhouse was maintained at a temperature range of 21 to 27°C. Seedlings were transplanted into a field nursery the first week of July 1994. The field evaluation nursery was located at the Univ. of Nebraska Agricultural Research and Development Center, Mead, Neb. (41° 4' N, 96° 5' W) which is located about 35 km west of Omaha, Neb. The soil type was Sharpsburg silty clay loam (silty clay Typic Argiudoll). Plots were single rows of space-transplanted plants on 1.1m centers. Previous research evaluating *Agropyron*, *Thinopyrum*, and *Bromus* perennial grass germplasm accessions in the central Great Plains demonstrated that a small number of replicates harvested for more than 1 year provided adequate statistical precision (Lamb et al. 1984, Vogel 1980, 1983, Vogel et al. 1986). The experimental design was a randomized complete block with 2 replicates. Accessions were blocked by genus. Genera, and species and accessions within a genus were randomized within each replicate.

Hand weeding and herbicides were used for weed control. Since some of the species are highly rhizomatous, periodic roto-tilling with a heavy duty roto-tiller was used to keep plants cut back to an area of 0.2 m^2. The herbicides metolachlor [2-chloro-N-(2-ethyl-6-methyl-phenyl)-N-(2-methoxy-1-methylethyl)acetamide] and imazethapyr {2-[4,5-dihydro-4-methyl-4-(1-methylethyl)-5-oxo-1H-imidazol-2-yl]-5-ethyl-3-pyridinecarboxylic acid} were applied 2 weeks prior to transplanting and in May of 1995 and 1996 at rates of 2 kg ha^{-1} and 0.03 kg ha^{-1}, respectively. The herbicide 2,4-D (2,4-dichlorophenoxyacetic acid) was applied in July of 1994 and May of 1996 for broadleaf weed control. Nitrogen fertilizer was not applied the establishment year. In 1995 and 1996, 112 kg N ha^{-1} (NH_4NO_3) was applied the last week of April. No other fertilizers were used.

Plots were harvested after flowering with a flail type plot harvester on 15 August 1995 and 11 July 1996 at a height of approximately 10 cm. Harvest was delayed in 1995 because of our unfamiliarity with the plant material. Some accessions produced only limited seed heads and it was difficult to initially ascertain when flowering had occurred. A subsample from each plot was dried in a forced draft oven at 50°C to determine dry matter concentration of the harvested forage, which was used to convert fresh weight yields to a dry weight basis. Because some plants did not survive the establishment year or post-establishment years, yields were expressed on a single-plant basis by dividing plot dry weight by the number of plants harvested per plot each year. Number of plants harvested was determined at the time of harvest. Forage yields are expressed as grams/plant on a dry weight basis. Survival percentage was determined as the percentage of plants surviving at the time of the final forage harvest in 1996. A plant was scored as surviving if any green leaf tissue was present.

Analysis of variance procedures were used to assess the statistical significance of variation among genera and accessions within genera using plot means over years (Snedecor and Cochran 1989). The error variances for genera and accessions nested within genera was used to calculate LSD values for each trait where the F tests for genera or accessions were significant at

Table 1. Mean forage yields and survival percentages for perennial Triticeae species grown at Mead, Nebraska, 1994 to 1996.

