EVIDENCE OF CLIMATE NICHE CREATION IN THE NORTHERN GREAT PLAINS: THE HISTORY OF INVASION, POPULATION GENETICS, COMPETITIVE EFFECT, AND LONG-TERM TRENDS OF *POA PRATENSIS* L.

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Title

Evidence of climate niche creation in the northern Great Plains: The history of invasion, population genetics, competitive effect, and long-term trends of *Poa pratensis* L.

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The Supervisory Committee certifies that this ***disquisition*** complies with North Dakota State University's regulations and meets the accepted standards for the degree of

DOCTOR OF PHILOSOPHY

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ABSTRACT

Understanding the mechanisms of invasion is critical in order to control an invasive species. *Poa pratensis* L. (Kentucky bluegrass) is an invasive species that has been present in the northern Great Plains (NGP) for over 100 years, but has become a dominant species in the mixed grass region recently. My dissertation seeks to answer one critical question—why has *P. pratensis* become such a successful invasive species in the NGP?

I first asked if the invasion was caused by adaptation and/or propagule pressure. I screened the genetic fingerprint of invasive *P. pratensis* in the NGP along with measuring the genomic content of wild plants and compared them to common cultivars. I found virtually no overlap between lawn cultivars and invasive *P. pratensis* populations. This was further supported by a narrow range of genomic content in wild individuals compared to the lawn cultivars. I also found no evidence of geographical patterning which is consistent with the hypothesis that local adaptation is not pervasive in *P. pratensis*.

I then asked whether *P. pratensis* was a strong competitor compared to dominant plant species native to the tallgrass prairie. I studied competitive effect between *Poa pratensis, Nassella viridula, Pascopyrum smithii,* and *Bouteloua gracilis* through a species-pair competition experiment. Based on the relative interaction indices, *P. smithii* and *P. pratensis* were competitive against *B. gracilis,* and *P. smithii* was competitive against *N. viridula*. Additionally, *P. pratensis* was facilitated by all three species in the experiment. This study indicates that *P. pratensis* may be somewhat competitive.

Finally, I asked whether the increase in the frequency of *P. pratensis* in the NGP may be attributed to environmental factors. In order to understand long-term correlations between *P. pratensis* invasion and environmental variables, I resampled plots that were previously sampled

for species composition in 1978, 1979, and 1999. I found that *P. pratensis* levels did increase across plots and was corrrelated with higher levels of precipitation. My research indicates that increased precipitation in the NGP as a result of climate change is correlated with *P. pratensis* invasion in the NGP.

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Thank you to my friends and colleagues from the Kentucky bluegrass working group and the United States Fish and Wildlife Service (FWS-R6-POAPRATENSISGENETICS). They have helped with funding, knowledge, and enthusiasm for Kentucky bluegrass research. A special thank you to Cami Dixon and John Hendrickson for their financial and technical support. Thank you to the Department of Biological Sciences for the summer financial support and teaching opportunities, the College of Natural Resource Management for summer funding, the

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Finally, I would like to thank my Grandma Rapheal and Uncle Rob for pushing me to get my PhD and knowing I would do it before I knew (somehow). My Grandma Rapheal sparked my love and curiosity of the natural world and science by taking me camping, bringing me to the science museum, and signing me up for science classes. Thank you to my Mom, Michelle Trayer, for teaching me to be tough and my Dad, Denny Dennhardt, for teaching me to be kind. Thank you to my husband Dacotah Melicher who met me my first day of graduate school and married me four years later. He has been a constant source of humor, love, and support. I could not imagine a better partner.

I would not have been able to complete this project without all these wonderful people. Thank you.

DEDICATION

This Dissertation is dedicated to

My husband, Dacotah Melicher,

My Grandma, Janice Rapheal,

And

My parents, Michelle Trayer and Walter Dennhardt

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LIST OF ABBREVIATIONS

BOGR……*Bouteloua gracilis*

dbRDA……...Distance based redundancy analysis

DNA…….. Deoxyribonucleic acid

NASM……*Nassella viridula*

NRCS…….Natural Resource Conservation Services

NDSU……North Dakota State University

NGP……..Northern Great Plains

PASM…….*Pascopyrum smithii*

POPR…….*Poa pratensis*

PPR……Prairie pothole region

USFWS……..United States Fish and Wildlife Service

USDA……United States Department of Agriculture

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CHAPTER 1. GENERAL INTRODUCTION

The importance of *Poa pratensis* for conservation and management

The tallgrass and mixed grass prairies of the northern Great Plains (NGP) are increasingly endangered ecosystems due in part to invasive species (Samson & Knopf 1994a). Invasive species impact ecosystems by driving biodiversity loss and threatening global conservation efforts (Pimentel *et al.* 2001). The prairies of the NGP are often inundated by invasive grass species which can turn a healthy, diverse prairie into nearly a monoculture. This transition of the land affects plant cover and forage for cattle grazing, small mammals, and grassland birds, along with food resources for pollinating insects. The cause of invasion is often unknown, although many reasons (e.g. lack of grazing (nonuse), too few fires, human transport, disturbance, and climate change) have been suggested. Considering less than 1% of the tallgrass and 20% of the mixed grass prairie remain in the NGP, the biology of these invasive grasses needs to be better understood for conservation efforts to be successful.

Poa pratensis L. (Kentucky bluegrass) is a major noxious species in the NGP (Murphy & Grant 2005a; Larson & Larson 2010a; Bahm *et al.* 2011a; DeKeyser *et al.* 2015). The recent evidence on the extent of distribution raises concerns about the effectiveness of past prairie management techniques in controlling this particular species (Cully *et al.* 2003; Bahm *et al.* 2011a; DeKeyser *et al.* 2013a). In one study, *P. pratensis* accounted for half of all non-native plant cover in the tallgrass prairie (Cully *et al.* 2003). A survey from 2014 revealed that in North and South Dakota 20-35% of rangelands consisted of more than 50% soil surface cover of "invasive bluegrasses", which includes both *Poa pratensis* and *Poa compressa* L. (Canada bluegrass) (United States Department of Agriculture Natural Resources Conservation Service

2014). *Poa compressa* is also a species that is introduced in the northern Great Plains and has been reported to hybridize with *P. pratensis* (Uchytil 1993).

While *P. pratensis* has been an invasive grass in the tallgrass prairie over the past 100 years, in the past 20 years *Poa pratensis* has also become an invasive species in the mixed grass regions of the NGP. In many of the prairies of the NGP Kentucky bluegrass can form nearly monotypic stands which reduces the abundance of native plant species (Fig. 1.1, 1.2). The loss of native plant diversity can have major ramifications for soil health, wildlife habitat, ecosystem services, grazing nutrition, and water resources. In order to preserve the diversity of the northern tall and mixed grass prairie land managers need a better understanding of the reasons for this expansion and work on controlling Kentucky bluegrass invasion in the NGP.

Figure 1.1. A private rangeland in North Dakota that is heavily invaded with Kentucky bluegrass. Photo credit: Carl Piper.

Figure 1.2. A heavily invaded native prairie at Arrowwood National Wildlife refuge in 2011. The yellow flowering heads are *P. pratensis.* Photo credit: Lauren Dennhardt.

Poa pratensis' root system is different from most native tallgrass prairie plants (Fig. 1.3). *Poa pratensis* only occupies the first few inches of soil, whereas many native species occupy several feet of soil. Root systems and soil interact with each other. Roots harbor microorganisms, decompose (which renews the nutrients in the soil), and stabilize soil. A prairie dominated by *P. pratensis* may jeopardize all these specialized root services by outcompeting and replacing native species. Additionally, *P. pratensis* is known to develop a thick thatch (dead plant material) in only a few years after invasion. This thick thatch may choke out many native plant species by preventing seedlings access to light resources. Once *P. pratensis* has invaded a prairie it can change the availability of habitat for a number of bird, mammal, and insect species, and thus be a threat to biodiversity.

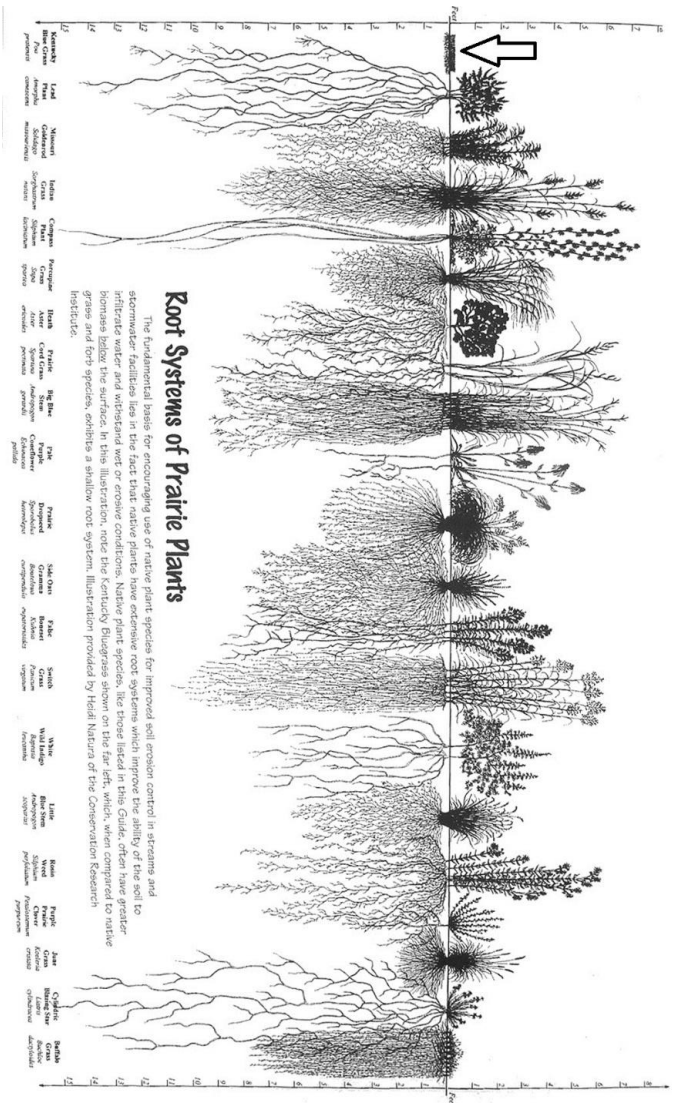

Figure 1.3. Image of a number of native species' root systems next to *Poa pratensis* on the far left, indicated by an arrow. Photo credit to Heidi Natura (http://www.shootingstarnativeseed.com/documents/native-roots.pdf). Image from: http://www.eatcology.com/wp-content/uploads/2011/11/prairie-root-systems_large.jpg

Poa pratensis is a C3 grass native to Eurasia. It has been in the United States for over 250 years (DeKeyser *et al.* 2015). An early introduction of *P. pratensis* was initiated by European settlers in the 1700s (Huff 2003a). From there, *P. pratensis* is thought to have moved west from its original establishment on the East coast via settlers using it as a packaging material. There

has been some debate about whether *P. pratensis* was native in some regions of the United States, but now it is believed the United States is occupied predominantly by the invasive *P. pratensis* (Huff 2003a). This subject will be discussed in greater detail in Chapter 2.

Before the 1950s, *P. pratensis* was distributed using a "stripping" procedure (collecting seeds using flailing method) from already established stands in Wisconsin, Minnesota, North Dakota, and Kentucky to eastern Kansas. This practice was used for 75 years (Huff 2003a; Honig *et al.* 2010a). The current method of growth and distribution relies on intensive agriculture and development focused in the Midwest and the Pacific Northwest (90% of U.S. production comes from Washington) in which fields are planted using some combination of burning, irrigation, fertilization, herbicide, and insecticide (Huff 2003a; Holman & Thill 2005). Modern biotechnology advances have led to cultivars that are highly competitive and now, genetically engineered to withstand glyphosate (Huff 2003a; Kaplan 2011a).

Invasive grasses are particularly difficult to manage because they are often reintroduced by Department of Transportation personnel for erosion control, ranchers for forage production, and managers of turf and lawn grasses, creating a continual propagule pressure, which inhibits and complicates control. Invasive grasses are not as conspicuous to humans, as some flashy invasive dicots (e.g. purple loosestrife (*Lythrum salicaria* L.), spotted knapweed (*Centaurea stoebe* L. subsp. *Micranthos* (Gugler) Hayek), and crownvetch (*Securigera varia* (L.) Lassen). Many invasive species, such as Canada thistle are easy to identify and can be targeted individually with herbicide treatment resulting in effective management strategies at a reasonable cost. Invasive grasses require a broad management technique such as grazing, burning, mowing, and in extreme cases, entire herbicidal wipeout for a clean start (United States Fish and Wildlife

Service 2009). Such efforts often require a lot of money, time, and are not always feasible in a land manager's annual budget (Hartnett *et al.* 1996).

Poa pratensis' current distribution in the United States is a broad one. It grows in a wide range of habitats, in every state and province within the United States and Canada (United States Department of Agriculture & Natural Resource Conservation Service 2014). It has been categorized as an understory dominant in aspen communities, riparian and wetland sites, meadow sites, mountainous sites, grassland range, and forested sites (Uchytil 1993), which illustrates the wide range of ecosystems it can inhabit. Planting of *P. pratensis* has been widely done as a turf grass, forage grass, and lawn grass. Quality of *P. pratensis* as a forage grass varies depending on the precipitation regime of the area. In the Dakotas, forage quality of *P. pratensis* is low compared to other grasses (Uchytil 1993), making it an interest of ranchers to replace *P. pratensis* with higher quality forage.

Organization of dissertation

My research project will promote understanding of an invasive commercial species from an ecological perspective. Through the use of tools developed in the turf grass industry, molecular biology, long-term data, and greenhouse experimentation, I have examined the evolutionary mechanisms (or lack thereof) behind the invasion of *P. pratensis* in the NGP. My main research question is how has *Poa pratensis* become a dominant species of grasslands in the tallgrass and mixed grass prairies of the NGP. I attempt to answer this question with four chapters.

The second chapter focuses on the history of *P. pratensis* in the NGP. My coauthors and I assembled a variety of sources to disentangle the introduction and later invasion of the species.

Our goal was to understand whether *P. pratensis* was truly introduced or not and whether there are any historical documents on invasion in the past 100 years.

The third chapter asks two major questions: Is *P. pratensis* invasion partially due to propagule pressure and has adaptation occurred? We answer this question by using neutral genetic markers and flow cytometry across populations in North Dakota, South Dakota, and Minnesota.

The fourth chapter addresses the competitive ability of *P. pratensis* through paired competition experiments. I chose three grass species that have been documented to be in decline when *P. pratensis* invades. I quantified both competitive and facilitative ability of each species paired with one another.

The fifth chapter disentangles the environmental and management effects on *P. pratensis* and a few other notable plant categories. We resampled a tallgrass prairie with plant community data from 1978, 1979, and 1999. We found correlations between our sampled plant categories and our environmental variables.

The sixth and final chapter concludes the original question proposed by this dissertation—why is *Poa pratensis* invading in the NGP?

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CHAPTER 2. KENTUCKY BLUEGRASS (*POA PRATENSIS)* INVASION IN THE PRAIRIE POTHOLE REGION: A STORY OF RAPID DOMINANCE IN AN ENDANGERED ECOSYSTEM[1]

DeKeyser ES, Dennhardt LA, Hendrickson J (2015) Kentucky bluegrass (Poa pratensis) Invasion in the Northern Great Plains: A Story of Rapid Dominance in an Endangered Ecosystem. *Invasive Plant Science and Management*, **8**, 255–261.

Abstract

Kentucky bluegrass was introduced into the present day United States in the 1600s. Since that time, Kentucky bluegrass has spread throughout the United States and Canada becoming prolific in some areas. In the last century, Kentucky bluegrass has been a presence and oftentimes a dominant species in some prairies in the Prairie Pothole Region (PPR). Sometime within the last few decades, Kentucky bluegrass has become the most common species on the untilled, native prairie sites of the PPR of North and South Dakota. In this paper we hypothesize how Kentucky bluegrass has come to dominate one of the most endangered ecosystems in North America—the prairie through a historical, climatological, and ecological lens. We urge others to start addressing the invasion of Kentucky bluegrass with both new research and management strategies.

Introduction

Kentucky bluegrass (*Poa pratensis* L.) is arguably one of the most recognized and widespread perennial grasses in North America, occurring in all 50 states and all Canadian

[1] Lauren Dennhardt wrote at least a third and formatted two out of three graphics. Edited and prepared for publication. Figure 2.2 was modified slightly in order to provide data for chapter four. Published in Invasive Plant Science and Management (Appendix 2.1).

provinces (Uchytil 1993; United States Department of Agriculture & Natural Resource Conservation Service 2014). This grass, which is a native to the more temperate and northern latitudes of Eurasia, has been established in favorable climates worldwide because of its strongly rhizomatous mat forming characteristics (Uchytil 1993). Recently, the increased abundance of Kentucky bluegrass in many natural areas, especially in the Prairie Pothole Region (PPR) and other eastern areas of the Northern Great Plains has resulted in heightened attention to potential negative attributes (Grant *et al.* 2009a; Larson & Larson 2010b; DeKeyser *et al.* 2013a). While the extent of the invasion is becoming clearer, what is not understood is 1) the history and causes of widespread invasion into natural areas, 2) where the contributing sources of propagules supplying the invasion originate from, and 3) the potential impacts to the ecosystem. In this paper, we address these questions using historical documentation concerning Kentucky bluegrass and long term data sets obtained within the region, and discuss potential mechanisms for the unanticipated spread of this species.

Kentucky bluegrass was widespread and well known in Europe before receiving the scientific name *Poa pratensis* in the 1700s (Schery 1959). Linnaeus appropriately gave the epithet *pratensis* meaning meadow because of the general proclivity of the grass (Lowe 1858; Wedin & Huff 1996). High palatability and yield made Kentucky bluegrass an important pasture grass for hundreds of years in the British Isles (Lowe 1858; Plues 1867). With proper maintenance, Kentucky bluegrass was reported to produce hay for cattle in June and provide an attractive lawn grass (Lowe 1858; Plues 1867).

Because of the popularity and widespread use in Europe and parts of Asia, it has been convincingly speculated that initial introduction into the United States happened during Western European colonization (mid to late 1600s) through seed mixtures, hay, and bedding (Lowe 1858;

Plues 1867; Carrier & Bort 1916; Bashaw & Funk 1987a; Casler & Duncan 2003). In fact, the grass was common in Kentucky prior to extensive European settlement and rapidly spread from that point (Bashaw & Funk 1987a; Dunn 2004). Kentucky bluegrass often was unintentionally spread by people because of use as a packaging material and bedding, but was also a sought after grass for utilitarian reasons (Bashaw & Funk 1987a; Dunn 2004). Henry Clay (1838) pointed out the popularity as a lawn grass in the southeast and noted a lack of Kentucky bluegrass in Virginia, New York, and Maryland, indicating a limited range at the time (Dunbar 1977). Clay offered to send a friend in New York Kentucky bluegrass because of a demand in New York for the grass (Dunbar 1977). There are reports of Thomas Jefferson having Kentucky bluegrass planted in his lawn at Monticello (Dunn 2004). By 1847, bluegrass was a widely used pasture grass as far as western New York, suggesting the popularity of the grass aided in the distribution into more northern states (Dunbar 1977; S.B. Buckley 1847). Piper (1916) reported, up to 90% of Kentucky bluegrass pastures were "spontaneous" events generally resulting from disturbance and colonization (Piper 1916). By the early 1900s, Kentucky bluegrass was recognized as the "most important pasture grass in North America" (Piper 1916).

Kentucky bluegrass most likely first occurred in the PPR during the mid to late 1800s. By 1896, Kentucky bluegrass was considered "common southward to the central United States" (Wright & Upham 1896). In Iowa, along the Missouri river, bluegrass was classified as a weed by 1909 and was "everywhere" and "common" (Shimek 1909). There were already reports in 1884 of Kentucky bluegrass taking over prairies in southwestern Minnesota and moving westward into Nebraska (Upham 1884). During a survey of western Minnesota and eastern North Dakota, Warren Upham (1890) predicted that bluegrass would spread into the region and become a predominant grass based on what was being experienced by others in the east. In 1891,

herbarium specimens were collected in the eastern municipalities of Fargo and Wahpeton, ND along the Red River by L.R. Waldron (Williams 1891). The North Dakota State University (NDSU) herbarium has other specimens collected along railways as far west as Medora, ND within the first decade of the 1900s (Williams 1891), although bluegrass wasn't noted at all in a botanical survey of two townships of southeastern ND in 1917 (Shunk 1917). In the publication "The Flora of North Dakota," Bergman (1918) called *P. pratensis* "a very common species, general throughout the state in all kinds of situations." By 1933, bluegrass was listed as a common plant in western ND (Edwards & Ableiter 1942). O.A. Stevens noted in his first publication of the "Handbook of North Dakota Plants" that *P. pratensis* "has spread so rapidly that it appears like a native plant" (Stevens 1950).

An ecological threat?

These same sources illustrate several attributes of Kentucky bluegrass which shed light on possible plant community and ecosystem impacts. Henry Clay (1838) pointed out that bluegrass would invade disturbed areas (e.g. salt licks) and would then quickly spread to dominate (Dunbar 1977). Clay also discussed competitive ability, noting Kentucky bluegrass would rapidly outcompete timothy (*Phleum pratense* L.) and clover (*Trifolium* spp.) when seeded together (Dunbar 1977). Lowe (1858) discouraged agriculturalists from using Kentucky bluegrass (Lowe 1858) because some thought the bluegrass root system would impoverish the soil. Others commented on the ability of Kentucky bluegrass to maintain growth early in the spring and late in the fall, and produce a lot of long foliage (up to 60 centimeters) (Buckley 1847). Stevens (1950) stated in the PPR "It invades and practically takes possession of moist prairie."

After the natural and the anthropogenic spread, there was a need among turf managers for a Kentucky bluegrass that was not as susceptible to drought or leafspot. In the 75 years prior to the 1950s, Kentucky bluegrass was distributed using a "stripping" procedure (collecting seeds using a flailing method) from already established stands in Wisconsin, Minnesota, North Dakota, and Kentucky to eastern Kansas (Casler & Duncan 2003; Huff 2003b). In the mid-1930s, the first Kentucky bluegrass cultivar, 'Merion' was discovered in a golf course in Pennsylvania and became available in 1947 (Dunn 2004; Stang *et al.* 2004). The 'Merion' cultivar was widely used until cool-season, turfgrass genetic improvement programs, initially started in 1962 at Rutgers University, began to provide a wider variety of cultivars. The emergence of turfgrass breeding programs at universities throughout the United States has resulted in hundreds of varieties of Kentucky bluegrass being developed. The current method of growth and distribution relies on intensive agriculture and development focused in the Midwest and the Pacific Northwest (90% of U.S. production comes from Washington) in which fields are planted using some combination of burning, irrigation, fertilization, herbicide, and insecticide use (Casler & Duncan 2003; Holman & Thill 2005). Modern biotechnology has made cultivars that are highly competitive and now, genetically engineered to withstand glyphosate (Casler & Duncan 2003; Kaplan 2011b).

More recently the invasion of Kentucky bluegrass has gained a great deal of attention throughout the PPR (Murphy & Grant 2005b; Grant *et al.* 2009a; Larson & Larson 2010b; Bahm *et al.* 2011b; DeKeyser *et al.* 2013a; White *et al.* 2013). Over the last two to three decades, a major shift seems to have occurred in the PPR, resulting in large changes in the frequency of Kentucky bluegrass in the prairie (Fig. 2.1). Demonstrating this increase are 28 native prairie sites sampled in central North Dakota both in 1984 and 2007. Out of the 28, Kentucky bluegrass

increased in frequency at 22 sites. Often, this increase is more pronounced than the decreases seen at the six other sites (Fig. 2.1). The overall frequency of Kentucky bluegrass in the 23 year period increased by 35% across all sites. Anecdotal evidence amongst many land managers indicates Kentucky bluegrass has increased in frequency over the last 20 years. A rangeland site monitored by North Dakota State University and Glenharold Mine in central North Dakota provides a detailed look into the expansion of Kentucky bluegrass (Fig. 2.2). In a decade, bluegrass rose from not present in 1988 to the most abundant species in 2009 (Fig. 2.2) demonstrating the ability to quickly establish in a site. Increases in Kentucky bluegrass appear to be at the expense of native species. Unpublished data from the United States Department of Agriculture's Agricultural Services (USDA ARS) in Mandan, ND indicate increases in Kentucky bluegrass often coincide with decreases in blue grama grass (*Bouteloua gracilis*), a grazing tolerant short statured native grass (Fig. 2.3). Finally, a recent study by DeKeyser of US Fish and Wildlife Service native prairie sites in the PPR, showed Kentucky bluegrass was the most abundant species across 37 sampled sites (unpublished).

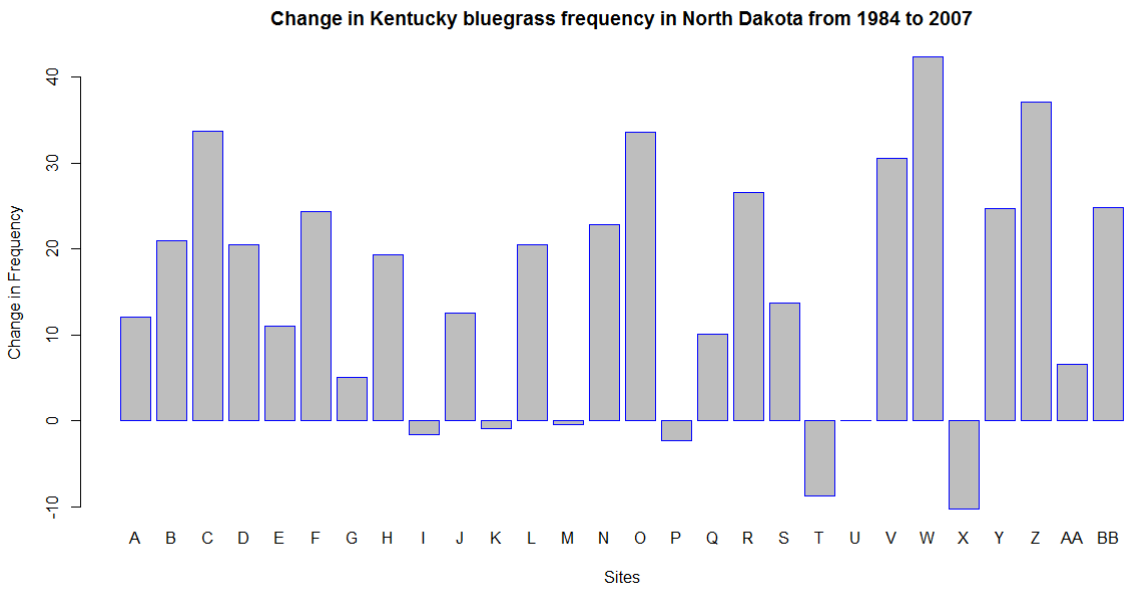

Figure 2.1. Change in Kentucky bluegrass frequency at 28 native prairie sites in North Dakota. Data from the 2007 and 1984 field collections have been subtracted to show the overall increase in Kentucky bluegrass invasion.

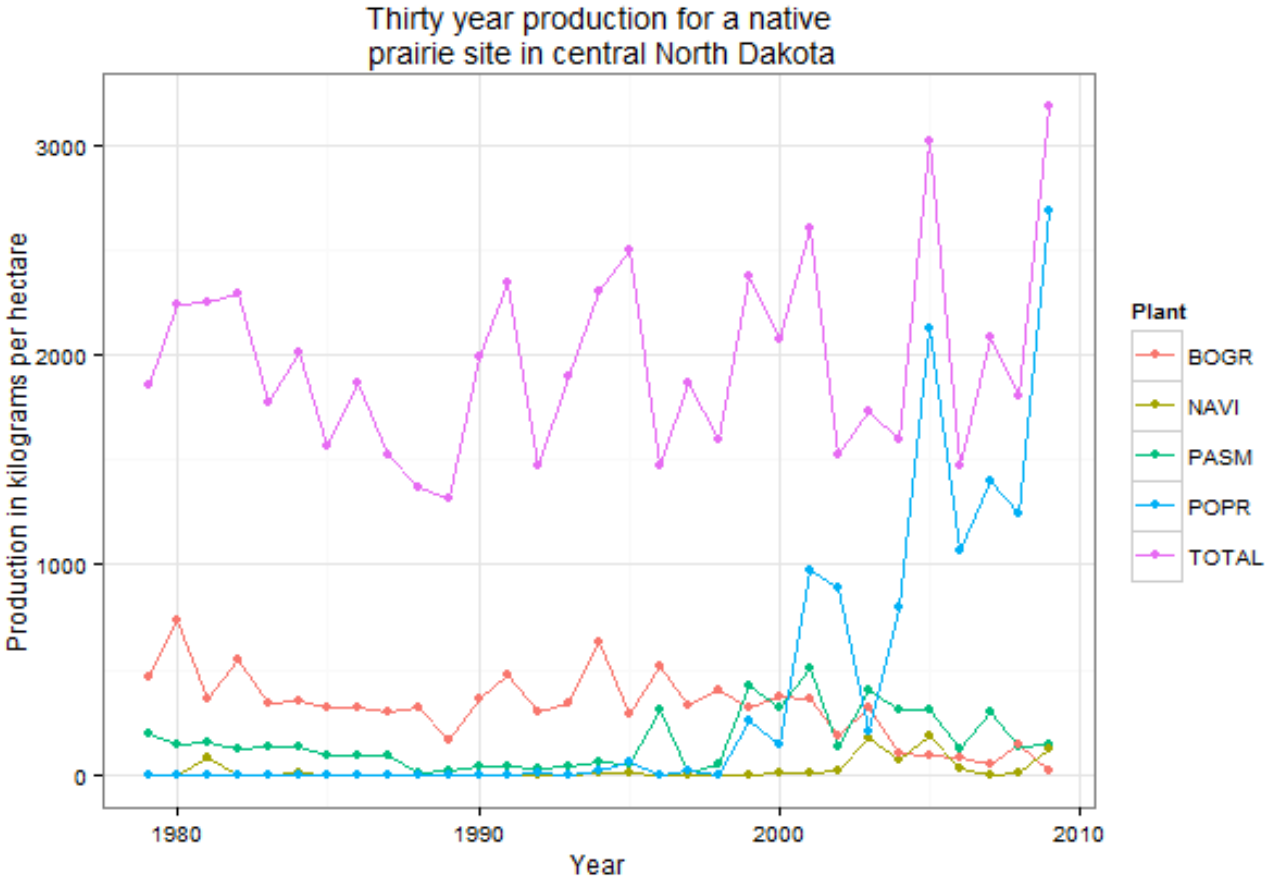

Figure 2.2. Production at an old mine site in Stanton, ND form 1979-2009 monitored by Kelly Krabbenhoft and Dave Neilson of Glenharold mine. Plant codes: *Bouteloua gracilis* (BOGR), *Pascopyrum smithii* (PASM), *Nassella viridula* (NAVI), *Poa pratensis* (POPR), and the total production (TOTAL).

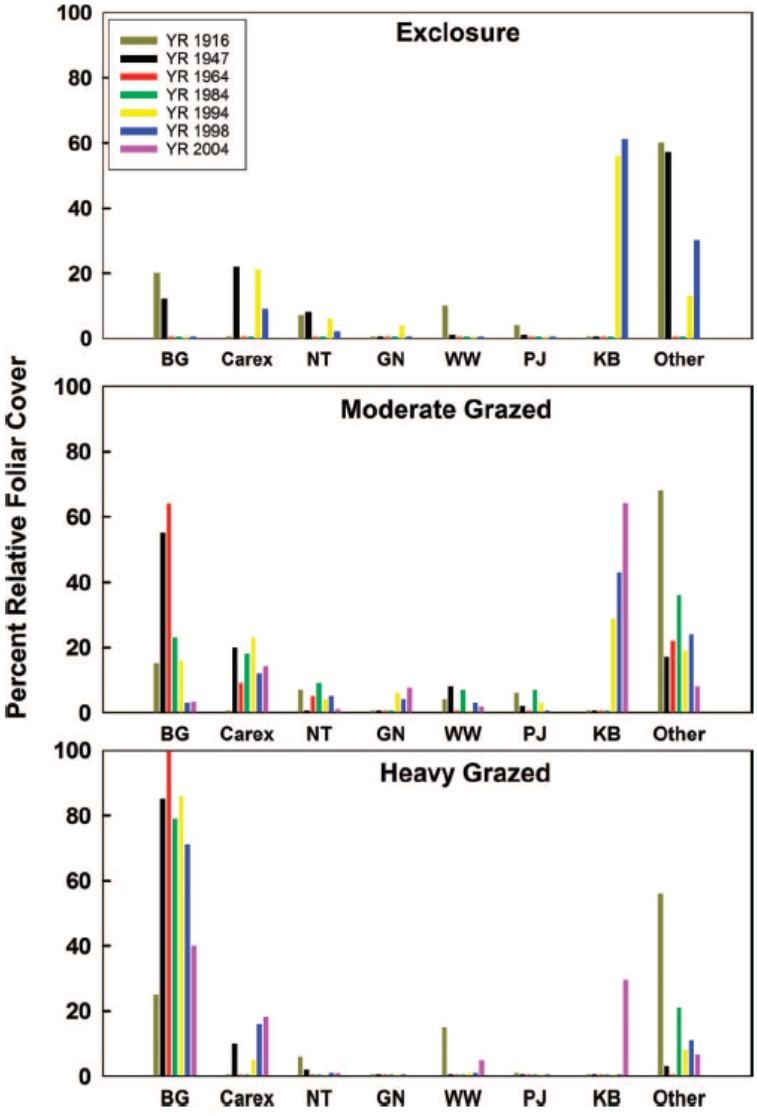

Figure 2.3. Relative foliar cover of individual species in an exclosure, moderately grazed, and heavily grazed pastures at the ARS USDA research center in Mandan, ND. BG=*Bouteloua gracilis*, Carex=*Carex* species, NT=*Hesperostipa comata*, GN=*Nassella viridula*, WW=*Pascopyron smithii*, PJ=*Koeleria macrantha*, KB=*Poa pratensis*. Exclosure data for 1964, 1984, and 2004 were not available.

The authors of this paper are mostly concerned with invasion in the PPR, an area stretching from Western Minnesota to Montana and north into Canada. In this highly fragmented, endangered ecosystem, major changes in species community composition are cause for concern and Kentucky bluegrass exemplifies that major ecosystem shift (Samson & Knopf 1994b; Murphy & Grant 2005b; Grant *et al.* 2009a). The control of cool-season invasive grasses such as Kentucky bluegrass, smooth brome grass (*Bromus inermis*), and reed canary grass (*Phalaris arundinacea*) (DeKeyser *et al.* 2013a) is the goal of many parties interested in prairie preservation in the PPR. Daehler (2003) suggested most introduced plants are not 'super invaders' so to speak but rather their performance is enhanced under certain human disturbance regimes (Daehler 2003; González-Moreno *et al.* 2014). Considering the popularity of Kentucky bluegrass amongst homeowners, cities, ranchers, and turfgrass managers, the changing climatic conditions, and the highly disturbed and fragmented prairie that remains, it seems very likely anthropogenic behavior has enhanced the invasion of Kentucky bluegrass.

Potential explanations for the invasion

Successful invasions need propagules. This is not an issue with Kentucky bluegrass because of the increased propagule pressure from the popularity of Kentucky bluegrass as a lawn and turf grass. Currently, Kentucky bluegrass is the most popular lawngrass in the United States and is especially popular in temperate regions such as the PPR (Uchytil 1993; Dunn 2004; Haydu *et al.* 2006). There are over 247 individual Kentucky bluegrass cultivars planted in the United States (Honig *et al.* 2010b). Kentucky bluegrass is the largest contributor to the $57.9 billion turfgrass industry meaning the likelihood for continual escape in the United States is high (Haydu *et al.* 2006).

Another potential contributor may be changing climate patterns in the PPR. The growing season has increased by 12 days over the last 120 years in parts of North Dakota (Badh *et al.* 2009). The increase in season length can potentially provide an opening for Kentucky bluegrass to invade in the early spring or late fall when bluegrass is photosynthetically active (Uchytil 1993). The additional growing days occur in the spring and fall, cool season months, with the fall gaining more days than the spring. Kentucky bluegrass produces the most rhizomes in the fall, which may provide reproductive advantages to long cool falls (Etter 1951). Kentucky bluegrass begins photosynthesizing earlier than many native species in the spring and an earlier spring may aid in rapid invasion.

Atmospheric CO_2 levels have increased greatly in the last 100 years (Etheridge *et al.* 1996; Global Greenhouse Gas Reference Network: National Oceanic and Atmospheric Administration 2014) and Kentucky bluegrass, a C_3 species, may perform more efficiently under these higher CO_2 concentrations. A study of the family Poaceae growing in higher concentrations of CO_2 indicated that while both C_4 and C_3 grass species increased in overall biomass production, C_3 grasses produced approximately 10% more biomass overall (Wand *et al.* 1999). Additionally, C_3 Poaceae species increased production of tillers by 27% in the higher CO_2 environment (Wand *et al.* 1999). From a broader perspective, across the plant kingdom, the literature supports herbaceous, fast growing, C3 species increasing their biomass more than slow growing C3 plants or C4 plants under increased CO_2 conditions (Poorter & Navas 2003). Because Kentucky bluegrass is a fast growing C_3 grass known for producing many tillers through rhizomatous growth, the increased levels of CO_2 in the atmosphere are likely facilitating productivity.

Finally, historic data from central North Dakota has indicated an increase in precipitation over the last 130 years. In the last 20 years, 15 years had above average precipitation levels (National Climate Data Center - National Oceanic and Atmospheric Administration 2014; National Oceanic and Atmospheric Administration 2014). In particular precipitation data from Mandan, ND indicate the 10 year average annual precipitation for the 1990s and 2000s are 25 and 15% greater than average annual precipitation for the previous 75 years (Regional Climate Centers *et al.* 2014). This time period corresponds with the previously mentioned increase in Kentucky bluegrass observed in the PPR. Stevens (1950) observed Kentucky bluegrass invading moist prairie and other historical records indicate Kentucky bluegrass is a hydrophilic, drought intolerant grass (Lowe 1858; Stevens 1950; Uchytil 1993; Jackson *et al.* 2002; Huff 2003b).

A host of other contributors may be changing these communities as well, such as plant-soil positive feedback cycles (Callaway 2000). Kentucky bluegrass has been shown to have significantly higher aboveground N production over native warm season grasses (Wedin & Tilman 1990). The decaying plant matter for other cool-season invasive grasses has been shown to facilitate invasion (Vinton & Goergen 2006).

Ecosystem impacts

As noted in figure 2.1 there was a 35% increase in Kentucky bluegrass frequency over 23 years. The same sites in figure 2.1 had an overall drop in species richness from an average of 25 in 1984 to 17 in 2007, and a drop in Shannon's diversity from 2.5 in 1984 to 1.6 in 2007. Species of graminoids and forbs decreased or were eliminated from the native prairie sites. For example, the native grass blue grama (*Bouteloua gracilis*) was found at 25 sites in 1984 and only 13 in 2007, prairie Junegrass (*Koeleria macrantha*) was at 24 sites in 1984 and 9 in 2007, threadleaf sedge (*Carex filifolia*) was at 20 sites in 1984 and 11 sites in 2007, and sun

sedge (*Carex inops*) was at 21 sites in 1984 and only 9 by 2007. Figure 2.2 further supports the fact that Kentucky bluegrass is replacing native graminoids, where before 1990 bluegrass wasn't even found at the site and by 2009 made up 84% of the annual production. The same native species showed clear reductions in total biomass post invasion versus prior to invasion. Before 1990 blue grama averaged 384 kg/ha and by 2009 was only 24 kg/ha, prairie Junegrass averaged 252 kg/ha prior to 1990 and was 6 kg/ha by 1990, and sedge species combined were 166 kg/ha prior to 1990 and only 4 kg/ha by 2009. The loss of these species in the plant community is also a loss of valuable functional forms important to ecosystem processes. For example, blue grama is one of the few common warm season grasses of the cool season dominated Northern Great Plains. Heitschmidt and Vermeire (2006) showed that blue grama can more than make up for losses of production due to spring drought, if precipitation returns during the blue grama's active growing period in July and August. The loss of this species due to Kentucky bluegrass invasion, may negatively impact the prairie's ability to maintain steady production due to variable weather patterns.

There is little argument that Kentucky bluegrass is probably the predominant grass of the Prairie Pothole Region today (Murphy & Grant 2005b; Grant *et al.* 2009a; United States Department of Agriculture Natural Resources Conservation Service 2014). Alarmingly, the USDA (2014) noted that Kentucky bluegrass along with Canada bluegrass (*Poa compressa*) has spread throughout the Northern Great Plains including occupying the majority of private rangelands in North Dakota (82%) and South Dakota (61%). Setter and Lym (2013) showed over a 250% increase in Kentucky bluegrass in the seedbank of certain soils on federal lands in western North Dakota over a ten year period (Setter & Lym 2013). This rate of increase shown by all of the aforementioned research arguably surpasses other invasive species within the region

including leafy spurge (Dunn 1979) and spotted knapweed (Sheley *et al.* 1998). The potential loss of species richness and species diversity becomes shocking. There is still a great deal unknown about the effects of this Kentucky bluegrass invasion, beyond the loss of species it is suspected that bluegrass may affect nitrogen cycling, pollinator diversity, and hydrology (Toledo *et al.* 2014b).

The need for understanding

More attention must be focused by the ecological community on the invasion of Kentucky bluegrass in the PPR. Even though Kentucky bluegrass's presence has been increasing in the PPR, the mechanism of the invasion is not known since Kentucky bluegrass is usually not classified as an invasive species because of its economic value (Kaplan 2011b; United States Department of Agriculture & Natural Resource Conservation Service 2014), therefore little research has been focused on this important aspect. The long lasting ecological impacts of Kentucky bluegrass invasion are also uncertain and need to be identified. The effect this invasion has on soil and community biology of the grasslands will be important information needed for future preservation of this important and endangered ecosystem (Samson & Knopf 1994b). Kentucky bluegrass is now a major component of the PPR and what that means for biodiversity and community composition will be a key area of research in the upcoming decades.

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CHAPTER 3. THERE IS NO EVIDENCE OF GEOGRAPHICAL PATTERNING AMONG INVASIVE *POA PRATENSIS* L. POPULATIONS IN THE NORTHERN GREAT PLAINS[2]

Dennhardt, LA, Tennefos, S, DeKeyser, ES, Travers, SE (2016) There is No Evidence of Geographical Patterning among Invasive *Poa pratensis* L. Populations in the Northern Great Plains. *Weed Science*, **in press**.

Abstract

The study of colonizing and dominant grass species is essential for prairie conservation efforts. We sought to answer how naturalized *Poa pratensis* L. in the northern Great Plains has become successful in the last twenty years despite its long history in the northern Great Plains. We tested for evidence of geographical differentiation using flow cytometry and microsatellite markers to ascertain the population genetics of *Poa pratensis*. Across all tested wild populations, high levels of genetic diversity (H_S = 0.823-0.906) were detected along with moderate levels of structure (Rho_{ST}=0.1263; p-value <0.001). Mantel tests of geographical patterns were not significant. Using clonal assignment we found two major clones which made up the majority of the tested wild populations. When we compared the wild individuals to pedigree cultivars, we found virtually no genetic overlap across all tests, which did not support our hypothesis of developed cultivars contributing to high genetic diversity in natural populations. Furthermore, DNA content tests indicated a narrow range in ploidy in wild populations compared to lawn cultivars further supporting a hypothesis of divergence between wild and pedigree cultivars.

[2] Lauren Dennhardt was the primary author, wrote the entire manuscript, collected and analyzed the data, prepared the manuscript for publication, and submitted the manuscript. Published in Weed Science (Appendix F).

