# Supplementary Information

**Appendix S1**. List of taxa examined in this study, voucher numbers from personal collections and NCBI accession numbers for all genes and taxa.

Taxa	Tissue source/Genbank gi numbers				
	ITS	matK	ndhF	rbcL	
Poa pratensis	Genbank/	Genbank/	Genbank/	Genbank/	
	HQ600540	HQ600012	AY589101	HQ600433	
Festuca octoflora	Genbank/ KF917280	-	-	-	
Agrostis hyemalis	Genbank/ HQ600526	Genbank/ HQ60053	-	Genbank/H Q600474	
Keoleria pyramidata	Genbank/ DQ336827	Genbank/ EF137505	-	Genbank/ AJ784825	
Sphenopholis obtusata	-	EJForrestel 300/ Pending	EJForrestel 300/ Pending	EJForrestel 300/ Pending	
Elymus smithii	Genbank/ GU557082	-	Genbank/ AF267703	Genbank/ JX848505	
Elymus canadensis	Genbank/ KJ028243	Genbank/ KJ028444	Genbank/ HM770846	Genbank/ KC237138	
Hordeum pusillum	Genbank/ HQ600534	Genbank/ AB078133	Genbank/ HQ619414	Genbank/ AY137452	
Bromus japonicus	Genbank/ KF713199	Genbank/ KF713100	-	Genbank/ KF12963	
Dactyloctenium aegyptium	Genbank/ EF153037	Genbank/ KF357745	Genbank/ GU359713	Genbank/ EF125106	
Chloris roxburghiana	-	EJForrestel 301/ Pending	EJForrestel 301/ Pending	EJForrestel 301/ Pending	

Chloris verticillata	-	EJForrestel 302/ Pending	EJForrestel 302/ Pending	EJForrestel 302/ Pending
Muhlenbergia paniculatus	Genbank/ EF153079	Genbank/ AF312335	Genbank/ GU359609	EJForrestel 303/ Pending
Muhlenbergia racemosa	Genbank/ GU359114	EJForrestel 304/ Pending	Genbank/ GU359638	Genbank/ AJ784836
Bouteloua curtipendula	Genbank/ GU359281	Genbank/ AF144578	Genbank/ EF422911	Genbank/ JN681654
Bouteloua gracilis	Genbank/ GU359285	Genbank/ HE575865	Genbank/ HE575771	Genbank/ JX848489
Tragus berteronianus	Genbank/ GU359224	Genbank/ AF144591	Genbank/ GU359675	EJForrestel 305/
Sporobolus compositus	-	EJForrestel 306/ Ponding	CSU:94198/ KJ740988	CSU:94198/ KJ740996
Sporobolus cryptandrus	Genbank/ GU359208	Genbank/ HQ593457	Genbank/ GU359674	Genbank/ HQ590286
Sporobolus heterolepis	-	Genbank/ AF164429	YU:EJForre stel41/ KJ740989	YU:EJForre stel41/ KJ740997
Sporobolus nitens	Genbank/ HM347023	EJForrestel 308/ Pending	Genbank/ HM346997	EJForrestel 308/ Pending
Eragrostis spectabilis	-	Genbank/ HE577884	Genbank/ HE577868	Genbank/ HE577858
Eragrostis nindensis	-	EJForrestel 309/ Pending	EJForrestel 309/ Pending	EJForrestel 309/ Pending

Eragrostis lehmanniana	Genbank/ DQ655819	EJForrestel 310/ Pending	Genbank/ HM346984	EJForrestel 310/ Pending
Eragrostis superba	Genbank/ DQ655825	EJForrestel 311/ Pending	Genbank/ HM346988	EJForrestel 311/ Pending
Enneapogon cenchroides	Genbank/ DQ655841	-	Genbank/ HM346981	-
Schmidtia pappophoroides	Genbank/ DQ655844	Genbank/ AF312362	EJForrestel 312/ Pending	EJForrestel 312/ Pending
Aristida congesta	Genbank/	Genbank/	Genbank/	Genbank/
	GQ924154	FR821317	FR821351	U31359
Heteropogon contortus	Genbank/	Genbank/	Genbank/	Genbank/
	DQ005055	FR821324	HE573490	HE575844
Bothriochloa radicans	-	EJForrestel 279/ Pending	EJForrestel 279/ Pending	EJForrestel 279/ Pending
Themeda triandra	Genbank/	Genbank/	Genbank/	Genbank/
	DQ005083	HE574429	FR821358	FN870939
Sorghastrum nutans	Genbank/	Genbank/	Genbank/	Genbank/
	DQ005079	FR821326	AF117421	EF125121
Andropogon gerardii	Genbank/	Genbank/	Genbank/	Genbank/
	DQ005015	AF144577	AF117391	AJ784818
Schizachyrium scoparium	Genbank/	Genbank/	Genbank/	Genbank/
	68164139	390607922	407724267	407724247
Digitaria eriantha	-	Genbank/ HE574068	Genbank/ HE573497	Genbank/ HE73375
Setaria pumila	Genbank/	Genbank/	Genbank/	Genbank/
	HQ600500	HM850575	EF189984	KC164338