Species	Genome[1]	2n[2]	Accession or strain[3]	Forage yield	Survival	Origin[4]
				(g/plant)	(%)	
Agropyron Gaertner						
A. cristatum (L.) Gaertner [fairway crested wheatgrass][5]	PP	14	PI 297870	261	100	Romania
A. cristatum	PP	14	PI 314600	68	100	USSR
A. cristatum	PP	14	cv Ruff	233	100	USSR
A. mongolicum Keng	PP	14	PI 406450	92	100	USSR
A. mongolicum	PP	14	PI 499391	58	100	PRC
A. mongolicum	PP	14	PI 499392	63	100	PRC
A. desertorum (Fischer ex Link) Shultes [standard-type crested wheatgrass]	PPPP	28	PI 249143	166	100	Portugal
A. desertorum	PPPP	28	cv Nordan	208	100	USSR
A. desertorum	PPPP	28	PI 314057	188	100	USSR
A. fragile (Roth) Cond. [Siberian wheatgrass]	PPPP	28	PI 406449	189	100	USSR
Pseudoroegneria (Nevski) À. Löve						
P. strigosa (M. Bieb)	StSt	14	D3778	9	80	PRC
P. strigosa subsp. *aegilopoides* (Drobov.)À. Löve	StSt	14	PI 531755	19	80	PRC
P. strigosa subsp. *aegilopoides*	StSt	14	PI 499637	14	100	PRC
P. libanotica (Hackel) D.R. Dewey	StSt	14	PI 380644	24	54	Iran
P. libanotica	StSt	14	PI 380652	23	25	Iran
P. spicata (Pursh) À. Löve subsp.[bluebunch wheatgrass]	StSt	14	PI 232127	40	88	USA
P. spicata	StSt	14	PI 232134	15	82	USA
P. stipifolia (Czern ex Nevski)	StSt	14	PI 440000	35	89	USSR
P. geniculata (Trin.) À. Löve	StStStSt	28	DJ3875	9	100	USSR
P. geniculata	StStStSt	28	DJ3882	15	100	USSR
Hordeum L.						
H. bogdanii Wilensky	HH	14	PI 269406	44	22	Afganistan
Afganistan *H. bogdanii*	HH	14	PI 440413	49	19	USSR
H. brachyantherum Nevski	HH	14	D3571	38[6]	0[6]	USA
H. brevisubulatum subsp. *violaceum* (Boise & Hofenacker) Tzvelev	HH	14	PI 401374	31	83	Iran
H. brevisubulatum subsp. *violaceum*	HH	14	PI 531774	68	83	USSR
H. bulbosum L.	HH	14	PI 318649	4	66	Greece
H. bulbosum	HHHH	28	PI 343189	53	0[6]	USSR
H. californicum Covas & Stebbins	HH	14	PI 531778	20	25	USA
H. californicum	HH	14	PI 531779	40	17	USA
H. chilense Roemer & Schultes	HH	14	PI 531781	202	0[6]	Argentina
H. comosum K. Presl	HH	14	D2742	14	33	Argentina
H. flexuosum Nees	HH	14	Castelar730	146	12	Argentina
H. haplophilum Griseb.	HH	14	D2749	11	0[6]	Argentina
H. roshevitzii Bowden	HH	14	PI 499504	26	33	PRC
H. roshevitzii	HH	14	PI 531788	35	86	PRC
H. stenostachys Godron	HH	14	PI 531791	69	14	Argentina
H. stenostachys	HH	14	PI 531792	67	0[6]	Argentina
Psathyrostachys Nevski						
P. fragilis (Boise) Nevski	NsNs	14	PI 343190	42	72	Iran
P. fragilis	NsNs	14	343192	91	100	Iran
P. juncea (Fisher) Nevski [Russian wildrye]	NsNs	14	PI 406468	142	95	USSR
P. juncea	NsNs	14	PI 531824	116	100	PRC
P. stoloniformis C.Baden	NsNs	14	D2562	33	100	PRC
P. stoloniformis	NsNs	14	D3376	53	100	PRC
Thinopyrum À. Löve						
T. bessarabicum (Savul & Rayass) À. Löve	E^bE^b	14	PI 431711	10	100	USSR
T. bessarabicum	E^bE^b	14	AJC305	41	88	USSR
T. elongatum (Host) D.R. Dewey	E^eE^e	14	D3610	18	100	Israel
T. junceiforme (Löve & Löve) À Löve	$E^bE^bE^eE^e$	28	PI 297873	15	25	Portugal
T. junceiforme	$E^bE^bE^eE^e$	28	D3463	66	64	France
T. caespitosum Liu & Wang	EEStSt	28	PI 531716	56	79	USSR
T. caespitosum	EEStSt	28	Jasska 4	34	60	USSR
T. intermedium (Host) Barkw. & D.R. Dewey [intermediate wheatgrass]	EEEEStSt	42	cv Slate	362	100	USSR
T. intermedium subsp. *barbulatum* (Schur) Barkw. & D.R. Dewey [pubescent intermediate wheatgrass]	EEEEStSt	42	cv Manska	309	100	USSR
T. ponticum (Podp.) Barkw. & D.R. Dewey	EEEEEE-StStStSt	70	cv Platte	417	100	USSR
Elymus L.						
E. abolinii (Drob.) Tzvelev	StStYY	28	PI 531554	63	0[6]	PRC
E. abolinii	StStYY	28	PI 531555	47	50	PRC