These results indicate the recent invasion of *Poa pratensis* in the northern Great Plains was not because of adaptation or propagule pressure but rather an environmental shift has created an advantageous opening for *Poa pratensis.*

Introduction

In the prairies of the northern Great Plains *Poa pratensis* L. (Kentucky bluegrass) cover is currently reported as dominant in many fragments of remaining prairie, which is a recent change having occurred in the last 20 years (Toledo *et al.* 2014a; United States Department of Agriculture Natural Resources Conservation Service 2014). *Poa pratensis* is a clonal, apomicitic, highly polyploid C_3 grass from Europe, which most likely first arrived in the northern Great Plains (NGP) in the late 1800s (DeKeyser *et al.* 2015; Upham 1890; Uchytil 1993). It often forms nearly homogenous stands and replaces diverse plant communities (DeKeyser *et al.* 2009, 2013a; Toledo *et al.* 2014a). The recent evidence on the extent of distribution raises concerns about the future of prairie management (Cully *et al.* 2003; Bahm *et al.* 2011a; DeKeyser *et al.* 2013a). In one study, *P. pratensis* accounted for half of all non-native plant cover in the tallgrass prairie (Cully *et al.* 2003). A survey from 2014 revealed that in North and South Dakota 20-35% of rangelands consisted of more than 50% soil surface cover of "invasive bluegrasses", which includes both *Poa pratensis* and *Poa compressa* L. (Canada bluegrass) (United States Department of Agriculture Natural Resources Conservation Service 2014). *P. compressa* is also a species that is introduced in the northern Great Plains and has been reported to hybridize with *P. pratensis* (Uchytil 1993).

It has long been thought that *P. pratensis* abundance is largely due to high levels of propagule pressure, or the cumulative release of a non-native species into an area where it did not originate, because of its commercial popularity (Uchytil 1993). *Poa pratensis* is frequently

seeded across lawns, golf courses, and grazing fields in temperate regions of North America and is preferred by managers because of its relatively low maintenance requirements, high forage value, and aesthetics (Uchytil 1993). The assumption that propagule pressure from the great variety of *P. pratensis* cultivars has accounted for the rise of *P. pratensis* in the NGP has never been tested in the NGP (Sakai *et al.* 2001). If recruitment of new individuals to wild populations is occurring through seed dispersal from planted populations, then a high level of genetic diversity is likely in wild populations of *P. pratensis*, since there are over 247 unique commercially available cultivars (Honig *et al.* 2010b). Additionally, we would expect evidence of geographical differentiation in the more heavily invaded regions of North Dakota. However, we know nearly nothing about the levels of genetic diversity in wild populations or whether the propagules are escaping frequently.

In addition to *P. pratensis'* importance for conservation, it is also an advantageous invasive species to study because it is clonal and a polyploid. Polyploidy has long been assumed to be a feature of many colonizing species through events such as a genome duplication which may provide a fast lane for adaptation in some individuals through changes in gene interaction and transcription levels (Stebbins 1947; Soltis & Soltis 1999; Beest *et al.* 2012). However, natural, internal barriers to gene flow may occur via incompatible ploidy levels for species that vary widely in chromosomal loads (Beest *et al.* 2012). It is possible that species circumvent this problem using clonal, asexual modes of reproduction, allopolyploidy, and/or apomixis (Stebbins 1941, 1947; Soltis & Soltis 1999). All these mechanisms of reproduction can create a complicated population genetic structure, but one that is potentially advantageous to colonizing species (Baker 1965). The population genetics of apomictic, clonal, highly polyploid species are

important to understand so as to identify potentially noxious species before introduction and control their spread (Pappert *et al.* 2000; Lavergne & Molofsky 2007; Merrill *et al.* 2012).

It is critical to understand the rapid dominance of *P. pratensis* because of the habitat destruction of prairies in the United States over the past century (Samson & Knopf 1994b). In this paper, we attempt to answer three critical questions about the recent spread of *P. pratensis* in the NGP using molecular tools: (1) Is there evidence of adaptation or a different population in the more heavily invaded region of North Dakota? (2) Do we see evidence of lawn cultivars of *P. pratensis* escaping to wild populations? and (3) What is the genotypic and genetic diversity of *P. pratensis*? Our goal is to understand the gene flow of the invasive *P. pratensis* and to discern if the wild genotype has any genetic overlap with *P. pratensis* cultivars by using microsatellite markers and flow cytometry.

Methods

Microsatellite analysis

We collected samples during the summer of 2012 at eight National Wildlife Refuges (NWR; managed habitat for wildlife) in North and South Dakota (Table 3.1, Fig. 3.1). All eight of our sites are remnant prairie managed by the United States Fish and Wildlife Service (Table 3.1). At each NWR, we collected from two managed units. We randomly generated seven points in ArcGIS version 10 at each managed unit, laid out a 2.5 meter line at each point, and collected five samples along the line. If the point did not contain *P. pratensis*, that point was omitted and one of the additional sampling points generated by ArcGIS was used. If no *P. pratensis* was available at the predefined transects, *P. pratensis* was collected haphazardly at the site as near to the point as possible. Each sample was an 8-12 cm blade of grass and each sample used in the final analysis was at least 8m apart from any other sample. Managed units were from 70 to 7 km

away from each other. We did not treat these as a form of subsampling since we were trying to detect clonal character across a NWR. We stored samples in a 1.5 mL microcentrifuge tube filled halfway with silica gel for desiccation. After isolating DNA we chose the samples with the highest quality DNA for the analysis. Ten samples were used in the final analysis for each NWR.

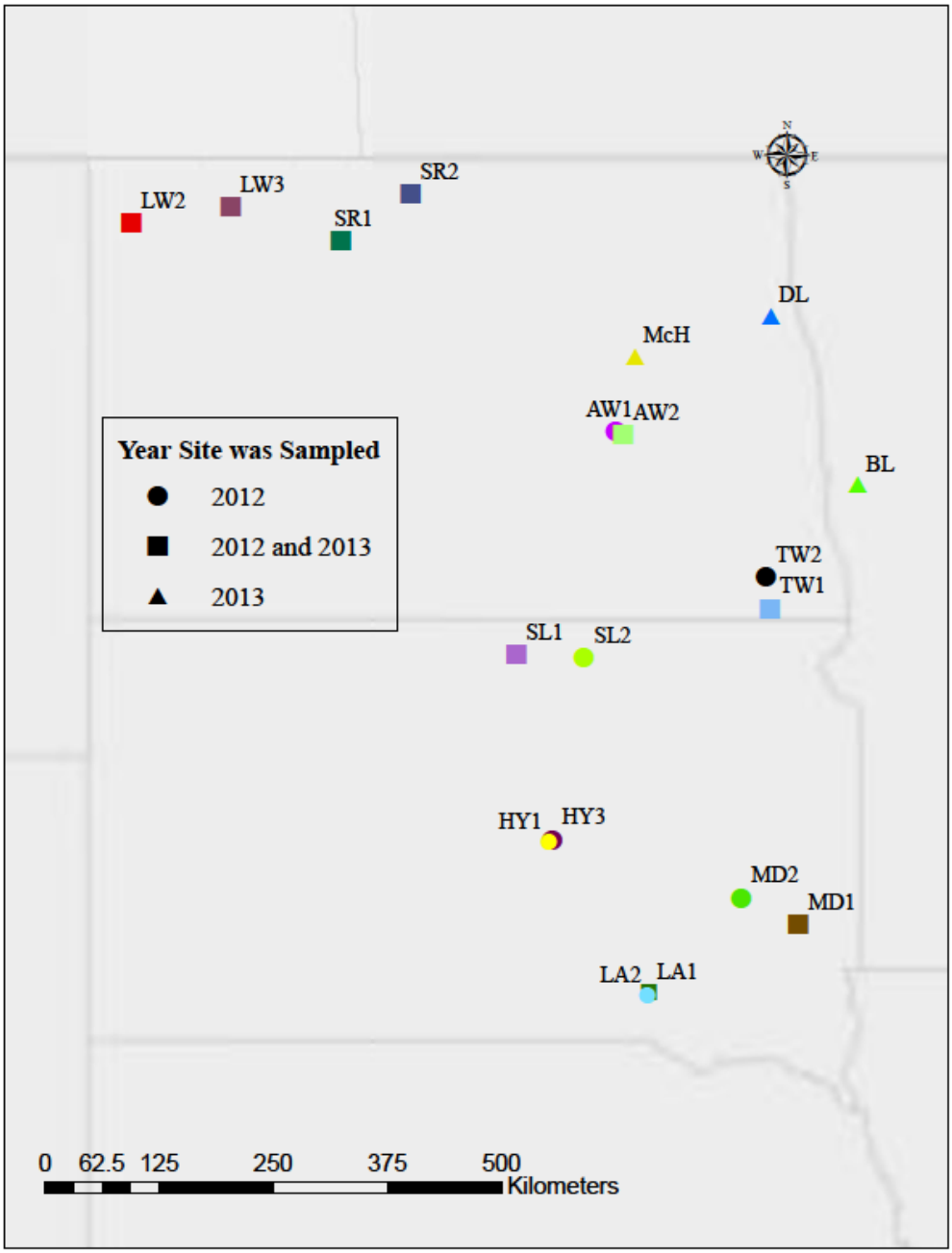

Figure 3.1. Location of sampling sites in North Dakota, South Dakota, and Minnesota. In 2012 we collected samples for the microsatellite analysis and in 2013 we collected samples for flow cytometry analysis.

Table 3.1. Location of the 19 sites where P. pratensis was sampled in 2012 and 2013. Codes are used to refer to sites in other table and figures. Data provided by the United States Fish and Wildlife Service (USFWS). Other acronyms in the table are National Wildlife Refuge (NWR), Wildlife Management District (WMD), and Waterfowl Production Area (WPA).

Code	Site	Year(s) sampled	Prairie type	Latitude	Longitude
SR2	Souris River Basin Complex: J. Clark Salyer NWR: GLT Plot A	2012 & 2013	Mixed	48.773	-100.879
LW3	Lostwood Complex: Mountrail County WPA: Coteau Prairie - G2 West half	2012 & 2013	Mixed	48.685	-102.651
LW2	Lostwood Complex: Burke County WPA: Swanson	2012 & 2013	Mixed	48.583	-103.627
SR1	Souris River Basin Complex: Upper Souris NWR: HB-24 Ekert Ranch South	2012 & 2013	Mixed	48.464	-101.566
DL	Devils Lake WMD: Grand Forks County WPA: Mekinock	2013	Tallgrass	47.971	-97.335
McH	Camp Grafton South: McHenry ND	2013	Tallgrass	47.703	-98.666
AW1	Arrowwood Complex: Arrowwood NWR: G14 Pasture 1 & 2	2012	Mixed	47.214	-98.864
AW2	Arrowwood Complex: Arrowwood NWR: G26 Paddocks 1, 2, 3 & 4	2012 & 2013	Mixed	47.187	-98.788
BL	Bluestem Prairie Scientific and Natural Area	2013	Tallgrass	46.85	-96.48
TW2	Tewaukon WMD: Sargent Country WPA: Gainor Unit B	2012	Tallgrass	46.231	-97.385
TW1	Tewaukon WMD: Sargent Country WPA: Krause	2012 & 2013	Tallgrass	46.019	-97.347
SL1	Sand Lake Complex: Campbell County WPA: Cooper North	2012 & 2013	Mixed	45.706	-99.839
SL2	Sand Lake Complex: Mcpherson County WPA: Charley-Harley	2012	Mixed	45.682	-99.173
HY3	Huron WMD: Hyde County WPA: Cowan Unit 4	2012	Mixed	44.426	-99.486
HY1	Huron WMD: Hyde County WPA: Cowan Unit 6	2012	Mixed	44.409	-99.518
MD2	Madison WMD: Miner County WPA: Hepner WPA	2012	Tallgrass	44.015	-97.624
MD1	Madison WMD: Minnehaha County WPA: Buffalo Lake 80	2012 & 2013	Tallgrass	43.824	-97.066
LA1	Lake Andes NWR: Douglas County WPA: Denning	2012 & 2013	Mixed	43.346	-98.534
LA2	Lake Andes NWR: Charles Mix County WPA: Trout	2012	Mixed	43.321	-98.553

In order to compare wild populations of *P. pratensis* with pedigree cultivars, we analyzed the genetic fingerprints of wild and greenhouse grown cultivars of *P. pratensis*. We planted

common cultivars of lawn *P. pratensis,* obtained from the Seed Superstore (https://www.seedsuperstore.com/, Buffalo, New York), in a greenhouse in 8 x 8 cm pots using standard potting soil (Miracle-Gro ® Moisture Control ® Potting Mix). Our cultivars represent the "Compact," "Compact-America," and "Midnight" clades out of the seven possible *P. pratensis* phylogenetic groups (Honig *et al.* 2012; Brett Young 2014). The Midnight clade contains "Award," and "Nuglade," the Compact clade contains, "Bewitched," and the Compact-America clade contains "Bedazzled." These three groups are commonly used as lawn grasses, but not as pasture grasses. We were attempting to detect a cultivar stock in naturalized populations, which is why we chose three pedigree phylogenetic groups.

Leaf samples were crushed in their microcentrifuge tubes with a grinding stick after adding a small volume of liquid nitrogen. We isolated the nuclear DNA using a DNeasy Plant Mini Kit (Qiagen©) extending the last incubation time in the protocol to 15 minutes to increase DNA yield (Qiagen 2012). The ten microsatellite primer pairs we used were identified for *P. pratensis* by Honig et al. 2010. In order to label amplified fragments we used the three primer CAG-tag of Oetting et al., 1995 whereby a CAG-specific tag is added to the 5' end of the forward primer rather than the M13 label (Oetting *et al.* 1995; Ross *et al.* 2013). Before initial primer screening, we entered the 88 primer pairs from Honigh et al., 2010 with the CAG-tag in OligoCalc (http://www.basic.northwestern.edu/biotools/oligocalc.html) in order to choose candidates that did not form hairpins (Kibbe 2007). The screening narrowed the potential primers to 26 pairs. We used six cultivars of *P. pratensis* and 10 wild samples from McHenry, ND collected in the fall of 2011 to further screen primers. The Plant-Microbe Genomics Facility at Ohio State University ran the 26 primer pairs on the 16 *P. pratensis* individuals using a 3730 DNA Analyzer (Applied Biosystems, Inc.) and recommended 10 primer pairs that consistently

amplified on the DNA Analyzer (Table 3.2). In order to test whether the markers were truly neutral, we conducted a BLAST search for primer sequences against records from all known life forms. All hits except for HM136764 produced no significant results. HM136764 produced hits on a number of grass species for the acetyltransferase protein feature, which is unlikely to be under selection.

Table 3.2 Primers used in analysis. Repeat motif represents the repetitive sequence, size range is the allele size range in base pairs, and the range is the range in polymorphism information content values for alleles (Honig *et al.* 2010b).

Poa pratensis primers				
GenBank	Primer Sequence (5' - 3')	Repeat motif	Size Range	Range
HM136689	F: GCCGTAAATAGTGGAGAAGAC	(CT)21	142-275	0.01-0.50
	R: AAAATCCTGACTGTTGGAGAC			
HM136697	F: CCAGCACATCTACGAGCAC	(CT)13	272-322	0.01-.48
	R: TTCGGAAGAACTTGATTTGG			
HM136706	F: GCACCGTGGACAAAGTTATT	(CT)17	244-335	0.01-0.41
	R: AGGGAAGGATGACATCAACA			
HM136712	F: ATCGTCACGGGGAGAATC	(CT)37	187-317	0.01-0.50
	R: AACTCCTGTCGCTGCGTA			
HM136723	F: CACTAAAAGCCAAACCACGA	(GA)13AA(GA)5	179-365	0.01-0.50
	R: AAATGGTAGCAGGAGATGGA			
HM136729	F: CCCCAAATCCCTACTCAAAT	(GA)19	274-353	0.01-0.50
	R: GATATGGACAACCACCATGC			
HM136764	F: GTTCTTGGGTAGTGTGCTGTAT	CAGA(CA)13	164-246	0.01-0.46
	R: CGTGTGAATCATTGCCTAAC			
HM136746	F: GAGACCCAAAAATCGTCCTC	(CT)18	285-342	0.01-0.50
	R: CGTCTCTTCGTTTGAGATGG			
HM136769	F: GCCGCTCTCTTGTGTCATT	(GT)29	132-241	0.01-0.50
	R: CGGGTAAGGTTTCTGCTTG			
HM136748	F: TGAGGAGTTGCTCGTCTAGG	(GA)26	240-365	0.01-0.42
	R: TCTGATGCAGACTTGGAACA			

All DNA was diluted to a concentration level of 5 ng/uL and 4 uL were added to each PCR reaction. Amplifications were performed in 26uL quantities containing 1 X Taq PCR buffer, 2.2 mM $MgCl_2$, 0.3 mM each dNTP, 1 U Taq DNA polymerase, 5 pmol forward primer with CAG addition, 10 pmol reverse primer, and 10 pmol forward florescent dye-labeled CAG primer (PET). Our thermacycler parameters were 94ºC for 30 s, 58ºC for 30 sec using step down by 0.5ºC, and 72ºC for 30 s for 16 cycles, then 94ºC for 30 s, 50ºC for 30 s, and 72ºC for 30 s for 24 cycles. We used the GoTaq® Flexi DNA Polymerase kit for PCR reactions and ordered our primers from Life Technologie®s. Only PCR products with high sizing quality (SQ) levels of

1.0 determined by GeneMapper were not sent in multiple times (192 of the 900), the rest were sent in twice for insurance of proper allele calls which is one way to handle ambiguous alleles and stutter. Many techniques for assessing polyploid alleles have been recommended in recent years (Pfeiffer *et al.* 2011; Narayan *et al.* 2015). We chose to send in ambiguous PCR products twice on difficult calls so as not to lose the resolution that microsatellite markers provide by using binary matrices (Pfeiffer *et al.* 2011).

Initial fragment analysis was conducted by the Plant-Microbe Genomics Facility at Ohio State University (http://pmgf.osu.edu/). Inconsistent peaks between the same sample at a single locus were judged by two criteria (1) consistency between other allele peaks amongst other samples at that locus and (2) an electropherogram peak height of at least 1000. If one or both of the criteria were met then the allele peak was accepted. Across all samples sent in twice there were 1363 instances of an allele matching and 561 instances of a new peak read detected. Out of the 1879 PCR products sent in, 144 returned no results.

We tested genetic differentiation amongst sample sites by calculating pairwise Rho_{ST} values using 5000 permutations with the program SPAGeDi v. 1.3a (Ronfort *et al.* 1998; Hardy & Vekemans 2002). We chose to use Rho_{ST} because it calculates population differentiation with a correlation approach independent of ploidy level, selfing rate, and type of inheritance instead of the infinite allele model of F_{ST} (Dufresne *et al.* 2014). The ambiguous chromosome copy numbers in our data would violate the assumptions of F_{ST} and G_{ST} values (Ronfort *et al.* 1998; Dufresne *et al.* 2014). Computation of inbreeding coefficients were corrected for allele dosage and executed in Genodive by jackknifing over loci (Nei 1978; Meirmans & Van Tienderen 2004). The observed heterozygosity (H_O) value was modified to reflect the "gametic heterozygosity" or the likelihood of randomly drawing a different allele from within an

individual as is typical with polyploids (Moody *et al.* 1993; Meirmans & Van Tienderen 2004). We created a principal coordinate analysis (PCoA) to visualize sample genetic structuring using Bruvo's distance model in Polysat, which is a distance matrix acceptable for individuals with unknown allele dosages (Bruvo *et al.* 2004; Clark & Jasieniuk 2011). Bruvo's distance matrix takes into account mutational distance between alleles at a locus by calculating the probability of mutation from one allele to another. The matrix also creates virtual alleles for those genotypes with unequal allele copy numbers at a single locus, thus bypassing the need to know copy number (Bruvo *et al.* 2004; Clark & Jasieniuk 2011). In order to test spatial and population correlations we conducted a Mantel test in Genodive using 1000 permutations and Mantel's r. Additonally, we tested whether predominant wind direction in June (when *P. pratensis*) is in flower could account for gene flow by running a separate mantel test on wind direction and bearing (Appendix B).

Because polyploid clones may have a slightly different PCR product because of scoring errors, we used the adapted method of Douhovikoff and Dodd (2003) and Meirmans and Tienderen (2004) described in Zhang et al., 2010. We estimated genotypic diversity using Genodive (Meirmans & Van Tienderen 2004). We first assigned clones using a stepwise mutation model where the absence of data was counted as one mutation step. We chose a threshold representing the maximum distance among samples from the same genet and the minimum distance among samples from different related genets (Douhovnikoff & Dodd 2003; Zhang *et al.* 2010). This is executed by using a bimodal selection method where the point between the two peaks is chosen for a threshold (supplementary material, (Arnaud-Haond *et al.* 2007)). We then tested for the probability of finding the observed clonal diversity using the corrected Nei's diversity index, 999 permutations, and randomized alleles over individuals

within the population. We manually calculated G/N, where G=number of genotypes and N=population size. We displayed the clonal diversity using a histogram in ggplot2 (Wickham 2009).

Flow cytometry

Plant samples for flow cytometry analysis were collected in the summer of 2013 (Fig. 3.1). We visited 12 sites across Minnesota, North Dakota, and South Dakota (Fig. 3.1 and Table 3.1). At each site, ten plant samples, at least ten meters apart, were randomly collected. We harvested 4x4 cm patches of *P. pratensis* and placed them in equally sized pots. Collections were brought back to NDSU and planted in 10 cm diameter pots filled with Miracle-Gro ® Moisture Control ® Potting Soil. Plants were maintained for two months in the greenhouse at the NDSU campus prior to flow cytometry analysis. We analyzed 20 of the 120 plants, because many died off following a greenhouse malfunction. A month before analysis, we planted seeds of *Glycine max* (L.) Merr. with known DNA content as a standard (Doležel *et al.* 2007).

Two weeks prior to analysis, propidium iodine (Sigma-Aldrich®), RNase (Sigma-Adlrich®), and Galbraith's buffer were prepared, vacuum-filtered through a 0.22-µm mesh to remove any contaminants, and stored at -20°C. Approximately 60 mg of plant material per sample was measured into separate 50x15mm petri dishes. In order to break open cells and reveal chromosomes for analysis, one mL of ice-cold Galbraith's buffer (45mM $MgCl_2$ (Sigma-Alrich®), 20 mM of MOPS (Sigma-Aldrich®), 30 mM sodium citrate (sodium citrate tribasic dihydrate Sigma-Aldrich®), 0.1% Triton X-100 (Sigma Aldrich®, adjusted to the pH to 7.0) was added to the material and chopped quickly using an autoclaved razor blade for two minutes. The resulting solution was pipetted slowly two times and squeezed through a 40 µm nylon mesh cell strainer into a 50 mL conical tube (Doležel *et al.* 2007). Within an hour, we stained the DNA

using 500 µL of the 1 mg ml^{-1} propidium iodine and dissipated RNA with 500 µL of the 1 mg ml^{-1} RNase solutions (Doležel *et al.* 2007). The solutions were incubated on ice for at least a half hour, aliquoted into microcentrifuge tubes, and stored on ice for no longer than two hours, until all samples were ready for analysis (Doležel *et al.* 2007). Half of the analyses were done on one day and the other half on the following.

Samples were run on a BD Accuri C6 Flow Cytometer (BD biosciences™) according to the manufacturer's instruction ("BD Accuri C6 Flow Cytometer Instrument Manual" 2012). Measurements at both FL2-A and FL3-A fluorescence were taken for 50,000 iterations and were only accepted if the coefficient of variation was at or below 5%. At the beginning of each run, at least two standards were run independently, followed by the *P. pratensis* samples. Although plants did not have an internal standardization, three ramets from each genotype were run independently three times. Estimations of DNA content were calculated using the soybean standardization and the 2C DNA content measurement provided with the sample (Doležel *et al.* 2007). We were able to estimate genome content from Eaton et al. 2004, in which they ran flow cytometry and conducted chromosomal counts on *Poa pratensis* (Eaton *et al.* 2004). Our methodology aligned with other *P. pratensis* flow cytometry protocols (Eaton *et al.* 2004; Raggi *et al.* 2015). Cultivar comparisons were done using previously published flow cytometry data (Eaton *et al.* 2004). Flow cytometry data were analyzed in R using the Agricolae package (Felip de Mendiburu 2015). An F-test on variance was used to compare the lawn varieties and wild plant samples.

Results

Genetic diversity

Wild populations of *P. pratensis* exhibited high levels of genetic diversity, but were heterozygote deficient at most populations. Our adjusted total expected heterozygosity was 0.898, indicating that expected heterozygosity within subpopulations (H_S) was only higher at Sandlake and Arrowwood (Table 3.3). The H_O values (0.763-0.870) across populations were lower than the H_S values (0.823-0.906) at all but one wild site (Table 3.3) (Nei 1978). The two populations with the highest average number of alleles (13) were Arrowwood and Sandlake, which also had high H_O values of 0.8 and 0.78 respectively (Table 3.3). The wild populations' inbreeding coefficients (G_{IS}) were positive, except for Hyde (Table 3.3). The effective number of alleles (Eff. Num.) was lowest for the lawn cultivars and the Hyde populations (Table 3.3).

Table 3.3. Genetic diversity of all populations. Average number of alleles (Num.), effective number of alleles (Eff. Num.), observed heterozygosity (H_O), heterozygosity within populations (H_S), inbreeding coefficient (G_{IS}), and the one sided p-value of the G_{IS} value calculated in Genodive and corrected for unknown allele dosage.

Population	Num	Eff. Num	HO	HS	Ht	Gis	p-value
Lostwood, ND	10.8	7.053	0.763	0.879	0.879	0.133	0.991
Souris, ND	11.6	7.614	0.78	0.882	0.882	0.116	0.995
Arrowwood, ND	11.9	9.051	0.8	0.906	0.906	0.117	0.994
Tewaukon, ND	9.4	6.171	0.78	0.838	0.838	0.069	1.001
Sandlake SD	12	8.908	0.78	0.9	0.9	0.134	0.96
Hyde, SD	7.8	5.079	0.81	0.807	0.807	-0.003	0.001
Madison, SD	11.4	7.645	0.708	0.883	0.883	0.198	0.535
Lake Andes, SD	8.6	6.062	0.77	0.825	0.825	0.067	1.001
Commercial varieties	7.2	5.257	0.87	0.823	0.823	-0.057	0.001

Genetic divergence among populations

Our results suggest some divergence among wild populations. The overall Rho_{ST} value along with the F_{ST} and G_{ST} values were significant (Rho_{ST}=0.1263; F_{ST} =0.0723; p-value<0.001 p-value <0.001; G_{ST}=0.0696 p-value<0.001). A majority of pairwise comparisons between populations (27 of 36) yielded significant differences (Table 3.4). The Mantel test for isolation by distance was not significant (r=-0.036, p=0.435). Additionally, there was no significant correlation between the wind direction and bearing coefficient matrix on both tests. Respectively, the pairwise RhoST values in both Mantel tests were not significant (r=-0.215, p=0.136; controlling for distance r=-0.216, p=0.591).

Among the wild populations there is little discernible differentiation in the PCoA plot, with some clustering between Hyde and Lake Andes, which are both South Dakota populations (Fig. 3.2). The wild samples were significantly different from each other in DNA content (F=17.61, p-value<0.001), although, compared to commercial varieties, wild populations have a narrow range of DNA content (Table 3.4; Fig. 3.3).

Lawn cultivars were distinct from the wild populations in the PCoA plot, pairwise Rho_{ST} values, and DNA content analyses (Figs. 3.2 & 3.3; Table 3.5). In the PCoA plot, the cultivars were the only group that clearly separated from all other samples (Fig. 3.2). The pairwise Rho_{ST} values were all significantly different from each sampled site (Table 3.5). DNA content of wild *P. pratensis*, had a narrower range than DNA content of cultivars (Fig. 3.3). Our flow cytometry results yielded ranges from 6.52 ± 0.127 to 10.47 ± 0.188 2C DNA content (Table 3.4), which is much more constricted compared to commercial varieties (Huff & Bara 1993; Barcaccia *et al.* 1997; Eaton *et al.* 2004). An Analysis of Variance of DNA content revealed significant differences between the wild and commercial groups (F=9.347, p-value=8.314×10^{-6}).

The threshold chosen for our clone assignment was a genetic distance of 55 out of 323 based on the bimodal histogram (Arnaud-Haond *et al.* 2007) Figure 3.1). Overall, the wild individuals were not significantly clonal (diversity observed=0.889, diversity expected=0.942, p=0.132) and consisted of 39 genotypes out of our 80 wild individuals (Fig. 3.4). We found three populations that were significantly clonal—Hyde, Souris, and Madison. Two of the genotypes (genotype one and four) represented nearly half the samples (Fig. 3.4). Genotype one represented 17 (21%) of the wild samples and genotype 4 represented 21 (26%) of the wild samples. Our overall uncorrected G/N value was 0.49 and populations ranged from 0.50-0.90 (Table 3.6).

Table 3.4 Flow cytometry results showing mean estimated DNA content in picograms per uL. Samples are listed from highest to lowest latitude. Each sample was run three times using three different leaf tissues.

Sample	Mean pictograms per uL	Standard error
SR2, ND	7.27	0.12
LW3, ND	8.31	0.04
SR1, ND #1	7.88	0.09
SR1, ND #2	7.81	0.08
DL, ND	7.58	0.13
McH, ND	7.20	0.33
AW2, ND #1	7.66	0.08
AW2, ND #2	10.47	0.11
BL, MN #1	8.65	0.06
BL, MN #2	7.45	0.04
BL, MN #3	7.25	0.42
TW1, ND #1	7.45	0.22
TW1, ND #2	8.16	0.26
SL1, SD #1	7.59	0.23
SL1, SD #2	7.55	0.09
MD1, SD #1	6.35	0.07
MD1, SD #2	7.12	0.51
MD1, SD #3	9.08	0.05
LA2, SD #1	7.68	0.09
LA2, SD #2	7.55	0.14

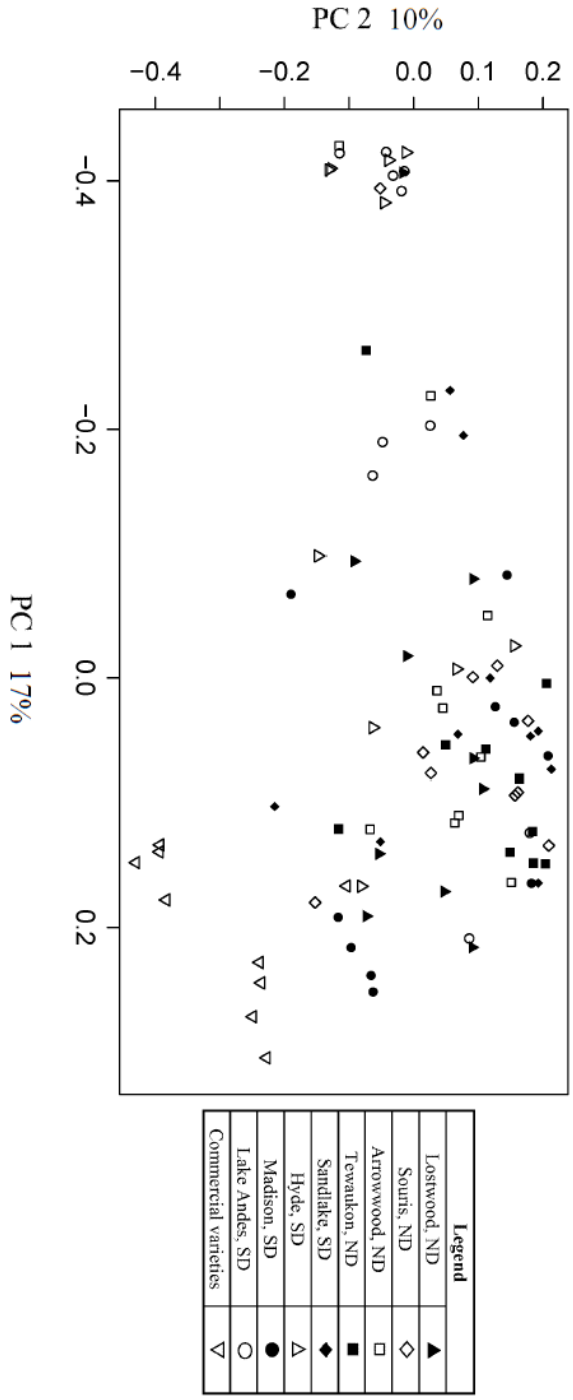

Figure 3.2. Principal coordinate analysis using Bruvo distance matrix. Each symbol represents an individual plant.

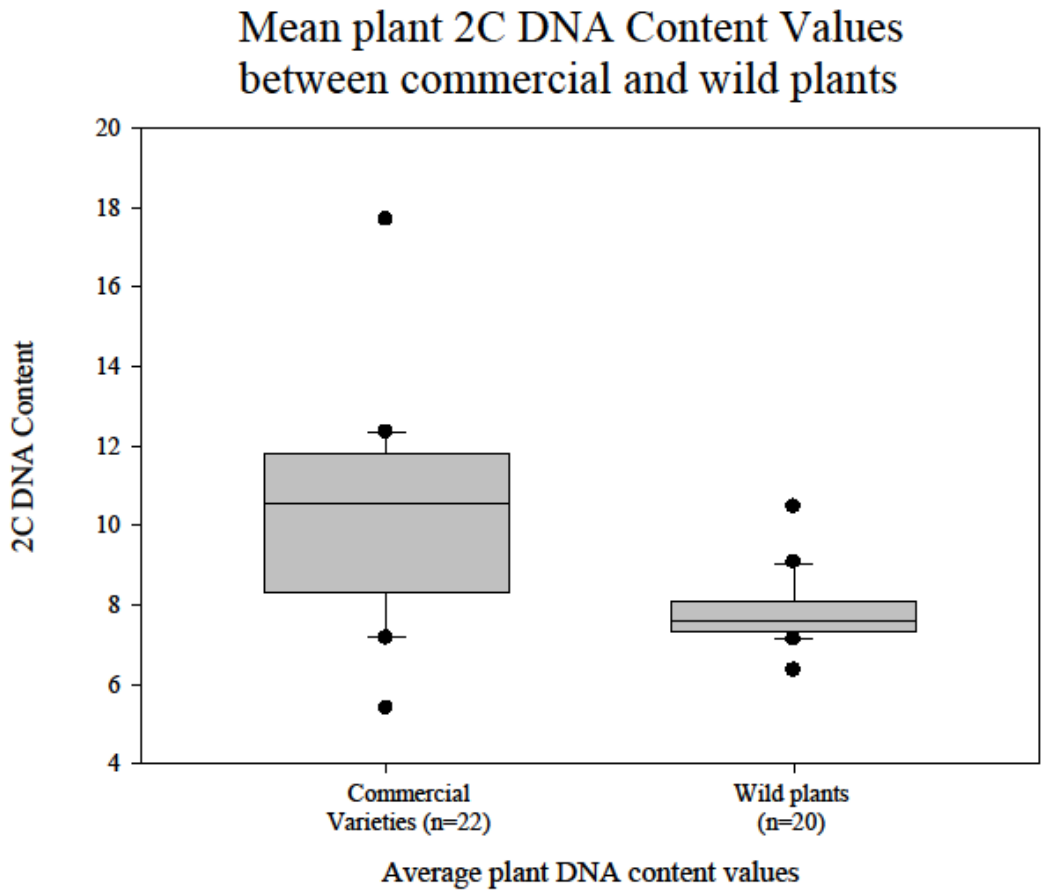

Figure 3.3. Boxplot depicting the mean picogram DNA content (picograms/uL) for both wild samples and commercial varieties.

Table 3.5. Pairwise RhoST values based on 5000 permutations calculated in SpageDi. These values show whether populations have significantly diverged from one another. RhoST was used because it uses the step-wise mutation model.

Rho and p-values									
Populations	Lostwood, ND	Souris, ND	Arrowwood, ND	Tewaukon, ND	Sandlake, SD	Hyde, SD	Madison, SD	Lake Andes, SD	Common Cultivars
Lostwood, ND		0.067*	0.030	0.128*	0.068*	0.131*	0.051	0.089*	0.247*
Souris, ND	0.008		0.023	0.083*	0.029	0.145*	0.038	0.086*	0.243*
Arrowwood, ND	0.229	0.312		0.072*	0.026	0.101*	0.031	0.074*	0.203*
Tewaukon, ND	0.000	0.006	0.009		0.091*	0.224*	0.061*	0.168*	0.263*
Sandlake, SD	0.011	0.188	0.249	0.001		0.142*	0.037	0.079*	0.240*
Hyde, SD	0.014	0.005	0.036	0.001	0.003		0.152*	0.030	0.354*
Madison, SD	0.053	0.138	0.215	0.043	0.135	0.003		0.144*	0.210*
Lake Andes, SD	0.033	0.019	0.041	0.001	0.030	0.392	0.002		0.326*
Common Cultivars	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

*A p-value of <0.05. P-values are listed below black bars.

Table 3.6. The genotypic diversity of all wild populations. The G/N value is uncorrected while the diversity observed and expected were calculated in Genodive by randomizing alleles over individuals within populations using Nei's diversity index (Nei 1978; Meirmans & Van Tienderen 2004).

Population	G/N	Observed diversity	Expected diversity	p-value
Lostwood, ND	0.80	0.933	0.947	0.397
Souris, ND	0.70	0.911	0.98	0.034
Arrowwood, ND	0.90	0.978	0.939	0.693
Tewaukon, ND	0.50	0.667	0.874	0.123
Sandlake, SD	0.90	0.978	0.96	0.506
Hyde, SD	0.50	0.756	0.931	0.045
Madison, SD	0.50	0.8	0.986	0.008
Lake Andes, SD	0.60	0.667	0.893	0.094
Overall	0.49	0.889	0.942	0.132

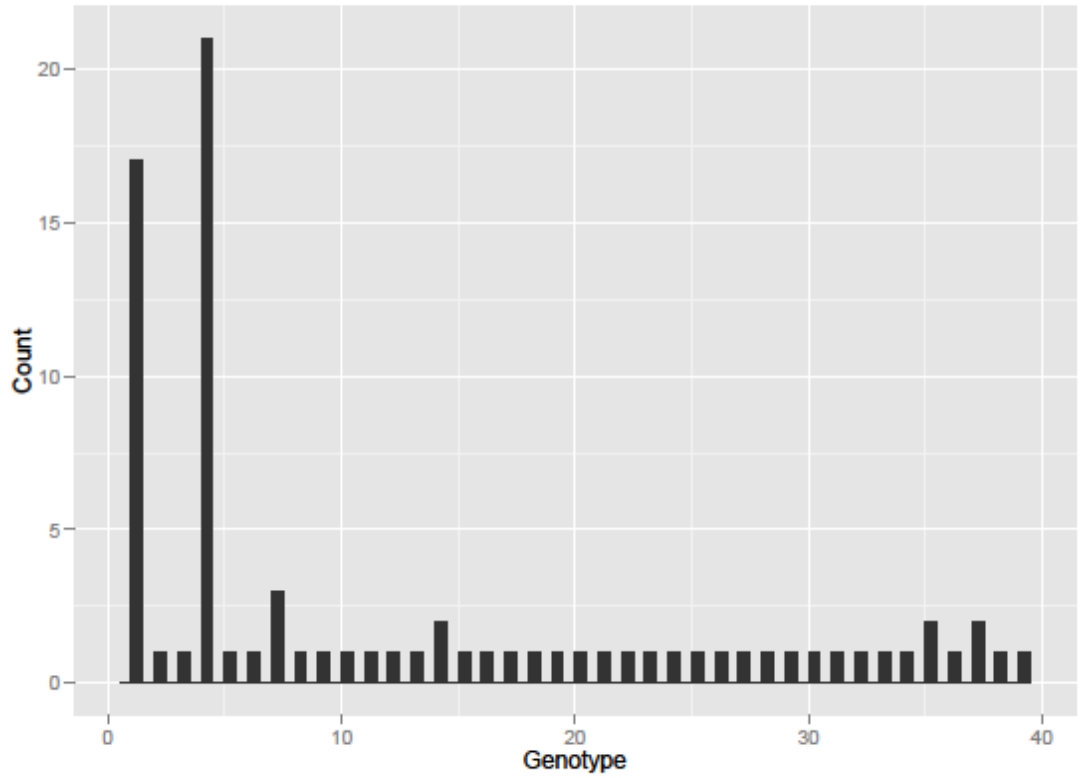

Figure 3.4. Histogram of clonal assignment and frequency of each clone. Clones were determined in Genodive using a step-wise mutation model. Clones 2 and 4 make up the majority of the individuals sampled.

Discussion

We found no evidence of local adaptation as evidenced by our lack of geographic distinctiveness. Although some populations of *P. pratensis* were genetically distinguishable, Mantel tests of both inter-individual distance and wind direction produced no significant patterns. One possible explanation is that populations that were not significantly different from one another are from similar source populations rather than connected by gene flow.

Our clonal assignment provided evidence that some populations were clonal (three of eight) (Table 3.6). Our histogram of clones indicated that there were two predominant clones throughout the region, both of which were distributed throughout the sampled area (Fig. 3.4). A possible explanation for the detection of two clones is that from either a subspecies and/or two separate founder populations. For example, one subspecies present in the NGP is *Poa pratensis* subspp. *pratensis* and is defined by the USDA as a noxious subspecies (United States Department of Agriculture & Natural Resource Conservation Service 2014). We also know that there are many sources of *P. pratensis* in the NGP and it is possible that at least one of the clones of *P. pratensis* came from planted *P. pratensis* used for pasture grass. Although recently *P. pratensis* is rarely planted for pasture grass in the Dakotas. Individuals falling outside of clones 2 and 4 could be the result of random mutations, escaped untested cultivars, or hybridization with other species of *Poa* such as *P. compressa* (Uchytill). Our G/N numbers were high, which is likely a combined result of small population size and distance between samples in each population (Table 3.6). Again, the G/N value was not corrected, but our Nei's genotypic diversity was adjusted making it a more reliable indicator (Meirmans & Van Tienderen 2004).

In contrast to many studies where clonal species are detected along with a negative inbreeding coefficient and low genotypic diversity, we found positive inbreeding coefficients in

all but one population (Pappert *et al.* 2000; Balloux *et al.* 2003; Stoeckel *et al.* 2006; Prugnolle & De Meeûs 2008). There are two explanations for these positive inbreeding coefficients. The first is the common challenge of proper allele calls in polyploids (Pfeiffer *et al.* 2011; Dufresne *et al.* 2014; Narayan *et al.* 2015). We may have overestimated genetic and genotypic diversity because of the ambiguous copies of each allele present in an individual. A second possible explanation for positive inbreeding coefficients is that a small sample size can lead to estimates of heterozygote deficiency. It is likely that our 10 samples per NWR where each sample was a great distance from each other lead to positive G_{IS} values in most population. It should be noted that we did detect a negative G_{IS} value in the Hyde population, which was also found to be clonal by our clonal assignment analysis.

The genetic (allelic) diversity was high compared to diploid plant species but typical for other polyploid plants with similar chromosome copy number (Ashley *et al.* 2003; Little 2005) Table 3.3). *Poa pratensis* has been present in the NGP since 1890, which is a long history for an introduced species. Additionally it has likely been introduced many times. In clonal kudzu, the authors found positive inbreeding coefficients and more genotypic diversity than most other clonal species (Pappert *et al.* 2000). It is possible that the starting genetic bank of *P. pratensis* lent a higher level of genotypic and genetic diversity than most clonal species because of multiple introductions and/or its long history in the NGP. As mentioned earlier, this may be why we detected two major clones. Finally, the fact that *P. pratensis* has seven copies of its chromosomes, means that genetic diversity should be higher to begin with which is why our H_O and H_S values are so high (Kirk *et al.* 2011). The genotypic diversity is comparable to that found in other polyploid invasive studies (Andreakis *et al.* 2009).

Despite the common use of *P. pratensis* in urban settings, we conclude that populations within regional natural areas are divergent from the tested lawn cultivars. In the PCoA, cultivars were distinct—the PCoA completely separated cultivated from naturalized individuals. From the PCoA, it is apparent that the level of genetic diversity is very limited among the tested lawn cultivars compared to the wild individuals. The limited overall genetic variation could be a result of the more selective needs of commercial breeders for desirable traits (Bashaw & Funk 1987b); Fig. 3.3). Another indication of differentiation between naturalized and lawn cultivars is derived from the cellular DNA content data. Naturalized *P. pratensis* had a narrow range of DNA content among samples (6.35-10.47 2C DNA content) compared to commercial varieties (5.39-17.69 2C DNA content; Fig. 3.3; Table 3.4). Other researchers reached the same conclusion. In one study, researchers found that *trn-L*, a chloroplast intron, contained mostly allele C in cultivated accessions while allele A was predominant in wild accessions of *P. pratensis* (Raggi *et al.* 2015). Additionally, our results align with other *P. pratensis* studies where clones and high levels of allelic diversity were detected along with wild individuals being different from the planted variety (Johnson *et al.* 2002; Honig *et al.* 2012; Bushman *et al.* 2014; Raggi *et al.* 2015).