Setaria viridis	Genbank/ HQ600485	Genbank/ FR832834	Genbank/ SVU21976	Genbank/ KC164340
Setaria incrassata	Genbank/ HM347019	EJForrestel 307/ Pending	EJForrestel 307/ Pending	EJForrestel 307/ Pending
Cenchrus ciliaris	Genbank/ AF019832	Genbank/ FR821328	Genbank/ EU741937	Genbank/ FR821344
Panicum deustum	Genbank/ AY129705	EJForrestel 313/ Pending	Genbank/ GU594631	EJForrestel 313/ Pending
Urochloa panicoides	-	Genbank/ HE574426	Genbank/ HE573544	Genbank/ HE573318
Urochloa mosambicensis	Genbank/ AY346338	EJForrestel 314/ Pending	Genbank/ FJ486516	EJForrestel 314/ Pending
Panicum virgatum	Genbank/ DQ005062	Genbank/ EU434294	Genbank/ U21986	Genbank/ EF125135
Panicum maximum	Genbank/ AY129712	Genbank/ HE574152	Genbank/ AY029649	Genbank/ AM849390
Panicum coloratum	Genbank/ KF805132	Genbank/ HE574090	Genbank/ AM849208	Genbank/ AM849415
Panicum oligosanthes	-	YU:EJForre stel34/ KJ740971	YU:EJForre stel34/ KJ740987	YU:EJForre stel34/ KJ740993
Panicum acuminatum	-	Genbank/ HF558501	Genbank/ AY188485	Genbank/ HQ590063

#### **Appendix S2.** Functional trait collection methods

Four fully expanded green leaves in full sun were collected per individual plant and immediately placed in plastic bags with a wet paper towel in a cooler. Two leaves were rehydrated for 24-48 hours following collection. Subsequently, leaf area and weight were recorded and the leaves were dried at 60 °C for at least 48 hours. Specific leaf area (leaf area divided by dry mass) and leaf dry matter content (dry mass divided by wet mass) were calculated for each leaf. The dried leaves were also ground for foliar C, N, C:N and C-13 isotope analysis. Organic carbon and nitrogen isotope samples were analyzed using a Costech ESC 4010 Elemental Combustion System (Costech Anlaytcial Technologies, Valencia, CA, USA) interfaced with a Thermo Finnigan Delta Plus Advantage isotope mass spectrometer (Thermo Finnigan-MAT, Bremen, Germany) at Yale University's Earth System Center for Stable Isotopic Studies. Ultimately, five of the ten leaves per species and treatment were subjected to leaf tissue analysis.

The other two leaves were preserved in 70% ethanol solution for analysis of stomatal size, density, and pore index. Dental putty (President Plus-light body; Coltene/Whaledent Ltd., Burgess Hill, West Sussex, UK) impressions were taken from the abaxial surface of the mid-section of five individuals and two preserved leaves per individual (N=10) from each species and treatment. Nail polish peels produced from the impressions were transferred onto microscope slides and imaged using a Zeiss SteREO Discovery.V12 Stereoscope and AxioCam HRc at 200X magnification. Along each peel, six stomata were measured for length and stomata were counted in two fields of view located on either side of the midrib to calculate stomatal density. Stomatal pore index, an index of total stomatal pore area per leaf area was quantified as stomatal density x the square of the mean guard cell length (Sack *et al.* 2003).