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Species	Genome[1]	2n[2]	Accession or strain[3]	Forage yield	Survival	Origin[4]
				(g/plant)	(%)	
E. ciliaris (Trin.) Tzvelev	StStYY	28	PI 531576	60	94	USSR
E. canadensis L. [Canada wildrye]	StStHH	28	PI 531564	154	100	USA
E. canadensis	StStHH	28	PI 531565	321	100	USA
E. caninus L.) L.	StStHH	28	PI 253290	38	65	Yugoslavia
E. caninus	StStHH	28	PI 439906	31	50	USSR
E. glaucus Buckley [blue wildrye]	StStHH	28	D3261	22	0[6]	USA
E. glaucus	StStHH	28	D3268	20	0[6]	USA
E. lanceolatus (Schribner & Smith) Gould [thickspike wheatgrass]	StStHH	28[fc]	D3626	109	100	Canada
E. lanceolatus	StStHH	28	D3627	46	100	USA
E. mutabilis (Drob.) Tzvelev	StStHH	28	PI 499449	48	67	PRC
E. mutabilis	StStHH	28	PI 499589	24	28	PRC
E. sibiricus L.	StStHH	28[fc]	PI 499613	100	67	PRC
E. sibiricus	StStHH	28[fc]	PI 499616	120	100	PRC
E. trachycaulus (Link) Gould ex Shinners [slender wheatgrass]	StStHH	28	PI 232168	52	100	USA
E. trachycaulus	StStHH	28	PI 276711	125	100	Hungary
E. trachycaulus	StStHH	28	PI 315368	196	100	USSR
E. alatavicus (Drob.) À. Löve	StStYYPP	42	PI 499475	7	44	PRC
E. alatavicus	StStYYPP	42	PI 531709	19	42	USSR
E. batalinii (Krasn.) À. Löve	StStYYPP	42[fc]	D3700	97	69	USSR
E. batalinii	StStYYPP	42	DJ4137	19	93	USSR
E. dahuricus Turez ex Griseb.	StStHHYY	42	PI 499592	122	81	PRC
E. dahuricus	StStHHYY	42	PI499593	78	81	PRC
Leymus Hochst.						
L. akmolinensis (Drob.) Tzvelev	NsNsXmXm	28	PI 440306	57	100	USSR
L. akmolinensis	NsNsXmXm	28	PI 531794	161	94	USSR
L. ambiguus (Vasey & Schribn.) D.R. Dewey	NsNsXmXm	28[fc]	KJ59	28	92	USA
L. ambiguus	NsNsXmXm	28	PI 531796	16	100	USA
L. chinensis (Trin.) Tzvelev	NsNsXmXm	28	PI 499515	273	100	PRC
L. chinensis	NsNsXmXm	28	PI 499518	227	100	PRC
L. cinereus (Scribn. & Merv.) À.. Löve [basin wildrye]	NsNsNsNs-XmXmXmXm	56[fc]	D3706	65	100	USA
L. cinereus	NsNsNsNs-	56[fc]	Magnar	100	100	Canada
L. cinereus	NsNsXmXm	28[fc]	KJ51	66	93	USA
L. *coreanus* (K.B.Jensen&R.R.-C. Wang)	NsNsXmXm		PI 531578	58	67	USSR
L. flavescens (Scribner & Smith) Pilger	NsNsXmXm	28	Has & Har	91	100	USA
L. racemosus (Lam.) Tzvelev [mammoth wildrye]	NsNsXmXm	28	PI 313965	44	86	USSR
L. racemosus	NsNsXmXm	28	PI 531812	416	100	USSR
L. cf. *racemous*	NsNsXmXm	28	DJ3801	294	100	USSR
L. racemosus	NsNsXmXm	28	PI 108491	290	95	USSR
L. cf. *ramosus* (Trin.) Tzvelev	NsNsXmXm	28	PI 499654	59	100	PRC
L. sabulosus (M. Bieb.) Tzvelev	NsNsXmXm	28	PI 531813	341	100	USSR
L. sabulosus	NsNsXmXm	28	PI 531814	234	100	USSR
L. salinus clone (M.E. Jones) À. Löve	NsNsNsNs-XmXmXmXm	56	PI 531816	81	100	USA
L. secalinus (Georgi) Tzvelev	NsNsXmXm	28	PI 499524	226	100	PRC
L. secalinus	NsNsXmXm	28	PI 499528	173	95	PRC
L. triticoides (Buckl) Pilger [beardless wheatgrass]	NsNsXmXm	28	PI531822	170	100	USA
L. tritcoides	NsNsXmXm	28	D2950	162	100	USA
L. tritcoides	NsNsXmXm	28	Asay M-9	125	100	USA
L. tritcoides	NsNsXmXm	28	cv. Shoshone	86	100	USA
Pascopyrum À. Löve						
P. smithii (Rydb.) À. Löve [western wheatgrass]	StStHHNsNs-XmXm.	56	cv. Flintlock	247	100	USA
P. smithii	StStHHNsNs-XmXm	56	cv Barton	183	100	USA
P. smithii	StStHHNsNs--XmXm	56	cv. Rodan	274	100	USA
F ratio for accessions				5.3**	3.6**	
LSD 0.05				103	34	