Since we found no evidence of geographical patterning or escaped cultivars, it is unlikely the recent invasion of *P. pratensis* in the NGP is a result of adaptation. Even though there were high levels of genetic diversity, we conclude that the genetic diversity is likely attributed to *P. pratensis* being polyploid rather than propagule pressure. The invasive populations are most likely a result of an earlier introduction, which means the recent invasion is likely caused by an environmental shift opening a niche for *P. pratensis.* In conclusion, more research will be

needed to identify an environmental change that could have facilitated the propagation of *Poa pratensis* in the northern Great Plains.

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CHAPTER 4. POA PRATENSIS IS FACILIATED BY THREE NATIVE GRASSES IN SPECIES PAIR COMPETITION EXPERIMENTS

Abstract

Poa pratensis is an invasive cool-season grass in the eastern tallgrass and mixed grass portion of the Northern Great Plains. Although it has been well documented as an invasive species, why it has become so prolific in recent decades is unknown. I hypothesize that the competitive ability of *P. pratensis* facilitated the invasion. I tested this by pairing *P. pratensis* with three native species reported to be in decline after *P. pratensis* invades. I tested whether *P. pratensis* was competitive against *Nassella viridula*, *Pascopyrum smithii*, and *Bouteloua gracilis* in paired competition experiments using loamy soil in a greenhouse and an early foliage trim. I found that the three competitors facilitated *Poa pratensis*, but *Poa pratensis* was only slightly competitive against *N. viridula*. It is possible cutting back *P. pratensis* at the beginning of the experiment helped facilitate *P. pratensis* because it is an increaser under grazing conditions. Additionally, *N. viridula* was outcompeted by all species in the experiment and *P. smithii* was competitive against *N. viridula* and *B. gracilis*. This study indicates that one potential factor facilitating the invasion of *P. pratensis* in the Northern Great Plains may be improper grazing management and facilitation by other grass species.

Introduction

Poa pratensis L. (Kentucky bluegrass) is a prolific invasive species that threatens conservation efforts in the tallgrass and mixed grass portion of the Northern Great Plains (United States Department of Agriculture Natural Resources Conservation Service 2014). There is evidence that *Poa pratensis* is negatively associated with grass biodiversity in those regions (Larson & Larson 2010). Once *P. pratensis* becomes established and spreads, it can become a

major fraction of the prairie, sometimes to the point of a monoculture (O'Brien 2014). Many have suggested and inferred from this evidence that *P. pratensis* is a strong competitor (DeKeyser *et al.* 2013; Toledo *et al.* 2014), but there is limited research investigating its competitive ability.

An important aspect of learning how species invade, is studying the mechanisms of invasion. As part of the invasion process, after introduction, species need to become established (Elton 1952). Establishment is an essential step of the invasion process and can only be overcome through successful competition with other species (Vasquez *et al.* 2010). Indeed, it is well known that many invasive species experience competition either directly or indirectly. Invasions exerting a competitive force on a native plant take many forms such as an invasive species attracting a herbivore away from a native plant, reducing pollinators by attracting them to itself, reducing the availability of nitrogen for other species, or performing better under increased nitrogen (D'Antonio & Mahall 1991; Brown *et al.* 2002; Vinton & Goergen 2006; Dangremond *et al.* 2010; Mangla *et al.* 2011). In one review, 17 out of 20 peer-reviewed studies found that competition played a role in invasion, which solidifies the importance of studying competition in invasion biology (Levine et al., 2003).

Typically, the limiting resources in the grasslands of the NGP are nitrogen and reliable precipitation (Weaver 1991; Wight 1976). In recent decades, precipitation and nitrogen levels in the eastern NGP have been increasing due to climactic changes that are altering the historical competitive landscape (Kochy & Wilson 2001; Morgan *et al.* 2008; Millett *et al.* 2009; Werner *et al.* 2013). Changing the nutrient availability and/or precipitation in a region can alter plant communities (Clark *et al.* 2002; Vinton & Goergen 2006; Adler & Levine 2007). Thus, it is

important to observe how plants compete when these resources are present in the proportions observable in a natural setting.

A recent study of *P. pratensis* competition found varied results. In the study, *P. pratensis* outcompeted *Elymus canadensis* L. when given priority, but was not competitive against *Bromus inermis* Leyss. (Ulrich & Perkins 2014). Priority in this case is logical since *P. pratensis* is one of the first species to emerge on the prairie in spring (Weaver 1991). This study tested species that were increasing in the region. My goal was to study *P. pratensis* competition with three species that have been observed to decline when *P. pratensis* increases in a region (Chapter 2-Fig 2.2).

In order to examine how competition may play a role in invasion by *P. pratensis,* I determined if *Poa pratensis* is competitive (reduces the biomass of the paired species compared to intraspecific growth) in a controlled, environment with three native plant species. My goal was to quantify the differences between *Poa pratensis* and native species growth when competing in paired greenhouse trials against species that may be in decline because of *P. pratensis* invasion. In this study I sought to examine whether competition between *Bouteloua gracilis* (Willd. ex Kunth) Lag. Ex Griffiths (blue grama), *Pascopyrum smithii* (Rydb.) Á. Löve (western wheatgrass), *Nassella viridula* (Trin.) Barkworth (green needlegrass), and *Poa pratensis* produced any competitive or facilitative effects when grown in conditions mimicking the current climate.

Methods

I chose three native grass species to use in this study--*Bouteloua gracilis* (BOGR), *Nassella viridula* (NAVI), and *Pascopyrum smithii* (PASM), which are all codominant species in the northern Great Plains and often co-occur with *Poa pratensis* (POPR) (Taylor 2001). Plants

were separately planted 14-21 days before the competition experiment began in pots with loamy soil. After germination, plants were transplanted to a separate 4 x 4 cm pot filled with loamy soil. Two plants were grown in each pot and each was trimmed to a height of eight cm to induce stress and begin the competition experiment at a similar level since germination times can vary. For example, POPR is documented to start germination between 14 and 21 days after sown in wet soil (Scotts Turfseed 2014). There were 10 treatments, replicated 14 times pairing the four species with each other (interspecific) and themselves (intraspecific) (Fig. 4.1). The growing medium was top soil collected from a site in Richland County 80 kilometers south of Fargo North Dakota (46.553834, -97.133522). The soil was classified as a prairie loam. Competitive pairings were grown on a greenhouse bench for two months under a 12 hour supplemental light cycle and were watered as necessary. Nitrogen was not added to the experiment.

At the end of the experiment, I measured above ground biomass by first cutting and washing the plant, drying the plants for 48 hours in an oven at 38°C, and weighing them. Plants were counted as dead in the experiment if more than 50% of plant material was desiccated at the end of the experiment. Thus, for each experimental treatment I calculated the percentage of plants that died as a dependent variable. In addition, the biomass of individual plants was a dependent variable for each replicate.

The normality of each dependent variable was tested using the Shapiro-Wilk test and visual confirmation of a unimodal distribution using R (Shapiro & Wilk 1965; R Core Team 2012). I log transformed the biomass data and created two datasets--samples including dead plants (any plants with no detectable biomass) and samples excluding dead plants. I executed a two-way ANOVA on the transformed data to test both the main effects and interactions of competitor and measured plant biomass. In order to see the effect of each interspecific

competition pair, I executed a one-way ANOVA comparing each competitor for each treatment. Finally, I conducted a Tukey's Highly Significant Difference (Tukey's HSD) test on each group using the Agricolae package in R (Felip de Mendiburu 2015). All of the ANOVAs were executed in R (R Core Team 2012).

In order to test if there were differences in survivorship between our treatments, I conducted a Pearson's X^2 heterogeneity test (Pearson 1900). I executed the test in R by testing the heterogeneity of all measured plants, all competitor plants, and the competitors against each species (R Core Team 2012). Additionally, I tested the relationship between percent survival and biomass without the dead plants to see whether both metrics were correlated. I ran a linear regression between the two variables in R (R Core Team 2012).

I measured competition effect and facilitation with the relative interaction index (RII) =(Bw-Bo)/(Bw+Bo), which is a robust index (Armas *et al.* 2004), where the treatment was the biomass of the plant of interest paired with a competitor (Bw) and the control (Bo) was the biomass of a plant paired against an individual of the same species. I measured the RII using four methods: with 50 pairwise measurements including dead plants, 50 pairwise measurements without dead plants, the pooled average plants including dead plants, and the pooled average without dead plants. For the pairwise index I used 50 random non-repeating pairwise comparisons between Bw and Bo.

I tested whether RII indices were significantly different from one another by comparing the median value of all four RII indices using a two-way ANOVA in R where the two main effects were competitors and measured plants (R Core Team 2012). I was only able to compare measured and competitor plants since each experimental category contained only one value.

Table 4.1. Experimental design of competition experiment. Each treatment was replicated 14 times. There were two plants in each pot. The control (Bo) was a plant grown with another individual of the same species and the treatment (Bw) was a plant grown with a plant of a different species.

		Competitor 1			
		POPR	NAVI	BOGR	PASM
Competitor 2	POPR	Bo=28	Bw=14	Bw=14	Bw=14
	NAVI		Bo=28	Bw=14	Bw=14
	BOGR			Bo=28	Bw=14
	PASM				Bo=28

Results

Overall, 43.44% of plants were alive at the end of the experiment. BOGR had the highest overall survival rate (53.78%), while POPR had the lowest (32.14%). PASM had an overall survival rate of 37.96% and NAVI had 49.88%. When comparing survival against paired competitors, POPR had the highest survival rate when paired with BOGR and the lowest against itself; NAVI had the highest survival rate when paired with NAVI and the lowest against POPR; PASM had the highest survival rate when paired with PASM and the lowest against POPR; BOGR had the highest survival rate when paired with BOGR and the lowest against PASM (Fig. 4.1; Table 4.2).

The overall X^2 heterogeneity test was significant for competitor plants (X^2=10.48 df=3, p-value=0.01499), but not significant for focal plants (X^2=5.80, df=3, p-value=0.1218). Meaning, the biomass of the focal plant when placed under competition with certain species is not random, but when the biomass of a focal plant is taken without consideration of the competitor it is random. On a finer scale, the X^2 heterogeneity tests within measured plant

categories were all not significant (Table 4.2). Finally there was no relationship between the percent survival and biomass without dead plants (R^2=.0000472, $F_{1,14}$=0.00066 p=0.9799).

The overall average biomass of the plants (without the dead plants) was 0.253 grams. In order from highest to lowest biomass was BOGR (0.30 g), NAVI (0.28 g), PASM (0.24 g), and POPR (0.19 g). POPR had the highest biomass when paired with PASM and the lowest with itself; NAVI had the highest biomass when paired with BOGR and the lowest with PASM; PASM had the highest biomass when paired with BOGR and NAVI and the lowest with POPR; and BOGR had the highest biomass when paired with NAVI and lowest with PASM (Fig. 4.3; Table 4.2).

The overall average biomass of the plants (including the dead plants) was 0.189 grams. From highest to lowest the average biomass for each plant species was BOGR and NAVI (0.23 g), PASM (0.16 g), and POPR (0.13 g). When comparing the paired plants, POPR had the highest biomass when paired with BOGR and the lowest with itself; NAVI had the highest biomass when paired with BOGR and the lowest with PASM; PASM had the highest biomass when paired with BOGR and NAVI and the lowest with POPR; and BOGR had the highest biomass when paired with NAVI and lowest with PASM (Fig. 4.2; Table 4.2).

Table 4.2. The average biomass for plants including dead plants and not including dead plants along with the percentage of plants that were alive or dead. The table includes standard deviation (SD), sample size (N), and standard error (SE).

Measured plant		***Poa pratensis***			**Measured plant**		***Pascopyrum smithii***		
Competitor	BOGR	POPR	PASM	NAVI	Competitor	BOGR	POPR	PASM	NAVI
Percent alive	50.00	21.43	28.57	42.86	Percent alive	50.00	28.57	51.85	40.00
Pearson's X^2 test	X^2=4.2738, df=3, p-value=0.2334				Pearson's X^2 test	X^2=2.3245, df=3, p-value=0.5078			
Biomass w/dead	0.32	0.15	0.24	0.25	Biomass w/dead	0.29	0.17	0.28	0.29
Median w/dead	0.37	0.13	0.14	0.22	Median w/dead	0.32	0.16	0.32	0.17
Tukey's assignment	a	a	a	a	Tukey's assignment	a	a	a	a
N	14.00	28.00	14.00	14.00	N	14.00	14.00	27.00	15.00
SE	0.06	0.03	0.08	0.06	SE	0.07	0.05	0.05	0.07
Biomass wo/dead	0.38	0.22	0.43	0.32	Biomass wo/dead	0.40	0.27	0.36	0.40
Median wo/dead	0.43	0.16	0.38	0.29	Median wo/dead	0.39	0.22	0.37	0.42
Tukey's assignment	a	a	a	a	Tukey's assignment	a	a	a	a
N	12.00	19.00	8.00	11.00	N	10.00	9.00	21.00	11.00
SE	0.05	0.03	0.10	0.07	SE	0.06	0.04	0.05	0.07
Measured plant		***Nassella viridula***			**Measured plant**		***Bouteloua gracilis***		
Competitor	BOGR	POPR	PASM	NAVI	Competitor	BOGR	POPR	PASM	NAVI
Percent alive	61.54	35.71	40.00	66.67	Percent alive	53.57	42.86	28.57	50.00
Pearson's X^2 test	X^2=4.8773, df=3, p-value=0.181				Pearson's X^2 test	X^2=2.5041, df=3, p-value=0.4745			
Biomass w/dead	0.17	0.08	0.06	0.16	Biomass w/dead	0.15	0.14	0.07	0.21
Median w/dead	0.12	0.08	0.05	0.16	Median w/dead	0.15	0.14	0.04	0.14
Tukey's assignment	ab	ab	b	a	Tukey's assignment	a	a	a	a
SD	0.14	0.06	0.05	0.08	SD	0.15	0.12	0.10	0.24
N	13.00	14.00	15.00	24.00	N	28.00	14.00	14.00	14.00
SE	0.04	0.02	0.01	0.02	SE	0.03	0.03	0.03	0.06
Biomass wo/dead	0.20	0.10	0.08	0.17	Biomass wo/dead	0.22	0.16	0.11	0.24
Median wo/dead	0.17	0.09	0.08	0.16	Median wo/dead	0.20	0.17	0.07	0.14
Tukey's assignment	a	ab	b	a	Tukey's assignment	a	a	a	a
SD	0.14	0.05	0.05	0.07	SD	0.12	0.11	0.10	0.24
N	11.00	11.00	12.00	22.00	N	19.00	12.00	9.00	12.00
SE	0.04	0.01	0.01	0.02	SE	0.03	0.03	0.03	0.07

The raw biomass of all plants including dead plants was not normal according to the Shapiro-Wilk normality test ($w=0.8589$, $p=3.79^{-15}$). Log transformation of the data improved normality ($w=0.92168$, $p=7.81^{-11}$). The raw biomass of all plants without dead plants was more normal than the raw biomass of plants including dead plants ($w=0.8889$, $p=2.835^{-11}$). When I plotted the histogram it did appear unimodal albeit skewed to the right (Figure G.1). Log transformation again improved normality ($w=0.97083$, $p=0.00026$) and the histogram appeared unimodal without skew (Figure G.1). Although ANOVA can still be fairly robust even when data is not normal (Glass *et al.* 1972; Harwell *et al.* 1992; Lix *et al.* 1996), I used the log transformed data without the dead plants for all reported ANOVAs (Table G.1-G.11). The results of ANOVAs on log transformed data with the dead plants are included in the appendix (Table G.12-G.22).

The two-way ANOVA of measured and competitor plants was significant for each main effect, but the interaction term was not significant (Table G.1). Tukey's tests indicated significant differences only between BOGR and both POPR and PASM as well as between NAVI and POPR and PASM. According to the one-way ANOVA on the competitors against each plant group, only NAVI was significant (Table G.10). PASM and POPR negatively affected NAVI's growth based on the two-way ANOVA (Table G.11).

Between the four RII measurements there were no significant differences ($F_{3,44}=0.003$, $p=0.999$). The two-way ANOVA indicated that measured plant identity was a significant effect, but competitor and the interaction between the two was not (Table G.24). Out of the measured plants, NAVI was significantly negatively affected by the presence of other plants and POPR was significantly facilitated by the presence of other plants (Table G.25). According to the RII numbers, overall, PASM and POPR are competitive with one another and POPR is facilitated by

many species (Fig. 4; Table 3). POPR was most greatly facilitated by BOGR. NAVI was negatively affected by POPR and PASM, but was not effected by BOGR. PASM was negatively affected by POPR, but was not affected by NAVI and BOGR. BOGR was negatively affected by PASM, but not NAVI or POPR.

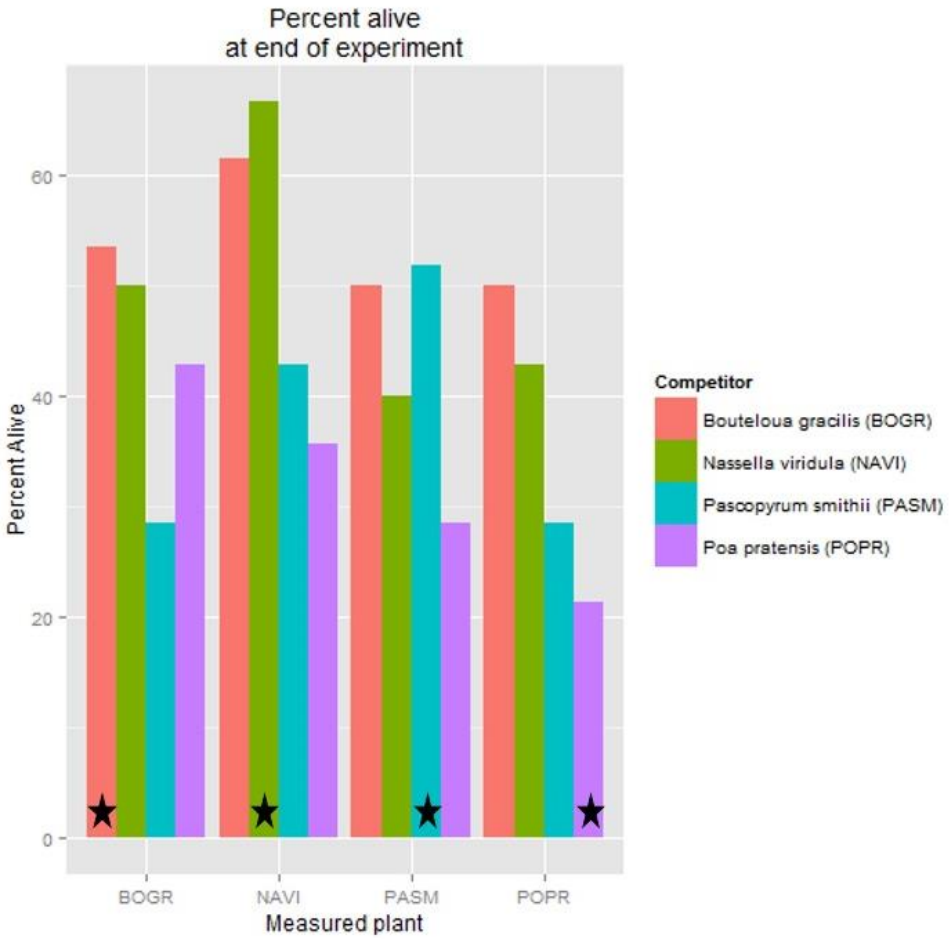

Figure 4.1. The percentage of plants alive at the end of the experiment. Black stars indicate conspecific pairings. The graph was represented in ggplot2 (Wickham 2009).

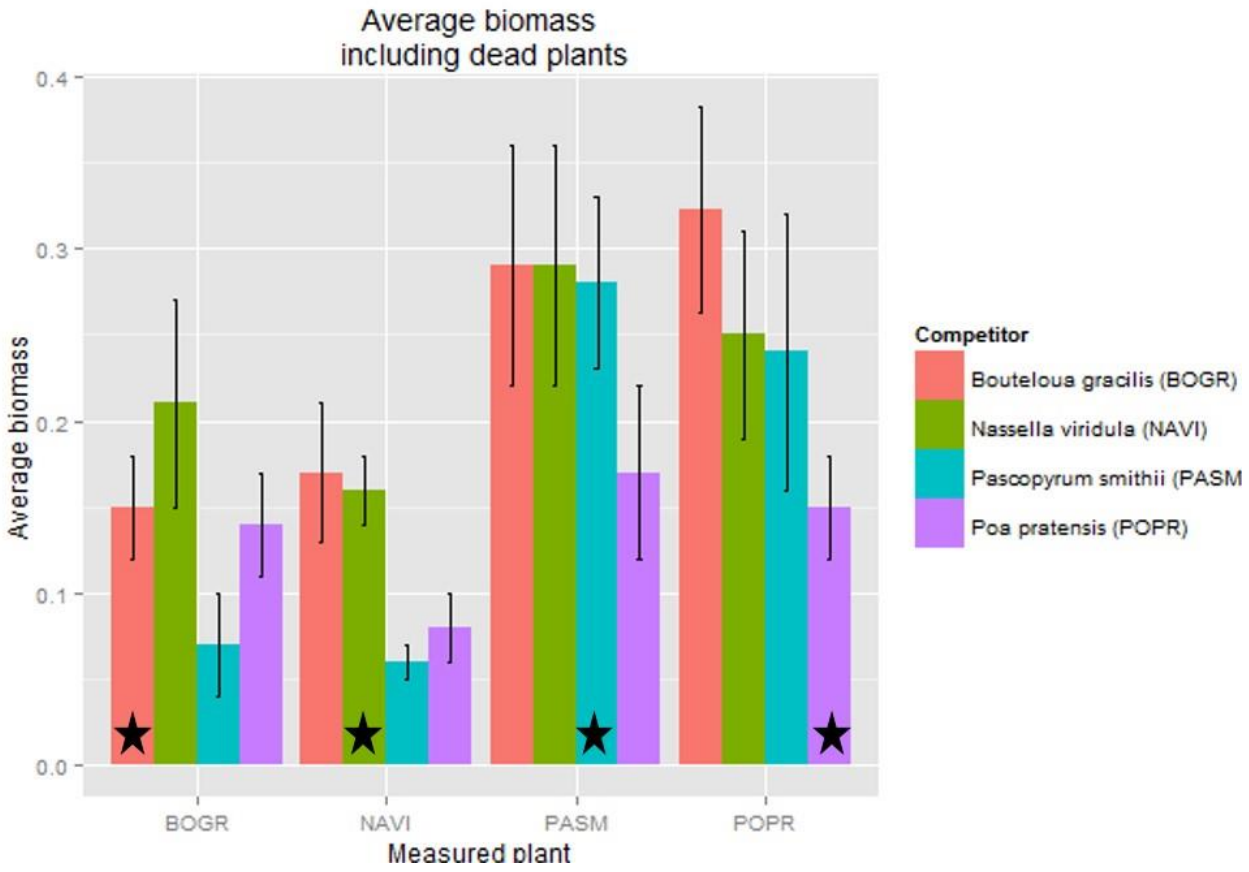

Figure 4.2. The average biomass for each plant competition pair including dead plants (measurements of zero). The bars represent $\pm$ 1 standard error. The graph was produced in ggplot2 (Wickham 2009).

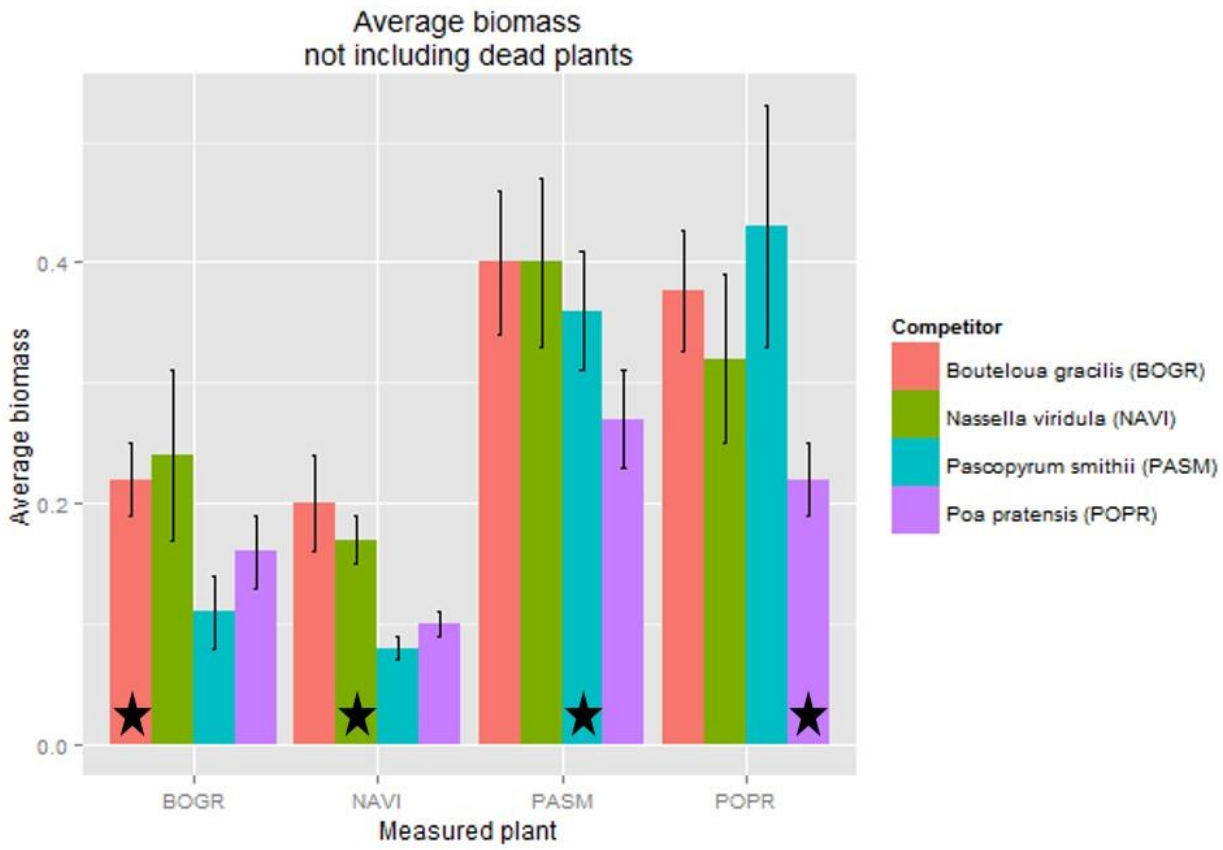

Figure 4.3. The average biomass of measured plants in all treatments not including dead plants (measurements of zero). The bars represent $\pm$ 1 standard error. The graph was produced in ggplot2 (Wickham 2009).

Table 4.3. The four RII statistic values including an average of the four and the median of the four RII statistics.

Measured plant	*Poa pratensis*			*Poa pratensis*			*Poa pratensis*		
Competitor	NAVI RII	SD	SE	PASM RII	SD	SE	BOGR RII	SD	SE
Including dead pairwise RII	0.26	0.68	0.10	-0.01	0.87	0.12	0.37	0.62	0.09
Not including dead pairwise RII	0.14	0.44	0.06	0.39	0.26	0.04	0.28	0.38	0.05
Including dead pooled RII	0.26	0.19	0.03	0.25	0.22	0.03	0.37	0.19	0.03
Not including dead pooled RII	0.19	0.17	0.03	0.33	0.21	0.04	0.27	0.17	0.03
Average	0.21	0.37	0.05	0.24	0.39	0.06	0.32	0.34	0.05
Median	0.22	0.32	0.05	0.29	0.24	0.04	0.33	0.28	0.04
Measured plant	*Nassella viridula*			*Nassella viridula*			*Nassella viridula*		
Competitor	POPR RII	SD	SE	PASM RII	SD	SE	BOGR RII	SD	SE
Including dead pairwise RII	-0.29	0.56	0.08	-0.38	0.55	0.08	-0.09	0.58	0.08
Not including dead pairwise RII	-0.25	0.28	0.04	-0.37	0.31	0.04	0.00	0.39	0.06
Including dead pooled RII	-0.34	0.08	0.01	-0.44	0.09	0.01	0.02	0.11	0.02
Not including dead pooled RII	-0.27	0.07	0.01	-0.38	0.08	0.01	0.06	0.10	0.02
Average	-0.29	0.25	0.04	-0.39	0.26	0.04	0.00	0.29	0.04
Median	-0.28	0.18	0.03	-0.38	0.20	0.03	0.01	0.25	0.04

Table 4.3. The four RII statistic values including an average of the four and the median of the four RII statistics (continued).

Measured plant	*Pascopyrum smithii*			*Pascopyrum smithii*			*Pascopyrum smithii*		
Competitor	POPR RII	SD	SE	NAVI RII	SD	SE	BOGR RII	SD	SE
Including dead pairwise RII	-0.19	0.74	0.10	-0.02	0.69	0.10	-0.01	0.72	0.10
Not including dead pairwise RII	-0.08	0.40	0.06	0.03	0.48	0.07	0.07	0.41	0.06
Including dead pooled RII	-0.24	0.23	0.04	0.02	0.26	0.04	0.01	0.24	0.04
Not including dead pooled RII	-0.15	0.20	0.04	0.05	0.23	0.04	0.05	0.21	0.04
Average	-0.16	0.39	0.06	0.02	0.41	0.06	0.03	0.39	0.06
Median	-0.17	0.31	0.05	0.02	0.37	0.05	0.03	0.33	0.05
Measured plant	*Bouteloua gracilis*			*Bouteloua gracilis*			*Bouteloua gracilis*		
Competitor	POPR RII	SD	SE	NAVI RII	SD	SE	PASM RII	SD	SE
Including dead pairwise RII	0.10	0.65	0.09	0.11	0.70	0.10	-0.23	0.79	0.11
Not including dead pairwise RII	-0.17	0.38	0.05	-0.03	0.49	0.07	-0.35	0.43	0.06
Including dead pooled RII	-0.03	0.14	0.02	0.16	0.18	0.03	-0.36	0.14	0.02
Not including dead pooled RII	-0.15	0.12	0.02	0.05	0.17	0.03	-0.33	0.13	0.02
Average	-0.06	0.32	0.05	0.07	0.39	0.06	-0.32	0.37	0.05
Median	-0.09	0.26	0.04	0.08	0.33	0.05	-0.34	0.28	0.04

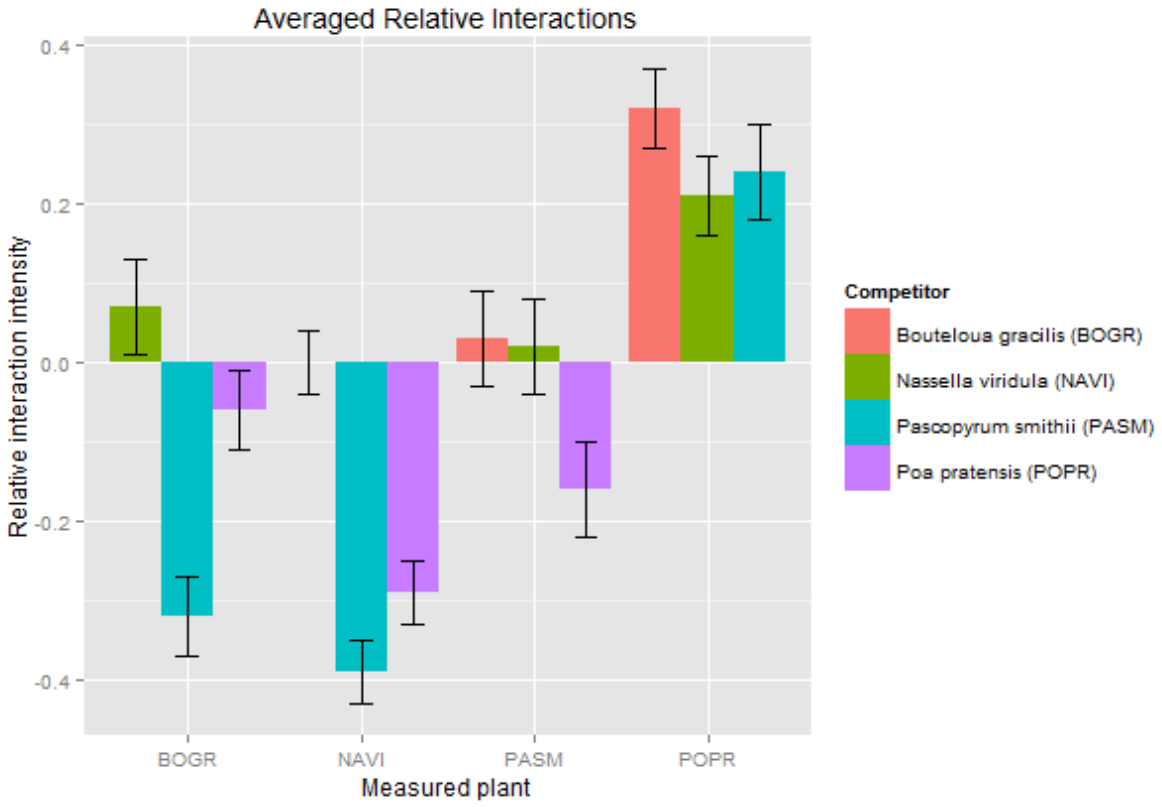

Figure 4.4. Mean RII organized by species paired (± 1 SE). A positive RII value implies that the measured species is facilitated by the competitor species and a negative RII indicates the paired species is competitive against the measured species.

Discussion

In this study, I sought to objectively measure whether POPR was competitive against three native plant species using aboveground biomass. BOGR and NAVI were not competitive against any other species and were not facilitated by their interaction with any other species based on the biomass ANOVA and RII; although, BOGR did have the highest survival rate compared to the other tested species. The high survival rate may be because the species were often grown in dry conditions because of the loamy soil and BOGR is a C_4 species. One study found that BOGR is twice as water efficient in dry conditions than PASM (a C_3 species), which

may be why BOGR had the highest survival rate of all four species (Monson *et al.* 1986). In our study, PASM only had a survival rate of 38% compared to BOGR's 54%. But when it came to PASM competition with BOGR, PASM successfully outcompeted BOGR. This result is consistent with a similar study in which BOGR and PASM were grown in competition with each other and both BOGR and PASM reduced each other's biomass (Samuel & Hart, 1992). There were differences in biomass for PASM when paired with BOGR, but RII of these interactions in my experiment indicated no real competition (Samuel & Hart 1992). Samuel and Hart did not calculate an interaction index and only reported biomass. In another study, BOGR growth was reduced by 60% in a natural prairie and by 50% in a PASM seeded prairie, while PASM was reduced by 30% by BOGR and by 50% in the PASM seeded community (Bakker & Wilson 2001).

Not as much is known about competition in NAVI. I found that NAVI was negatively affected by POPR and PASM. Counter to my results, a study found that NAVI frequency was positively associated with frequency in annual bromes and PASM, which suggests that PASM may not be competitive against NAVI in natural areas (Ogle & Reiner 2002). One possible disadvantage for NAVI may be the cutting at the beginning of the experiment. NAVI has been documented to perform poorly under heavy grazing (Reed 1961).

PASM successfully outcompeted BOGR and NAVI. This is expected since PASM is known to be a fairly competitive species (Samuel & Hart 1992; Bakker & Wilson 2001). My study may be a conservative measure of PASM competitiveness because, although I watered the plants as needed, the soil was often dry. The dry soil may have reduced the number of successful PASM individuals in our study since PASM is a C_3 species (Monson *et al.* 1986). PASM was

negatively affected by POPR in my study. Similarly, a study of plants grown in fertilized soil found that POPR was facilitated by PASM (Kanaan & Butler 2012).

My study found that POPR was facilitated by the three native species and competitive against NAVI. The relative facilitation of growth in POPR when it was paired with other species may be because POPR did not perform as well when it was grown with itself. One study found that *Poa pratensis* did not have much of a competitive effect on *Elymus canadensis* or *Bromus inermis* except when it was started before species (priority effect against *Elymus canadensis*; Ulrich & Perkins 2014). Other studies have indicate that POPR's competitive effect increases with the biomass of other species, supporting our finding that other species facilitate POPR invasion (Reader *et al.*, 1994). POPR is considered invasive and thought to be competitive against other species but the mixed results on competition suggest something more complicated is occurring. It is possible that POPR is more competitive only when there are high levels of nitrogen as demonstrated by previous studies (Wilson & Tilman, 1991).

In conclusion, it does appear that POPR is somewhat competitive, but not as competitive as PASM, while NAVI and BOGR appear to be negatively affected by the presence of competitors (Fig. 4.4). Our results may be partially driven by the clipping at the beginning of the experiment. The clipping may have stimulated POPR and PASM growth since they are classified increasers under grazing conditions (Weaver 1991). However, BOGR is also classified as an increaser (Weaver 1991) and did not perform well in this experiment under competition. This seemingly contradictive result may be caused by the early clipping in the experiment. BOGR is a C4 grass while POPR and PASM are C3 grasses, thus early clipping may have stimulated the cool-season grasses while stunting the C4 grasses. There has been some research that early intensive grazing can reduce POPR, but light or season long grazing may increase

POPR (Patton *et al.* 2013). Thus, it may be important for land managers to be cautious about time and intensity of grazing along with the competitive landscape in grasslands.

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CHAPTER 5. HIGHER PERCENT COVER OF *POA PRATENSIS L.* AND OTHER GRASSES IS CORRELATED WITH CLIMACTIC CHANGES IN THE TALLGRASS PRAIRIE OF THE NORTHERN GREAT PLAINS[3]

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Abstract

The effects of climate change are already observable in many regions. In the tallgrass region of the Northern Great Plains (NGP), they are being observed through increased annual precipitation and temperature. We quantified the composition of a tallgrass prairie in western Minnesota in order to better understand both plant cover changes and what environmental variables are correlated with these changes. We found a major shift from a forb to a grass dominated prairie, which was correlated with both fire management and an increase in precipitation in the region. We also found that the cover of *Poa pratensis* increased significantly and was associated with rising precipitation. Our study indicates that in the NGP, precipitation changes may be more of a driver of plant community changes than temperature changes.

Introduction

Over the past 40 years, the eastern tallgrass portion of the Northern Great Plains which includes eastern North Dakota, western Minnesota, and portions of Canada (hereafter NGP), has trended and is continuing to trend toward a climate higher in precipitation and annual temperature (Morgan *et al.* 2008; Millett *et al.* 2009; Werner *et al.* 2013). There was an increase in annual average precipitation from 1958-2008 of 5-15% in the NGP (U.S. Global Change

[3] Lauren Dennhardt wrote this manuscript, prepared the experimental design, organized field assistants, conducted the analysis, prepared graphs, and prepared the manuscript for publication. Other authors provided field assistance and editing help.

Research Program 2009). Precipitation in the spring and winter is projected to increase by another 10-30% by 2080 (U.S. Global Change Research Program 2009). In western Minnesota, the temperature has risen an average of 1.3°C over the last century with that rate increasing in recent decades (Minnesota Department of Health 2015). These climactic shifts have effects on the plant communities in the region including shifting flowering times for nearly a third of species (Dunnell & Travers 2011).

The vegetation of the NGP has adapted to periods of little rain fall with long, costly root systems (Weaver 1991). Typically, the NGP will undergo wet-dry cycles lasting 10-20 years in which succession between drought resistant and opportunistic species fluctuate (Weaver 1991; Valk 2005). However, the NGP is currently in a multi-decade higher precipitation trend (Valk 2005). This high precipitation trend may have serious implications for vegetation communities. In wetlands of the NGP, *Typha* species will dominate wet cycles and *Phragmites australis* (Cav.) Trin. ex Steud. will favor dry cycles (Valk 2005). This current high precipitation trend has increased *Typha glauca* in the region considerably since the 1960s (Valk 2005). There are historical reports on some of the wet-dry cycle changes in plant communities. It has long been documented that productivity on a grassland increases as precipitation levels rise (Branson 1985). Droughts were an important event in prairies that have led to an increase in the percent composition of native over invasive species (Weaver 1954), although there has been little research in recent decades on community shifts for terrestrial plant species in the region. Moreover, if climate predications are accurate and the wet-dry cycle has been disrupted, it is likely that vegetation communities will be altered. Annual temperature is projected to continue to rise in the region, which could desiccate wetlands if temperature changes outpace precipitation level increases (Johnson *et al.* 2005).

Since climate change may threaten biodiversity (Solomon *et al.* 2007; Primack & Miller-Rushing 2009), many land managers are expected to be confronted with plant community effects in the future. Mitigation of plant community composition is accomplished through a variety of management tools including burning, mowing, herbicide application, and grazing. These methods can ameliorate the undesirable effects of invasive species, climate change, and disturbance. As prairie management and climate change exert forces on the prairie in the future, successful management will depend on untangling separate effects (Hellmann *et al.* 2008).

Our goal in this study is to better understand different effects of management and climactic change on plant community composition in the NGP. In this paper, we compare current vegetation characteristics with past communities and examine correlations among the observed patterns. Additionally, we analyze both environmental and management treatment variables to determine how these two factors affect the vegetation community of a mesic tallgrass prairie.

Methods

Data Collection

In order to characterize the relationship between plant communities, climactic changes, and management history in a tallgrass prairie, we evaluated the plant cover of dominant plant categories at six plots at a 2,700 hectare tallgrass prairie preserve in Clay county, Minnesota (Bluestem prairie, Nature Conservancy, 46.844683, -96.463276). The six 25 X 25 m plots were originally studied in 1978, 1979, and 1999 and represent six different plant communities with variable burn histories and soil types (Table 5.1; Fig. 5.1; Dziadyk 1981; Miller 2000). From previous studies, we acquired percent plant cover and percent soil moisture data (Dziadyk 1981; Miller 2000).

Table 5.1. Description of soil type, parent material, dominant plant species for each plot. The dominant plant species were determined in 1978 and 1979 (Dziadyk 1981).

Plot	NRCS Soils	Parent material	Dominant plants	Years burned
1	Rockwell clay loam	Glaciolacustrine deposits over loamy glacial till	*Bouteloua gracilis* *Stipa spartea*	1977, 1996, 1999, 2003, 2008, 2012
2	Rockwell clay loam	Glaciolacustrine deposits over loamy glacial till	*Sporobolus heterolepis* *Schizachyrium scoparium*	1996, 2002, 2007, 2011
3	Foldahl loamy fine sand	Sandy glaciolacusrine deposits over loamy till	*Schizachyrium scoparium* *Sporobolus heterolepis*	1996, 2000, 2005, 2009
4	Rockwell clay loam	Glaciolacustrine deposits over loamy glacial till	*Andropogon gerardii* *Calamagrostis stricta*	1977, 1996, 1999, 2003, 2008, 2012
5	Fossum loamy sand	Sandy glaciofluvial deposits	*Carex* spp.	1996, 2000, 2005, 2009
6	Foldahl loamy fine sand	Sandy glaciolacusrine deposits over loamy till	*Elymus repens* Forbs	1996, 2000, 2005, 2009

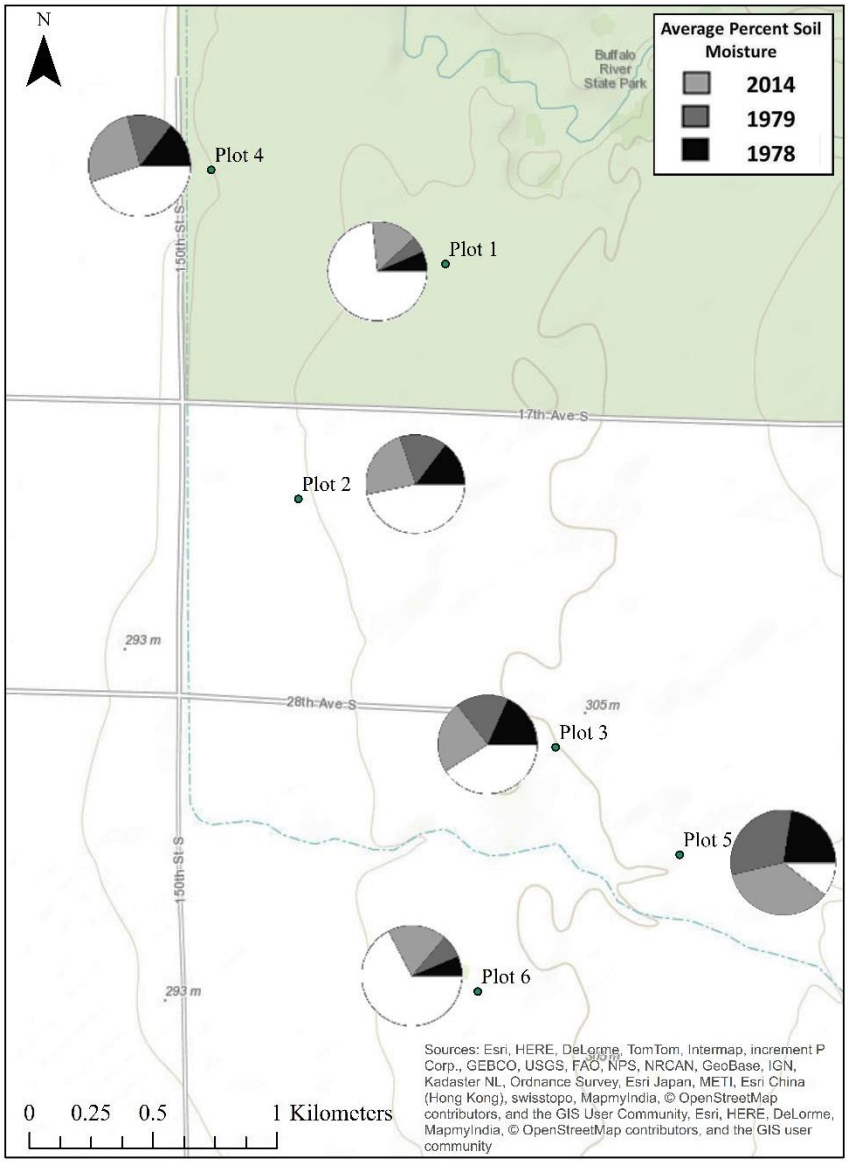

Figure 5.1. Plot location in Glyndon, Minnesota. The six locations were all on land managed by the Nature Conservancy. Each plot was 25 x 25 meters. The pie charts represent percent soil moisture in 1978, 1979, and 2014. We collected data twice from each plot in the summer of 2014.