#### Appendix S3. Details of Phylogenetic Inference

Total genomic DNA was isolated from dried plant tissue and amplified following the protocol and using the primers specified in GPWG (2011). PCR products were sequenced using Applied Biosystems Big Dye Chemistry & 3730 xL DNA analyzers (Applied Biosystems) at the Keck Biotechnology Resource Laboratory (Yale University). 38 new sequences from 18 species were deposited in Genbank; voucher specimen information and Genbank accession numbers are listed in Table S1. The four markers were aligned using MUSCLE v 3.7 (Edgar 2004) and manually edited. Individual alignment files were concatenated using Phyutility (Smith & Dunn 2008). Our aligned sequence matrix consisted of 8,606 base pairs. Models of nucleotide substitution and optimal partitioning strategies were chosen simultaneously under the Bayesian Information Criterion (BIC) using heuristic search algorithms in PartitionFinder (Lanfear et al. 2012). The non-coding nuclear gene region ITS was treated as its own partition. For the coding genes *rbcL*, *mat*K and *ndh*F, all five combinations of codon partitions were considered as candidate partitions. Alternative nucleotide substitution models considered were those available in BEAST v.1.6. (Drummond & Rambaut 2007). The best fit partition strategy according to BIC was a GTR+I+G model for all partitions. As we were interested in obtaining a dated tree, phylogenetic relationships were inferred using Bayesian methods in BEAST v.1.6.2 (Drummond & Rambaut 2007). Mixed partition analyses were performed for each of the sampled genes and on the concatenated matrices using the optimal partition strategies identified by PartitionFinder (Lanfear et al. 2012). Trees were unlinked by gene region and analyses were conducted under a model of uncorrelated rates and a log-normal distribution. The tree was time-calibrated using normally distributed calibrations for the following four clades in the tree: i) BEP-PACMAD split (mean=49.8, sd=3.0), ii) Andropogoneae (mean=18.0, sd=3.7), iii) Chloridoideae (mean=34.7, sd=3.75), and iv) Aristideae (mean=8.6, sd=10.5) following the BEAST dating analysis of Christin et al. (2014) (Christin et al. 2014) based on macrofossil evidence. The MCMC chain was run for 20,000,000 generations and sampled every 10,000 generations. Convergence of the chain was assessed by visualizations of the state likelihoods using Tracer v1.5 (Drummond & Rambaut 2007). Effective sample sizes for all model parameter estimates were examined to ensure adequate mixing of the chain, with ESS values above 200 indicating appropriate sampling. 2,000,000 generations were discarded as burn-in and the remaining trees were combined to generate a maximum clade credibility tree that was used for all analyses.

### **Appendix S4. Cleaning of GBIF records**

To quantify the precipitation niche of each species across their entire ranges, georeferenced herbarium specimens point records were downloaded from the Global Biodiversity Information Facility (http:// www.gbif.org, accessed on 8 April 2014). Records that did not fit the following criteria were culled from the final list: 1) Records with less than a tenth of a degree accuracy; 2) duplicate coordinate values as another record for a given species; 3) Records that fell within a body of water; and, 4) records for which the country of specimen origin field did not match the actual location of the coordinates. After cleaning, our median number of records for species included in the principal components analysis (constituted over 5% mean cover in any treatment) was 285, with number of records ranging from 47 to 61,814. Using this cleaned set of coordinates, we extracted mean annual precipitation (MAP) from the WorldClim database ((Hijmans, Cameron & Parra 2005) at 30 arc degree resolution. To remove outliers, the mid-90% of the range of each species set of points was used to calculate the mean and range of MAP for each species. As there was no correlation between number of records and range of mean precipitation values (r=-0.07, df=38, p=,.654), we also included the range of the mid-90% of all values in our principal components analysis.

**Appendix S5.** Rank abundance curves of grass species in mesic grassland sites of North America (Konza) and South Africa (Kruger) subjected to grazing release and fire frequency treatments. Relative abundance values for each treatment are mean values from the 2012 field season. Those species that consist of the top 90% of grass cover at each site are labeled on each panel.





**Appendix S6.** Analysis of similarity percentage (SIMPER) results for each site and treatment contrast with significant PERMANOVA results. Species that contributed to the top 90% of dissimilarity in percent cover between different fire and grazing treatments are presented for each comparison. Fire and grazing constrasts were analyzed independently. See Table S1 for complete species names.