[1]Superscript on genome letters refers to a subset of that genome.
[2]Ploidy level determined by conventional chromosome counts except where superscript fc indicates ploidy level was estimated by flow cytometry.
[3]PI numbers are accession numbers of the USDA Plant Germplasm system; other accession/strain numbers are from the USDA Triticeae collection at Logan, Utah (K.Jensen).
[4]PRC = Peoples Republic of China, USSR = area occupied by former Soviet Union, USA = United States of America followed by postal abbreviation of indivual states. See Germplasm Information Network (GRIN) at http://www/ars-grin.gov/ for specific accession information.
[5]USA common name is in brackets [ ].
[6]Some accessions produced forage yields in 1995 but did not have any surviving plants at the time when final stands were determined in July of 1996. Yields are means for 1995 and 1996.

Year/ location	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Sep.	Oct.	Nov.	Dec.	Annual
	Monthly precipitation (mm)												
1994	12	6	0	32	36	230	107	43	95	34	62	16	674
1995	20	10	62	109	145	33	26	34	63	35	12	9	558
1996	130	2	23	82	185	140	37	76	51	17	59	10	694
Omaha	17	20	54	70	111	99	83	82	93	61	34	24	747
Lincoln	14	18	53	70	99	99	81	87	88	54	32	22	717
	Average monthly temperature (C)												
1994	–7.2	–6.7	4.7	10.1	16.9	22.4	21.7	21.6	18.3	12.6	5.1	–2.6	9.7
1995	–6.1	–0.4	3.0	7.7	13.0	21.2	24.9	25.6	17	11.5	0.5	–2.2	9.6
1996	–7.8	–2.7	–0.6	8.5	14.3	22.1	22.2	21.6	16.4	11.9	–0.4	–5.9	8.3
Omaha	–6.3	–3.4	3.1	10.8	16.9	22.1	24.7	23.3	18.2	12.0	3.7	–4.2	10.3
Lincoln	–5.9	–3.0	–1.9	10.9	16.7	22.4	25.6	213.8	18.5	12.0	3.8	–3.6	10.4

Data from National Climatic Data Center at http://www.ncdc.noaa/gov.

the 0.05 probability level. Means over years were used because average performance of a perennial over years is the most important indicator of agronomic value, and in previous perennial grass germplasm evaluation research, accession by year interaction effects were either not significant or small (Lamb et al. 1984, Vogel, 1983, Vogel et al. 1986).

Results and Discussion

In the central Great Plains, the most important trait for a perennial grass is the ability to survive. The temperature of the region can vary from 40°C during the summer months to -40°C during winter, sometimes without snow cover (Lawson et al. 1977). During the late fall, winter, and spring there can be large and rapid changes in temperature. Temperature changes of more than 30°C can occur within 48 hours. Climatic conditions during this study were typical for the region (Table 2).

Plots were established with transplanted seedlings instead of by direct seeding because of potential differences in seedling vigor and we wanted to ensure that seedlings became well established during the first growing season. There were visible differences among accessions for seedling growth at the time of transplanting. Consequently, we did not collect any first year data but instead used the first growing season to allow the seedlings to become well established. There were significant differences among genera and accessions for survival (Table 1, 3, and 4). As expected based on their previous use in the region, crested wheatgrasses (*Agropyron* species, P genome) had 100% survival. Other genera that had species with excellent survival were *Pseudoroegneria* (St genome), *Psathyrostachys* (Ns genome) which includes Russian wildrye (*P. juncea*), *Thinopyrum* (E and E+St genome) species that have both the E and St genomes (the intermediate and tall wheatgrasses), some *Elymus* (St + Y,H, or P genomes) species, and most *Leymus* (Ns+Xm genomes) species. All of the *Pascopyrum* (St,H,N, and Xm genomes) accessions had survival percentages of 100%. *Hordeum* (H genome) species had the lowest average survival percentages and no *Hordeum* species had 100% survival (mean = 34%; range = 0 to 86%). The *Pseudoroegneria* species with the best survival were from Eurasia while the *Elymus* species with the best survival were native North American species such as *E. canadensis*, *E. lanceolatus*, and *E. trachycaulus* (Table 1). Eighteen of the 24 *Leymus* accessions had survival percentages of 100% and only 1 had a survival percentage less than 90%.