In the summer of 2014 five of the original six plots were identified by the presence of metal poles that were placed at the plot corners in 1999 (Dziadyk 1981; Miller 2000). Plot six was not marked with poles because it was not sampled in 1999. We determined the location of plot six using coordinates from the 1978-79 study. Plots were sampled twice throughout the summer of 2014; once from June 9th to 13th and again from July 21st to the 24th. At each plot,

we copied the sampling protocol used in the past by systematically mapping and sampling 100 1m x 1m quadrats in a grid. There was an approximately 1m wide buffer between quadrats. A surveyor's flag was dropped pin-first at ten haphazardly chosen locations within each quadrat. The category of the plant or bare ground was recorded at each quadrat depending on the most basal point of contact with the pin. In 1978, 100 quadrats were sampled per plot; in 1979 and 1999 120 quadrats were sampled per plot. In each of these previous studies, plots were sampled once in late summer. In 2014, at the end of each sampling period at each plot we had 1000 individual data points, which resulted in a total of 12,000 data points.

Unlike the studies of these plots prior to 2000, which sought to characterize plant communities varying in dominant plant species, we were interested in changes in plant communities that may have occurred because of climactic changes or management. We chose to focus on the following six plant categories: *Spartina pectinata* Bosc ex Link (prairie cordgrass), *Poa pratensis* L. (Kentucky bluegrass), *Bromus inermis* Leyss (smooth brome), other graminoid species (members of Poaceae and the genus Equisteum; hereafter referred to as grasses), forbs, and members of the sedge family (Cyperaceae). We chose *Spartina pectinata* and sedges because both categories are wetland plants which perform well in high soil moisture conditions (Weaver 1991). *Poa pratensis* and *Bromus inermis* are invasive species that have been documented as dominant in many regions of the NGP (Bahm *et al.* 2011a; United States Department of Agriculture Natural Resources Conservation Service 2014). Additionally, we chose to categorize the differences between forbs and grasses in order to see large scale changes.

In addition to recording plant cover, we measured percent soil moisture at all six plots. We used a coring tool with a 7 cm column to iteratively collect soil samples at ten locations across each plot. Approximately 1,155 mL of soil were thus collected from depths of 0-30, 30-

60, and 60-90 cm each. These samples were then placed in plastic bags and returned to the lab in a cooler. On the same day as collection the soil samples were weighed, dried in an oven at 100°C for 48 hours, and weighed again. Percent soil moisture was calculated as the difference between wet soil mass and dry mass divided by the dry mass and multiplied by 100. Percent soil moisture was similarly measured at each depth at one location per plot in 1978 and three locations per plot in 1979. We collected ten cores per plot in order to ascertain a more representative average.

We also acquired data on temperature, precipitation, and snow accumulation for the region of the study. Daily values for each of these three variables were available from the National Climactic Data Center database (http://www.ncdc.noaa.gov/cag/time-series/us/32/00/pcp/12/06/1895-2014?base_prd=true&firstbaseyear=1901&lastbaseyear=2000) dating back to before the first study in 1978. The data originated from a weather station in Clay County, Minnesota located 8.4 kilometers from our study plots (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015). Elevation data was collected from the Minnesota Geospatial Information Office (Minnesota Geospatial Information Office 2010). Soil type data was from the Geospatial Data Gateway managed by the United States Department of Agriculture (Geospatial Data Gateway, https://gdg.sc.egov.usda.gov/). A list of all the data used in our full model can be found in Table 5.1.

Data analysis

We used the plant census data to calculate percent basal cover of the six plant categories at each plot in both early and late summer 2014. Percent basal cover was calculated as the total number of pin hits for a given plant category divided by the total number of pin drops at that plot multiplied by 100 (Silvy 2012). In order to choose which plant categories were to be included in

further analysis, we performed an ANOVA on percent cover estimates with year as the independent variable and a second ANOVA with plot as the independent variable. In this way we tested for spatial, temporal, and sampling period differences across plant basal cover as well as percent soil moisture. In order to not weaken our final model, we chose to only include variables that were significantly affected by either year or plot (in 2014 and across years) (McCune & Grace 2002). If a difference was significant, we explored the data further using Tukey's honest significant difference (HSD) test to decipher how years and plots were grouped for each plant and soil group. Both the Tukey's HSD and ANOVA were executed in R using the 'agricolae' package (Mendiburu 2012).

In order to identify correlations between percent cover estimates and environmental factors, we executed a distance based redundancy analysis (dbRDA). We sought to identify meaningful correlations between plant communities and environmental factors. A problem with any analysis of correlations between plant and environmental variables is covariation among individual variables. This is commonly remedied with a multivariate analysis such as a redundancy analysis (RDA) or canonical correspondence analysis (CCA), which simultaneously accounts for covariation among multiple variables while still performing multiple linear regressions allowing the user to decipher meaningful relationships. CCAs are criticized for using chi-square distance measurements and RDAs require data to be linear. We bypassed this linear requirement by using a distance-based RDA (dbRDA). Before a RDA is performed, the response matrix is transformed by calculating a constrained dissimilarity matrix, which creates a principal coordinate analysis (PCoA; Legendre & Anderson, 1999). This data transformation is necessary because a requirement of a RDA is for the data to be linear, which is rare in environmental data (McCune *et al.* 2002; Borcard 2011; Legendre 2012). We chose which

explanatory variables to include in the dbRDA by systematically adding variables to the dbRDA from our full list of explanatory variables until a model emerged with the most explanatory power (Table 5.2). This systematic model selection of variables included each permutation of order and inclusion/exclusion of every variable. We judged the power of our model by the value of our first two eigenvalues. For example, if adding an explanatory variable did not add any value to the eigenvalues we did not include that variable. The dbRDA was performed in 'vegan' using the CAPSCALE argument and a Bray-Curtis distance matrix (Oksanen *et al.* 2015). We assessed whether models were significant based on ANOVAs run on the whole model, the axes, and the explanatory variables with 200 permutations.

Table 5.2. Environmental variables included in full model of dbRDA. Variables were removed from the final analysis if they did not contribute to the eigenvalues.

Variable	Description
Plot	The 25m x 25m location at Bluestem Prairie sampled in 1978, 1979, 1998, 2014.
Year	The year data was collected.
Thirty	The percent soil moisture at 0-30 cm collected in 1978, 1979, and 2014.
Sixty	The percent soil moisture at 30-60 cm collected in 1978, 1979, and 2014.
Ninety	The percent soil moisture at 60-90 cm collected in 1978, 1979, and 2014.
AvePr	The average precipitation for five years prior to the year sampled (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
Spring	The average temperature for April through June in the sampling year (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
logElevation	The log of the elevation in meters (Minnesota Geospatial Information Office 2010).
logAGDU	The log of the average growing degree units (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
Precipitation	The average precipitation for the sampling year (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
Snow	The average snowfall for the sampling year (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
Temp	The average temperature for the sampling year (National Oceanic and Atmospheric Administration-National Climatic Data Center 2015).
Burn	Years since the last burn at each plot (The Nature Conservancy).
Soil	The soil type at the plot (Geospatial Data Gateway).

A dbRDA does not handle missing data well and since we did not have data for soil moisture from 1998, we ran a separate dbRDA on soil moisture. Because there were not many

explanatory variables (soil moisture at 0-30, 30-60, and 60-90 cm) and the number of explanatory variables cannot exceed the response variables, we split up the data into two groups—species level (POPR, BRIN, and Sedges) and functional groups (forbs and grasses). From those results, we executed a linear regression in R on the significant components when appropriate (R Core Team 2012).

Results

Spatial and temporal changes in plant communities and soil moisture levels

Both ANOVAs on year and plot revealed that percent cover of *S. pectinata* was not significantly affected by either component, so we removed it from further analysis ($F_{1,21}$=3.284; p=0.0843; $F_{5,17}$=1.135; p=0.0602). All other plant categories were significantly affected by one or both and thus remained in the analysis (Table 5.3).

Basal cover of most of our tested plant categories increased over the last four decades (Fig. 5.2). *Poa pratensis* and *B. inermis* cover were significantly affected by year where *P. pratensis* was higher in 2014 compared to other sampled years ($F_{1,21}$=15.33; p=0.0008; $F_{1,21}$=6.45, p=0.019; Table 5.3; Table H.1, H.2). Cyperaceae members did not change over the last four decades ($F_{1,21}$=3.985, p=0.059). The other change we documented was a shift from a forb to a grass dominated community (Fig. 5.3). Overall, the cover of grasses increased significantly in 2014 compared to previous years ($F_{1,21}$=43.12; p<.0001; S3). Soil moisture levels were significantly affected by year for soil depths of 30-60 cm and 60-90 cm, but not 0-30 cm ($F_{1,16}$=10.56, p=0.005; $F_{1,16}$=8.12, p=0.012; $F_{1,16}$=1.98, p=0.178; S4). For 30-60 cm the soil moisture content was higher in 2014 compared to other years (Table H.4).

Table 5.3. ANOVA in basal percent cover by each plant category by year and plot. Year was included as a random variable and plot was a fixed variable. *Spartina pectinata* was not significant for year or plot so it was not included in further analysis. Although sedges were not significant for the below categories, they were across plots for 2014 (Table H.5).

By year					
Plant category	df	SS	MS	F	P
POPR	1	1678	1678	15.33	0.0008*
Sedges	1	473.5	473.5	3.985	0.059^{NS}
SPPE	1	1.843	1.8434	3.284	0.0843^{NS}
BRIN	1	44.18	44.18	6.45	0.019*
Grasses	1	13864	13864	43.12	0.0001*
Forbs	1	15104.7	15104.7	37.972	0.0001*
By plot					
POPR	5	622	124.3	0.63	0.68^{NS}
Sedges	5	1317	263.41	2.711	0.056^{NS}
SPPE	5	5.967	1.1935	2.648	0.0602^{NS}
BRIN	5	47.03	9.406	1.135	0.38^{NS}
Grasses	5	217.6	43.52	0.0387	0.999^{NS}
Forbs	5	961.3	192.26	0.1512	0.977^{NS}

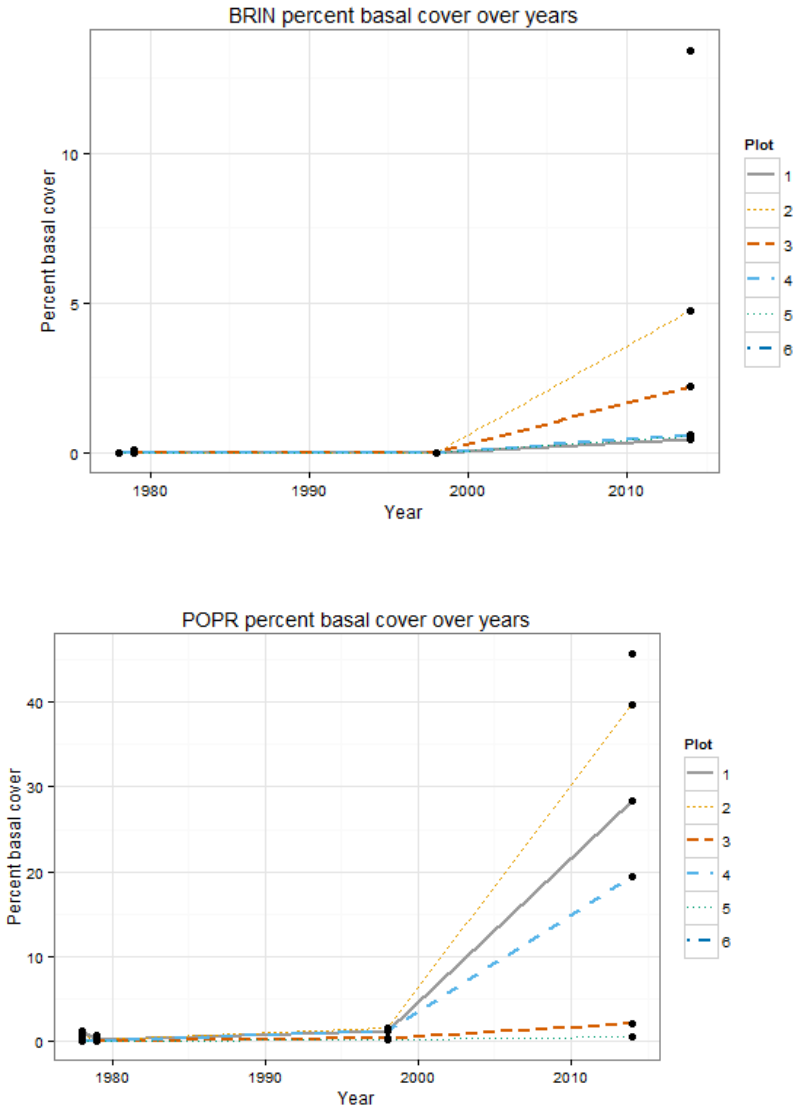

Figure 5.2. Percent cover of three plant categories over time. Estimates are based on the number of intercepts divided by the total number per plot per year. The graph was created in ggplot2 (Wickham 2009).

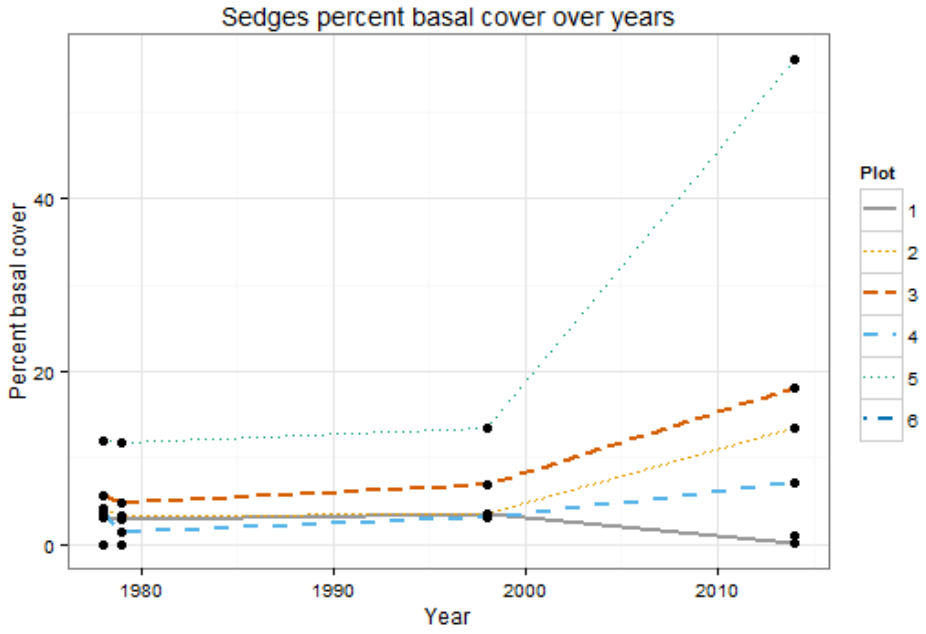

Figure 5.2. Percent cover of three plant categories over time (continued). Estimates are based on the number of intercepts divided by the total number per plot per year. The graph was created in ggplot2 (Wickham 2009).

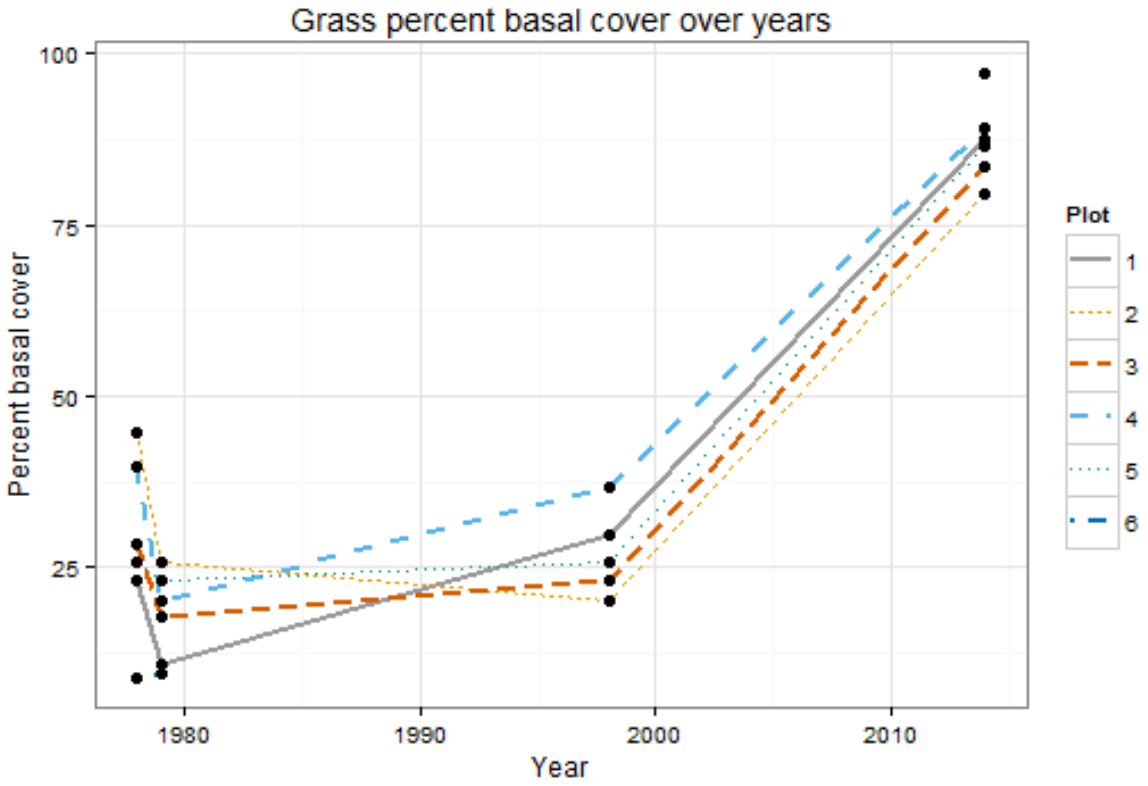

Figure 5.3. Grass percent basal cover at each plot including POPR, Cyperace, and BRIN. Estimates are based on the number of intercepts divided by the total number per plot per year. The graph was created in ggplot2 (Wickham 2009).

Plot differences were important for sedges and forbs in 2014 ($F_{5,5}$=86.192, p<0.001; $F_{5,5}$=6.291, p=0.0324). Cover of sedges was higher on plot five compared to other plots, but the Tukey's posthoc test produced no spatial separation for forbs (Table H.5; H.6). For all plant categories plot differences across years was not significant (Table H.1-H.3, H.5, H.6). Plot differences were found to be an important component in percent soil moisture both in 2014 and across years for 0-30 cm and 60-90 cm depths and for 2014 0-30 cm was significant as well (Table H.4, H.7).

In 2014, our plant measurements between early and late summer did not change significantly for all plant categories (S1-S3, S5, S6). There were significant differences for soil depths of 30-60 cm and 60-90 cm between the early and late sampling period in 2014 (S7).

Environment and cover correlations

The final dbRDA model contained precipitation, spring time temperature, plot, and years since the last burn. In west-central Minnesota, annual precipitation has increased while annual spring time temperature has decreased (Fig. 5.4). Precipitation, spring time annual temperature, and years since last burn were all significant at the 95% confidence level within our model (Table 5.4). Our only explanatory variable which was not significant was plot, but we kept it in the model because it did contribute to our eigenvalues. We had three axes that were significant, but the third only accounted for 3.5% of the variance so it was not analyzed (Legendre et al., 2011). Our first two axes accounted for a total of 73% of the variance.

Environmental variables did correlate with some plant species in our overall dbRDA (Fig. 5.5). *Poa pratensis* demonstrated a positive relationship to annual precipitation and plot six. Cyperaceae is correlated with annual spring temperature. Forbs are negatively correlated with grasses and annual precipitation, while grasses are positively correlated with annual precipitation. Two to three years after a burn, is correlated with grasses more so than forbs. Whereas, forbs are more closely associated with one year after a burn or zero (never has been burned). *Bromus inermis* did not show an association with any variables.

The dbRDA on just soil moisture was significant for *P. pratensis*, *B. inermis,* and Cyperaceae ($F_{1,16}$=3.12, p=0.003; S8). It was not significant for the forb and graminoids matrix ($F_{3,14}$=2.38, p=0.092; S8). We removed 0-30 cm and 60-90 cm from the species model because it did not contribute to the eigenvalues. The dbRDA was significant for only 30-60 cm soil

moisture levels for both dbRDAs ($F_{1,14}$=6.70, p=0.021; $F_{1,16}$=3.12, p=0.01). Because only the first axis on both dbRDAs had any explanatory power we conducted a linear regression on each plant category and the only significant soil moisture level which was 30-60 cm. Only sedges and grasses/forbs displayed a significant positive correlation (Fig. 5.6).

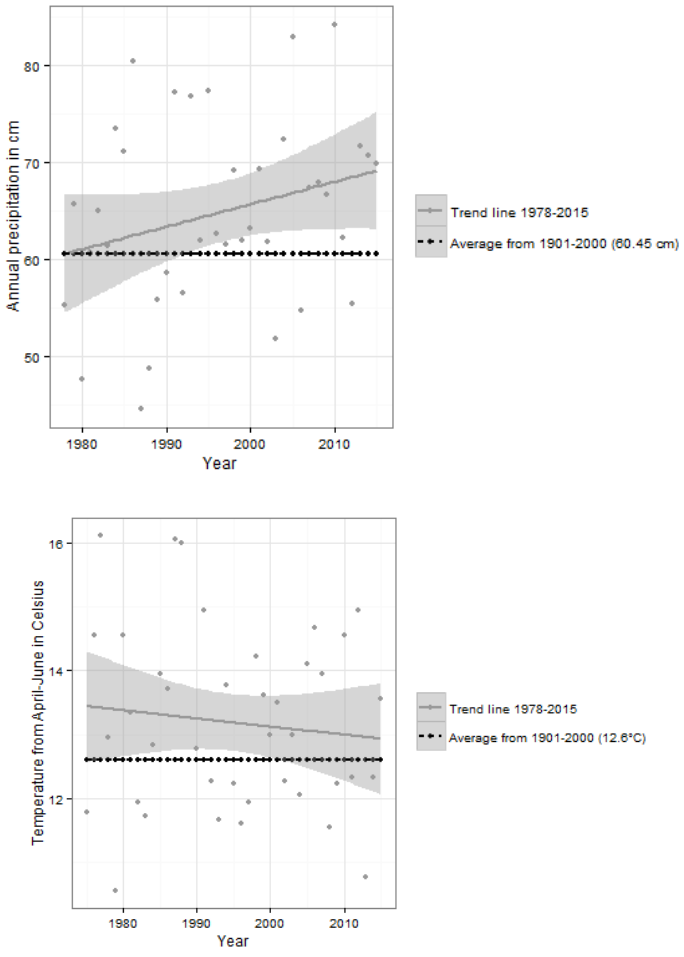

Figure 5.4. Average spring temperature and average annual precipitation by year from multiple weather stations in west-central Minnesota. Data was collected from NOAA. Precipitation r^2=0.072, $F_{1,36}$=2.80, p=0.10 and annual spring time temperature r^2=0.001, $F_{1,39}$=0.468, p=0.498. (http://www.ncdc.noaa.gov/cag/time-series/us/21/4/pcp/12/12/1975-2015?base_prd=true&firstbaseyear=1901&lastbaseyear=2000&trend=true&trend_base=10&firsttrendyear=1975&lasttrendyear=2015)

Table 5.4. The ANOVAs for model including all environmental variables. The data includes the overall model, explanatory variables, and individual axes. Each ANOVA was permuted 999 times within the 'vegan' package.

Overall model				
	Df	Variance	F	p-value
Model	11	3.78	5.48	0.001
Residual	11	0.69		
Explanatory variables				
Precipitation	1	1.47	23.49	0.001
Spring Temp	1	0.57	9.07	0.002
Plot	5	0.52	1.66	0.139
Years since last burn	4	1.22	14.86	0.001
Residual	11	0.69		
Individual Axes				
CAP1	1	2.95	47.18	0.001*
CAP2	1	0.31	4.98	0.001*
CAP3	1	0.16	2.52	0.019*
CAP4	1	0.07	1.19	0.280
CAP5	1	0.06	0.99	0.405
CAP6	1	0.05	0.84	0.622
CAP7	1	0.05	0.72	0.743
CAP8	1	0.03	0.54	0.904
CAP9	1	0.03	0.51	0.904
CAP10	1	0.03	0.44	0.956
CAP11	1	0.02	0.37	0.973
Residual	11	0.69		

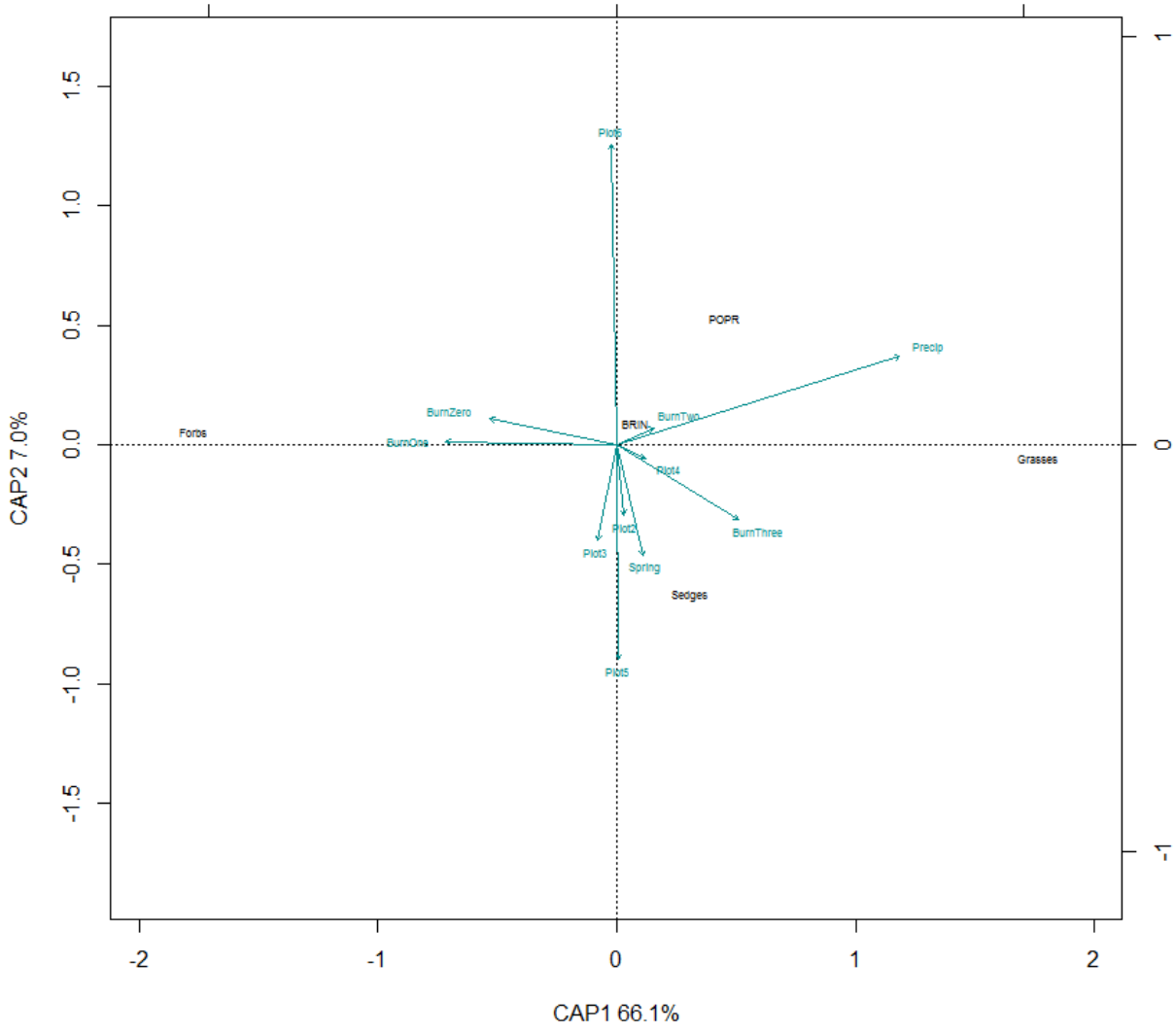

Figure 5.5. Distance based redundancy analysis (dbRDA) on selected for environmental and plant data using a Bray-Curtis dissimilarity matrix. CAP1 and CAP2 were both statistically significant and account for 73.1% of the total variance.

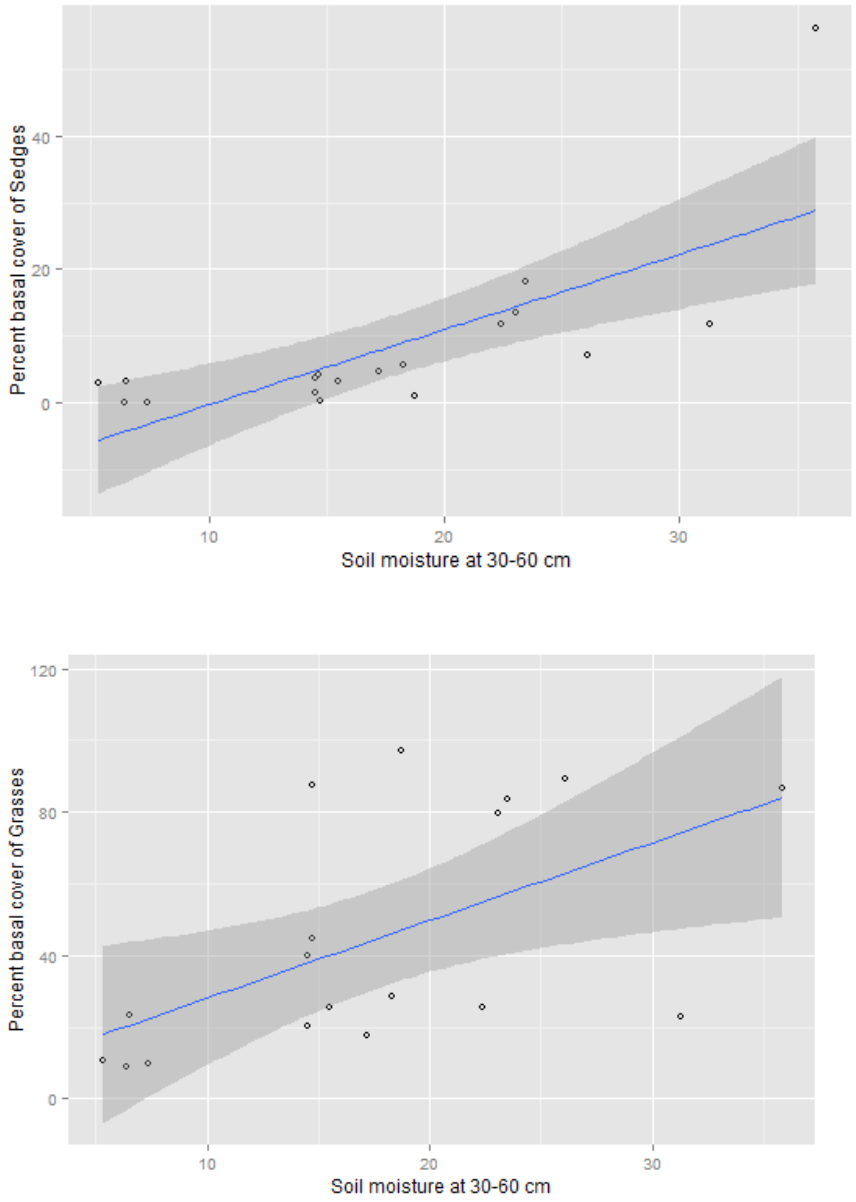

Figure 5.6. Percent basal cover of sedges and grasses as a function of soil moisture at 30-60 cm. Best fit regression lines and 95% confidence intervals are indicated. Significant linear regressions on 30-60 cm in all plots and all years. Percent soil moisture and plant cover for sedges (r^2=0.5418, SE=9.074, $F_{1,16}$=18.92, p<0.001) and grasses (r^2=0.32, SE=27.65, $F_{1,16}$=12.89, p=0.01).

Discussion

Our dbRDA attributed two major explanatory variables to the conversion from a forb to grass dominated community—fire management and rising precipitation levels. The productivity of grasses often increases with fire management. When regular fire management is absent from a tallgrass prairie, it is often dominated by forbs or woody species (Gibson & Hulbert 1987; Vinton *et al.* 1993; Briggs & Knapp 2001; Peterson *et al.* 2007). Because the Nature Conservancy has burned the prairie every four years the cumulative effect of management has likely increased the cover of grasses, which can be seen in our study (Fig. 5.5).

In our analysis, annual precipitation is a stronger explanatory variable than fire management. Evidence of precipitation regimes affecting forb versus grass dominated grasslands can be found during the Holocence (Clark *et al.* 2002). At the time the NGP was arid and dominated by forb species rather than grasses, which supports the opposite trend of what we are currently observing (Clark *et al.* 2002). Furthermore, a modern comparison of the Great Plains with the Great Basin verified that grass cover was positively correlated with higher levels of summer precipitation (Cook & Irwin 1992). Studies that manipulated precipitation regimes consistently support C4 grasses favoring higher levels of precipitation (Nie *et al.* 1992; Collins *et al.* 2012). C3 grasses have been found to increase under higher precipitation levels as well, but only when CO_2 concentrations were also increased (Nie *et al.* 1992). This same study found that C4 grasses increase in frequency under only increased precipitation (Nie *et al.* 1992). Collins et al., highlighted the strongest positive response to increased precipitation in a mesic prairie were C4 grasses. Our results are consistent with previous findings of increased grass cover associated with increased precipitation in a prairie community. Both the fire and precipitation levels may account for the extreme shift from a forb to grass dominated community we documented.

The positive relationship we found between percent grass cover and percent soil moisture (30-60 cm) was found in another tallgrass prairie study where the authors compared percent soil moisture with annual aboveground biomass of grasses (Briggs & Knapp 1995). Sedges also showed a strong positive relationship with percent soil moisture in our study, perhaps because the sedge species we commonly encountered may have been hydrophilic. Most of the interactions we tested with our plant communities and percent soil moisture proved to be statistically insignificant. It is possible that our comparison of percent soil moisture and some plant community characteristics were not significant because soil moisture may have been more dependent on soil type rather than precipitation levels.

Changing temperatures may play a role in the spread of some species in our study. Our climate dbRDA did indicate a relationship between basal cover of members of the Cyperaceae and spring annual temperature (Fig. 5.5). Most (63%) sedges are C3 species (Bruhl & Wilson 2007). However, previous studies have not found that C3 grass species respond positively to climate changes (Owensby *et al.* 1999; Epstein *et al.* 2002). Predictive climate change models focusing on vegetation characteristics have forecasted a 10-20% increase of C4 grasses and a 10-20% decrease of C3 species when considering precipitation, temperature, and seasonality in North and South America (Epstein *et al.* 2002). One untested possibility for the trend we observed with Cyperaceae is an increase of CO_2 in the atmosphere. A study comparing Cyperaceae grown in ambient and twice ambient conditions found that Cyperaceae nearly doubled in percent basal cover under increased CO_2 conditions (Owensby *et al.* 1999). Another relationship we discovered was that basal cover of Cyperaceae was strongly correlated with plot five. Plot five was located in a low elevation area that was extremely wet, which likely provided ideal growing conditions for Cyperaceae.

The increase in *P. pratensis* we found over time follows regional trends. An increase in *P. pratensis* invasion has been documented by many studies (Cully *et al.* 2003; Grant *et al.* 2009b; DeKeyser *et al.* 2013b, 2015; O'Brien 2014; Toledo *et al.* 2014a). Notably, one survey from 2014 found that 20-35% of rangelands consisted of more than 50% soil surface cover of "invasive bluegrasses", which includes both *Poa pratensis* and *Poa compressa* L. (Canada bluegrass; United States Department of Agriculture Natural Resources Conservation Service 2014). Our analysis indicated a positive relationship between annual precipitation levels and *P. pratensis.* In one study, under increased precipitation and CO2 levels, *P. pratensis* increased in frequency (Nie et al., 1989). Further evidence that *P. pratensis* is increasing because of precipitation is a study from 1954 where a heavily invaded prairie consisted of over 50% *P. pratensis* in 1937, but after a three year drought, *P. pratensis* dropped to 3% (Weaver 1954). Since the NGP is higher in precipitation now compared to the past 100 years, *P. pratensis* may be increasing in frequency due to precipitation levels.

Although most climate studies on plant communities focus on changes in temperature, annual growing degree days and phenology, changes in precipitation may be more consequential in some areas. We conclude that the increasing annual precipitation in the NGP over the last 20 years has impacted the plant composition of the prairie. Although land managers may be able to reverse some of these climactic effects with prescribed burning or grazing, it does indicate as long as the NGP continues this higher precipitation trend, intense management should be maintained. The major caveat of our study is that we only observed one grassland preserve. More long-term data in the NGP is needed to draw major conclusions. As for the future, predictions of precipitation regimes are variable, although for northern climates the general

prediction is increased precipitation (Johnson *et al.* 2005, 2010). Overall, increased precipitation may increase the presence of invasive grass species in the NGP.

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CHAPTER 6. CONCLUSIONS

The goal of this dissertation was to specify the reasons *Poa pratensis* is invading plant communities in the NGP. The list of potential reasons include: climactic changes, human disturbance, adaptation, or some combination of the three. I have presented evidence that *P. pratensis* performs well in competition experiments and that rising precipitation levels are correlated with increased *Poa pratensis* frequency in the region.

Poa pratensis invasion is at least partially a result of increased precipitation in the NGP (Chapter 5). In addition to a correlation between annual precipitation and *P. pratensis* frequency, there is plenty of evidence from the literature that *P. pratensis* is limited by water availability. As mentioned earlier, the major invasion shift in ND is the westward movement of *P. pratensis* into mixed grass prairie. Western North Dakota had an average annual precipitation level of 406 mm from 1901-2000 and has been rising by +63.5mm/decade from 1895 to 2014 (National Oceanic and Atmospheric Administration 2014). The average precipitation from 2000-2014 in Western North Dakota has been 443mm (National Oceanic and Atmospheric Administration 2014). This rise is notable since *P. pratensis* grown in lawns need at least 400 mm of precipitation a year (Bush 2002) for successful growth. Further supporting the link between precipitation and invasion are studies that indicate *P. pratensis* competes better under increased precipitation (e.g. Nie *et al.* 1992), along with historical data supporting this trend (Weaver 1954). One aspect that is lacking is reliable long-term data on *P. pratensis* in the NGP, but there is currently work being conducted on resampling plots from the 1970s (Personal communication, John Hendrickson and Cami Dixon). Although, looking at the available data for the change in precipitation and *P. pratensis* at multiple sites in ND there is a visible connection between precipitation and grass frequency (Fig. 6.1).

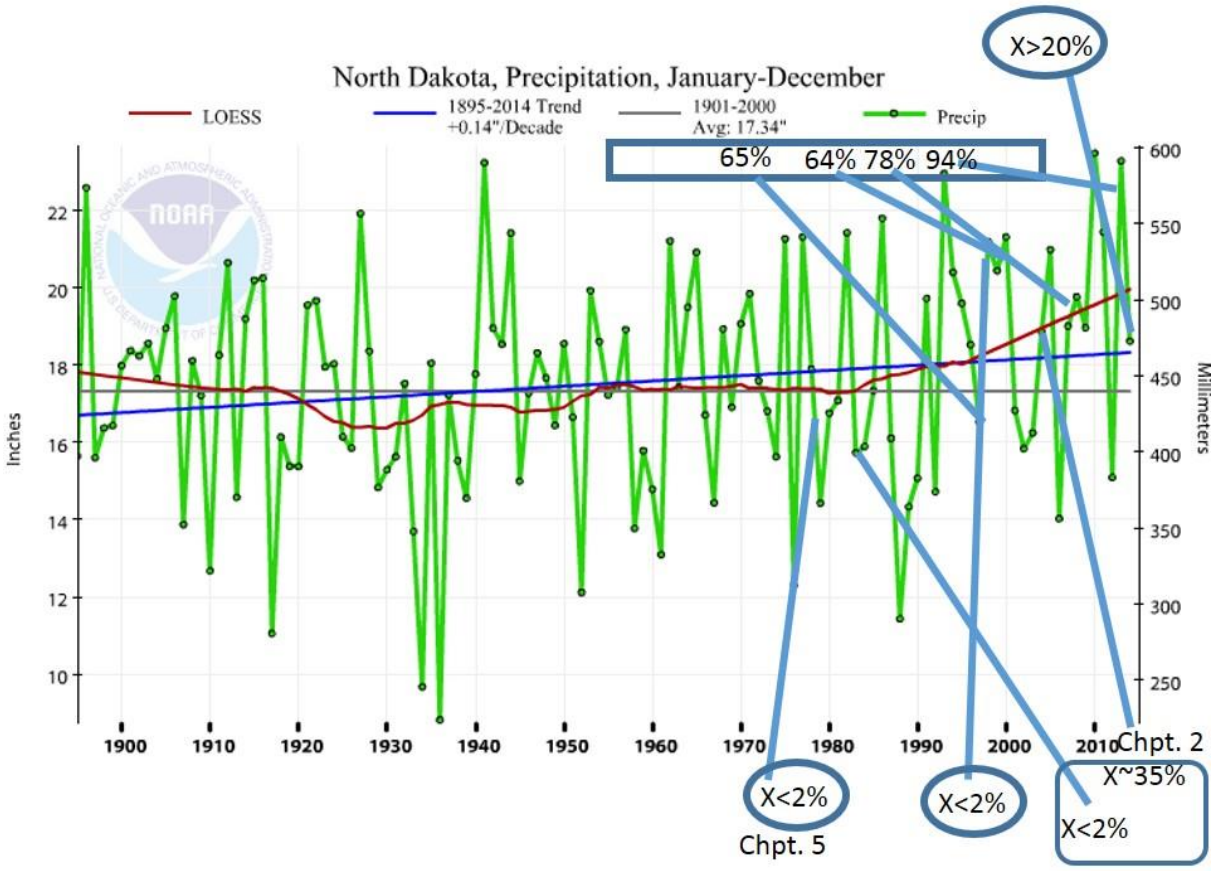

Figure 6.1. The annual precipitation for the state of North Dakota plotted from 1895-2015 with an 1895-2015 trend line (blue line), a LOESS (locally weighted scatterplot smoothing; red line), and the average between 1901-2014 (flat gray line). The percentages on this figure are estimated percentages at which *P. pratensis* was found in each study: the percentages in the blue circle are from chapter five of this dissertation, the two percentages in the rounded square are from chapter two, and the four percentages in the square are from O'Brien 2014.