	Konza			
Contrast	Species	Contribution	Species	Contribution
Grazed- Ungrazed	A. gerardii	0.36	NS	NS
C	S. asper	0.15		
	B. japonicus	0.09		
	S. nutans	0.08		
	P. pratensis	0.04		
	B. gracilis	0.06		
	S. scoparium	0.04		
	B. curtipendula	0.04		
Annual- Intermediate	A. gerardii	0.35	B. radicans	0.43
Intermediate	B. japonicus	0.16	U. mosambicensis	0.15
	S. asper	0.11	A. congesta	0.14
	S. nutans	0.08	P. coloratum	0.11
	B. gracilis	0.07	T. triandra	0.07
	P. pratensis	0.05		
	S. scoparium	0.04		
	B. curtipendula	0.04		
Annual – Unburned	A. gerardii	0.33	B. radicans	0.36

	S. asper	0.21	P. coloratum	0.17
	B. japonicus	0.11	U. mosambicensis	0.12
	S. nutans	0.07	D. eriantha	0.10
	B. gracilis	0.06	P. maximum	0.07
	P. pratensis	0.06	T. triandra	0.06
	S. scoparium	0.04	A. congesta	0.05
	B. curtipendula	0.04		
Intermediate-	A. gerardii	0.30	B. radicans	0.33
Unburned	S. asper	0.20	P. coloratum	0.17
	B. japonicus	0.16	U. mosambicensis	0.11
	S. nutans	0.12	A. congesta	0.10
	P. pratensis	0.07	D. eriantha	0.09
	S. scoparium	0.05	T. triandra	0.08
	B. gracilis	0.03	P. maximum	0.06
	B. curtipendula	0.03		

**Appendix S7.** Effects of grazing removal of large herbivores on taxonomic, phylogenetic and functional diversity of the grass communities in mesic savanna grasslands of North America (Konza) and South Africa (Kruger). Mean pair-wise plot differences (ungrazed –grazed paired plots) with 95% confidence intervals through time for the annual, intermediate (3/4 year), and unburned fire treatments in a) taxonomic richness, b) taxonomic diversity (Shannon's diversity), c) taxonomic evenness (J'), d) taxonomic dominance (Berger-Parker index), e) mean phylogenetic distance (MPD, in millions of years), f) functional dispersion (FDis), g) community-weighted trait means of principal component 1 species values and h) community-weighted trait means of principal component 2 species values (for g & h, see Figure 2a in the main text). The horizontal black line indicates zero change in each panel.





Species	Grazing response	References	
Andropogon_gerardii	D	Koerner <i>et al.</i> 2014 Eby <i>et al.</i> 2014	
Andropogon_greenwayi	Ι	McNaughton 1979	
Bothriochloa_decipiens	D/I	Vesk & Westoby 2001	
Bothriochloa_ewartiana	D/I	Vesk & Westoby 2001	
Bothriochloa_macra	D/I	Vesk & Westoby 2001	
Bothriochloa_pertusa	Ι	Vesk & Westoby 2001	
Bothriochloa_radicans	D/I	Koerner et al. 2014	
Bothriochloa_saccharoides	Ι	Anderdon & Briske 1995	
Chrysopogon_fallax	I,D/I	Vesk & Westoby 2001 McIntyre & Lavorel 2001	
Cymboopgon_flexuosus	Ι	Sankaran 2005	
Cymboopgon_refractus	Ι	McIntyre & Lavorel 2001	
Cymbopogon_exacvatus	Ι	McNaughton 1978	
Cymbopogon_nardus	Ι	Harrington & Pratchett 1974	
Cymbopogon_refractus	D	Vesk & Westoby 2001	
Diheteropogon_filifolius	D	Martindale 2007	
		McNaughton 1983 Vesk & Westoby 2001	
Heteropogon_contortus	D,D,D	McIntyre & Lavorel 2001	
Hyparrhenia_filipendula	D	McNaughton 1983	
Schizachyrium_scoparium Sorghum leiocladum	D,D/I D	Anderson & Briske 1995 N'Guessan & Hartnett 2011 Vesk & Westoby 2001	

**Appendix S8.** Grazing studies compiled from other studies reporting either significant increases (I), decreases (D) or inconsistent (I/D) shifts in abundance for Andropogoneae species in response to active grazing.

Sorghum_nervosum	D	Vesk & Westoby 2001
Sorghum_plumosum	D	Vesk & Westoby 2001
Sorghum_timorense	Ι	Vesk & Westoby 2001
		Martindale 2007 McNaughton 1983
Themeda_triandra	D,D,D,D	Eby <i>et al.</i> 2014

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