The genera with the highest forage yields were *Agropyron*, *Thinopyrum*, *Leymus*, and *Pascopyrum* (Table 1 and 4). Some species, including *Hordeum* taxa, had high forage yields the first year of harvest but did not survive the second year. Check cultivars of *Agropyrons*, Ruff and Nordan, are well adapted standards for identifying species and genomic combinations that had equivalent forage yields (> 100 g/plant) and more than 90% survival. None of the *Pseudoroegneria* (St genome) or *Hordeum* (H genome) species had comparable forage yields or survival percentage. The only *Psathyrostachys* species (Ns genome) that survived both years of the study was Russian wildrye, (*P. juncea*). The hexaploid and decaploid *Thinopyrum* species *T. intermedium* and *T. ponticum* had high forage yields and survivability (Table 1). Other genomic combinations within *Thinopyrum* were not as well adapted. The only *Elymus* accessions that had yields and survival percentages equivalent to the 2 crested wheatgrass cultivars belonged to species that had the StStHH genomic configuration. These included Canada wildrye (*E. canadensis*) which is native to Great Plains grasslands, slender wheatgrass (*E. trachycaulus*) which is native to some North American grasslands, and *E. sibiricus*, which is an Eurasian counterpart to Canada wildrye. None of the other Eurasian or North American species with the StStHH genomic configuration were as well adapted based on survival scores and forage yields. Many *Leymus* species with the NsNsXmXm genomic configuration from Eurasia had excellent survival percentages and high forage yields. Many of these species had not been evaluated previously in the Central Great Plains.

Table 3. Analysis of variance for plant yield and survival of Triticeae species grown at Mead, Nebr. from 1994 to 1996.

Source	df	Mean Squares	
		Yield (g/plant)	Survival (%)
Replicate	1	29805	679
Genus	7	80124	13407
Replicate x genus	7	2517	686
Entry (genus)	98	14307	1091
Error	98	2695	301
F for genus		31.8**	19.5**
F for species		5.3**	3.6**

*,** Indicate significance at the 0.05 and 0.01 levels of probability respectively.

Table 4. Mean forage yields and survival percentages for perennial Triticeae genera averaged over species grown in a space-planted trail at Mead, Nebr. in 1995 and 1996.

Genus	Accessions	Forage yield	Survival
	(n)	(g/plant)	(%)
Agropyron	10	153	100
Pseudoroegeneria	10	20	80
Hordeum	17	57	34
Psathyrostachys	6	80	94
Thinopyrum	10	153	85
Elymus	24	80	68
Leymus	25	154	97
Pascopyrum	3	235	100
F ratio for genera		31.8**	19.5**
LSD	0.05	118	44

** Indicates statistical significance at the 0.01 level of probability.

Pascopyrum is a monotypic genus (*P. smithii* - western wheatgrass) that is native to the prairies and plains of North America. The western wheatgrass accessions that were evaluated were representative of Great Plains germplasm and had high forage yields and excellent survival. 'Barton' western wheatgrass was developed by direct increase of a collection from Barton County, Kan., 'Flintlock' was developed by breeding from collection in Kansas and Nebraska, while Rodan was developed by breeding at Mandan, N.D. (Alderson and Sharp 1993)

The adaptability to the central Great Plains and productivity of some of these species such as the crested, intermediate, tall, and western wheatgrasses and Russian wildrye's was known before their genomic configurations were determined (Asay and Jensen 1996a, 1996b). The results of this study correspond with the previously known adaptation and productivity of these species and their constituent genomes. Western wheatgrass apparently gets its adaptability to the central Great Plains from its *Leymus* genomes (NsNsXmXm). Most species with the HH, HHHH (*Hordeum*) and StSt, StStStSt (*Pseudoroegneria*) genomic configurations do not appear to be adapted to the central Great Plains. Several *Leymus* species showed considerable potential and merit additional evaluation in the central Great Plains. The promising species and the number of accessions of each in the USDA Germplasm System (in parentheses) include *Leymus chinensis* (36), *L. sabulosus* (4), *L. akmolinensi* (3), *L. racemosus* (30) and *L. secalinus* (50). In addition to having high forage yields following anthesis, they also had excellent regrowth which stayed green late into the fall. The leaves of some of these species are relatively coarse and their palatability to livestock will need to be determined. According to Asay and Jensen (1996b) many of the *Leymus* species are characterized by seed dormancy and poor seedling vigor. These traits also will need to be evaluated. In this study, we evaluated only a few of the available accessions of the most promising species. The accessions of these species that are available in the USDA Germplasm System should be evaluated at several locations in the Central Great Plains to identify the most suitable accessions for use in the region and in breeding programs.

The previous work by geneticists such as Douglas Dewey, which has resulted in the genomic characterization of the Triticeae, enabled this study to be structured so that we could characterize grasses by their constituent genomes rather than geographic origin. It provides an example of how the rapidly emerging field of genomics can have practical applications to grasslands and rangelands.

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