Further support for climactic changes influencing the change in *P. pratensis* frequencies comes from a study of a grassland at the military training base Camp Grafton in Ramsey County, ND. O'Brien found that levels of *P. pratensis* increased in frequency since the 1990's (O'Brien 2014). From 1998-2001 *P. pratensis* composed 65% of the percent cover of the grassland. However, in 2011-2013 it composed 93.8% on the upland site, remained steady at the midland site, and rose from 58.1% to 86.5% at the lowland site. This study attributed the change in *P.*

pratensis to increases in precipitation, annual growing degree days, and temperature (O'Brien 2014). One of the major differences between our studies is that I used a methodology in which environmental variables were selected whereas his study kept all variables in the model. This means, that in my study the stronger covariate is the one that is chosen to stay in the model—in my case precipitation.

It is possible that the increase in annual temperature in the region may also be contributing to invasion. Priority, the start of growth at an earlier time, has been shown to give *P. pratensis* a competitive advantage (Ulrich & Perkins 2014). Since *P. pratensis* is an early emerging species and germinates in fall, it is logical to assume that the increased numbers of growing degree days in the region provide a growth advantage relative to other species. This hypothesis needs further empirical study.

There is evidence for other contributing factors in *P. pratensis* invasion that were not addressed in this thesis such as soil type and land use. From other studies we know that *P. pratensis* performs well on loamy soil (Klempel 2015) which is a soil type found extensively throughout North Dakota (Yang *et al.* 2007). There is also research that indicates that traditional grazing practices which discourage ranchers from grazing too early in the season allow for increased levels of invasion (Patton *et al.* 2013; Hendrickson & Printz 2015).

Finally, the work described here led to multiple rejected hypotheses. The most notable was the lack of evidence for adaptation by *P. pratensis* that was presented in Chapter three. I found no evidence of detectable geographic patterning in the population genetics of this species. This conclusion led me to the consideration of an environmental shift being a cause for invasion. Another hypothesis rejected in Chapter three was that invasion was occurring because of propagule pressure. There was virtually no genetic overlap between the tested cultivars and wild

individuals; the amount of nuclear genetic diversity points to a long history of *P. pratensis* presence in the prairie. The other rejected hypotheses is that *Poa pratensis* is extremely competitive. Although it was facilitated by native species, it was less competitive relative to other native plant species in paired experiments.

One certainty is that over the past century, *Poa pratensis* has become a major portion of the prairie. This is evidenced from a few important places—the literature, reports from land managers, and warnings from senior ecologists in the region. Whether the cause of invasion is a climactic shift in temperature and precipitation or changing land-use, management strategies will need to be more deliberate and extensive in the future. North Dakota's west is a major cattle ranching territory and efforts should be maintained to increase high-intensity spring grazing and/or frequent burn regimes to keep maintain the tallgrass and mixed grass prairie. Both management strategies have been shown to be effective and will be needed in the future (Hendrickson & Lund 2010; Patton *et al.* 2013).

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APPENDIX B. SUPPLEMENTARY MATERIAL FOR CHAPTER 3

The methodology and calculation used for calculating a mantel test on wind direction

In order to test the hypothesis of whether gene flow could be explained by predominant wind direction in June, we ran a Mantel test on wind direction and our pairwise Rho^{ST} values.

We tested whether wind pollination may explain the population landscape by first calculating the bearing between all tested NWRs in the study. We then calculated the predominant wind direction in June using nearby historical data for all sites. The North Dakota sites were the most robust. We picked the four weather stations closest to the NWR, calculated the average wind direction from 2001-2011, then found the average of the four sites. In South Dakota, the data was more limited. We took the closest average wind direction for June in 2002 or 2005 depending on what was available. We calculated the average wind direction using the equation below.

We first calculated u and v.

u = -wspd*sin(wdir)

v = -wspd*cos(wdir)

We then calculated the monthly mean for each month by calculating uave and vave.

We then transformed the data to wspd and wdir.

rad=4.0*atan(1.0)/180

wspd=sqrt(uave^2+vAve^2)/rad+180

We then calculated a matrix representing a coefficient of similarity between compass bearing and wind direction between two sites. We took the bearing between two points and separately calculated the least difference between the bearing and the wind direction of the first

site. Then we did the same for the second site. We took the two calculated numbers and added them together. We then ran two mantel tests. The first was on our wind direction and compass bearing similarity matrix and the pairwise RhoST values. The second mantel test was the same, but it was a paired Mantel test and included a distance matrix.

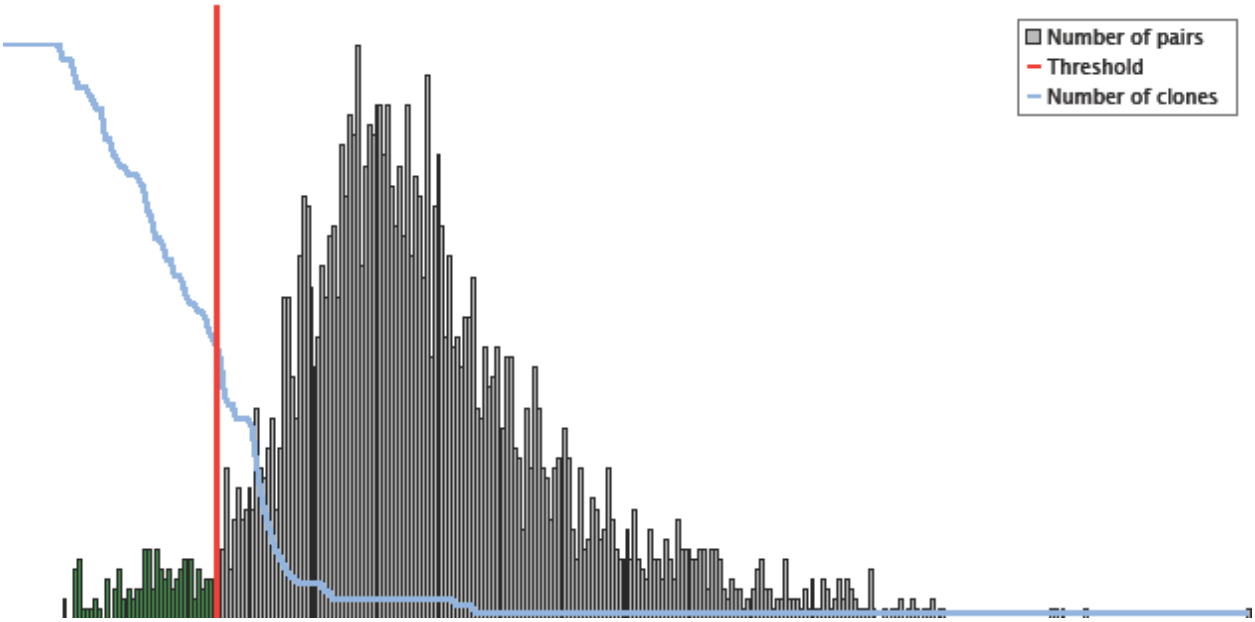


Figure B.1. The histogram showing the cutoff point for what a clone is considered to be using Genodive. The red line is the chosen threshold between the two bimodal peaks.

Table B.1. Paired F_{ST} values based on 5000 permutations calculated in SpageDi. Highlighted values with asterisk indicate a p-value of >0.05, thus non-significant values. P-values are listed below black bars.

	F_{ST} values								
Populations	Lostwood, ND	Souris, ND	Arrowwood, ND	Tewaukon, ND	Sandlake, SD	Hyde, SD	Madison, SD	Lake Andes, SD	Common Cultivars
Lostwood, ND		0.051*	0.048*	0.089*	0.065*	0.099*	0.084*	0.075*	0.154*
Souris, ND	0.038		0.000	0.035	0.023	0.049	0.010	0.053*	0.093*
Arrowwood, ND	0.025	0.361		0.042*	0.021	0.054*	0.016*	0.055*	0.110*
Tewaukon, ND	0.007	0.078	0.032		0.052*	0.127	0.047	0.104*	0.127*
Sandlake, SD	0.001	0.302	0.324	0.008		0.087*	0.034	0.064*	0.124*
Hyde, SD	0.006	0.072	0.040	0.000	0.002		0.087*	0.027	0.176*
Madison, SD	0.001	0.880	0.635	0.077	0.123	0.004		0.105*	0.104*
Lake Andes, SD	0.009	0.029	0.009	0.000	0.005	0.265	0.000		0.179*
Common Cultivars	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	

Table B.2. Paired G_{ST} values based on 5000 permutations calculated in SpageDi. Highlighted values with asterisk indicate a p-value of >0.05, thus non-significant values. P-values are listed below black bars.

	G_{ST} values								
Populations	Lostwood, ND	Souris, ND	Arrowwood, ND	Tewaukon, ND	Sandlake, SD	Hyde, SD	Madison, SD	Lake Andes, SD	Common Cultivars
Lostwood, ND		0.047*	0.030*	0.074*	0.048*	0.068*	0.043*	0.053*	0.119*
Souris, ND	0.009		0.026*	0.051*	0.029*	0.074*	0.035*	0.051*	0.117*
Arrowwood, ND	0.217	0.318		0.046*	0.027*	0.054*	0.033*	0.046*	0.099*
Tewaukon, ND	0.000	0.005	0.01		0.058*	0.111*	0.044*	0.089*	0.124*
Sandlake, SD	0.006	0.187	0.249	0		0.074*	0.036*	0.049*	0.118*
Hyde, SD	0.009	0.009	0.035	0.001	0.003		0.082*	0.019*	0.160*
Madison, SD	0.044	0.15	0.226	0.051	0.128	0.003		0.084*	0.105*
Lake Andes, SD	0.035	0.024	0.049	0.001	0.029	0.381	0.001		0.155*
Common Cultivars	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

Table B.3. Allele lengths for each locus for each sample. A "-9" indicates missing data in which a peak was detected but unreadable. Many samples were sent in more than once for consistency tests. Site Code meanings are available in Table 3.1. Samples were named based upon site, transect number, and location on transect.

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW1	A2.8	28	292							
TW1	A2.8	28	-9							
TW1	A2.8	28	292							
TW1	A3.2	28	286	292	304					
TW1	A3.2	28	286	292						
TW1	A3.2	28	286	292	304					
TW1	A3.8	28	270							
TW1	A3.8	28	270	292						
TW1	A4.2	28	-9							
TW1	A4.2	28	270							
TW1	A5.0	28	270	304						
TW1	A5.0	28	270	304						
TW1	A5.0	28	270	304						
TW1	A2.8	21	-9							
TW1	A2.8	21	181							
TW1	A2.8	21	173	181						
TW1	A3.2	21	-9							
TW1	A3.2	21	179							
TW1	A3.8	21	179	186						
TW1	A3.8	21	179	186	196					
TW1	A4.2	21	181	184						
TW1	A4.2	21	181	184						
TW1	A5.0	21	181							
TW1	A5.0	21	181	183						
TW1	A5.0	21	181	183						
TW1	A2.8	23	-9							
TW1	A2.8	23	302	312						
TW1	A2.8	23	302	312						
TW1	A3.2	23	286	291						
TW1	A3.2	23	286	291						
TW1	A3.8	23	329							
TW1	A3.8	23	312	320	327	329				
TW1	A4.2	23	293							
TW1	A4.2	23	288	293						
TW1	A5.0	23	290	293						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW1	A5.0	23	290							
TW1	A5.0	23	290							
TW1	A2.8	8	-9							
TW1	A2.8	8	200	208	216	226				
TW1	A2.8	8	-9							
TW1	A2.8	8	178	200	208	216	226			
TW1	A3.2	8	214	218	228	269				
TW1	A3.2	8	214	218	228	269				
TW1	A3.8	8	212	216	269					
TW1	A3.8	8	206	212	216	228	239	269		
TW1	A4.2	8	172	203	214	269				
TW1	A4.2	8	172	203	214	239	269			
TW1	A5.0	8	208	222						
TW1	A5.0	8	200	208	222					
TW1	A5.0	8	200	208	222					
TW1	A2.8	9	-9							
TW1	A2.8	9	301							
TW1	A3.2	9	299							
TW1	A3.2	9	299							
TW1	A3.8	9	298-2	305						
TW1	A3.8	9	299	306	310					
TW1	A4.2	9	306							
TW1	A4.2	9	306							
TW1	A5.0	9	299	305						
TW1	A5.0	9	299	305						
TW1	A5.0	9	299	305						
TW1	A2.8	15	-9							
TW1	A2.8	15	-9							
TW1	A2.8	15	260	277						
TW1	A3.2	15	213	277						
TW1	A3.2	15	198	213	244	260	277	282	363	
TW1	A3.8	15	277							
TW1	A3.8	15	277	282						
TW1	A4.2	15	284							
TW1	A4.2	15	277	284						
TW1	A5.0	15	-9							
TW1	A5.0	15	284	290						
TW1	A5.0	15	284	290						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW1	A2.8	17	-9							
TW1	A2.8	17	-9							
TW1	A3.2	17	290							
TW1	A3.2	17	290	305						
TW1	A3.8	17	284	305						
TW1	A3.8	17	284	305	290	306				
TW1	A4.2	17	280	296						
TW1	A4.2	17	280	296	306	341				
TW1	A5.0	17	295	306	320	334				
TW1	A5.0	17	295	306	320	?	334			
TW1	A5.0	17	295	306	320	334				
TW1	A2.8	10	260							
TW1	A2.8	10	251	263						
TW1	A2.8	10	251	263						
TW1	A3.2	10	260							
TW1	A3.2	10	260	245	251	268	273			
TW1	A3.8	10	251	257						
TW1	A3.8	10	251	257	257	260	268			
TW1	A4.2	10	251	255						
TW1	A4.2	10	251	255						
TW1	A5.0	10	260							
TW1	A5.0	10	255	260						
TW1	A5.0	10	260							
TW1	A2.8	25	151	160	170	203				
TW1	A2.8	25	203							
TW1	A2.8	25	151	158	168	201				
TW1	A3.2	25	160	175	195	205				
TW1	A3.2	25	158	160	175	195	203	205		
TW1	A3.8	25	160	175	197	201	205			
TW1	A3.8	25	160	175	201	205	207			
TW1	A4.2	25	151	160	168	201				
TW1	A4.2	25	151	160	168	201	205	207		
TW1	A5.0	25	151	160	162	168	175	191	203	
TW1	A5.0	25	151	160	162	168	175	191	203	
TW1	A5.0	25	151	160	162	168	175	191	203	
TW1	A2.8	11	261	283						
TW1	A2.8	11	-9							
TW1	A2.8	11	261	283	263	268				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW1	A3.2	11	256	263						
TW1	A3.2	11	256	263	265					
TW1	A3.8	11	263							
TW1	A3.8	11	263							
TW1	A4.2	11	254	256	261	265	265			
TW1	A4.2	11	254	256	261	265				
TW1	A5.0	11	202	211	226	243	256	261		
TW1	A5.0	11	202	?	226	256	261			
TW1	A5.0	11	202	211	226	243	256	261		
TW1			270	288						
TW2	B1.8	28	270	288						
TW2			270	284						
TW2	B2.0	28	270	284						
TW2			270	288						
TW2			270	288						
TW2			276							
TW2	B2.4	28	270							
TW2	B2.6	28	270	288						
TW2		2	270	288						
TW2	B3.4	28	270	288						
TW2			181	183	192					
TW2	B1.8	21	181	183	192					
TW2			183	184	186	192				
TW2	B2.0	21	183	184	186	192				
TW2			181	183	186	192				
TW2			-9							
TW2			179	192						
TW2	B2.4	21	181	186	192					
TW2	B2.6	21	181	183	186	192				
TW2		1	181							
TW2	B3.4	21	179	183	192					
TW2			291							
TW2	B1.8	23	291							
TW2			286	293						
TW2	B2.0	23	286	293						
TW2			291							
TW2			291							
TW2			-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW2	B2.4	23	286	293						
TW2	B2.6	23	291							
TW2	1		291							
TW2	B3.4	23	291							
TW2			192	203						
TW2	B1.8	8	192	203						
TW2			206	208						
TW2	B2.0	8	206	208						
TW2			192	196	203					
TW2			203							
TW2			203							
TW2	B2.4	8	172	192	208	252				
TW2	B2.6	8	192	196	203					
TW2	1		-9							
TW2	B3.4	8	200	203						
TW2			293	306						
TW2	B1.8	9	293	306						
TW2			?	306						
TW2	B2.0	9	295	306						
TW2			293	306						
TW2			306							
TW2			-9							
TW2	B2.4	9	295	306						
TW2	B2.6	9	293	306						
TW2	B3.4	1	-9							
TW2	B3.4	9	305							
TW2			277	308						
TW2	B1.8	15	277	308						
TW2			277	308						
TW2	B2.0	15	277	308						
TW2			277	308						
TW2			277	308						
TW2			-9							
TW2	B2.4	15	277	308						
TW2	B2.6	15	277	308						
TW2	B3.4	1	277	308						
TW2	B3.4	15	277	308						
TW2			286	296	306	339				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW2	B1.8	17	286	296	306	339				
TW2			284	292	302					
TW2	B2.0	17	284	292	302					
TW2			286	296	306					
TW2			286	296	306	339				
TW2			286	296	306					
TW2	B2.4	17	275	284	292	302	339			
TW2	B2.6	17	286	296	306					
TW2	B3.4	1	286	296						
TW2	B3.4	17	286	296	306					
TW2			251	260						
TW2	B1.8	10	251	260						
TW2			251	260						
TW2	B2.0	10	251	260						
TW2			251	260						
TW2			251	260						
TW2			?	251	260	273	?	?		
TW2	B2.4	10	251	260	277					
TW2	B2.6	10	251	260						
TW2	B3.4	1	250	260						
TW2	B3.4	10	250	260						
TW2			149	156	164	168	170	201		
TW2	B1.8	25	149	156	164	168	170	201		
TW2			160	201						
TW2	B2.0	25	160	201						
TW2			201							
TW2			-9							
TW2			149	156	164	201				
TW2	B2.4	25	154	160	164	170	187	193	199	207
TW2	B2.6	25	201							
TW2		1	-9							
TW2	B3.4	25	205	207						
TW2			243	256	261	293	311			
TW2	B1.8	11	243	256	261	293	311			
TW2			?	261						
TW2	B2.0	11	258	261						
TW2			261							
TW2			261							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
TW2			256	261	313					
TW2	B2.4	11	256	261	263	293				
TW2	B2.6	11	261							
TW2	B3.4	11	250	256	261					
TW2			276							
TW2			276							
MD1	C2.4	28	276							
MD1			288							
MD1	C4.0	28	288							
MD1			292							
MD1	C4.2	28	292							
MD1			270							
MD1	C4.4	28	270							
MD1			?	292						
MD1	C4.6	28	290	292						
MD1			181							
MD1			181	196						
MD1	C2.4	21	181	196						
MD1			173	181	186	192				
MD1	C4.0	21	173	181	186	192				
MD1			173	181	186	192				
MD1	C4.2	21	173	181	186	192				
MD1			173	181	186	192				
MD1	C4.4	21	173	181	186	192				
MD1			173	181	186	189				
MD1	C4.6	21	173	181	186	189				
MD1			289	312						
MD1			289	312						
MD1	C2.4	23	289	312						
MD1			286	291						
MD1	C4.0	23	286	291						
MD1			286	291						
MD1	C4.2	23	286	291						
MD1			286	293-2						
MD1	C4.4	23	286	293						
MD1			286	291						
MD1	C4.6	23	286	291						
MD1		1	206	216	226					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD1			206	216	226					
MD1	C2.4	8	206	216	226					
MD1			196	203	208	212	226			
MD1	C4.0	8	196	203	208	212	226			
MD1			194	208	226					
MD1	C4.2	8	194	208	226					
MD1			172	192	202	208				
MD1	C4.4	8	172	192	202	208				
MD1			170	194	196	214	218	228		
MD1	C4.6	8	170	194	196	214	218	228		
MD1			287	298-2						
MD1			287	298-2						
MD1	C2.4	9	287	297						
MD1			303	306						
MD1	C4.0	9	303	306						
MD1			303							
MD1	C4.2	9	303							
MD1			295	306						
MD1	C4.4	9	295	306						
MD1			299							
MD1	C4.6	9	299							
MD1			213	286						
MD1			183	213	286					
MD1	C2.4	15	183	213	286					
MD1			198	292	312	328				
MD1	C4.0	15	198	292	312	328				
MD1			292	312						
MD1	C4.2	15	292	312						
MD1			277	308						
MD1	C4.4	15	277	308						
MD1			198	277						
MD1	C4.6	15	198	277						
MD1			284							
MD1			284							
MD1	C2.4	17	284							
MD1			277	292	296-2					
MD1	C4.0	17	277	292	296					
MD1			277	292	296-2					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD1	C4.2	17	277	292	296					
MD1			275	284						
MD1	C4.4	17	275	284						
MD1			290							
MD1	C4.6	17	290							
MD1			251	273						
MD1			251	273						
MD1	C2.4	10	251	273						
MD1			250	258	268	288				
MD1	C4.0	10	250	258	268	288				
MD1			250	258	268	288				
MD1	C4.2	10	250	258	268	288				
MD1			251	260						
MD1	C4.4	10	251	260						
MD1			260							
MD1	C4.6	10	260							
MD1			149	160	162	168	201	227		
MD1			149	160	168	201	?	227		
MD1	C2.4	25	149	160	168	201	215	227		
MD1			151	160	164	168	184	191	208	
MD1	C4.0	25	151	160	164	168	184	191	208	
MD1			151	160	164	184	191	208		
MD1	C4.2	25	151	160	164	184	191	208		
MD1			160	187	193	199	207			
MD1	C4.4	25	160	187	193	199	207			
MD1			160	175	177	195	203			
MD1	C4.6	25	160	175	177	195	203			
MD1	C2.4		263							
MD1			263							
MD1	C2.4	11	263							
MD1			254	256	263	265	283	316		
MD1	C4.0	11	254	256	263	265	283	316		
MD1			263	283						
MD1	C4.2	11	263	283						
MD1			261							
MD1	C4.4	11	261							
MD1			263							
MD1	C4.6	11	263							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD1			-9							
MD2	D4.0	28	270							
MD2			-9							
MD2			270	286	308	333	333	350		
MD2	D3.0	28	270	286	308	333	333	350		
MD2			-9							
MD2			288							
MD2	D3.2	28	288							
MD2			?							
MD2			270	333						
MD2	D3.4	28	270	333						
MD2			270							
MD2	D4.2	28	270							
MD2			-9							
MD2	D4.0	21	181							
MD2			183							
MD2			183	186						
MD2	D3.0	21	183	186						
MD2			181							
MD2			181	186	192					
MD2	D3.2	21	181	186	192					
MD2			181							
MD2			173	179	184	192				
MD2	D3.4	21	173	179	184	192				
MD2			184							
MD2	D4.2	21	184							
MD2			-9							
MD2	D4.0	23	-9							
MD2			-9							
MD2			286							
MD2	D3.0	23	286							
MD2			302	312						
MD2			286	291						
MD2	D3.2	23	286	291						
MD2			288							
MD2			286	327						
MD2	D3.4	23	286	327						
MD2			-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD2	D4.2	23	286							
MD2			192	194	206	216				
MD2	D4.0	8	192	194	206	216				
MD2			-9							
MD2			192	202	206	216				
MD2	D3.0	8	192	202	206	216				
MD2			200	208	216	226				
MD2			?	196	203	208	219	226		
MD2	D3.2	8	180	196	203	208	219	226		
MD2			-9							
MD2			196	203	210	218	228			
MD2	D3.4	8	196	203	210	218	228			
MD2			203	212						
MD2	D4.2	8	203	212						
MD2			303	310	319					
MD2	D4.0	9	303	310	319					
MD2			-9							
MD2			?							
MD2	D3.0	9	305							
MD2			287	298-2	303					
MD2			303							
MD2	D3.2	9	303							
MD2			-9							
MD2			298-2	303						
MD2	D3.4	9	298	303						
MD2			303	310						
MD2	D4.2	9	303	310						
MD2			-9							
MD2	D4.0	15	290							
MD2			-9							
MD2			290							
MD2	D3.0	15	290							
MD2			277	286						
MD2			198	292	312	328				
MD2	D3.2	15	198	292	312	328				
MD2			277	286						
MD2			209	258	274					
MD2	D3.4	15	209	258	274					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD2			290							
MD2	D4.2	15	290							
MD2			280	295	305	330	341			
MD2	D4.0	17	280	295	305	330	341			
MD2			-9							
MD2			295							
MD2	D3.0	17	295							
MD2			-9							
MD2			277	292	296-2					
MD2	D3.2	17	277	292	296					
MD2			-9							
MD2			284	296						
MD2	D3.4	17	284	296						
MD2			280	288						
MD2	D4.2	17	280	288						
MD2			260							
MD2	D4.0	10	260							
MD2			-9							
MD2			250							
MD2	D3.0	10	250							
MD2			251	263						
MD2			250	258	268	277	288			
MD2	D3.2	10	250	258	268	277	288			
MD2			250							
MD2			251							
MD2	D3.4	10	251							
MD2			251	257						
MD2	D4.2	10	251	257						
MD2			160							
MD2	D4.0	25	160							
MD2			-9							
MD2			151	160	162	178	201			
MD2	D3.0	25	151	160	162	178	201			
MD2			160	170	201					
MD2			151	160	164	168	184	208		
MD2	D3.2	25	151	160	164	168	184	208		
MD2			151	160	170	201				
MD2			154	160	168	170	184	193	199	205

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
MD2	D3.4	25	154	160	168	170	184	193	199	205
MD2			151	160	187	201				
MD2	D4.2	25	151	160	187	201				
MD2			226	261						
MD2	D4.0	11	226	261						
MD2			251	265						
MD2			261	303						
MD2	D3.0	11	261	303						
MD2			-9							
MD2			256	263	283	316				
MD2	D3.2	11	256	263	283	316				
MD2			226	261						
MD2			261	268						
MD2	D3.4	11	261	268						
MD2			256	261	297					
MD2	D4.2	11	256	261	297					
MD2			-9							
MD2			270	306						
LW3	E1.6	28	270	306						
LW3			181							
LW3			179							
LW3	E1.6	21	179							
LW3			302	312						
LW3			300	311						
LW3	E1.6	23	300	311						
LW3			200	208	226					
LW3			198	206	214	224				
LW3	E1.6	8	198	206	214	224				
LW3			287	295	298-2	301				
LW3			-9							
LW3	E1.6	9	287	295	298	301				
LW3			286							
LW3			286							
LW3	E1.6	15	286							
LW3			301	305-2						
LW3			301	305-2						
LW3			278	299	305					
LW3	E1.6	17	278	299	305					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW3			263							
LW3			250	262						
LW3	E1.6	10	250	262						
LW3			151	158	170	195	201			
LW3			149	156	168	199	201			
LW3	E1.6	25	149	156	168	199	201			
LW3			261	283						
LW3			261	283						
LW3	E1.6	11	261	283						
LW3			276	290						
LW3			276	290						
LW3	E1.8	28	276	290						
LW3			179	183	192					
LW3			179	184	194					
LW3	E1.8	21	179	183	192					
LW3			288							
LW3			288							
LW3	E1.8	23	288							
LW3			203	218						
LW3			218							
LW3	E1.8	8	218							
LW3			295	303						
LW3			295	303						
LW3	E1.8	9	295	303						
LW3			325							
LW3			325							
LW3	E1.8	15	325							
LW3			277	284	292	308				
LW3			277	284	292	308				
LW3	E1.8	17	277	284	292	308				
LW3			251	255						
LW3			250	255						
LW3	E1.8	10	250	255						
LW3			158	164	194					
LW3			158	164	195					
LW3	E1.8	25	158	164	194					
LW3			261							
LW3			256	261						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW3	E1.8	11	256	261						
LW3			276	290						
LW3			276	290						
LW3			276	290						
LW3	E2.2	28	276	290						
LW3			181	186	196					
LW3			179	184	194					
LW3	E2.2	21	179	183	194					
LW3			286	289	296					
LW3			288	295						
LW3	E2.2	23	288	295						
LW3			194	206	212	219				
LW3			192	203	210	218				
LW3	E2.2	8	192	203	210	218				
LW3			298-2	305						
LW3			295	303						
LW3	E2.2	9	295	303						
LW3			-9							
LW3			325							
LW3	E2.2	15	325							
LW3			278	284	294	308				
LW3			277	284	292	308				
LW3	E2.2	17	277	284	292	308				
LW3			251	257						
LW3			251	255						
LW3	E2.2	10	251	255						
LW3			160	168	197					
LW3			158	164	194					
LW3	E2.2	25	158	164	194					
LW3			263							
LW3			256	261						
LW3	E2.2	11	256	261						
LW3			276	292						
LW3			276	290						
LW3	E2.4	28	276	290						
LW3			181	186	196					
LW3			179	183	192					
LW3	E2.4	21	179	183	192					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW3			286	289	296					
LW3			288							
LW3	E2.4	23	288							
LW3			189	194	206	212	219			
LW3			203	218						
LW3	E2.4	8	203	218						
LW3			298-2	305						
LW3										
LW3	E2.4	9	-9							
LW3			183	310	326					
LW3			325							
LW3	E2.4	15	325							
LW3			278	284	294	306				
LW3			277	284	292	306				
LW3	E2.4	17	277	284	292	306				
LW3			251	257						
LW3			251	255						
LW3	E2.4	10	251	255						
LW3			160	168	197					
LW3			158	164	194					
LW3	E2.4	25	158	164	194					
LW3			263							
LW3			261							
LW3	E2.4	11	261							
LW3			270	292						
LW3			270	292						
LW3	E2.0	28	270	292						
LW3			179	184	199					
LW3			179	183	199					
LW3	E2.0	21	179	184	199					
LW3			296							
LW3			-9							
LW3	E2.0	23	296							
LW3			203	218						
LW3			-9							
LW3	E2.0	8	203	218						
LW3			-9							
LW3			298-2							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW3	E2.0	9	298							
LW3			221	286	308	347				
LW3			290							
LW3	E2.0	15	290							
LW3			288	292						
LW3			-9							
LW3	E2.0	17	288	292						
LW3			251							
LW3			289	292						
LW3	E2.0	10	289	292						
LW3			149	158	195					
LW3			151	164						
LW3	E2.0	25	149	158	195					
LW3			265	268						
LW3			261	263	268					
LW3	E2.0	11	261	263	268					
LW3			-9							
LW3			270	308						
LW2	F2.6	28	270	308						
LW2			270							
LW2			308	333						
LW2	F2.8	28	308	333						
LW2			270							
LW2			270							
LW2	F3.0	28	270							
LW2			-9							
LW2			270	284						
LW2	F3.4	28	270	284						
LW2			270	286						
LW2	F3.8	28	270	286						
LW2			181	186	192					
LW2			179	181	186					
LW2	F2.6	21	179	181	186					
LW2			181	186	192					
LW2			179	181	186					
LW2	F2.8	21	179	181	186					
LW2			181	186	192					
LW2			179	186						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW2	F3.0	21	179	186						
LW2			181	186	192					
LW2			173	181						
LW2	F3.4	21	173	181						
LW2			181	186	192					
LW2	F3.8	21	181	186	192					
LW2			286	291						
LW2			286	289	302					
LW2	F2.6	23	286	289	302					
LW2			286	291						
LW2			286	289	302					
LW2	F2.8	23	286	289	302					
LW2			286	291						
LW2			289	302						
LW2	F3.0	23	289	302						
LW2			286							
LW2			289							
LW2	F3.4	23	289							
LW2			289	302	312					
LW2	F3.8	23	289	302	312					
LW2			208	219	226					
LW2			200	206	208	218				
LW2	F2.6	8	200	206	208	218				
LW2			208	219	224					
LW2			?	200	206	208	218			
LW2	F2.8	8	170	200	206	208	218			
LW2			208	219	224					
LW2			194	206						
LW2	F3.0	8	194	206						
LW2			208							
LW2			164	219	228	269				
LW2			164	176	184	203	232	247	263	274
LW2	F3.8	8	164	219	228	269				
LW2			298-2	303						
LW2			287	298-2						
LW2	F2.6	9	287	298						
LW2			303							
LW2			287	298-2						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW2	F2.8	9	287	298						
LW2			303							
LW2			-9							
LW2	F3.0	9	287							
LW2			295	305						
LW2			290							
LW2	F3.4	9	290							
LW2			-9							
LW2			-9							
LW2	F3.8	9	287							
LW2			292							
LW2			286							
LW2	F2.6	15	286							
LW2			292							
LW2			-9							
LW2	F2.8	15	-9							
LW2			-9							
LW2			-9							
LW2	F3.0	15	-9							
LW2			277	308						
LW2			-9							
LW2	F3.4	15	-9							
LW2			-9							
LW2	F3.8	15	-9							
LW2			-9							
LW2			284	301						
LW2	F2.6	17	284	301						
LW2			-9							
LW2			284	301						
LW2	F2.8	17	284	301						
LW2			277	292	296-2					
LW2			284	322						
LW2	F3.0	17	284	322						
LW2			284	292						
LW2			286	306						
LW2	F3.4	17	286	306						
LW2			341							
LW2	F3.8	17	341							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW2			250	268	288					
LW2			257							
LW2	F2.6	10	257							
LW2			250	?	268	288				
LW2			257							
LW2	F2.8	10	257							
LW2			250	268	288					
LW2			251	273	276	343				
LW2	F3.0	10	251	273	276	343				
LW2			251	260	268	273	277			
LW2			268	285						
LW2	F3.4	10	268	285						
LW2			251	260						
LW2	F3.8	10	251	260						
LW2			160	164	184	191	208			
LW2			151	160	168	197	203			
LW2	F2.6	25	151	160	168	197	203			
LW2			151	160	164	184	191	208		
LW2			151	160	168	177	197	203	227	
LW2	F2.8	25	151	160	168	177	197	203	227	
LW2			151	160	164	168	184	191	208	
LW2			151	160	170	175	227			
LW2	F3.0	25	151	160	170	175	227			
LW2			154	160	164	187	193	199	207	
LW2			160	170	177	203	218	238		
LW2	F3.4	25	160	170	177	203	218	238		
LW2			160	170	178	201				
LW2	F3.8	25	160	170	178	201				
LW2			263							
LW2			261	263						
LW2	F2.6	11	261	263						
LW2			-9							
LW2			256	263	283					
LW2	F2.8	11	256	263	283					
LW2			-9							
LW2			226	263	283					
LW2	F3.0	11	226	263	283					
LW2			261	263						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LW2			226	245	256	263				
LW2	F3.4	11	226	245	256	263				
LW2			206	226	251					
LW2	F3.8	11	206	226	251					
LW2			-9							
LW2			270	276						
SL1	G2.8	28	270	276						
SL1			181	186						
SL1			179	183						
SL1	G2.8	21	179	186						
SL1			296							
SL1			296							
SL1			296							
SL1	G2.8	23	296							
SL1			194	203	210					
SL1			192	208						
SL1	G2.8	8	192	208						
SL1			305	313						
SL1			-9							
SL1			-9							
SL1	G2.8	9	305	313						
SL1			271	282	310					
SL1			198							
SL1			-9							
SL1	G2.8	15	271	282	310					
SL1			275	288	291					
SL1			341							
SL1			275	284	288					
SL1			275	284	288					
SL1	G2.8	17	275	288	291					
SL1			262							
SL1			251							
SL1			258							
SL1	G2.8	10	251							
SL1			163	193	197	205				
SL1			146	162	170	191	203			
SL1	G2.8	25	163	193	197	205				
SL1			261	268	283	297	316			

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL1			261	283	297	316				
SL1			261	283	297	316				
SL1	G2.8	11	261	269	283	297	316			
SL1			270	276						
SL1			270	276						
SL1	G3.2	28	270	276						
SL1			181	186						
SL1			181	186						
SL1	G3.2	21	181	186						
SL1			296							
SL1			296							
SL1	G3.2	23	296							
SL1			194	203	210					
SL1			194							
SL1	G3.2	8	194	203	210					
SL1			306	313						
SL1			-9							
SL1	G3.2	9	306	313						
SL1			277							
SL1			266							
SL1			198	303						
SL1			-9							
SL1	G3.2	15	266							
SL1			275	288	291					
SL1			275	288	291					
SL1	G3.2	17	275	288	291					
SL1			262							
SL1			260							
SL1	G3.2	10	262							
SL1			160	163	197	205				
SL1			149	163	175	193	205			
SL1	G3.2	25	149	163	175	193	205			
SL1			261	283	297	316				
SL1			261	265	283	297	316			
SL1	G3.2	11	261	283	297	316				
SL1			270	276						
SL1			270							
SL1	G3.6	28	270	276						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL1			-9							
SL1			179	184	186	189				
SL1	G3.6	21	179	184	186	189				
SL1			-9							
SL1			286							
SL1	G3.6	23	286							
SL1			178-2							
SL1			-9							
SL1	G3.6	8	178							
SL1			305	313						
SL1			-9							
SL1	G3.6	9	305	313						
SL1			292	299						
SL1	G3.6	15	266	299						
SL1			275	288						
SL1			339							
SL1	G3.6	17	275	288						
SL1			260	332						
SL1			260							
SL1	G3.6	10	260	332						
SL1			149	156						
SL1			170	215	163	193	201	215		
SL1			199							
SL1	G3.6	25	149	156						
SL1			261	265	163	193	201	215		
SL1			251	261						
SL1	G3.6	11	261	265						
SL1			270	288						
SL1			270	284	308					
SL1	G3.8	28	270	284						
SL1			-9		308					
SL1			179	184						
SL1	G3.8	21	179	184						
SL1			-9							
SL1			286	299						
SL1	G3.8	23	286	299						
SL1			-9							
SL1			216	236	269	274				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL1	G3.8	8	216	236	269	274				
SL1			301							
SL1	G3.8	9	301							
SL1			231	297						
SL1	G3.8	15	231	297						
SL1			339							
SL1	G3.8	17	339							
SL1			260	332						
SL1			316	327						
SL1	G3.8	10	316	327						
SL1			170	215						
SL1			-9							
SL1	G3.8	25	170							
SL1			251	256	261	265	277			
SL1			261							
SL1	G3.8	11	251	256	261	265	277			
SL1			270	276						
SL1			270	276						
SL1	G2.6	28	270	276						
SL1			179	183						
SL1			179	183						
SL1	G2.6	21	179	183						
SL1			296							
SL1	G2.6	23	296							
SL1			192	208						
SL1			192	202	208					
SL1	G2.6	8	192	202	208					
SL1			303	311						
SL1			303	311						
SL1	G2.6	9	303	311						
SL1			277							
SL1			196							
SL1	G2.6	15	277							
SL1			275	284	290					
SL1				275	288	290				
SL1	G2.6	17	275	284	290					
SL1			258							
SL1			260							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL1	G2.6	10	258							
SL1			144	160	191	203				
SL1			146	158	162	170	191	195	203	
SL1	G2.6	25	144	160	191	203				
SL1			261	265						
SL1			261	265	283	297	316			
SL1	G2.6	11	261	265						
SL1			270							
SL1			?							
SL2	H1.0	28	270							
SL2			175	181						
SL2			175	181						
SL2	H1.0	21	175	181						
SL2			290	299						
SL2			289	299						
SL2	H1.0	23	290	299						
SL2			200	216	236					
SL2			200	236						
SL2	H1.0	8	200	236						
SL2			301	303						
SL2			301							
SL2	H1.0	9	301	303						
SL2			299	318						
SL2			299	318						
SL2	H1.0	15	299	318						
SL2			275	284	296	311				
SL2			275	284	296	311				
SL2	H1.0	17	275	284	296	311				
SL2			-9							
SL2			250							
SL2	H1.0	10	250							
SL2			-9							
SL2			168	181	205					
SL2	H1.0	25	168	181	205					
SL2			224	263	275					
SL2			224	261	263	275				
SL2	H1.0	11	224	263	275					
SL2			261	270	306	348				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL2			270	306						
SL2			288	309						
SL2	H2.2	28	261	270	306	348				
SL2			179							
SL2			179	184	189					
SL2	H2.2	21	179							
SL2			300	311						
SL2			286	290						
SL2	H2.2	23	300	311						
SL2			198	224						
SL2			-9							
SL2	H2.2	8	198	224						
SL2			287	295	301					
SL2			301							
SL2	H2.2	9	287	295	301					
SL2			286							
SL2			286	310						
SL2	H2.2	15	286							
SL2			299	305						
SL2			275	292	295					
SL2	H2.2	17	299	305						
SL2			250	262						
SL2			250	262						
SL2			248	268						
SL2	H2.2	10	250	262						
SL2			198							
SL2			149	?	160	181	207			
SL2	H2.2	25	198							
SL2			261	283	311					
SL2			256	261	283					
SL2	H2.2	11	261	283	311					
SL2			288							
SL2	H2.6	28	288							
SL2			173	179	184	189				
SL2	H2.6	21	173	179	184	189				
SL2			286	290						
SL2	H2.6	23	286	290						
SL2			-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL2			192	206	224					
SL2	H2.6	8	192	206	224					
SL2			301	303						
SL2	H2.6	9	301	303						
SL2			290	310	326					
SL2	H2.6	15	290	310	326					
SL2			275	292	295					
SL2			275	295						
SL2	H2.6	17	275	292	295					
SL2			248	268	285					
SL2	H2.6	10	248	268	285					
SL2			158	160						
SL2			149	158	160	181	207			
SL2	H2.6	25	149	158	160	181	207			
SL2			261	283						
SL2	H2.6	11	261	283						
SL2		-9								
SL2			270	306						
SL2	H2.0	28	270	306						
SL2			179	184						
SL2			179							
SL2	H2.0	21	179	184						
SL2			290	299						
SL2			300	311						
SL2	H2.0	23	290	299	311					
SL2			202	218	236					
SL2			192	206	224					
SL2	H2.0	8	198	206	224					
SL2			303							
SL2			287	298-2						
SL2	H2.0	9	303							
SL2			318							
SL2			286							
SL2	H2.0	15	318							
SL2			-9							
SL2			278	299	303	328				
SL2	H2.0	17	278	299	303	328				
SL2			-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL2			250	262						
SL2	H2.0	10	251	262						
SL2			-9							
SL2			160							
SL2	H2.0	25	160							
SL2			224	265						
SL2			263	270	283					
SL2	H2.0	11	224	265						
SL2			288							
SL2			288							
SL2	H2.8	28	288							
SL2			181	192						
SL2			181	192						
SL2	H2.8	21	179	191						
SL2			286	291						
SL2			286	291						
SL2	H2.8	23	286	291						
SL2			208	219	226					
SL2			208	219	226					
SL2	H2.8	8	208	219	226					
SL2			303							
SL2			287	298	303					
SL2	H2.8	9	287	298	303					
SL2			286	290	312	328	340			
SL2			292	312	328	340				
SL2	H2.8	15	286	292	312	328	340			
SL2			-9							
SL2			286	295	305	339				
SL2	H2.8	17	286	295	305	339				
SL2			-9							
SL2			250	258	268	285				
SL2	H2.8	10	250	258	268	285				
SL2			-9							
SL2			160	164	184	191	208	218		
SL2	H2.8	25	160	164	184	191	208	218		
SL2			256	263	283					
SL2			256	261	283	313				
SL2	H2.8	11	256	263	283	313				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SL2			306							
LA1	I2.4	28	306							
LA1			179							
LA1			306							
LA1			181	186						
LA1			181	186						
LA1	I2.4	21	181	186						
LA1			293-2							
LA1			302							
LA1			302							
LA1	I2.4	23	302							
LA1			214	222						
LA1			200	208	212					
LA1			-9							
LA1			192	194	208	212	218	226		
LA1	I2.4	8	192	194	208	212	218	226		
LA1			-9							
LA1			298-2							
LA1			298-2							
LA1	I2.4	9	298							
LA1			288							
LA1			277	282						
LA1			277	282	363					
LA1	I2.4	15	277	282	363					
LA1			292	320						
LA1			278	290	301					
LA1			278	288	301	305				
LA1	I2.4	17	278	288	301	305				
LA1			257							
LA1			251	263						
LA1			250	263						
LA1	I2.4	10	250	263						
LA1			158	163	170	181	201			
LA1			160	170	201					
LA1			160	170	181	203				
LA1	I2.4	25	160	170	181	201				
LA1			256							
LA1			261							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA1			256	261						
LA1	I2.4	11	256	261						
LA1			270	306						
LA1			270	286	306					
LA1	I2.8	28	270	286	306					
LA1			181							
LA1			181							
LA1	I2.8	21	181							
LA1			302	312						
LA1			302	312						
LA1	I2.8	23	302	312						
LA1			200	208	226					
LA1			200	208	216	226				
LA1	I2.8	8	200	208	216	226				
LA1			287	298-2	303					
LA1			287	298-2	303					
LA1	I2.8	9	287	297	303					
LA1			286							
LA1			286							
LA1	I2.8	15	286							
LA1			301	305-2	341					
LA1			301	305	341					
LA1	I2.8	17	301	305	341					
LA1			251	263						
LA1			251	263						
LA1	I2.8	10	251	263						
LA1			158	170	201					
LA1			151	158	170	201				
LA1	I2.8	25	151	158	170	201				
LA1			261	283						
LA1			261	283						
LA1	I2.8	11	261	283						
LA1			306							
LA1			276	306						
LA1	I3.0	28	276	306						
LA1			179							
LA1			181							
LA1	I3.0	21	181							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA1			302	312						
LA1			302	312						
LA1	I3.0	23	302	312						
LA1			200	208	226					
LA1			200	208	216	226				
LA1	I3.0	8	200	208	216	226				
LA1			287	298	303					
LA1			287	298-2	303					
LA1	I3.0	9	287	297	303					
LA1			286							
LA1			286							
LA1	I3.0	15	286							
LA1			301	305	341					
LA1			301	305						
LA1	I3.0	17	301	305						
LA1			251	263						
LA1			251	263						
LA1	I3.0	10	251	263						
LA1			158	170	201					
LA1			151	158	170	201				
LA1	I3.0	25	151	158	170	201				
LA1			261	283						
LA1			261	275	283	316				
LA1	I3.0	11	261	275	283	316				
LA1			261	270	306					
LA1			257	270						
LA1	I3.2	28	260	270	306					
LA1			181							
LA1			181							
LA1	I3.2	21	181							
LA1			296	312						
LA1			296	312						
LA1	I3.2	23	296	312						
LA1			211	216	226					
LA1			194	210	216	226				
LA1	I3.2	8	194	210	216	226				
LA1			287	298-2	298	303				
LA1			287	298-2	303					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA1	I3.2	9	287	297	299	303				
LA1			300	326						
LA1			300	326						
LA1	I3.2	15	300	326						
LA1			294	301	302	341				
LA1			294	301	341					
LA1	I3.2	17	294	301	303	341				
LA1			251	263	277					
LA1			251	263	277					
LA1	I3.2	10	251	263	277					
LA1			160	168	201	203				
LA1			160	168	203					
LA1	I3.2	25	160	168	200	202				
LA1			261							
LA1			261							
LA1	I3.2	11	261							
LA1			270							
LA1			270							
LA1	I3.4	28	270							
LA1			181	186						
LA1			181	186						
LA1	I3.4	21	181	186						
LA1			302							
LA1			302							
LA1	I3.4	23	302							
LA1			194	208	212	226				
LA1			208	212	226					
LA1	I3.4	8	194	208	212	226				
LA1			287	293	303					
LA1			287	293	303					
LA1	I3.4	9	287	293	303					
LA1			286	300						
LA1			286	300						
LA1	I3.4	15	286	300						
LA1			302	305						
LA1			302	311	341					
LA1	I3.4	17	302	304	312	340				
LA1			251							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA1			251	260						
LA1	I3.4	10	251	261						
LA1			158	170	184	199				
LA1			151	158	170	187	199			
LA1	I3.4	25	152	158	170	184	199			
LA1			256	261	283					
LA1			258	261	283					
LA1	I3.4	11	257	261	283					
LA1			270	306	348					
LA2	J1.0	28	270	306	348					
LA2			179							
LA2			179							
LA2	J1.0	21	179							
LA2			300	311						
LA2			300	311						
LA2	J1.0	23	300	311						
LA2			-9							
LA2			198	206	224					
LA2	J1.0	8	198	206	224					
LA2			287	298-2	301					
LA2			287	298-2	301					
LA2	J1.0	9	287	297	301					
LA2			286							
LA2			286							
LA2	J1.0	15	286							
LA2			278	299	303	306				
LA2			299	303	306					
LA2	J1.0	17	278	299	303	306				
LA2			-9							
LA2			250	262						
LA2	J1.0	10	250	262						
LA2			149	154	164	199				
LA2			149	154	168	178	199			
LA2	J1.0	25	149	154	164	199				
LA2			261	283	316					
LA2			261	283						
LA2	J1.0	11	261	283	316					
LA2			270	306						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA2			270	306						
LA2	J1.2	28	270	306						
LA2			179							
LA2			179							
LA2	J1.2	21	179							
LA2			300	311						
LA2			300	311						
LA2	J1.2	23	300	311						
LA2			198	224						
LA2			198	206	224					
LA2	J1.2	8	198	206	224					
LA2			287	298-2	301					
LA2			287	298-2						
LA2	J1.2	9	287	297	301					
LA2			286							
LA2			286							
LA2	J1.2	15	286							
LA2			299	303						
LA2			299	306						
LA2	J1.2	17	299	303						
LA2			250	262						
LA2			250	262						
LA2	J1.2	10	250	262						
LA2			158	168	199					
LA2			149	158	168	199				
LA2	J1.2	25	149	154	164	199				
LA2			261	283	316					
LA2			261	283						
LA2	J1.2	11	261	283	316					
LA2			270	306						
LA2	J1.4	28	270	306						
LA2			179							
LA2	J1.4	21	179							
LA2			300	311						
LA2	J1.4	23	300	311						
LA2			198	206	224					
LA2	J1.4	8	198	206	224					
LA2			287	298-2						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA2	J1.4	9	287	297						
LA2			286							
LA2	J1.4	15	286							
LA2			299							
LA2	J1.4	17	299							
LA2			250	262						
LA2	J1.4	10	250	262						
LA2			149	154	164	199				
LA2	J1.4	25	149	154	164	199				
LA2			261	283						
LA2	J1.4	11	261	283						
LA2			270							
LA2			270							
LA2	J2.6	28	270							
LA2			181	186	192					
LA2			179	184	189					
LA2	J2.6	21	181	186	192					
LA2			286	293-2						
LA2			286	293						
LA2	J2.6	23	286	294						
LA2			203	208						
LA2			206							
LA2	J2.6	8	204	208						
LA2			293	305						
LA2			293	303						
LA2	J2.6	9	293	303						
LA2			277	308						
LA2			277	307						
LA2	J2.6	15	277	307						
LA2			284	292	302					
LA2			284	291	301					
LA2	J2.6	17	284	291	301					
LA2			260	277						
LA2			-9							
LA2	J2.6	10	260	278						
LA2			154	160	187	193	199	207		
LA2			-9							
LA2	J2.6	25	153	159	187	193	199	207		

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
LA2			263							
LA2			261							
LA2	J2.6	11	261							
LA2			270							
LA2	J2.8	28	270							
LA2			184	189						
LA2	J2.8	21	184	189						
LA2			286	293						
LA2	J2.8	23	286	293						
LA2			192	206						
LA2	J2.8	8	192	206						
LA2			293	303						
LA2	J2.8	9	293	303						
LA2			277	307						
LA2	J2.8	15	277	307						
LA2			284	291	301					
LA2	J2.8	17	284	290	300					
LA2			251	258						
LA2	J2.8	10	251	258						
LA2			158	197	205					
LA2	J2.8	25	158	197	205					
LA2			261							
LA2	J2.8	11	261							
LA2			-9							
LA2			-9							
LA2			270	?	333					
AW1	K1.0	28	270	306	333					
AW1			181	189						
AW1			179	181	186					
AW1	K1.0	21	179	181	186					
AW1			286	316						
AW1			286							
AW1	K1.0	23	286							
AW1			206							
AW1	K1.0	8	206							
AW1			305							
AW1			-9							
AW1	K1.0	9	-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW1			284	290	310					
AW1			288							
AW1	K1.0	15	288							
AW1			291	305-2	311					
AW1			286	291	305-2	311				
AW1			-9							
AW1	K1.0	17	-9							
AW1			251	260						
AW1			251	260						
AW1			250	258	260					
AW1	K1.0	10	250	258	260					
AW1			160	177	191	197				
AW1			149	160	164	178	191	213		
AW1			146	158	175	187	194	210		
AW1	K1.0	25	146	158	175	187	194	210		
AW1			256	268	277					
AW1			256	268	277					
AW1			256	268	277					
AW1	K1.0	11	256	268	277					
AW1			270	276						
AW1			270	276						
AW1			-9							
AW1	K1.2	28	270	276						
AW1			183							
AW1			183							
AW1			179							
AW1	K1.2	21	183							
AW1			291							
AW1			291							
AW1			290							
AW1	K1.2	23	292							
AW1			226							
AW1			200	226						
AW1			224							
AW1	K1.2	8	200	224						
AW1			298	305						
AW1			298	305						
AW1			-9							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW1	K1.2	9	298	304						
AW1			266	277						
AW1			183	266	307					
AW1			-9							
AW1	K1.2	15	184	266	278	306				
AW1			282	288	295	311	341			
AW1			288	295	311					
AW1			286	294	311					
AW1	K1.2	17	288	295	311					
AW1			247	255						
AW1			247	255						
AW1			245							
AW1	K1.2	10	245	255						
AW1			154	160	170	181	193	203		
AW1			154	160	168	168	178	193	203	
AW1			149	158	175	191	201			
AW1	K1.2	25	154	158	170	180	193	203		
AW1			265	275						
AW1			265	275						
AW1			263	275						
AW1	K1.2	11	265	275						
AW1			286	309						
AW1			270	?	306	309	333			
AW1	K1.4	28	270	286	309	333				
AW1			179							
AW1			179	183						
AW1	K1.4	21	179	183						
AW1			290	295						
AW1			290	295						
AW1	K1.4	23	290	295						
AW1			200							
AW1			200							
AW1	K1.4	8	200							
AW1			-9							
AW1			299	303						
AW1	K1.4	9	299	303						
AW1			274	288	292	307				
AW1			277	286	292	307				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW1	K1.4	15	274	288	292	307				
AW1			275	284	296-2					
AW1			275	284	296-2					
AW1	K1.4	17	275	284	297					
AW1			251							
AW1			251							
AW1	K1.4	10	250							
AW1			151	158	175	191	194			
AW1			151	158	175	191	194			
AW1	K1.4	25	151	158	175	191	194			
AW1			256	261	283					
AW1			256	261	283					
AW1	K1.4	11	256	261	283					
AW1			286							
AW1			286							
AW1	K2.4	28	286							
AW1			181	184						
AW1			181	184						
AW1	K2.4	21	181	185						
AW1			286	293						
AW1			286	293						
AW1	K2.4	23	286	292						
AW1			194	206	216					
AW1			206	216						
AW1	K2.4	8	194	206	216					
AW1			303	310						
AW1			303	310						
AW1	K2.4	9	303	310						
AW1			290							
AW1			290							
AW1	K2.4	15	290							
AW1			295	330						
AW1			295	305						
AW1	K2.4	17	295	305	330					
AW1			260							
AW1			251	260						
AW1	K2.4	10	251	260						
AW1			151	156	160	177	201			

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW1			160	178	201					
AW1	K2.4	25	151	155	160	178	201			
AW1			261							
AW1			261	297						
AW1	K2.4	11	261	297						
AW1			-9							
AW1			282							
AW1			270	276						
AW1	K2.6	28	270	276						
AW1			183							
AW1			183							
AW1			183							
AW1	K2.6	21	183							
AW1			291							
AW1			291							
AW1			291							
AW1	K2.6	23	291							
AW1			189	194	212	226				
AW1			192	226						
AW1			192	226						
AW1	K2.6	8	192	226						
AW1			298	305						
AW1			298	305						
AW1			298	305						
AW1	K2.6	9	298	305						
AW1			182	266	318					
AW1			183	318						
AW1	K2.6	15	182	266	318					
AW1			288	296-2	311					
AW1			288	296-2	311					
AW1	K2.6	17	288	296	312					
AW1			247	255						
AW1			247							
AW1	K2.6	10	247	255						
AW1			151	160	168	177	193	203		
AW1			154	160	168	178	193	203		
AW1	K2.6	25	151	160	168	178	192	202		
AW1			265	275						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW1			265	275						
AW1	K2.6	11	265	275						
AW1			270	276						
AW1			270	276						
AW2	L2.6	28	270	276						
AW2			-9							
AW2			181							
AW2			181	186						
AW2	L2.6	21	181	186						
AW2			289							
AW2			289							
AW2			-9							
AW2	L2.6	23	289							
AW2			206	214						
AW2			169	192	196	202	206	212	214	224
AW2	L2.6	8	206	214						
AW2			298	305						
AW2			298	305	307					
AW2	L2.6	9	298	305	307	288				
AW2			288							
AW2			183	288						
AW2	L2.6	15	183	288		301				
AW2			282	286	290	301				
AW2			282	286	301					
AW2	L2.6	17	282	286	290					
AW2			251							
AW2			248	277	296					
AW2			251	263						
AW2			251	258						
AW2	L2.6	10	251	263						
AW2			154	160	177	197				
AW2			154	160	177	197				
AW2			215							
AW2	L2.6	25	154	160	177					
AW2			261	268	285					
AW2			206	238	251	261	277			
AW2	L2.6	11	261	268	285					
AW2			270	306						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW2			270	306						
AW2	L4.4	28	270	306						
AW2			179	181						
AW2			179	181						
AW2	L4.4	21	179	181						
AW2			300							
AW2			300							
AW2	L4.4	23	300							
AW2			198	219						
AW2			198	219						
AW2	L4.4	8	198	219						
AW2			-9							
AW2			298	303						
AW2	L4.4	9	299	303						
AW2			286							
AW2			286	300						
AW2	L4.4	15	286	300						
AW2			296	306						
AW2			296	306						
AW2	L4.4	17	296	306						
AW2			260							
AW2			250	262						
AW2	L4.4	10	250	262		194	201			
AW2			149	158	170	194	201			
AW2			158	170	194	201				
AW2	L4.4	25	149	158	170	303	316			
AW2			256	261	283	303	316			
AW2			256	261	283	303	316			
AW2	L4.4	11	256	261	283					
AW2			276	292						
AW2			276	290						
AW2	L4.6	28	276	290						
AW2			181	186	196					
AW2			179	183	194					
AW2	L4.6	21	181	186	196					
AW2			286	289	296					
AW2			288	295						
AW2	L4.6	23	286	300	296					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW2			206	219						
AW2			203	218						
AW2	L4.6	8	203	219						
AW2			298-2	305						
AW2				-9						
AW2	L4.6	9	296	304						
AW2			326							
AW2			325							
AW2	L4.6	15	326							
AW2			278	284	294	306				
AW2			277	284	292	306				
AW2	L4.6	17	278	284	294					
AW2			251	257						
AW2			250	254						
AW2	L4.6	10	250	254						
AW2			160							
AW2			158	164	194					
AW2	L4.6	25	158	164	194					
AW2			261	263						
AW2			256	261						
AW2	L4.6	11	261	263		333	348			
AW2			306							
AW2			270	290	306	333	348			
AW2	L4.8	28	270	290	306					
AW2			179	179						
AW2			181							
AW2	L4.8	21	181							
AW2			300	311						
AW2			300	311						
AW2	L4.8	23	300	311		224				
AW2			184	198	206	224				
AW2			198	206	214	224				
AW2	L4.8	8	198	206	214	301				
AW2			287	295	298-2	301				
AW2			-9							
AW2	L4.8	9	287	295	297					
AW2			286							
AW2			286							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW2	L4.8	15	286							
AW2			299	305	306					
AW2			299	305	306					
AW2	L4.8	17	299	305	306					
AW2			250	262						
AW2			250	262						
AW2	L4.8	10	250	262						
AW2			168	199						
AW2			149	154	168	199				
AW2	L4.8	25	168	199						
AW2			261							
AW2			261	283						
AW2	L4.8	11	261	283						
AW2			270	276						
AW2	L5.2	28	270	276						
AW2			179	183	192					
AW2			333							
AW2	L5.2	21	179	183	192					
AW2			288							
AW2			-9							
AW2	L5.2	23	-9							
AW2			194	203						
AW2			194	203	209					
AW2			203	219						
AW2	L5.2	8	194	203	209					
AW2			303							
AW2			-9							
AW2	L5.2	9	303							
AW2			191	303						
AW2	L5.2	15	191	303						
AW2			311	341						
AW2			282	284	288	292	301	305-2	341	
AW2	L5.2	17	282	284	292	301	306	342		
AW2			258	332						
AW2			250	257	263	304	332			
AW2			251	260						
AW2			304							
AW2	L5.2	10	250	257	263	304	332			

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
AW2			160							
AW2			168	175	229					
AW2	L5.2	25	160							
AW2			223	263						
AW2			206	275						
AW2	L5.2	11	223	263						
AW2			270							
AW2			270	280						
SR1	M1.2	28	270	280						
SR1			173	179	220					
SR1			179	220						
SR1	M1.2	21	173	179	220					
SR1			-9							
SR1			-9							
SR1	M1.2	23	-9							
SR1			206	212						
SR1			206	212						
SR1	M1.2	8	206	212						
SR1			303							
SR1			303							
SR1	M1.2	9	303							
SR1			224							
SR1			-9							
SR1			-9							
SR1	M1.2	15	224							
SR1			303							
SR1			303							
SR1	M1.2	17	303							
SR1			255	264						
SR1			254	264						
SR1	M1.2	10	254	264						
SR1			146	151	160	175	199			
SR1	M1.2	25	146	151	160	175	199			
SR1			261	263						
SR1			261	285						
SR1	M1.2	11	261	285						
SR1			280							
SR1	M1.0	28	280							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR1			179							
SR1	M1.0	21	179							
SR1			291							
SR1	M1.0	23	291							
SR1			206	206						
SR1	M1.0	8	206							
SR1			303							
SR1	M1.0	9	303							
SR1			224							
SR1	M1.0	15	224							
SR1			303	?						
SR1	M1.0	17	303	305						
SR1			264							
SR1	M1.0	10	264							
SR1			168	203						
SR1	M1.0	25	168	203						
SR1			261	285						
SR1	M1.0	11	261	285						
SR1			270	282						
SR1			280							
SR1	M1.4	28	270	282						
SR1			181	220						
SR1			181							
SR1			179	184						
SR1	M1.4	21	181							
SR1			-9							
SR1			-9							
SR1			290							
SR1	M1.4	23	290							
SR1			208	214						
SR1			208							
SR1			202	206						
SR1	M1.4	8	208							
SR1			305							
SR1			306							
SR1			-9							
SR1			303							
SR1	M1.4	9	303							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR1			185							
SR1			196	266	288					
SR1			-9							
SR1			292	299						
SR1	M1.4	15	196	266	288					
SR1			305	306						
SR1			305							
SR1			286	339						
SR1			305	306						
SR1			286	296-2						
SR1	M1.4	17	286	304	306					
SR1			257	265						
SR1			257	265						
SR1			257	265						
SR1			254							
SR1	M1.4	10	257	265						
SR1			151	160	164	170	205			
SR1			151	160	164	170	205			
SR1			-9							
SR1			-9							
SR1	M1.4	25	151	160	164	170	205			
SR1			261	287						
SR1			261	265						
SR1			252	261	277					
SR1	M1.4	11	261	287						
SR1			-9							
SR1			270							
SR1	M1.6	28	270							
SR1			179							
SR1			179	181						
SR1	M1.6	21	179	181						
SR1			-9							
SR1			288							
SR1	M1.6	23	288							
SR1			-9							
SR1			198	214						
SR1	M1.6	8	198	214						
SR1			298	305						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR1			295	303						
SR1	M1.6	9	298	305						
SR1			277	286						
SR1			286							
SR1	M1.6	15	286							
SR1			292	315	322					
SR1			?							
SR1	M1.6	17	292	315	322					
SR1			250	251						
SR1			248							
SR1	M1.6	10	248							
SR1			151	162	170	187	199			
SR1			-9							
SR1	M1.6	25	151	162	170	187	199			
SR1			261	284	303					
SR1			-9							
SR1	M1.6	11	261	284	303					
SR1			276	288						
SR1			270	276						
SR1	M1.8	28	276	288						
SR1			181	183						
SR1			179							
SR1			175							
SR1	M1.8	21	181	183						
SR1			-9							
SR1			-9							
SR1			-9							
SR1	M1.8	23	-9							
SR1			218							
SR1			-9							
SR1			202	216	242					
SR1	M1.8	8	202	216	242					
SR1			303	307						
SR1			306							
SR1			306							
SR1	M1.8	9	303	307						
SR1			183	286	310					
SR1			286	308						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR1			286	308						
SR1	M1.8	15	183	286	310					
SR1			286	292	305	311	315			
SR1			286	291	303					
SR1			286	291	303					
SR1	M1.8	17	286	292	305	311	315			
SR1			251							
SR1			251							
SR1			251							
SR1	M1.8	10	251							
SR1			160	170						
SR1			149	158	168					
SR1			-9							
SR1	M1.8	25	149	158	168					
SR1			256	261	303	311				
SR1			256	261						
SR1			202	256	261	303				
SR1	M1.8	11	256	261	303	311				
SR1			270							
SR1			270	280						
SR1			290							
SR2	N1.4	28	290							
SR2			179	184						
SR2			179	220						
SR2			179	184	194					
SR2	N1.4	21	179	184	194					
SR2			290							
SR2			-9							
SR2			288							
SR2	N1.4	23	288							
SR2			202	214						
SR2			-9							
SR2			203	216						
SR2	N1.4	8	203	216						
SR2			303	310						
SR2			303							
SR2			303	305						
SR2	N1.4	9	303	305						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR2			292	299						
SR2			277							
SR2			271							
SR2	N1.4	15	271							
SR2			286	296-2	306					
SR2			303							
SR2			286	294						
SR2	N1.4	17	286	294						
SR2			254							
SR2			255	265						
SR2			250							
SR2	N1.4	10	250							
SR2			-9							
SR2			146	158	163	191	203			
SR2			144	158	164	191	203			
SR2	N1.4	25	144	158	164	191	203			
SR2			252	261	277					
SR2			265	283	297					
SR2			261	275						
SR2	N1.4	11	261	275						
SR2			290	315						
SR2			282	292	315					
SR2			290							
SR2	N1.6	28	282	292	315					
SR2			181							
SR2			179	181						
SR2			179							
SR2	N1.6	21	179	181						
SR2			286	291						
SR2			286	291						
SR2			286	290						
SR2	N1.6	23	286	290						
SR2			202	226						
SR2			202	218	226					
SR2			200	224						
SR2	N1.6	8	202	226						
SR2			305							
SR2			305							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR2			-9							
SR2	N1.6	9	305							
SR2			286	299	308	326				
SR2			183	286	299	307				
SR2			286	307	325					
SR2	N1.6	15	286	308	326					
SR2			292	314	328					
SR2			292	314	328					
SR2			292	294	311	328				
SR2	N1.6	17	292	314	328					
SR2			255	273						
SR2			255	273						
SR2			-9							
SR2	N1.6	10	255	273						
SR2			146	151	160	170	177	184	199	
SR2			146	151	160	170	177	187	199	
SR2			144	158	168	175	184	197		
SR2	N1.6	25	146	151	160	170	177	186	198	
SR2			263							
SR2			263							
SR2			261							
SR2	N1.6	11	263							
SR2			270	306	333					
SR2			261	270	306					
SR2	N2.4	28	270	306						
SR2			181							
SR2			181							
SR2	N2.4	21	181							
SR2			302	312						
SR2			302	312						
SR2	N2.4	23	302	312						
SR2			178	200	208	216	226			
SR2			200	208	216	226				
SR2	N2.4	8	178	200	208	216	226			
SR2			287	298-2	303					
SR2			287	298-2	303					
SR2	N2.4	9	287	297	303					
SR2			286							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR2			264	286	318					
SR2	N2.4	15	286							
SR2			301	305-2						
SR2			301	305-2	339					
SR2	N2.4	17	301	305	339					
SR2			251	263						
SR2			251	263						
SR2	N2.4	10	251	263						
SR2			151	158	170	201				
SR2			151	158	170	201				
SR2	N2.4	25	151	158	170	200				
SR2			243	261	283					
SR2			261	283						
SR2	N2.4	11	243	261	283					
SR2			270	276						
SR2			-9							
SR2	N2.6	28	270	276						
SR2			181	186	199					
SR2			-9							
SR2	N2.6	21	181	186	199					
SR2			289	291	312					
SR2			-9							
SR2	N2.6	23	289	291	312					
SR2			200	208	226					
SR2			212	224						
SR2	N2.6	8	200	208	226					
SR2			-9							
SR2			298-2							
SR2	N2.6	9	297							
SR2			197							
SR2			277							
SR2	N2.6	15	277							
SR2			282	290						
SR2			290	306						
SR2	N2.6	17	282	290						
SR2			251	255	263	332				
SR2			-9							
SR2	N2.6	10	251	255	263	332				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
SR2			160	177	203	215	229			
SR2	N2.6	25	160	177	203	215	229			
SR2			261							
SR2	N2.6	11	261							
SR2			270							
SR2			270	292						
SR2	N2.8	28	270	292						
SR2			179	186						
SR2			181	186						
SR2	N2.8	21	181	186						
SR2			293-2							
SR2			289	293-2						
SR2	N2.8	23	289	293						
SR2			203	212						
SR2			203	212						
SR2	N2.8	8	203	212						
SR2			-9							
SR2			298	305						
SR2	N2.8	9	298	305						
SR2			290							
SR2			290							
SR2	N2.8	15	290							
SR2			275	282	286	290	301	306	318	
SR2			286	306						
SR2			282	286	290	306	318			
SR2	N2.8	17	282	286	290	306	318			
SR2			251	260						
SR2			251	263						
SR2	N2.8	10	251	263						
SR2			146	151	160	164	181	184	197	
SR2			146	151	160	164	181	184	197	
SR2	N2.8	25	146	151	160	164	181	184	197	
SR2			256	297						
SR2			256	298						
SR2	N2.8	11	256	298						
SR2			270							
SR2			270	280						
HY1	P1.0	28	270							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY1			183	186						
HY1			183	186						
HY1	P1.0	21	183	186						
HY1			286	302						
HY1			286	302						
HY1	P1.0	23	286	302						
HY1			206	214	219					
HY1			192	206	214	219				
HY1	P1.0	8	192	206	214	219				
HY1			289	298-2	305					
HY1			289	298-2	306					
HY1	P1.0	9	289	297	305					
HY1			271							
HY1			-9							
HY1	P1.0	15	271							
HY1			275							
HY1			277							
HY1	P1.0	17	277							
HY1			251							
HY1			251							
HY1	P1.0	10	251							
HY1			151	160	164	170	184	201		
HY1			151	160	168	172	184	201		
HY1	P1.0	25	151	160	168	172	184	201		
HY1			256	316						
HY1			256	316						
HY1	P1.0	11	256	316						
HY1			306							
HY1			276	308						
HY1	P1.2	28	306							
HY1			181							
HY1			181							
HY1	P1.2	21	181							
HY1			302	312						
HY1			302	312						
HY1	P1.2	23	302	312						
HY1			200	208	216	226				
HY1			200	208	216	226				

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY1	P1.2	8	200	208	216	226				
HY1			298-2	303						
HY1			298-2	303						
HY1	P1.2	9	297	303						
HY1			286							
HY1			286							
HY1	P1.2	15	286							
HY1			301	305-2						
HY1			301	305						
HY1	P1.2	17	301	305						
HY1			251	263						
HY1			251	263						
HY1	P1.2	10	251	263						
HY1			151	158	170	201				
HY1			158	170	201					
HY1	P1.2	25	151	158	170	201				
HY1			261	283						
HY1			261	283						
HY1	P1.2	11	261	283						
HY1			270							
HY1			270							
HY1	P1.4	28	270							
HY1			181	186						
HY1			183	186						
HY1	P1.4	21	181	186						
HY1			286	302						
HY1			286	302						
HY1	P1.4	23	286	302						
HY1			206	214	219					
HY1			206	214	219					
HY1	P1.4	8	206	214	219					
HY1			289	298-2	305					
HY1			288	298-2	306					
HY1	P1.4	9	289	297	305					
HY1			271							
HY1			271	304						
HY1	P1.4	15	271	305						
HY1			275							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY1			275							
HY1			275							
HY1			284	305	330					
HY1			284	301						
HY1	P1.4	17	275							
HY1			251	340						
HY1			251							
HY1	P1.4	10	251	340						
HY1			151	160	164	170	184	201		
HY1			160	175	187	201	215			
HY1	P1.4	25	151	160	164	170	184	201		
HY1			256	316						
HY1			256	316						
HY1	P1.4	11	256	316						
HY1			270	276						
HY1			270	276						
HY1	P2.4	28	270	276						
HY1			181							
HY1			181							
HY1	P2.4	21	181							
HY1			286	291						
HY1			286	291						
HY1	P2.4	23	286	291						
HY1			214	224						
HY1			214	224						
HY1	P2.4	8	214	224						
HY1			299	303						
HY1			301	305						
HY1	P2.4	9	301	303						
HY1			320	328						
HY1			303	318	328					
HY1	P2.4	15	303	318	328					
HY1			284	302						
HY1			284	305						
HY1	P2.4	17	284	303						
HY1			250	285						
HY1			250	285						
HY1	P2.4	10	250	285						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY1			151	160	170	177	187			
HY1			160	170	178	187	208			
HY1	P2.4	25	160	170	177	187	208			
HY1			256	263	297					
HY1			256	263	297					
HY1	P2.4	11	256	263	297					
HY1			276							
HY1			276							
HY1	P2.6	28	276							
HY1			181	186	196					
HY1			181	186	196					
HY1	P2.6	21	181	186	196					
HY1			286	302						
HY1			286	302						
HY1	P2.6	23	286	302						
HY1			206	212	219	226				
HY1			206	219	226					
HY1	P2.6	8	206	212	219	226				
HY1			287	298-2						
HY1			287	298-2						
HY1	P2.6	9	287	297						
HY1			264	286						
HY1			286							
HY1	P2.6	15	264	286						
HY1			384	301						
HY1			284	294	301					
HY1	P2.6	17	284	301						
HY1			251	257						
HY1			251	257						
HY1	P2.6	10	251	257						
HY1			151	160	168	197				
HY1			160	170	197					
HY1	P2.6	25	151	160	170	197				
HY1			256	263	283					
HY1			263	283						
HY1	P2.6	11	256	263	283					
HY1			270	308						
HY1			270	308						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY3	Q1.8	28	270	308						
HY3			181							
HY3			181							
HY3	Q1.8	21	181							
HY3			302	312						
HY3			302	312						
HY3	Q1.8	23	302	312						
HY3			200	208	216	226				
HY3			200	208	216	226				
HY3	Q1.8	8	200	208	216	226				
HY3			287	298-2	303					
HY3			287	298-2	303					
HY3	Q1.8	9	287	297	303					
HY3			286							
HY3			286							
HY3	Q1.8	15	286							
HY3			301	305-2	330					
HY3			301	305-2	341					
HY3	Q1.8	17	301	305	330					
HY3			251	263						
HY3			251	263						
HY3	Q1.8	10	251	263						
HY3			151	158	168	201				
HY3			151	158	170	201				
HY3	Q1.8	25	151	158	170	201				
HY3			243	261	283	316				
HY3			261	283	316					
HY3	Q1.8	11	243	261	283	316				
HY3			270	306						
HY3			270	308						
HY3	Q2.0	28	270	308						
HY3			181							
HY3			181							
HY3	Q2.0	21	181							
HY3			302	312						
HY3			302	312						
HY3	Q2.0	23	302	312						
HY3			158	194	200	203	208	216	226	

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY3			194	200	203	208	212	216	226	
HY3	Q2.0	8	194	200	203	208	216	226		
HY3			287	298-2	303	310				
HY3			287	298-2	303					
HY3	Q2.0	9	287	297	303					
HY3			286							
HY3			286							
HY3	Q2.0	15	286							
HY3			301	305	341					
HY3			301	305-2						
HY3	Q2.0	17	301	305	341					
HY3			251	263						
HY3			251	263						
HY3	Q2.0	10	251	263						
HY3			151	158	170	201				
HY3			151	158	170	201				
HY3	Q2.0	25	151	158	170	201				
HY3			251	283						
HY3			261	283	316					
HY3	Q2.0	11	261	283	316					
HY3			306							
HY3			263	270	308					
HY3	Q2.2	28	306							
HY3			181							
HY3			181							
HY3	Q2.2	21	181							
HY3			302	312						
HY3			302	312						
HY3	Q2.2	23	302	312						
HY3			200	216	226					
HY3			200	216	226					
HY3	Q2.2	8	200	216	226					
HY3			298-2	303						
HY3			298-2	303						
HY3	Q2.2	9	297	303						
HY3			286							
HY3			286							
HY3	Q2.2	15	286							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY3			301	305						
HY3			301	305						
HY3	Q2.2	17	301	305						
HY3			251	263						
HY3			251	263						
HY3	Q2.2	10	251	263						
HY3			151	158	170	201				
HY3			151	158	170	201				
HY3	Q2.2	25	151	158	170	201				
HY3			261	283						
HY3			261	283	316					
HY3	Q2.2	11	261	283	316					
HY3			-9							
HY3			261	270	276	306				
HY3	Q2.4	28	261	270	276	306				
HY3			179	181						
HY3			179	181						
HY3	Q2.4	21	179	181						
HY3			302	312						
HY3			302	312						
HY3	Q2.4	23	302	312						
HY3			200	208	216	226				
HY3			200	208	216	226				
HY3	Q2.4	8	200	208	216	226				
HY3			287	298-2	303					
HY3			287	298-2	303					
HY3	Q2.4	9	287	297	303					
HY3			286							
HY3			286							
HY3	Q2.4	15	286							
HY3			301	305						
HY3			290	301	305	341				
HY3	Q2.4	17	301	305						
HY3			251	263						
HY3			251	263						
HY3	Q2.4	10	251	263						
HY3			151	158	170	201				
HY3			158	170	201					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
HY3	Q2.4	25	151	158	170	201				
HY3			261	283						
HY3			261	283	316					
HY3	Q2.4	11	261	283	316					
HY3			276	290						
HY3			276	290						
HY3	Q2.6	28	276	290						
HY3			181	186	196					
HY3			181	186	196					
HY3	Q2.6	21	181	186	196					
HY3			286	289						
HY3			286	289						
HY3	Q2.6	23	286	289						
HY3			206	219						
HY3			206	219						
HY3	Q2.6	8	206	219						
HY3			298-2	305						
HY3			298-2	305						
HY3	Q2.6	9	297	305						
HY3			326							
HY3			310	326						
HY3	Q2.6	15	310	326						
HY3			278	284	294	306				
HY3			278	284	294	306				
HY3	Q2.6	17	278	284	294	306				
HY3			251	257						
HY3			251	257						
HY3	Q2.6	10	251	257						
HY3			160	168	197					
HY3			160	168	197					
HY3	Q2.6	25	160	168	197					
HY3			263							
HY3			261	263						
HY3	Q2.6	11	261	263						
HY3			257	280						
HY3			257	288						
Bewitched	R1.0	28	257	280						
Bewitched			181	196						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Bewitched			181	196						
Bewitched	R1.0	21	181	196						
Bewitched			286	293-2						
Bewitched			286	289	296					
Bewitched	R1.0	23	286	294						
Bewitched			210	226	252					
Bewitched			226							
Bewitched	R1.0	8	210	226	252					
Bewitched			299	311						
Bewitched			293	305						
Bewitched	R1.0	9	299	311						
Bewitched			288	304						
Bewitched			277	282	304					
Bewitched	R1.0	15	288	304						
Bewitched			298	328						
Bewitched			278	291	296	311				
Bewitched	R1.0	17	298	326						
Bewitched			255	268	311					
Bewitched			251	308						
Bewitched	R1.0	10	255	268	311					
Bewitched			158	164	170	184	191	210		
Bewitched			158	164	184	191	199			
Bewitched	R1.0	25	158	164	170	184	191	210		
Bewitched			256	263						
Bewitched			256	263	293					
Bewitched	R1.0	11	256	263						
Bewitched	R1.2	28	257	288						
Bewitched	R1.2	21	181	196						
Bewitched	R1.2	23	286	289	296					
Bewitched	R1.2	8	226							
Bewitched	R1.2	9	293	305						
Bewitched	R1.2	15	277	282	304					
Bewitched	R1.2	17	278	291	296	311				
Bewitched	R1.2	10	251	308						
Bewitched	R1.2	25	158	164	184	191	199			
Bewitched	R1.2	11	256	263	293					
Bewitched			254	284	288	315				
Bewitched			288							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Award	R1.4	28	254	284	288	315				
Award			181							
Award			181	196						
Award	R1.4	21	181							
Award			286	291						
Award			286	289	296	326				
Award	R1.4	23	286	291						
Award			203	212	216					
Award			226							
Award	R1.4	8	203	212	216					
Award			298	306						
Award			293	305						
Award	R1.4	9	298	306						
Award			277	282	292					
Award			277	282	304					
Award	R1.4	15	277	282	292					
Award			278	284	295	306				
Award			278	291	311					
Award	R1.4	17	278	284	295	306				
Award			255	260						
Award			308							
Award	R1.4	10	255	260						
Award			149	160	164	177	191	199		
Award			158	163	164	184	191	199		
Award	R1.4	25	149	160	164	177	191	199		
Award			254	263						
Award			256	261	293					
Award	R1.4	11	254	263						
Award	R1.6	28	288							
Award	R1.6	21	181	196						
Award	R1.6	23	286	289	296	326				
Award	R1.6	8	226							
Award	R1.6	9	293	305						
Award	R1.6	15	277	282	304					
Award	R1.6	17	278	291	311					
Award	R1.6	10	308							
Award	R1.6	25	158	163	165	184	191	199		
Award	R1.6	11	256	261	293					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Award			257	280						
Award			257	288						
Nuglade	R2.0	28	257	288						
Nuglade			179	196						
Nuglade			179	194	196					
Nuglade	R2.0	21	179	196						
Nuglade			286	289	296					
Nuglade			286	289						
Nuglade	R2.0	23	286	289	296					
Nuglade			219	226						
Nuglade			219	226						
Nuglade	R2.0	8	219	226						
Nuglade			293	305						
Nuglade			293	305						
Nuglade	R2.0	9	293	305						
Nuglade			277	282	304					
Nuglade			277	282	304					
Nuglade	R2.0	15	277	282	304					
Nuglade			278	291	296	311				
Nuglade			278	291	196	311				
Nuglade	R2.0	17	278	291	296	311				
Nuglade			308							
Nuglade			308							
Nuglade	R2.0	10	308							
Nuglade			158	163	184	191	199			
Nuglade			158	163	184	191	199			
Nuglade	R2.0	25	158	163	184	191	199			
Nuglade			256	263	293					
Nuglade			256	263	293					
Nuglade	R2.0	11	256	263	293					
Nuglade	S2.2	28	257	288						
Nuglade	S2.2	21	179	194	196					
Nuglade	S2.2	23	286	289						
Nuglade	S2.2	8	219	226						
Nuglade	S2.2	9	293	305						
Nuglade	S2.2	15	277	282	303					
Nuglade	S2.2	17	278	291	296	311				
Nuglade	S2.2	10	308							

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Nuglade	S2.2	25	158	163	184	191	199			
Nuglade	S2.2	11	256	263	293					
Nuglade			280							
Nuglade			280							
Bedazzled	S3.0	28	280							
Bedazzled			181	196	199					
Bedazzled			181	196	199					
Bedazzled	S3.0	21	181	196	199					
Bedazzled			286	291	293-2					
Bedazzled			286	291	293-2					
Bedazzled	S3.0	23	286	291	293					
Bedazzled			210	226	252					
Bedazzled			210	226	242	252				
Bedazzled	S3.0	8	210	226	252					
Bedazzled			299	311						
Bedazzled			299	311						
Bedazzled	S3.0	9	299	311						
Bedazzled			288	304						
Bedazzled			288	304						
Bedazzled	S3.0	15	288	304						
Bedazzled			298	306	328					
Bedazzled			298	302	306	328				
Bedazzled	S3.0	17	298	306	328					
Bedazzled			255	268	277	311				
Bedazzled			255	268	276	311				
Bedazzled	S3.0	10	255	268	277	311				
Bedazzled			158	164	170	186	210			
Bedazzled			158	164	170	187	210			
Bedazzled	S3.0	25	158	164	170	186	210			
Bedazzled			261	263						
Bedazzled			261	263						
Bedazzled	S3.0	11	261	263						
Bedazzled	S3.2	28	280							
Bedazzled	S3.2	21	181	196	199					
Bedazzled	S3.2	23	286	291	293					
Bedazzled	S3.2	8	210	226	242	252				
Bedazzled	S3.2	9	299	311						
Bedazzled	S3.2	15	288	304						

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Bedazzled	S3.2	17	298	302	306	328				
Bedazzled	S3.2	10	255	268	276	311				
Bedazzled	S3.2	25	158	164	170	187	210			
Bedazzled	S3.2	11	261	263						
Bedazzled			257	280						
Bedazzled			280							
Bedazzled			280							
Bedazzled	S3.4	28	280							
Bedazzled			179	199						
Bedazzled			181	199						
Bedazzled			181	199						
Bedazzled	S3.4	21	181	199						
Bedazzled			286	291						
Bedazzled			286	289	291					
Bedazzled			286	289	291					
Bedazzled	S3.4	23	286	289	291					
Bedazzled			226	252						
Bedazzled			226	252						
Bedazzled			226	252						
Bedazzled	S3.4	8	226	252						
Bedazzled			299	311						
Bedazzled			299	311						
Bedazzled			299	311						
Bedazzled	S3.4	9	299	311						
Bedazzled			288	304						
Bedazzled			288	304						
Bedazzled			288	304						
Bedazzled	S3.4	15	288	304						
Bedazzled			302	306						
Bedazzled			302	306						
Bedazzled			302	306						
Bedazzled	S3.4	17	302	306						
Bedazzled			255	268						
Bedazzled			255	268	276	311				
Bedazzled			255	268	276	311				
Bedazzled	S3.4	10	255	268	276	311				
Bedazzled			162	164	184	191	210			
Bedazzled			164	187	210					

Table B.3. Allele lengths for each locus for each sample (continued).

Site Code	Sample Name	Marker	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8
Bedazzled			164	187	210					
Bedazzled	S3.4	25	164	187	210					
Bedazzled			261							
Bedazzled			263							
Bedazzled			263							
Bedazzled	S3.4	11	263							
Bedazzled	S3.6	28	280							
Bedazzled	S3.6	21	181	199						
Bedazzled	S3.6	23	286	289	291					
Bedazzled	S3.6	8	226	252						
Bedazzled	S3.6	9	299	311						
Bedazzled	S3.6	15	288	304						
Bedazzled	S3.6	17	302	306						
Bedazzled	S3.6	10	255	268	276	311				
Bedazzled	S3.6	25	164	187	210					
Bedazzled	S3.6	11	263							

APPENDIX C. PERMIT FOR COLLECTING PLANT SAMPLES FOR THE GENETIC DIVERSITY AND FLOW CYTOMETRY STUDY IN 2012 AND 2013

United States Department of the Interior
FISH AND WILDLIFE SERVICE
Audubon National Wildlife Refuge
3275 11th St. NW
Coleharbor, ND 58531-9419

May 7, 2012

Dr. Shawn Dekeyser
North Dakota State University
131 Walster Hall, PO Box 6050
Fargo, ND 58108

Dear Dr. Dekeyser,

This letter will serve as your authorization to conduct survey and research activities on Waterfowl Production Areas and National Wildlife Refuges in North Dakota and South Dakota in coordination with the Native Prairie Adaptive Management Project. The planned studies include: 1) Kentucky bluegrass response to management techniques; 2) Abiotic factors associated with Kentucky bluegrass invasion; 3) Kentucky bluegrass genetics analysis.

This authorization will be for 2012- 2013. Conditions of this authorization include:

*contacting the appropriate management office prior to any field activities to receive final approval and any special conditions.

*no vehicle travel off of established trails will be allowed.

*all information, data, studies or project reports must be provided to the Service.

If we can be of any further assistance, please let me know.

Sincerely,

Lloyd Jones
Project Leader

cc: ND & SD WMD's & NWR's

APPENDIX D. PERMIT FOR COLLECTING PLANT SAMPLES FROM BLUESTEM PRAIRIE IN 2013. SAMPLES WERE USED FOR FLOW CYTOMETERY PROJECT

The Nature Conservancy
Protecting nature. Preserving life.

The Nature Conservancy in Minnesota
11101 West River Parkway, Suite 200
Minneapolis, MN 55415

tel [612] 331-0750
fax [612] 331-0770

nature.org

RESEARCH PERMIT

May 21, 2013

Lauren Dennhardt
North Dakota State University,
Department of Biological Sciences 651-503-6979 lauren.dennhardt*at* ndsu.edu
1340 Bolley Drive,
Stevens 218,
Fargo, ND 58102

RE: The competitive behavior, population genetics, and ploidy of an important invasive species in native prairies of the prairie pothole region, Kentucky bluegrass (*Poa pratensis* L.)

This Research Permit ("Permit") serves as permission for you to conduct research on The competitive behavior, population genetics, and ploidy of an important invasive species in native prairies of the prairie pothole region, Kentucky bluegrass (*Poa pratensis* L.) as described in the attached Permit Application (the "Research") at the following TNC Preserve(s)(s): Bluestem Prairie SNA (the "Preserve(s)"). Since Bluestem Prairie SNA is also a Scientific and Natural Area(s), you will need a separate permit from the Minnesota Department of Natural Resources. Please call or e-mail Mark Cleveland, DNR Scientific and Natural Areas Management Coordinator, at 651-259-5094 or mark.cleveland*at* state.mn.us regarding this separate permit. The Research is subject to the following requirements:

1. **Contact stewardship staff (listed below) before entering the Preserve(s)** to avoid conflicts with stewardship management activities such as prescribed burning.
2. The Research must be completed by June 20, 2013. Research activities and sampling methods will be carried out as outlined in the attached Permit Application. All field markers, equipment, and other materials must be removed from the Preserve(s) by this date.
3. Minimize the spread of invasive species while conducting the Research (Please refer to http://mipn.org prevention.html for helpful tips and information from the Midwest Invasive Plant Network).
4. No vehicles may be driven on the Preserve(s).
5. Carry this letter while on the Preserve(s) – with an attached copy of your Permit Application- and extend courtesy to other site visitors, explaining the Research when necessary.
6. You and/or your assistants are using the Preserve(s) at your own risk. You agree to take all necessary safety precautions to protect yourself, your assistants, and other Preserve(s) visitors. The Conservancy makes no warranties or representations concerning the suitability of the Preserve(s) for any purpose. You hereby indemnify the Conservancy against any loss or damage arising from your presence on the Preserve(s).
7. Acknowledge The Nature Conservancy in any presentations or publications generated by this work.
8. Submit electronic copies of: a preliminary research summary by December 31, 2013, and a final report upon completion of your work, to jpastika*at* tnc.org and mcornett*at* tnc.org. Include maps and spatial data with your report. We would also appreciate receiving a copy of any future peer-reviewed publications that summarize work conducted on our lands – in pdf format if possible.
9. If you have questions about the Preserve(s)' management history or planned management activities (e.g. prescribed fire, weed control, mowing), please feel free to contact **Matt Mecklenburg, Land Steward at 218-498-2679.**
10. The Conservancy may terminate this Permit at any time upon two weeks written notice. In addition, if you default in performance of this Permit, whether for circumstances within or beyond your control, the Conservancy may immediately terminate this Permit by written notice to you.
11. This Permit is not effective until you sign and date below to acknowledge your agreement with the terms and conditions set forth in this Permit.

If you have any questions or comments about this permit, please feel free to call me at 219-727-6119.

Sincerely,

Meredith Cornett
Director of Conservation Science, TNC

ec/cc: Brian Winter, Matt Mecklenburg, Marissa Ahlering, Phil Gerla, Mark Cleveland

I agree to abide by the terms and conditions set forth in this Research Permit

Signature Date 5-21-13

Lauren Dennhardt
Print Name

APPENDIX E. MINNESOTA DEPARTMENT OF NATURAL RESOURCES SCIENTIFIC AND NATURAL AREAS PERMIT FOR 2013. THIS PERMIT ALLOWS FOR THE COLLECTION OF PLANTS FOR THE FLOW CYTOMETRY STUDY IN 2013

STATE OF MINNESOTA
DEPARTMENT OF NATURAL RESOURCES
DIVISION OF ECOLOGICAL & WATER RESOURCES
SCIENTIFIC AND NATURAL AREAS PROGRAM

SPECIAL PERMIT NUMBER: **2013-23R**
SCIENTIFIC AND NATURAL AREAS: **Bluestem Prairie Scientific and Natural Areas**

DATE: May 23, 2013

By virtue of the authority conferred on me by the Commissioner of Natural Resources relative to Scientific and Natural Areas, I grant permission to:

Lauren Dennhardt
North Dakota State University, Department of Biological Sciences
1340 Bolley Drive, Stevens 218, Fargo, ND 58102
Work Telephone: 651-503-6979
E-mail: lauren.dennhardt@ndsu.edu

With field crew members: TBA

to enter upon the above Scientific and Natural Area (SNA) to conduct a study of **The competitive behavior, population genetics, and ploidy of an important invasive species in native prairies of the prairie pothole region, Kentucky bluegrass** as described in the 2013 application (dated 5/17/13), and under the conditions listed below:

It is understood that the above named persons have a clear understanding of the purpose and long-term goal of state Scientific and Natural Areas. In keeping with this purpose, they shall always conduct their activities in a manner that is least disruptive to the on-going natural processes of these areas. All activities carried out must be in accordance with the proposal submitted. Permission must be received from the SNA Program if the permitee desires or anticipates deviating from this permit. In addition, the following conditions are placed on the proposal submitted:

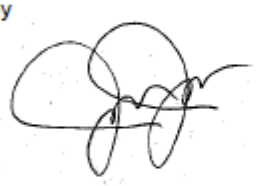
1. **All work shall be done to prevent the inadvertent transport of invasive species**. Order 113 is incorporated into this permit by reference and may be found at http://files.dnr.state.mn.us/assistance/grants/habitat/heritage/oporder_113.pdf. **Please note**: There are pockets of exotic invasive plants on all of these sites. The permitee shall prevent invasive species from entering into or spreading within a project site by **cleaning equipment, foot gear, and clothing prior to arriving at the project site and before moving from area to area in the project site**
2. No motorized vehicle may be used within the SNA boundary.
3. Soil samples will be taken as described in the permit application at **Bluestem Prairie Scientific and Natural Areas**.
4. Contact site manager to coordinate placement of these instruments: Bluestem Prairie SNA: Shelley Hedtke, SNA Specialist, shelley.hedtke@state.mn.us, 218-739-7576 ex. 262 (o)
5. All markers, equipment, and other items used during the research shall be removed at the end of the study and disturbed soil replaced in a manner as close to its original arrangement as possible
6. Equipment and procedures used to collect soil samples or mark plots or other features should be placed or used so as not to cause damage to the resources
7. **Any soil boring holes, soil sample spots, or sensor soil slits must be back filled, or closed (e.g. with a boot heel)**
8. Please carry this permit while on the SNA and extend courtesy to any other site visitors, explaining this research work when necessary.
9. You are using the SNA at your own risk. You agree to take all necessary safety precautions to protect yourself, your assistants, and any other SNA visitors.
10. Please acknowledge the Minnesota DNR, Scientific and Natural Areas Program in any articles and presentations concerning this research.

11. Please submit electronic copies of: a preliminary research summary December 31, 2013; and a final report upon completion of your work, to mark.cleveland@state.mn.us. We would also appreciate receiving a copy of any future peer-reviewed publications that summarize work conducted on our lands – in pdf format if possible.

As with all SNAs, the site you have selected may be subject to planned management activities (e.g. brush and tree removal, prescribed burns, seed harvest, etc) during the duration of your permitted activities.

This permit is valid through December 31, 2013 and may be revoked at any time to protect the resources of the SNA upon verbal or written communication. This permit may be renewed for fieldwork in 2013.

By



James Japs
Division of Ecological & Water Resources
500 Lafayette Rd., Box 25
St. Paul, MN 55155-4025

This SCIENTIFIC AND NATURAL AREA was established to protect and perpetuate Minnesota's rare and unique natural resources for nature observation, education and research purposes.

Principal activities which are **UNLAWFUL** in the use of this area are listed below:

* Collecting plants, animals, rocks or fossils
* Camping, picnicking, and swimming
* Horses, dogs, and other pets
* Snowmobiles and other motorized vehicles
* Hunting, trapping, fishing and boating
* Entry into restricted areas and sanctuaries

APPENDIX F. COPYRIGHT FORM TO USE CHAPTER THREE IN THE DISSERTATION

allen press™
PUBLISHING SERVICES

Date: January 13, 2016

Dear Lauren Dennhardt,

On behalf of Allen Press Publishing Services, I am pleased to grant permission to you for the reprinting of the following:

"There is no evidence of geographical patterning among invasive Poa pratensis L. populations in the northern Great Plains." by Lauren Dennhardt, Edward DeKeyser, Sarah Tennefos, and Steven Travers appearing in *Weed Science* (in-press) (2016).

For use in PhD dissertation.

This permission is a one-time, non-exclusive, electronic worldwide grant for English language use as described in this letter, and is subject to the following conditions:

1. No payment required.
2. Each copy containing our material that you reproduce or distribute must bear the appropriate copyright information, crediting the author, journal, and publisher (*Weed Science,* Allen Press Publishing Services).

If these terms are acceptable, please sign and date, and fax back to my attention at 785-843-1853. This permission will be effective upon our receipt of the signed contract. If applicable, when sending payment, please make clear reference to our title and author. Materials should be addressed to *Weed Science*, c/o Marilyn Kearney, P.O. Box 1897, Lawrence, KS 66044.

Sincerely,

Marilyn Kearney
Publishing Specialist
Allen Press Publishing Services

AGREED: _____ DATE: 1/20/16

_____ We have elected not to use this material

APPENDIX G. SUPPLEMENTARY MATERIAL FOR CHAPTER 4

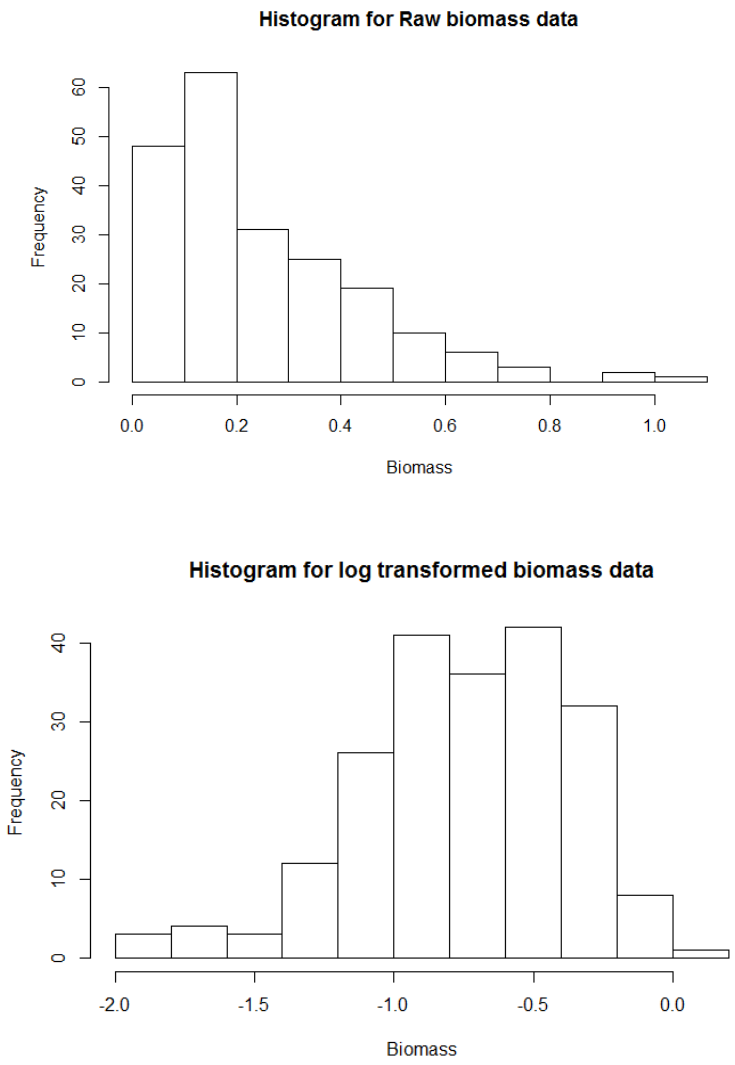


Figure G.1. Histograms of the raw (top) and transformed (bottom) biomass data for the data which did not included undetectable biomass (less than 0.00).

Table G.1. Two-way ANOVA on the log transformed data without the dead plants for both the measured and competitor plants. Analysis was conducted in R (R Core Team 2012).

	df	MS	F -value	P-value
Measured	3	1.87	17.50	<0.001***
Competitor	3	0.69	6.42	<0.001***
Measured X Competitor	9	0.14	1.28	0.252^{NS}
Residuals	192	0.11		

Table G.2. Tukey's HSD on all measured plants without the dead plants after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log	SD	Sample size	Min	Max	Tukey's Assignment
BOGR	-0.85	0.38	52	-1.95	-0.04	b
NAVI	-0.94	0.32	55	-1.85	-0.36	b
PASM	-0.54	0.34	51	-1.73	0.01	a
POPR	-0.62	0.33	50	-1.32	-0.03	a

Table G.3. Tukey's HSD on all competitor plants without the dead plants after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's Assignment
BOGR	-0.64	0.31	52	-1.59	-0.12	a
NAVI	-0.71	0.35	56	-1.95	-0.04	ab
PASM	-0.79	0.48	49	-1.85	0.01	ab
POPR	-0.83	0.34	51	-1.83	-0.24	a

Table G.4. Overall one-way ANOVA on Poa pratensis competitors without the dead plants using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.242	2.475	0.0733
Residuals	46	0.098		

Table G.5. Tukey's HSD on all competitors without the dead plants against Poa pratensis after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.48	0.09	12	-1.00	-0.21	a
NAVI	-0.63	0.38	11	-1.28	-0.16	a
PASM	-0.47	0.33	8	-0.90	-0.03	a
POPR	-0.75	0.29	19	-1.32	-0.24	a

Table G.6. Overall one-way ANOVA on Bouteloua gracilis competitors without the dead plants using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.334	2.600	0.063
Residuals	48	0.128		

Table G.7. Tukey's HSD on all competitors without the dead plants against Bouteloua gracilis after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's Assignment
BOGR	-0.72	0.23	19	-1.11	-0.23	a
NAVI	-0.79	0.46	12	-1.95	-0.04	a
PASM	-1.10	0.36	9	-1.63	-0.53	a
POPR	-0.92	0.41	12	-1.83	-0.42	a

Table G.8. Overall one-way ANOVA on Pascopyrum smithii competitors without the dead plants using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.055	0.463	0.710
Residuals	47	0.119		

Table G.9. Tukey's HSD on all competitors without the dead plants against Pascopyrum smithii after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.44	0.24	10	-0.98	-0.12	a
NAVI	-0.51	0.36	11	-1.17	-0.15	a
PASM	-0.57	0.42	21	-1.73	0.01	a
POPR	-0.61	0.20	9	-0.86	-0.31	a

Tale G.10. Overall one-way ANOVA on Nassella viridula competitors without the dead plants using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.423	5.564	0.002
Residuals	51	0.083		

Table G.11. Tukey's HSD on all competitors without the dead plants against Nassella viridula after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.83	0.38	11	-1.59	-0.36	a
NAVI	-0.80	0.20	22	-1.36	-0.50	a
PASM	-1.19	0.34	11	-1.85	-0.79	b
POPR	-1.07	0.29	11	-1.74	-0.76	ab

Table G.12. Two-way ANOVA on the log transformed data for both the measured and competitor plants. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Measured	3	0.437	3.174	0.0248*
Competitor	3	0.504	3.661	0.013*
Measured X Competitor	9	0.128	0.930	0.4994^{NS}
Residuals	259	0.138		

Table G.13. Tukey's HSD on all measured plants after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	Log of biomass	SD	Sample size	Min	Max	Tukey's Assignment
BOGR	-0.84	0.34	70	-1.30	-0.02	b
NAVI	-0.84	0.27	65	-1.30	-0.31	ab
PASM	-0.68	0.44	70	-1.30	0.03	a
POPR	-0.74	0.42	70	-1.30	-0.00	ab

Table G.14. Tukey's HSD on all competitor plants after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.72	0.39	69	-1.30	-0.09	a
NAVI	-0.70	0.36	67	-1.30	-0.02	a
PASM	-0.82	0.42	69	-1.30	0.03	a
POPR	-0.85	0.34	70	-1.30	0.21	a

Table G.15. Overall one-way ANOVA on Poa pratensis competitors using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.31	1.83	0.1506
Residuals	66	0.17		

Table G.16. Tukey's HSD on all competitors against Poa pratensis after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.54	0.38	14	-1.30	-0.17	a
NAVI	-0.69	0.42	14	-1.30	-0.13	a
PASM	0.79	0.51	14	-1.30	-0.00	a
POPR	-0.84	0.37	28	-1.30	-0.21	a

Table G.17. Overall one-way ANOVA on Bouteloua gracilis competitors using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.209	1.826	0.151
Residuals	66	0.114		

Table G.18. Tukey's HSD on all competitors against Bouteloua gracilis after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log	std	r	Min	Max	Tukey's HSD
BOGR	-0.54	0.38	14	-1.30	-0.17	a
NAVI	-0.69	0.42	14	-1.30	-0.13	a
PASM	-0.79	0.51	14	-1.30	-0.00	a
POPR	-0.84	0.37	28	-1.30	-0.21	a

Table G.19. Overall one-way ANOVA on Pascopyrum smithii competitors using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.086	0.432	0.731
Residuals	66	0.199		

Table G.20. Tukey's HSD on all competitors against Pascopyrum smithii after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.64	0.46	14	-1.30	-0.09	a
NAVI	-0.66	0.47	15	-1.30	-0.12	a
PASM	-0.65	0.44	27	-1.30	0.03	a
POPR	-0.80	0.41	14	-1.30	-0.27	a

Table G.21. Overall one-way ANOVA on Nassella viridula competitors using log transformed data. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Competitor	3	0.285	4.501	0.006
Residuals	61	0.063		

Table G.22. Tukey's HSD on all competitors against Nassella viridula after log transformation. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

	log of biomass	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.77	0.33	13	-1.30	-0.31	ab
NAVI	-0.73	0.23	24	-1.30	-0.44	a
PASM	-0.99	0.22	14	-1.30	-0.67	b
POPR	-0.95	0.24	14	-1.30	-0.65	ab

Table G.23. ANOVA on linear regression for percent survival against average biomass without dead plants.

	df	MS	F-value	P-value
Average biomass	1	0.113	0.001	0.980
Residuals	14	170.712		

Table G.24. Two way ANOVA on the median RII values between the measured plants and competitors. Analysis was conducted in R (R Core Team 2012).

	df	MS	F-value	P-value
Measured	3	0.138	8.677	0.012*
Competitor	3	0.041	2.575	0.167^{NS}
Residuals	5	0.016		

Table G.25. Tukey's HSD on all measured plants using the median RII values. Tukey's HSD was conducted using the Agricolae package in R (R Core Team 2012; Felip de Mendiburu 2015).

Measured plant	Median	SD	Sample size	Min	Max	Tukey's assignment
BOGR	-0.12	0.21	3	-0.34	0.08	ab
NAVI	-0.22	0.2	3	-0.38	0.01	b
PASM	-0.04	0.11	3	-0.17	0.03	ab
POPR	0.28	0.06	3	0.22	0.33	a

Table G.26. The biomass data for the end of the competition experiment after the plants were washed then dried for 48 hours.

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
NAVI	1	0.8394	0.1108	0.9502	27.1	Alive
BOGR	1	0.0497	0.909	0.9587	27	Alive
BOGR	2	0.07379	0.13348	0.20727	36	Dead
BOGR	2	0.05083	0.07976	0.13059	30	Dead
PASM	3	0.09665	0.22917	0.32582	32	Alive
BOGR	3	0.02051	0.05331	0.07382	0	Dead
NAVI	4	0.0231	0.01802	0.04112	0	Dead
POPR	4	0.01803	0.0524	0.07043	0	Dead
NAVI	5	0.04235	0.09273	0.13508	23	Alive
PASM	5	0.38638	0.65278	1.03916	39.1	Alive
PASM	6	0.15961	0.46519	0.6248	30.2	Alive
PASM	6	0.3082	0.60381	0.91201	37.2	Alive
BOGR	7	0.09481	0.17083	0.26564	31.2	Alive
POPR	7	0.13492	0.44224	0.57716	29	Alive
NAVI	8	0.09346	0.1643	0.25776	27.6	Alive
NAVI	8	0.08679	0.11931	0.2061	23.6	Alive
POPR	9	0.05868	0.15341	0.21209	26	Dead
PASM	9	0.22794	0.47372	0.70166	47.5	Alive
POPR	10	0.06646	0.29477	0.36123	26.5	Alive
POPR	10	0.108	0.33549	0.44349	25.7	Alive
POPR	11	0.25487	0.62564	0.88051	35	Alive
NAVI	11	0.03788	0.11792	0.1558	29.5	Alive
PASM	12	0.07708	0.16804	0.24512	27.5	Alive
NAVI	12	0.04301	0.16187	0.20488	28	Alive
POPR	12	0.05085	0.10709	0.15794		?
PASM	13	0.18822	0.32651	0.51473	35	Alive
BOGR	13	0.10679	0.26145	0.36824	39.5	Alive
POPR	14	0.16545	0.70206	0.86751	30.5	Alive
PASM	14	0.05533	0.19743	0.25276	31	Alive
PASM	15	0.12141	0.46508	0.58649	36.5	Alive
PASM	15	0.12478	0.44323	0.56801	33.5	Alive
POPR	16	0.20542	0.38436	0.58978	24.5	Alive
POPR	16	0.02214	0.04797	0.07011	17.5	Dead
POPR	17	0.07693	0.21235	0.28928	20.5	Alive
BOGR	17	0.05727	0.1958	0.25307	25.2	Alive
NAVI	18	0.06897	0.1571	0.22607	23.8	Alive
NAVI	18	0.01189	0.25933	0.27122	28.5	Alive
NAVI	19	0.12129	0.27828	0.39957	28.1	Alive

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
BOGR	19	0.04929	0.13791	0.1872	29.4	Alive
BOGR	20	0.06359	0.17904	0.24263	30.5	Alive
BOGR	20	0.07184	0.14782	0.21966	33.5	Alive
BOGR	21	0	0	0	0	Dead
BOGR	21	0	0	0	0	Dead
POPR	22	0.05134	0.11448	0.16582	0	Dead
POPR	22	0.02489	0.06109	0.08598	0	Dead
NAVI	23	0	0	0	0	Dead
PASM	23	0	0	0	0	Dead
NAVI	24	0	0	0	0	Dead
NAVI	24	0	0	0	0	Dead
BOGR	25	0	0	0	0	Dead
NAVI	25	0	0	0	0	Dead
NAVI	26	0	0	0	0	Dead
POPR	26	0	0	0	0	Dead
BOGR	27	0	0	0	0	Dead
PASM	27	0	0	0	0	Dead
POPR	28	0	0	0	0	Dead
PASM	28	0	0	0	0	Dead
PASM	29	0	0	0	0	Dead
PASM	29	0	0	0	0	Dead
BOGR	30	0.04854	0.16643	0.21497	34.5	Alive
POPR	30	0.1426	0.47487	0.61747	29.5	Alive
NAVI	31	0.03921	0.11655	0.15576	19.5	Alive
PASM	31	0.12278	0.33871	0.46149	30.2	Alive
POPR	32	0	0	0	0	Dead
POPR	32	0.06036	0.15457	0.21493	22.1	Dead
POPR	33	0.1478	0.41903	0.56683	27.2	Dead
PASM	33	0.06286	0.30148	0.36434	33.3	Dead
NAVI	34	0.0215	0.09047	0.11197	20	Dead
POPR	34	0.2316	0.69746	0.92906	32.2	Dead
NAVI	35	0.09544	0.29221	0.38765	37.5	Alive
NAVI	35	0.10403	0.1954	0.29943	35.5	Alive
NAVI	36	0.08285	0.18419	0.26704	31.7	Alive
BOGR	36	0.0945	0.14747	0.24197	32.2	Alive
POPR	37	0.23433	0.57299	0.80732	33	Alive
BOGR	37	0.01058	0.03258	0.04316	22.1	Dead
PASM	38	0.21304	0.43034	0.64338	33.8	Alive
BOGR	38	0.11759	0.29792	0.41551	36	Dead

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
BOGR	39	0.11654	0.28595	0.40249	55	Alive
BOGR	39	0.08408	0.18701	0.27109	36.5	Alive
PASM	40	0.0872	0.37462	0.46182	31	Alive
PASM	40	0.19469	0.51031	0.705	55	Alive
NAVI	41	0.16793	0.33391	0.50184	30.5	Alive
BOGR	41	0.13731	0.38549	0.5228	35.5	Alive
BOGR	42	0.21305	0.5928	0.80585	43.4	Alive
BOGR	42	0.15937	0.28741	0.44678	31.5	Alive
PASM	43	0.08986	0.28183	0.37169	30.1	Alive
POPR	43	0.22495	0.94074	1.16569	32.5	Alive
PASM	44	0.05537	0.29832	0.35369	43.5	Alive
PASM	44	0.21143	0.51542	0.72685	43.2	Alive
PASM	45	0.20817	0.48413	0.6923	34	Alive
BOGR	45	0	0	0	0	Dead
POPR	46	0.14191	0.62404	0.76595	31	Alive
BOGR	46	0.06197	0.19434	0.25631	29	Alive
POPR	47	0.08319	0.28021	0.3634	25	Alive
NAVI	47	0.0481	0.13151	0.17961	18	Alive
NAVI	48	0.1224	0.20927	0.33167	31	Alive
NAVI	48	0.17962	0.15951	0.33913	30.1	Alive
NAVI	49	0.02171	0.04754	0.06925	9.5	Alive
PASM	49	0	0	0	0	Dead
POPR	50	0	0	0	0	Dead
POPR	50	0	0	0	0	Dead
PASM	51	0.0428	0.05442	0.09722	24.5	Alive
PASM	51	0.09638	0.15193	0.24831	29.5	Alive
PASM	52	0.19349	0.34394	0.53743	43.1	Alive
BOGR	52	0.01316	0.03441	0.04757	17	Alive
BOGR	53	0.00841	0.01127	0.01968	0	Dead
NAVI	53	0.01424	0.02555	0.03979	9.5	Alive
PASM	54	0.03533	0.06701	0.10234	19.2	Dead
NAVI	54	0.035	0.05288	0.08788	11.5	Dead
BOGR	55	0.04517	0.07753	0.1227	0	Dead
BOGR	55	0	0	0	0	Dead
PASM	56	0	0	0	0	Dead
POPR	56	0	0	0	0	Dead
BOGR	57	0	0	0	0	Dead
POPR	57	0	0	0	0	Dead
NAVI	58	0.08014	0.17314	0.25328	19.2	Alive

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
NAVI	58	0.1104	0.15299	0.26339	21	Alive
NAVI	59	0.08429	0.09274	0.17703	23	Alive
POPR	59	0.03154	0.0832	0.11474	22.1	Alive
POPR	60	0	0	0	0	Dead
POPR	60	0.04284	0.05962	0.10246	17.2	Alive
POPR	61	0.16054	0.41212	0.57266	21.5	Alive
BOGR	61	0.14331	0.22991	0.37322	29	Alive
POPR	62	0.18681	0.58744	0.77425	24.5	?
PASM	62	0.10858	0.14503	0.25361	0	?
POPR	63	0.13917	0.15565	0.29482	0	Dead
POPR	63	0.06816	0.15765	0.22581	0	Dead
POPR	64	0.2152	0.48689	0.70209	27.5	Alive
NAVI	64	0.0426	0.05536	0.09796	20.2	Alive
BOGR	65	0.05	0.09545	0.14545	27	Alive
PASM	65	0.27581	0.48679	0.7626	28	Alive
BOGR	66	0.14508	0.43756	0.58264	41.5	Alive
BOGR	66	0.06144	0.14256	0.204	36.2	Alive
BOGR	67	0.08889	0.16093	0.24982	31.7	Alive
NAVI	67	0.36427	0.44111	0.80538	34	Alive
PASM	68	0.49255	0.71053	1.20308	38	Alive
NAVI	68	0.01935	0.0725	0.09185	22	Alive
PASM	69	0.04884	0.37513	0.42397	20.5	Alive
PASM	69	0.29992	0.25227	0.55219	36.5	Alive
NAVI	70	0.07111	0.18056	0.25167	9.3	Alive
NAVI	70	0.14427	0.31357	0.45784	0	Alive
BOGR	71	0.08039	0.29226	0.37265	0	Alive
POPR	71	0.12342	0.24143	0.36485	27	Alive
BOGR	72	0.06154	0.11977	0.18131	27.5	Dead
NAVI	72	0.27207	0.35093	0.623	33.5	Dead
BOGR	73	0	0	0	0	Dead
PASM	73	0	0	0	0	Dead
BOGR	74	0.1139	0.2182	0.3321	31.5	Alive
BOGR	74	0.11414	0.15067	0.26481	22.8	Alive
POPR	75	0.10916	0.33372	0.44288	24	Alive
NAVI	75	0.04024	0.15817	0.19841	24	Dead
POPR	76	0	0	0	0	Dead
PASM	76	0.10329	0.18294	0.28623	36.5	Alive
POPR	77	0	0	0	0	Dead
POPR	77	0	0	0	0	Dead

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
NAVI	78	0.1099	0.18779	0.29769	25.7	Alive
NAVI	78	0.04057	0.11694	0.15751	24.5	Dead
NAVI	79	0	0	0	0	Dead
PASM	79	0	0	0	0	Dead
PASM	80	0.05309	0.07236	0.12545	22.5	Dead
PASM	80	0.08812	0.07412	0.16224	23.4	Dead
BOGR	81	0	0	0	0	Dead
BOGR	81	0	0	0	0	Dead
PASM	82	0	0	0	0	Dead
BOGR	82	0	0	0	0	Dead
BOGR	83	0	0	0	0	Dead
POPR	83	0	0	0	0	Dead
BOGR	84	0	0	0	0	Dead
NAVI	84	0	0	0	0	Dead
PASM	85	0	0	0	0	Dead
NAVI	85	0	0	0	0	Dead
POPR	86	0	0	0	0	Dead
PASM	86	0.16229	0.22331	0.3856	42.5	Dead
POPR	87	0	0	0	0	Dead
NAVI	87	0	0	0	0	Dead
POPR	88		0.22758	0.22758	4.7	Dead
POPR	88	0	0	0	0	Dead
NAVI	89	0.01978	0.08997	0.10975	22.2	Dead
PASM	89	0.20558	0.54674	0.75232	53	Alive
PASM	90	0.21633	0.37005	0.58638	24	Dead
PASM	90	0.08898	0.45393	0.54291	29.5	Dead
POPR	91	0.11726	0.33473	0.45199	25	Dead
PASM	91	0.16155	0.49125	0.6528	37.6	Dead
POPR	92	0.1052	0.43882	0.54402	18	Dead
BOGR	92	0.08347	0.38504	0.46851	34.5	Dead
NAVI	93	0.03457	0.13545	0.17002	6.2	Dead
POPR	93	0.2118	0.37726	0.58906	9	Dead
POPR	94	0	0	0	0	Dead
POPR	94	0.26385	0.57258	0.83643	4.6	Dead
BOGR	95	0	0	0	0	Dead
PASM	95	0	0	0	0	Dead
BOGR	96	0.10583	0.20296	0.30879	43.5	Alive
BOGR	96	0.09903	0.24083	0.33986	51.5	Alive
BOGR	97	0.16824	0.34387	0.51211	30	Dead

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
NAVI	97	0.03332	0.09313	0.12645	19.3	Dead
PASM	98	0.18284	0.54544	0.72828	16	Dead
NAVI	98	0.02273	0.13075	0.15348	27.5	Dead
PASM	99	0.12775	0.37044	0.49819	19	Dead
PASM	99	0.13781	0.31617	0.45398	14.2	Dead
NAVI	100	0.08548	0.30346	0.38894	24.1	Dead
NAVI	100	0.04611	0.12534	0.17145	23	Dead
POPR	101	0.11884	0.16435	0.28319	20	Dead
PASM	101	0	0	0	0	Dead
POPR	102	0.0607	0.33626	0.39696	0	Dead
BOGR	102	0.02649	0.07997	0.10646	0	Dead
POPR	103	0.10457	0.28736	0.39193	21.6	Dead
NAVI	103	0.08819	0.17342	0.26161	21.7	Dead
POPR	104	0.07804	0.25322	0.33126	26	Dead
POPR	104	0.05978	0.24871	0.30849	25.8	Dead
NAVI	105	0.04791	0.05568	0.10359	21.6	Alive
BOGR	105	0.02752	0.14229	0.16981	27.5	Dead
NAVI	106	0.00314	0.01416	0.0173	0	Dead
PASM	106	0.08108	0.15377	0.23485	45	Dead
NAVI	107	0.09029	0.21964	0.30993	26	Alive
NAVI	107	0.03575	0.09084	0.12659	19.5	Alive
BOGR	108	0.07672	0.22162	0.29834	38.6	Alive
BOGR	108	0.11924	0.22244	0.34168	45	Alive
BOGR	109	0.01198	0.02335	0.03533	7	Dead
PASM	109	0.04125	0.10487	0.14612	20.5	Alive
PASM	110	0	0	0	0	Dead
PASM	110	0	0	0	0	Dead
POPR	111	0	0	0	0	Dead
NAVI	111	0	0	0	0	Dead
POPR	112	0.04837	0.0993	0.14767	0	Dead
BOGR	112	0.00589	0.01492	0.02081	0	Dead
POPR	113	0.05609	0.12483	0.18092	19.5	Alive
PASM	113	0.04001	0.13891	0.17892	37	Dead
POPR	114	0	0	0	0	Dead
POPR	114		0.36996	0.36996	0	Dead
NAVI	115	0.02048	0.09485	0.11533	24	Alive
PASM	115	0.11114	0.42312	0.53426	60	Alive
NAVI	116	0.04748	0.11588	0.16336	19.9	Dead
BOGR	116	0.11244	0.09865	0.21109	31.5	Dead

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
NAVI	117	0	0	0	0	Dead
NAVI	117	0.04505	0.23021	0.27526	28.2	Alive
BOGR	118	0.02788	0.07349	0.10137	17	Alive
PASM	118	0.26707	0.7573	1.02437	38.5	Dead
BOGR	119	0.07958	0.26307	0.34265	29.5	Dead
BOGR	119	0.09461		0.09461	48	Dead
PASM	120			0	35.5	Alive
PASM	120	0.31519	1.01881	1.334	44.5	Alive
NAVI	121	0.01133	0.0499	0.06123	24.5	Alive
POPR	121	0.05443	0.08295	0.13738	16.6	Alive
NAVI	122		0	0	0	Dead
BOGR	122	0.16258	0.31647	0.47905	51.2	Alive
NAVI	123	0.01016	0.01829	0.02845	10	Dead
PASM	123	0.22785	0.65047	0.87832	50	Dead
NAVI	124	0.05271	0.10363	0.15634	20.5	Dead
NAVI	124	0.1366	0.14858	0.28518	26.2	Dead
POPR	125	0.05666	0.12121	0.17787	6.5	Dead
POPR	125	0.07972	0.27965	0.35937	4.5	Dead
POPR	126	0.18274	0.53242	0.71516	9.3	Dead
BOGR	126	0.02549	0.07381	0.0993	0	Dead
POPR	127	0	0	0	0	Dead
PASM	127	0	0	0	0	Dead
BOGR	128	0.025	0.06436	0.08936	25	Alive
PASM	128	0.30074	0.56613	0.86687	45.2	Dead
BOGR	129	0.03873	0.08868	0.12741	15.4	Alive
BOGR	129	0	0	0	0	Dead
PASM	130	0.00341	0.01882	0.02223	0	Dead
PASM	130	0.14227	0.4133	0.55557	9.1	Alive
NAVI	131	0.10982	0.17275	0.28257	22	Alive
BOGR	131	0.05774	0.12576	0.1835	40	Alive
NAVI	132	0.02742	0.07558	0.103	19.7	Dead
POPR	132	0.08138	0.16547	0.24685	23	Dead
NAVI	133	0.00891	0.03909	0.048	0	Dead
PASM	133	0.04593	0.11461	0.16054	0	Dead
NAVI	134	0.01305	0.04362	0.05667	20.2	Dead
NAVI	134	0.05374	0.08354	0.13728	22.6	Dead
BOGR	135	0.06309	0.12321	0.1863	32	Dead
POPR	135	0.05384	0.12815	0.18199	20	Dead
BOGR	136	0.06973	0.07798	0.14771	0	Dead

Table G.26. The biomass data for the end of the competition experiment (continued).

Plant	ID	Root biomass	Stem biomass	Total	Height	Notes
PASM	136	0.04838	0.30647	0.35485	0	Dead
BOGR	137	0	0	0	0	Dead
BOGR	137	0	0	0	0	Dead
POPR	138	0	0	0	0	Dead
PASM	138	0	0	0	0	Dead
POPR	139	0.08579	0.13642	0.22221	22	Alive
POPR	139	0.05728	0.1334	0.19068	23	Alive
PASM	140	0	0	0	0	Dead
PASM	140	0	0	0	0	Dead

APPENDIX H. SUPPLEMENTARY MATERIAL FOR CHAPTER 5

Table H.1. Summary ANOVAs for Poa pratensis across years, plots across years, plots for 2014, and early and late sampling in 2014. Poa pratensis significantly changed in 2014, although not spatially or across early or late sampling in 2014. Tukey's honest significant difference test was executed in the R package Agricolae for each year (Felip de Mendiburu 2015).

	df	MS	F-value	P-value
Year	1	1678	15.33	0.000796
Residuals	21	109.5		
Plot (78-14)	5	124.3	0.63	0.68
Residuals	17	197.4		
Plot ('14 only)	5	715.6	2.178	0.207
Early or late	1	114.7	0.349	0.58
Residuals	5	328.6		

Year	Mean	SD	Sample size	Min	Max	Tukey's assignment
1978	0.33	0.51	6	0	1.2	b
1979	0.15	0.27	6	0	0.7	b
1998	0.9	0.62	5	0.1	1.6	b
2014	22.63	18.91	6	0.5	45.8	a

Table H.2. Summary ANOVAs for Bromus inermis across years, plots across years, plots for 2014, and early and late sampling in 2014. Bromus inermis significantly changed over the years, but was not detected in the Tukey's HSD test. Bromus inermis did not change spatially or across early or late sampling in 2014. Tukey's honest significant difference test was executed in the R package Agricolae for each year (Felip de Mendiburu 2015).

	df	MS	F-value	P-value
Year	1	44.18	6.45	0.019
Residuals	21	6.85		
Plot (78-14)	5	9.406	1.135	0.38
Residuals	17	8.289		
Plot ('14 only)	5	51.4	2.56	0.163
Early or late	1	79.05	3.937	0.104
Residuals	5	20.08		

Year	Mean	SD	Sample Size	Min	Max	Tukey's assignment
1978	0	0	6	0	0	a
1979	0.017	0.0408	6	0	0.1	a
1998	0	0	5	0	0	a
2014	3.6667	5.0696	6	0.45	13.45	a

Table H.3. Summary ANOVAs for grasses across years, plots across years, plots for 2014, and early and late sampling in 2014. Grasses significantly changed across years, specifically 2014 contained a larger percent cover than other years. Grasses did not change spatially over the years, spatially in 2014, or across early or late sampling in 2014. Tukey's honest significant difference test was executed in the R package Agricolae for each year (Felip de Mendiburu 2015).

	df	MS	F-value	P-value
Year	1	13864	43.12	<.0001
Residuals	21	261		
Plot (78-14)	5	43.52	0.0387	0.999
Residuals	17	1125.16		
Plot ('14 only)	5	106.58	2.112	0.216
Early or late	1	296.01	5.865	0.06
Residuals	5	50.47		

Year	Mean	SD	Sample Size	Min	Max	Tukey's Assignment
1978	28.45	12.70	6	8.9	44.6	b
1979	17.85	6.50	6	9.6	25.7	b
1998	27.06	6.44	5	20.1	36.7	b
2014	87.28	5.98	6	79.5	97.3	a

Table H.4. Summary ANOVAs for percent soil moisture across years. Differences in soil moisture were found between years for depths of 30-60 cm and 60-90 cm and spatially for depths of 0-30 cm and 60-90 cm. For the depth of 30-60 cm, 2014 was significantly different. Tukey's honest significant difference test was executed in the R package Agricolae for each depth when ANOVA was significant (Felip de Mendiburu 2015).

0-30 cm soils across years

	df	MS	F-value	P-value
Year	1	799.1	1.984	0.178
Residuals	16	402.9		
Plot	5	1088.2	7.237	0.00244
Residuals	12	150.4		

Plot	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	8.54	4.49	3	5.6	13.71	b
2	32.23	7.16	3	24.1	37.6	ab
3	20.36	8.10	3	15.1	29.69	b
4	29.57	11.47	3	21.6	42.72	b
5	63.42	11.54	3	51.5	76.5	a
6	17.79	21.82	3	4.2	42.96	b

30-60 cm soils across years

	df	MS	F-value	P-value
Year	1	587.80	10.56	0.00503
Residuals	16	55.70		
Plot	5	155.68	2.668	0.076
Residuals	12	58.35		

Year	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1978	13.8	6.38	6	6.4	22.4	b
1979	15.2	9.19	6	5.3	31.3	b
2014	26.6	7.23	6	14.95	35.81	a

Table H.4. Summary ANOVAs for percent soil moisture across years (continued).

60-90 cm soils across years

	df	MS	F- value	P-value
Year	1	205.99	8.12	0.01161
Residuals	16	25.38		
Plot	5	70.631	3.27	0.04286
Residuals	12	21.576		

Year	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1978	14.58	5.57	6	7.8	23.2	a
1979	14.27	5.46	6	4.9	20.4	a
2014	21.61	4.49	6	15.14	27.09	a

Plot	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	10.31	7.02	3	4.9	18.24	b
2	15.97	5.32	3	12.6	22.1	ab
3	17.11	3.7	3	14.4	21.33	ab
4	21.36	4.98	3	18	27.09	ab
5	23.12	2.68	3	20.4	25.76	a
6	13.05	2.49	3	10.3	15.14	ab

Table H.5. Summary ANOVAs for sedges across years, plots across years, plots for 2014, and early and late sampling in 2014. Sedges significantly changed across the plots in 2014, specifically plot 5 contained a larger percent cover than other plots. Sedges did not change spatially over the years, across time, or across early or late sampling in 2014. Tukey's honest significant difference test was executed in the R package Agricolae for each year (Felip de Mendiburu 2015).

	df	MS	F-value	P-value
Year	1	473.5	3.985	0.059
Residuals	21	118.8		
Plot (78-14)	5	263.41	2.711	0.056
Residuals	17	97.17		
Plot ('14 only)	5	869.1	86.192	<0.0001
Early or late	1	9.5	0.946	0.375
Residuals	5	10.1		

Plot ('14 only)	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	0.2	0.28	2	0	0.4	d
2	13.4	2.12	2	11.9	14.9	bc
3	18.15	2.76	2	16.2	20.1	bc
4	7.05	1.20	2	6.2	7.9	bcd
5	56.1	6.79	2	51.3	60.9	a
6	1.05	0.49	2	0.7	1.4	cd

Table H.6. Summary ANOVAs for forbs across years, plots across years, plots for 2014, and early and late sampling in 2014. Forbs significantly changed across years and spatially in 2014, specifically 2014 contained a lower percent cover than other years. Forbs did not change spatially over the years or across early or late sampling in 2014. Tukey's honest significant difference test was executed in the R package Agricolae for each year (Felip de Mendiburu 2015).

	df	MS	F-value	P-value
Year	1	15104.70	37.972	<0.0001
Residuals	22	397.80		
Plot (78-14)	5	192.26	0.1512	0.977
Residuals	18	1271.93		
Plot ('14 only)	5	71.64	6.291	0.0324
Early or late	1	34	2.986	0.1446
Residuals	5	11.39		

Year	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1978	71.55	12.69594	6	55.4	91.1	a
1979	82.15	6.052846	6	74.3	90.4	a
1998	59.2833	33.9441	6	9	79.9	a
2014	12.6333	5.98487	6	2.7	20.5	b

Plot (2014)	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	83.3	10.32	2	76	90.6	a
2	75.15	10.39	2	67.8	82.5	a
3	76.45	16.48	2	64.8	88.1	a
4	86.25	6.72	2	81.5	91	a
5	86	3.68	2	83.4	88.6	a
6	95.05	1.91	2	93.7	96.4	a

Table H.7. Summary ANOVAs on the 2014 percent soil data moisture data. Differences in soil moisture were found between early and late summer for depths of 30-60 cm and 60-90 cm. Tukey's honest significant difference test was executed in the R package Agricolae for each depth (Felip de Mendiburu 2015).

0-30 cm soils in 2014

	df	MS	F-value	P-value
Plot	5	2708.3	47.67	<.0001
Residuals	87	56.8		
Early or Late	1	93.93	0.465	0.497
Residuals	91	202.09		

Plot	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	13.7	3.47	20	8.8	20.8	d
2	37.61	5.45	20	29.1	49.1	b
3	29.7	4.92	20	18.6	40.3	c
4	42.73	7.93	20	32.9	61.4	b
5	62.27	31.66	3	43	98.8	a
6	42.96	7.38	10	34.4	59.5	b

30-60 cm soils in 2014

	df	MS	F-value	P-value
Plot	5	708.40	24.45	<.0001
Residuals	87	29.00		
Early or Late	1	737.30	12.60	<0.001
Residuals	91	58.50		

Plot	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	14.95	3.83	20	8.63	20.37	c
2	27.08	4.98	20	19.5	36.86	ab
3	24.77	3.48	20	19.96	30.61	b
4	32.36	7.51	20	24.04	49.48	ab
5	35.81	4.74	3	32.97	41.28	ab
6	24.62	6.88	10	16.11	35.86	b

Table H.7. Summary ANOVAs on the 2014 percent soil data moisture data (continued).

60-90 cm soils in 2014

	df	MS	F-value	P-value
Plot	5	256	26.39	<.0001
Residuals	80	9.7		
Early or Late	1	248.48	11.55	0.001
Residuals	84	21.52		

Plot	Mean	SD	Sample size	Min	Max	Tukey's Assignment
1	18.16	2.41	17	13.6	21.8	c
2	22.21	3.80	17	15.9	29.1	b
3	21.25	2.81	19	17.3	26.3	b
4	27.09	3.36	20	20.6	33.5	a
5	25.73	2.70	3	23.7	28.8	ab
6	15.14	3.00	10	9	19.5	c

Table H.8. Six separate ANOVAs on the two dbRDAs performed on plant and percent soil moisture data. The dbRDA was performed in vegan using the CAPSCALE argument and a Bray-Curtis dissimilarity matrix and ANOVAs were done using 200 permutations and a seed set of 44. Only the first axis of both dbRDAs was significant so we concluded a linear regression should be completed to visualize the interaction.

Functional Group Level

	df	variance	F-value	P-value
Model	3	0.62	2.38	0.092
Residuals	14	1.22		
30-60 cm	1	0.58	6.70	0.021
0-30 cm	1	0.03	0.31	0.647
60-90 cm	1	0.01	0.13	0.718
Residuals	14	1.25		
CAP1	1	0.62	7.13	0.018
CAP2	1	0.00	0.01	0.984
CAP3	1	0.00	0.00	1.000
Residual	14	1.22		

Species Level

	df	variance	F-value	P-value
Model	1	1.42	3.12	0.003
Residuals	16	7.29		
30-60 cm	1	1.42	3.12	0.01
Residuals	16	7.29		
CAP1	1	1.42	3.12	0.004
Residuals	16	7.29		

Table H.9. Data collected in 2014 for long-term climate change study. There were six plots at Bluestem prairie. We dropped 10 pins at 100 quadrats per plot. We collected data twice that summer. POPR=Poa pratensis, Sedge=Sedge family, SPPE=Spartina pectinata, BRIN=Bromus inermis, GR=Other grasses, FO=Forbs, and BR=Bare ground.

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O (0-30)	% H2O (30-60)	% H2O (60-90)
6/9/2014	1	1	1	0	0	0	9	0	0	13.2	16.0	14.1
6/9/2014	1	2	4	0	0	0	2	3	1			
6/9/2014	1	3	1	0	0	0	7	1	1			
6/9/2014	1	4	2	0	0	0	4	2	2			
6/9/2014	1	5	3	0	1	0	4	2	0			
6/9/2014	1	6	5	0	1	0	3	0	1			
6/9/2014	1	7	1	0	1	0	7	1	0			
6/9/2014	1	8	3	0	1	0	4	2	0			
6/9/2014	1	9	3	0	0	0	5	1	1			
6/9/2014	1	10	1	0	0	0	8	0	1			
6/9/2014	1	11	1	0	0	0	2	3	4	14.4	14.0	17.7
6/9/2014	1	12	2	0	0	0	7	1	0			
6/9/2014	1	13	0	0	0	0	9	1	0			
6/9/2014	1	14	2	0	0	0	7	1	0			
6/9/2014	1	15	2	0	1	0	6	1	0			
6/9/2014	1	16	2	0	0	0	6	2	0			
6/9/2014	1	17	1	0	0	0	7	2	0			
6/9/2014	1	18	2	0	0	0	5	0	3			
6/9/2014	1	19	3	0	0	0	5	1	1			
6/9/2014	1	20	3	0	3	0	4	0	0			
6/9/2014	1	21	3	0	1	0	4	2	0			
6/9/2014	1	22	7	0	0	0	1	1	1	17.2	15.8	x
6/9/2014	1	23	1	0	0	0	8	1	0			
6/9/2014	1	24	4	0	0	0	3	3	0			
6/9/2014	1	25	4	0	3	0	3	0	0			
6/9/2014	1	26	4	0	0	0	4	0	2			
6/9/2014	1	27	1	0	1	0	5	3	0			
6/9/2014	1	28	1	0	0	0	3	3	3			
6/9/2014	1	29	2	0	0	0	7	1	0			
6/9/2014	1	30	3	0	0	0	5	1	1			
6/9/2014	1	31	0	0	2	1	6	1	0			
6/9/2014	1	32	3	0	0	0	6	1	0			
6/9/2014	1	33	4	0	0	0	2	3	1			
6/9/2014	1	34	3	0	0	0	5	2	0	14.9	14.0	x

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/9/2014	1	35	1	0	1	0	7	1	0			
6/9/2014	1	36	2	0	0	1	3	4	0			
6/9/2014	1	37	1	0	0	2	7	0	0			
6/9/2014	1	38	0	0	0	0	6	1	3			
6/9/2014	1	39	6	0	0	0	4	0	0			
6/9/2014	1	40	0	0	0	0	5	3	2			
6/9/2014	1	41	2	0	0	2	5	1	0			
6/9/2014	1	42	1	0	0	0	2	7	0			
6/9/2014	1	43	0	0	0	0	4	4	2			
6/9/2014	1	44	1	0	0	1	6	2	0			
6/9/2014	1	45	5	0	0	0	2	1	2			
6/9/2014	1	46	4	0	0	0	1	5	0	13.0	15.2	16.5
6/9/2014	1	47	3	0	2	0	3	2	0			
6/9/2014	1	48	4	0	0	0	4	1	1			
6/9/2014	1	49	6	0	0	1	2	1	0			
6/9/2014	1	50										
6/9/2014	1	51										
6/9/2014	1	52										
6/9/2014	1	53										
6/9/2014	1	54										
6/9/2014	1	55										
6/9/2014	1	56										
6/9/2014	1	57										
6/9/2014	1	58										
6/9/2014	1	59										
6/9/2014	1	60										
6/9/2014	1	61	0	0	0	0	6	2	2			
6/9/2014	1	62	1	0	0	0	3	3	3			
6/9/2014	1	63	2	0	0	0	3	4	1			
6/9/2014	1	64	2	0	0	0	3	2	3			
6/9/2014	1	65	3	0	0	0	5	2	0			
6/9/2014	1	66	4	0	0	0	2	2	2			
6/9/2014	1	67	2	0	0	0	6	2	0			
6/9/2014	1	68	0	0	0	0	7	2	1			
6/9/2014	1	69	3	0	0	0	5	0	2			
6/9/2014	1	70	1	0	0	0	5	2	2			
6/9/2014	1	71	5	0	0	0	3	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/9/2014	1	72	3	0	0	0	1	3	3			
6/9/2014	1	73	0	0	0	0	5	4	1	10.7	12.3	16.6
6/9/2014	1	74	2	0	0	0	2	2	4			
6/9/2014	1	75	0	0	0	0	8	1	1			
6/9/2014	1	76	6	0	0	0	4	0	0			
6/9/2014	1	77	2	0	0	0	7	0	1			
6/9/2014	1	78	2	0	0	0	6	0	2			
6/9/2014	1	79	3	0	0	0	5	1	1			
6/9/2014	1	80	2	0	0	0	7	0	1			
6/9/2014	1	81	4	0	0	0	3	0	3			
6/9/2014	1	82	2	0	0	0	6	2	0			
6/9/2014	1	83	5	0	0	0	1	2	2			
6/9/2014	1	84	3	0	0	0	6	0	1	11.3	12.9	17.9
6/9/2014	1	85	4	0	0	0	5	1	0			
6/9/2014	1	86	3	0	0	0	3	2	2			
6/9/2014	1	87	3	0	0	0	5	1	1			
6/9/2014	1	88	4	0	0	0	4	2	0			
6/9/2014	1	89	6	0	0	0	2	1	1			
6/9/2014	1	90	3	0	0	0	4	1	2			
6/9/2014	1	91										
6/9/2014	1	92										
6/9/2014	1	93										
6/9/2014	1	94										
6/9/2014	1	95										
6/9/2014	1	96								10.4	13.2	17.5
6/9/2014	1	97										
6/9/2014	1	98										
6/9/2014	1	99										
6/9/2014	1	100										
6/9/2014	1	101	2	0	0	0	5	2	1			
6/9/2014	1	102	3	0	0	0	4	1	2			
6/9/2014	1	103	5	0	0	0	1	2	2			
6/9/2014	1	104	2	0	0	0	5	1	2			
6/9/2014	1	105	3	0	0	0	5	2	0			
6/9/2014	1	106	0	0	0	0	7	2	1			
6/9/2014	1	107	1	0	0	0	8	1	0			
6/9/2014	1	108	5	0	0	0	5	0	0	9.2	8.8	15.2

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/9/2014	1	109	2	0	0	0	6	0	2			
6/9/2014	1	110	3	0	0	0	7	0	0			
6/9/2014	1	111	3	0	0	0	6	1	0			
6/9/2014	1	112	3	0	0	0	6	0	1			
6/9/2014	1	113	3	0	0	0	6	0	1			
6/9/2014	1	114	6	0	0	0	4	0	0			
6/9/2014	1	115	2	0	0	0	3	4	1			
6/9/2014	1	116	4	0	0	0	3	3	0			
6/9/2014	1	117	1	0	0	0	8	1	0			
6/9/2014	1	118	1	0	0	0	9	0	0			
6/9/2014	1	119	3	0	0	0	6	1	0			
6/9/2014	1	120	1	0	0	0	8	0	1	10.3	8.7	16.1
6/10/2014	2	1	0	1	3	2	0	3	1			
6/10/2014	2	2	4	0	2	0	1	3	0			
6/10/2014	2	3	2	0	4	1	1	2	0			
6/10/2014	2	4	2	1	2	1	1	3	0			
6/10/2014	2	5	0	0	5	1	2	2	0			
6/10/2014	2	6	0	0	3	0	3	4	0			
6/10/2014	2	7	2	1	5	0	1	1	0			
6/10/2014	2	8	0	2	4	0	3	1	0			
6/10/2014	2	9	1	1	2	1	1	4	0			
6/10/2014	2	10	2	1	3	0	3	1	0	27.7	23.0	22.6
6/10/2014	2	11	0	2	5	0	1	2	0			
6/10/2014	2	12	0	1	5	1	0	3	0			
6/10/2014	2	13	0	1	2	1	2	4	0			
6/10/2014	2	14	0	1	2	2	4	0	1			
6/10/2014	2	15	0	3	1	0	1	5	0			
6/10/2014	2	16	1	1	1	0	3	3	1			
6/10/2014	2	17	0	2	2	0	3	2	1			
6/10/2014	2	18	0	1	2	0	5	2	0			
6/10/2014	2	19	1	0	5	0	4	0	0	28.6	23.8	22.3
6/10/2014	2	20	0	3	3	0	3	0	1			
6/10/2014	2	21	1	3	3	0	1	2	0			
6/10/2014	2	22	0	2	1	0	2	5	0			
6/10/2014	2	23	0	2	1	0	1	6	0			
6/10/2014	2	24	2	2	1	0	3	2	0			
6/10/2014	2	25	3	0	3	0	0	3	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	2	26	2	0	0	3	1	4	0			
6/10/2014	2	27	0	1	3	0	0	5	1			
6/10/2014	2	28	0	0	5	0	0	4	1	27.4	21.9	19.1
6/10/2014	2	29	6	0	0	0	1	2	1			
6/10/2014	2	30	3	0	6	0	0	1	0			
6/10/2014	2	31	0	4	1	1	1	3	0			
6/10/2014	2	32	0	5	2	1	1	1	0			
6/10/2014	2	33	0	2	2	1	3	2	0			
6/10/2014	2	34	0	0	4	0	0	5	1			
6/10/2014	2	35	0	4	1	1	1	3	0			
6/10/2014	2	36	0	2	3	0	1	4	0			
6/10/2014	2	37	1	0	5	0	1	3	0	32.9	23.2	19.8
6/10/2014	2	38	2	1	4	1	0	1	1			
6/10/2014	2	39	3	1	3	0	1	1	1			
6/10/2014	2	40	5	2	1	0	0	1	1			
6/10/2014	2	41	0	1	2	1	2	4	0			
6/10/2014	2	42	1	4	1	2	1	1	0			
6/10/2014	2	43	1	1	1	0	0	6	1			
6/10/2014	2	44	3	2	0	1	1	3	0			
6/10/2014	2	45	0	4	2	1	1	1	1			
6/10/2014	2	46	1	2	2	0	0	4	1	28.8	20.7	15.1
6/10/2014	2	47	2	1	6	0	1	0	0			
6/10/2014	2	48	3	3	3	0	0	1	0			
6/10/2014	2	49	3	0	2	0	2	2	1			
6/10/2014	2	50	2	2	2	0	3	1	0			
6/10/2014	2	51	2	4	1	2	0	0	1			
6/10/2014	2	52	2	1	2	2	1	0	2			
6/10/2014	2	53	0	2	1	1	0	4	2			
6/10/2014	2	54	2	2	2	2	0	1	1			
6/10/2014	2	55	0	3	4	0	0	0	3	28.6	23.2	x
6/10/2014	2	56	1	2	0	1	0	1	5			
6/10/2014	2	57	1	0	3	0	1	3	2			
6/10/2014	2	58	0	2	3	0	1	3	1			
6/10/2014	2	59	2	3	3	0	1	1	0			
6/10/2014	2	60	0	1	2	3	1	3	0			
6/10/2014	2	61	2	0	4	1	0	3	0			
6/10/2014	2	62	3	0	1	4	0	1	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	2	63	1	0	2	1	2	4	0			
6/10/2014	2	64	2	0	2	1	0	4	1	26.8	26.7	15.8
6/10/2014	2	65	5	0	2	0	1	2	0			
6/10/2014	2	66	0	0	6	1	1	2	0			
6/10/2014	2	67	0	2	2	2	0	2	2			
6/10/2014	2	68	1	0	2	2	2	1	2			
6/10/2014	2	69	2	0	4	3	0	1	0			
6/10/2014	2	70	2	2	0	1	1	2	2			
6/10/2014	2	71	0	1	3	4	0	0	2			
6/10/2014	2	72	0	2	1	1	1	3	2			
6/10/2014	2	73	0	1	2	2	0	1	4	32.5	24.5	17.5
6/10/2014	2	74	0	2	2	0	0	6	0			
6/10/2014	2	75	0	1	1	0	0	4	4			
6/10/2014	2	76	1	4	2	0	0	3	0			
6/10/2014	2	77	1	0	1	2	1	3	2			
6/10/2014	2	78	0	0	3	1	1	5	0			
6/10/2014	2	79	2	1	0	1	1	1	4			
6/10/2014	2	80	0	5	2	0	1	2	0			
6/10/2014	2	81	1	2	1	0	2	1	3			
6/10/2014	2	82	1	3	1	0	1	3	1	26.8	26.9	22.2
6/10/2014	2	83	2	2	1	1	0	3	1			
6/10/2014	2	84	1	2	1	1	1	3	1			
6/10/2014	2	85	1	2	0	3	1	2	1			
6/10/2014	2	86	0	1	2	4	0	1	2			
6/10/2014	2	87	1	0	1	2	2	2	2			
6/10/2014	2	88	2	3	1	0	1	1	2			
6/10/2014	2	89	0	3	0	2	0	1	4			
6/10/2014	2	90	1	2	0	1	3	2	1			
6/10/2014	2	91	0	1	0	4	5	0	0	29.3	22.6	19.3
6/10/2014	2	92	0	3	2	1	1	3	0			
6/10/2014	2	93	2	2	2	1	1	2	0			
6/10/2014	2	94	3	0	2	0	0	5	0			
6/10/2014	2	95	2	2	4	0	0	2	0			
6/10/2014	2	96	4	0	0	1	1	4	0			
6/10/2014	2	97	0	2	0	2	1	3	2			
6/10/2014	2	98	1	2	2	1	0	1	3			
6/10/2014	2	99	0	3	2	1	0	2	2			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	2	100	1	0	2	2	1	2	2			
6/11/2014	3	1	0	0	2	4	1	0	3			
6/11/2014	3	2	1	1	1	1	1	2	3			
6/11/2014	3	3	2	1	2	2	1	0	2			
6/11/2014	3	4	0	0	0	0	6	1	3			
6/11/2014	3	5	0	0	1	1	4	1	3			
6/11/2014	3	6	0	0	1	0	4	4	1			
6/11/2014	3	7	0	1	1	0	4	2	2			
6/11/2014	3	8	0	1	1	0	2	3	3			
6/11/2014	3	9	0	0	1	0	2	5	2			
6/11/2014	3	10	0	0	0	0	4	3	3	22.3	19.7	20.8
6/11/2014	3	11	0	2	1	0	6	1	0			
6/11/2014	3	12	0	2	2	0	3	1	2			
6/11/2014	3	13	0	1	1	0	5	2	1			
6/11/2014	3	14	0	1	4	0	3	1	1			
6/11/2014	3	15	0	1	1	1	3	3	1			
6/11/2014	3	16	1	1	0	0	3	3	2			
6/11/2014	3	17	0	0	2	0	4	3	1			
6/11/2014	3	18	0	2	3	0	3	1	1			
6/11/2014	3	19	1	0	3	1	0	4	1	24.2	20.3	16.7
6/11/2014	3	20	0	0	2	2	1	4	1			
6/11/2014	3	21	0	2	1	0	3	0	4			
6/11/2014	3	22	0	3	3	0	2	2	0			
6/11/2014	3	23	0	5	1	1	2	1	0			
6/11/2014	3	24	2	4	1	1	0	2	0			
6/11/2014	3	25	0	2	1	0	2	5	0			
6/11/2014	3	26	0	2	3	0	3	2	0			
6/11/2014	3	27	0	1	3	1	1	4	0			
6/11/2014	3	28	3	2	3	0	1	1	0	22.9	19.7	x
6/11/2014	3	29	0	4	2	1	2	1	0			
6/11/2014	3	30	0	0	0	2	4	4	0			
6/11/2014	3	31	2	0	2	0	3	0	3			
6/11/2014	3	32	1	1	2	1	2	0	3			
6/11/2014	3	33	0	0	3	0	6	0	1			
6/11/2014	3	34	0	2	2	0	4	0	2			
6/11/2014	3	35	0	0	1	0	2	5	2			
6/11/2014	3	36	1	1	3	0	2	1	2			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/11/2014	3	37	2	1	1	1	1	2	2	25.8	20.9	18.1
6/11/2014	3	38	0	2	1	1	2	1	3			
6/11/2014	3	39	2	0	2	0	1	2	3			
6/11/2014	3	40	2	0	1	0	2	2	3			
6/11/2014	3	41	0	2	3	0	2	2	1			
6/11/2014	3	42	0	2	0	2	3	3	0			
6/11/2014	3	43	0	3	3	0	1	3	0			
6/11/2014	3	44	0	6	0	0	2	2	0			
6/11/2014	3	45	0	6	0	0	2	2	0			
6/11/2014	3	46	0	5	1	0	4	0	0	21.4	20.9	17.6
6/11/2014	3	47	0	2	1	0	2	2	3			
6/11/2014	3	48	0	4	1	0	4	1	0			
6/11/2014	3	49	0	2	3	0	1	3	1			
6/11/2014	3	50	0	3	2	2	1	1	1			
6/11/2014	3	51	0	0	0	2	4	1	3			
6/11/2014	3	52	0	3	0	1	4	0	2			
6/11/2014	3	53	0	5	2	0	2	1	0			
6/11/2014	3	54	0	3	0	0	3	4	0			
6/11/2014	3	55	5	0	0	0	3	2	0	19.9	23.4	17.2
6/11/2014	3	56	0	1	0	0	5	4	0			
6/11/2014	3	57	1	0	1	0	6	1	1			
6/11/2014	3	58	0	1	3	0	3	3	0			
6/11/2014	3	59	0	1	1	0	3	3	2			
6/11/2014	3	60	0	1	0	0	3	5	1			
6/11/2014	3	61	0	1	2	1	2	1	3			
6/11/2014	3	62	0	2	2	0	5	0	1			
6/11/2014	3	63	0	4	1	0	3	0	2			
6/11/2014	3	64	0	1	0	0	6	1	2	25.2	22.1	17.2
6/11/2014	3	65	0	1	0	4	2	3	0			
6/11/2014	3	66	0	5	2	0	0	1	2			
6/11/2014	3	67	0	1	1	0	1	6	1			
6/11/2014	3	68	0	1	2	0	3	4	0			
6/11/2014	3	69	0	1	3	0	2	1	3			
6/11/2014	3	70	1	1	1	0	2	2	3			
6/11/2014	3	71	0	0	4	0	3	0	3			
6/11/2014	3	72	0	0	5	0	1	0	4			
6/11/2014	3	73	0	2	0	2	4	1	1	15.7	18.9	20.5

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/11/2014	3	74	0	2	1	1	3	3	0			
6/11/2014	3	75	0	0	3	0	3	3	1			
6/11/2014	3	76	2	1	1	0	3	3	0			
6/11/2014	3	77	0	3	0	0	4	3	0			
6/11/2014	3	78	0	2	0	0	2	4	2			
6/11/2014	3	79	0	0	1	2	0	4	3			
6/11/2014	3	80	0	0	1	1	1	2	5			
6/11/2014	3	81	0	0	6	0	1	0	3			
6/11/2014	3	82	0	3	2	0	3	1	1	23.2	18.3	19.2
6/11/2014	3	83	0	0	2	0	3	4	1			
6/11/2014	3	84	0	2	2	0	1	3	2			
6/11/2014	3	85	1	0	3	0	2	3	1			
6/11/2014	3	86	0	4	4	0	0	2	0			
6/11/2014	3	87	1	2	1	0	3	1	2			
6/11/2014	3	88	0	2	1	0	0	5	2			
6/11/2014	3	89	0	1	0	1	0	4	4			
6/11/2014	3	90	0	1	1	0	2	3	3			
6/11/2014	3	91	0	4	1	0	3	1	1	24.3	22.2	18.5
6/11/2014	3	92	1	2	5	0	2	0	0			
6/11/2014	3	93	1	0	4	0	3	1	1			
6/11/2014	3	94	0	0	4	2	2	2	0			
6/11/2014	3	95	0	1	3	0	1	2	3			
6/11/2014	3	96	0	1	0	1	5	2	1			
6/11/2014	3	97	0	4	0	0	1	5	0			
6/11/2014	3	98	0	4	1	0	1	2	2			
6/11/2014	3	99	0	2	1	1	2	3	1			
6/11/2014	3	100	0	5	0	0	4	1	0			
6/10/2014	4	1	2	2	2	0	1	3	0			
6/10/2014	4	2	0	0	3	0	5	2	0			
6/10/2014	4	3	1	0	5	0	1	3	0			
6/10/2014	4	4	1	0	4	0	1	4	0			
6/10/2014	4	5	0	0	3	0	1	6	0			
6/10/2014	4	6	2	2	3	0	1	2	0			
6/10/2014	4	7	1	0	3	0	4	2	0			
6/10/2014	4	8	2	0	2	0	2	4	0			
6/10/2014	4	9	2	1	5	0	2	0	0			
6/10/2014	4	10	1	0	6	0	3	0	0	36.1	27.0	23.0

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	4	11	2	3	1	0	4	0	0			
6/10/2014	4	12	0	1	5	0	3	1	0			
6/10/2014	4	13	0	0	2	0	2	6	0			
6/10/2014	4	14	2	2	0	0	4	2	0			
6/10/2014	4	15	3	1	2	0	3	1	0			
6/10/2014	4	16	1	5	0	0	3	0	1			
6/10/2014	4	17	2	3	0	0	4	1	0			
6/10/2014	4	18	5	2	1	0	2	0	0			
6/10/2014	4	19	4	2	0	0	2	1	1	38.0	26.1	25.1
6/10/2014	4	20	0	2	6	0	2	0	0			
6/10/2014	4	21	2	4	2	0	1	1	0			
6/10/2014	4	22	2	3	0	0	1	3	1			
6/10/2014	4	23	4	2	2	0	0	2	0			
6/10/2014	4	24	3	0	0	0	2	2	3			
6/10/2014	4	25	0	1	5	0	1	0	3			
6/10/2014	4	26	2	3	4	0	1	0	0			
6/10/2014	4	27	1	1	3	0	2	2	1			
6/10/2014	4	28	0	3	2	0	2	1	2	31.5	33.1	25.0
6/10/2014	4	29	0	3	6	0	0	0	1			
6/10/2014	4	30	0	3	4	0	1	0	2			
6/10/2014	4	31	0	6	3	0	1	0	0			
6/10/2014	4	32	4	0	4	0	2	0	0			
6/10/2014	4	33	2	2	4	0	1	1	0			
6/10/2014	4	34	4	0	4	0	1	1	0			
6/10/2014	4	35	1	0	5	0	4	0	0			
6/10/2014	4	36	0	3	5	0	1	1	0			
6/10/2014	4	37	4	0	4	0	1	1	0	33.7	24.8	22.5
6/10/2014	4	38	1	2	3	0	4	0	0			
6/10/2014	4	39	2	2	2	0	3	0	1			
6/10/2014	4	40	3	0	4	0	3	0	0			
6/10/2014	4	41	1	0	1	0	5	3	0			
6/10/2014	4	42	2	1	2	0	2	3	0			
6/10/2014	4	43	1	0	4	0	2	3	0			
6/10/2014	4	44	6	0	3	0	0	1	0			
6/10/2014	4	45	3	0	4	0	3	0	0			
6/10/2014	4	46	5	0	1	0	3	0	1	25.3	24.9	22.4
6/10/2014	4	47	5	1	2	0	1	1	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	4	48	0	2	5	0	3	0	0			
6/10/2014	4	49	3	0	3	0	4	0	0			
6/10/2014	4	50	0	1	6	0	2	1	0			
6/10/2014	4	51	1	1	3	1	3	1	0			
6/10/2014	4	52	6	0	3	0	0	1	0			
6/10/2014	4	53	4	3	0	1	1	0	1			
6/10/2014	4	54	4	0	4	0	0	2	0			
6/10/2014	4	55	3	0	5	0	1	1	0	28.5	27.9	22.3
6/10/2014	4	56	0	2	3	0	5	0	0			
6/10/2014	4	57	1	1	4	0	2	2	0			
6/10/2014	4	58	2	0	6	0	2	0	0			
6/10/2014	4	59	0	1	7	0	2	0	0			
6/10/2014	4	60	3	2	4	0	0	1	0			
6/10/2014	4	61	2	0	1	0	3	0	4			
6/10/2014	4	62	4	0	0	0	3	0	3			
6/10/2014	4	63	1	0	5	0	0	0	4			
6/10/2014	4	64	3	0	4	0	2	1	0	32.8	29.8	22.8
6/10/2014	4	65	3	0	4	0	0	1	2			
6/10/2014	4	66	0	0	4	0	0	3	3			
6/10/2014	4	67	1	0	6	0	2	0	1			
6/10/2014	4	68	1	0	5	0	4	0	0			
6/10/2014	4	69	1	0	1	0	1	4	3			
6/10/2014	4	70	0	0	3	0	4	2	1			
6/10/2014	4	71	4	0	0	0	5	1	0			
6/10/2014	4	72	3	0	0	0	4	2	1			
6/10/2014	4	73	6	0	0	0	1	3	0	30.0	30.1	23.2
6/10/2014	4	74	6	0	0	0	3	1	0			
6/10/2014	4	75	2	0	0	0	7	1	0			
6/10/2014	4	76	5	0	0	0	2	3	0			
6/10/2014	4	77	3	0	1	0	6	0	0			
6/10/2014	4	78	4	0	0	4	2	0	0			
6/10/2014	4	79	4	0	3	0	2	1	0			
6/10/2014	4	80	4	0	4	0	2	0	0			
6/10/2014	4	81	3	0	0	0	5	1	1			
6/10/2014	4	82	1	0	2	0	2	1	4	32.2	27.9	22.7
6/10/2014	4	83	5	0	0	0	3	2	0			
6/10/2014	4	84	0	0	0	0	3	3	4			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/10/2014	4	85	5	0	0	0	4	0	1			
6/10/2014	4	86	4	0	0	0	2	2	2			
6/10/2014	4	87	3	0	0	0	2	4	1			
6/10/2014	4	88	5	0	0	0	5	0	0			
6/10/2014	4	89	6	0	0	0	3	0	1			
6/10/2014	4	90	8	0	0	0	2	0	0			
6/10/2014	4	91	4	0	0	0	5	0	1	33.1	26.1	21.1
6/10/2014	4	92	1	0	0	0	7	2	0			
6/10/2014	4	93	4	0	0	0	6	0	0			
6/10/2014	4	94	3	0	0	0	2	5	0			
6/10/2014	4	95	1	0	0	0	3	6	0			
6/10/2014	4	96	3	0	0	0	4	3	0			
6/10/2014	4	97	1	0	0	0	6	3	0			
6/10/2014	4	98	3	0	0	0	6	1	0			
6/10/2014	4	99	5	0	0	0	4	1	0			
6/10/2014	4	100	5	0	0	0	5	0	0			
6/12/2014	5	1	0	1	0	0	8	0	1			
6/12/2014	5	2	0	2	1	0	6	0	1			
6/12/2014	5	3	0	2	3	0	5	0	0			
6/12/2014	5	4	0	2	2	0	6	0	0			
6/12/2014	5	5	0	4	1	0	3	2	0			
6/12/2014	5	6	0	0	2	0	7	0	1			
6/12/2014	5	7	0	6	4	0	0	0	0			
6/12/2014	5	8	0	8	0	0	0	0	2			
6/12/2014	5	9	0	9	0	0	0	0	1			
6/12/2014	5	10	0	7	0	0	0	1	2			
6/12/2014	5	11	0	5	0	0	4	0	1			
6/12/2014	5	12	0	1	2	0	7	0	0			
6/12/2014	5	13	0	4	1	0	3	1	1			
6/12/2014	5	14	0	9	0	0	0	1	0			
6/12/2014	5	15	0	10	0	0	0	0	0			
6/12/2014	5	16	0	8	0	0	0	2	0			
6/12/2014	5	17	0	6	0	0	1	3	0			
6/12/2014	5	18	0	9	0	0	0	1	0			
6/12/2014	5	19	0	8	0	0	0	2	0			
6/12/2014	5	20	0	9	0	0	1	0	0			
6/12/2014	5	21	0	4	0	0	6	0	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/12/2014	5	22	0	4	1	0	4	1	0			
6/12/2014	5	23	0	9	0	0	0	1	0			
6/12/2014	5	24	0	6	0	0	4	0	0			
6/12/2014	5	25	0	6	0	0	2	2	0			
6/12/2014	5	26	0	3	0	0	0	7	0			
6/12/2014	5	27	0	2	0	0	0	8	0			
6/12/2014	5	28	0	6	0	0	0	3	1			
6/12/2014	5	29	0	6	0	0	0	2	2			
6/12/2014	5	30	0	8	0	0	0	2	0			
6/12/2014	5	31	0	4	0	0	6	0	0			
6/12/2014	5	32	0	5	1	1	3	0	0			
6/12/2014	5	33	0	7	0	0	2	1	0			
6/12/2014	5	34	0	8	0	0	2	0	0			
6/12/2014	5	35	0	9	0	0	1	0	0			
6/12/2014	5	36	0	8	0	0	2	0	0			
6/12/2014	5	37	0	6	1	0	3	0	0			
6/12/2014	5	38	0	8	0	0	0	0	2			
6/12/2014	5	39	0	2	0	0	0	7	1			
6/12/2014	5	40	0	7	0	0	0	3	0			
6/12/2014	5	41	0	3	0	1	5	1	0			
6/12/2014	5	42	0	5	0	0	3	1	1			
6/12/2014	5	43	0	7	0	0	1	1	1			
6/12/2014	5	44	0	8	1	0	1	0	0			
6/12/2014	5	45	0	7	0	0	2	1	0			
6/12/2014	5	46	0	5	0	0	2	2	1			
6/12/2014	5	47	0	9	0	0	0	1	0			
6/12/2014	5	48	0	6	0	0	2	1	1			
6/12/2014	5	49	0	8	0	0	1	1	0			
6/12/2014	5	50	0	7	0	0	1	1	1			
6/12/2014	5	51	0	0	1	0	4	0	5			
6/12/2014	5	52	0	1	0	1	2	2	4			
6/12/2014	5	53	0	4	1	0	0	0	5			
6/12/2014	5	54	0	6	0	0	1	3	0			
6/12/2014	5	55	0	5	0	0	0	3	2			
6/25/2014	5	56	0	7	1	0	1	1	0			
6/25/2014	5	57	0	7	0	0	0	3	0			
6/25/2014	5	58	0	6	1	0	1	1	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/25/2014	5	59	0	6	2	0	1	1	0			
6/25/2014	5	60	0	7	1	0	0	2	0			
6/12/2014	5	61	0	1	0	0	7	2	0			
6/12/2014	5	62	0	9	0	0	0	0	1			
6/12/2014	5	63	0	6	3	0	1	0	0			
6/12/2014	5	64	0	8	0	0	0	2	0			
6/12/2014	5	65	0	9	0	0	0	1	0			
6/12/2014	5	66	0	9	0	0	0	1	0			
6/12/2014	5	67	0	9	0	0	0	1	0			
6/12/2014	5	68	0	6	0	0	2	2	0			
6/12/2014	5	69	0	5	0	0	3	2	0			
6/12/2014	5	70	0	9	0	0	1	0	0			
6/25/2014	5	71	0	0	1	5	3	1	0			
6/25/2014	5	72	0	4	0	1	5	0	0			
6/25/2014	5	73	0	8	0	1	0	0	1			
6/25/2014	5	74	0	7	0	1	2	0	0			
6/25/2014	5	75	0	8	0	0	1	1	0			
6/25/2014	5	76	0	8	0	0	0	2	0			
6/25/2014	5	77	0	7	0	0	0	0	3			
6/25/2014	5	78	0	7	0	0	1	1	1			
6/25/2014	5	79	0	6	0	0	1	3	0			
6/25/2014	5	80	0	5	0	0	3	1	1			
6/12/2014	5	81	0	3	1	0	5	1	0			
6/12/2014	5	82	0	9	1	0	0	0	0			
6/12/2014	5	83	0	7	2	0	0	1	0			
6/12/2014	5	84	0	9	1	0	0	0	0			
6/12/2014	5	85	0	10	0	0	0	0	0			
6/12/2014	5	86	0	7	1	0	2	0	0			
6/12/2014	5	87	0	7	0	0	0	3	0			
6/12/2014	5	88	0	9	0	0	0	1	0			
6/12/2014	5	89	0	4	0	0	4	2	0			
6/12/2014	5	90	0	6	2	0	2	0	0			
6/25/2014	5	91	0	10	0	0	0	0	0			
6/25/2014	5	92	0	6	1	0	0	0	3			
6/25/2014	5	93	0	8	0	0	1	0	1			
6/25/2014	5	94	0	6	2	0	0	2	0			
6/25/2014	5	95	0	8	0	0	0	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/25/2014	5	96	0	7	2	0	0	1	0			
6/25/2014	5	97	0	7	2	0	0	1	0			
6/12/2014	5	98	0	7	0	0	2	1	0			
6/12/2014	5	99	0	6	0	0	2	2	0			
6/12/2014	5	100	8	0	1	0	0	1	0			
6/13/2014	6	1	2	0	4	4	0	0	0			
6/13/2014	6	2	6	0	0	3	0	0	1			
6/13/2014	6	3	2	0	2	5	1	0	0			
6/13/2014	6	4	3	0	1	4	1	1	0			
6/13/2014	6	5	4	0	4	2	0	0	0			
6/13/2014	6	6	5	0	3	2	0	0	0			
6/13/2014	6	7	7	0	0	3	0	0	0			
6/13/2014	6	8	5	0	0	3	2	0	0			
6/13/2014	6	9	7	0	0	3	0	0	0			
6/13/2014	6	10	7	0	0	2	0	1	0	30.6	26.4	13.8
6/13/2014	6	11	4	0	1	1	0	1	3			
6/13/2014	6	12	4	0	1	5	0	0	0			
6/13/2014	6	13	3	0	0	4	1	1	1			
6/13/2014	6	14	4	0	2	1	2	0	1			
6/13/2014	6	15	3	0	4	3	0	0	0			
6/13/2014	6	16	7	0	1	0	2	0	0			
6/13/2014	6	17	5	0	0	0	2	0	3			
6/13/2014	6	18	5	0	0	3	0	0	2			
6/13/2014	6	19	4	0	0	6	0	0	0			
6/13/2014	6	20	5	0	0	5	0	0	0			
6/13/2014	6	21	2	0	0	8	0	0	0			
6/13/2014	6	22	5	0	0	3	1	0	1			
6/13/2014	6	23	3	0	1	1	3	2	0			
6/13/2014	6	24	8	0	2	0	0	0	0			
6/13/2014	6	25	8	0	0	1	1	0	0			
6/13/2014	6	26	6	0	0	3	1	0	0			
6/13/2014	6	27	7	0	0	2	1	0	0			
6/13/2014	6	28	8	0	0	2	0	0	0	32.1	24.5	15.2
6/13/2014	6	29	3	0	3	3	1	0	0			
6/13/2014	6	30	1	0	2	5	1	0	1			
6/13/2014	6	31	1	0	0	4	3	1	1			
6/13/2014	6	32	3	0	0	0	3	1	3			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/13/2014	6	33	1	0	0	5	2	2	0			
6/13/2014	6	34	5	0	0	2	3	0	0			
6/13/2014	6	35	1	0	0	0	8	0	1			
6/13/2014	6	36	6	0	0	4	0	0	0			
6/13/2014	6	37	7	0	0	1	0	0	2			
6/13/2014	6	38	7	0	0	2	0	0	1			
6/13/2014	6	39	7	0	0	3	0	0	0			
6/13/2014	6	40	9	0	0	1	0	0	0			
6/13/2014	6	41	2	0	0	4	3	1	0			
6/13/2014	6	42	1	0	1	1	4	1	2			
6/13/2014	6	43	6	0	0	2	1	1	0			
6/13/2014	6	44	7	0	1	2	0	0	0			
6/13/2014	6	45	9	0	0	1	0	0	0			
6/13/2014	6	46	5	0	0	0	4	1	0	30.1	21.8	16.3
6/13/2014	6	47	9	0	0	0	1	0	0			
6/13/2014	6	48	7	0	0	0	3	0	0			
6/13/2014	6	49	8	0	0	0	2	0	0			
6/13/2014	6	50	10	0	0	0	0	0	0			
6/13/2014	6	51	3	0	1	3	0	1	2			
6/13/2014	6	52	1	0	1	4	2	0	2			
6/13/2014	6	53	7	0	0	2	1	0	0			
6/13/2014	6	54	6	0	0	3	0	1	0			
6/13/2014	6	55	4	0	0	4	1	0	1			
6/13/2014	6	56	6	0	0	1	1	2	0			
6/13/2014	6	57	5	0	0	2	1	0	2			
6/13/2014	6	58	10	0	0	0	0	0	0			
6/13/2014	6	59	5	0	0	0	0	0	5			
6/13/2014	6	60	7	0	0	2	1	0	0			
6/13/2014	6	61	5	0	0	0	4	1	0			
6/13/2014	6	62	1	8	0	1	0	0	0			
6/13/2014	6	63	2	3	0	2	1	1	1			
6/13/2014	6	64	5	0	0	3	2	0	0	32.4	23.9	14.0
6/13/2014	6	65	3	0	0	7	0	0	0			
6/13/2014	6	66	8	0	0	1	1	0	0			
6/13/2014	6	67	2	0	0	6	2	0	0			
6/13/2014	6	68	9	0	0	0	1	0	0			
6/13/2014	6	69	8	0	0	2	0	0	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
6/13/2014	6	70	6	0	1	2	1	0	0			
6/13/2014	6	71	8	0	0	2	0	0	0			
6/13/2014	6	72	8	0	1	1	0	0	0			
6/13/2014	6	73	3	1	0	4	1	0	1			
6/13/2014	6	74	5	1	0	3	1	0	0			
6/13/2014	6	75	7	1	0	1	1	0	0			
6/13/2014	6	76	6	0	0	1	3	0	0			
6/13/2014	6	77	4	0	0	5	1	0	0			
6/13/2014	6	78	8	0	0	1	1	0	0			
6/13/2014	6	79	7	0	0	3	0	0	0			
6/13/2014	6	80	9	0	0	1	0	0	0			
6/13/2014	6	81	7	0	0	3	0	0	0			
6/13/2014	6	82	8	0	0	1	1	0	0	28.1	19.9	12.6
6/13/2014	6	83	8	0	0	1	1	0	0			
6/13/2014	6	84	2	0	0	2	6	0	0			
6/13/2014	6	85	3	0	0	1	6	0	0			
6/13/2014	6	86	5	0	0	0	5	0	0			
6/13/2014	6	87	7	0	0	0	2	1	0			
6/13/2014	6	88	4	0	0	1	5	0	0			
6/13/2014	6	89	0	0	0	9	0	0	1			
6/13/2014	6	90	6	0	0	4	0	0	0			
6/13/2014	6	91	7	0	0	0	3	0	0			
6/13/2014	6	92	2	0	0	2	6	0	0			
6/13/2014	6	93	4	0	0	2	4	0	0			
6/13/2014	6	94	4	0	0	3	3	0	0			
6/13/2014	6	95	6	0	0	0	2	2	0			
6/13/2014	6	96	3	0	0	0	6	1	0			
6/13/2014	6	97	9	0	1	0	0	0	0			
6/13/2014	6	98	5	0	0	2	3	0	0			
6/13/2014	6	99	3	0	0	0	6	0	1			
6/13/2014	6	100	7	0	1	0	2	0	0			
7/22/2014	4	1	0	0	0	0	7	3	0			
7/22/2014	4	2	1	0	0	0	8	1	0			
7/22/2014	4	3	0	0	3	0	5	2	0			
7/22/2014	4	4	1	0	0	0	9	0	0			
7/22/2014	4	5	0	1	0	0	9	0	0			
7/22/2014	4	6	5	2	0	0	3	0	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/22/2014	4	7	1	0	0	0	8	1	0			
7/22/2014	4	8	2	0	0	0	6	2	0			
7/22/2014	4	9	0	0	0	0	9	1	0			
7/22/2014	4	10	0	0	1	0	8	1	0	24.9	21.4	20.1
7/22/2014	4	11	0	0	0	0	8	2	0			
7/22/2014	4	12	0	1	0	0	7	2	0			
7/22/2014	4	13	0	2	0	0	7	1	0			
7/22/2014	4	14	1	0	0	0	8	1	0			
7/22/2014	4	15	2	0	3	0	5	0	0			
7/22/2014	4	16	3	0	0	0	7	0	0			
7/22/2014	4	17	0	4	0	0	5	1	0			
7/22/2014	4	18	2	0	0	0	7	1	0			
7/22/2014	4	19	0	1	0	0	8	1	0	30.3	19.7	19.9
7/22/2014	4	20	0	0	0	0	9	1	0			
7/22/2014	4	21	3	0	0	0	5	2	0			
7/22/2014	4	22	1	0	0	0	8	1	0			
7/22/2014	4	23	1	1	0	0	8	0	0			
7/22/2014	4	24	1	1	0	0	8	0	0			
7/22/2014	4	25	5	0	0	0	5	0	0			
7/22/2014	4	26	3	0	0	0	7	0	0			
7/22/2014	4	27	4	0	0	0	6	0	0			
7/22/2014	4	28	4	2	0	0	4	0	0	25.4	19.9	19.1
7/22/2014	4	29	0	0	0	0	9	0	1			
7/22/2014	4	30	1	0	0	0	9	0	0			
7/22/2014	4	31	1	0	0	0	9	0	0			
7/22/2014	4	32	2	0	0	0	7	1	0			
7/22/2014	4	33	1	0	0	0	4	5	0			
7/22/2014	4	34	0	1	4	0	5	0	0			
7/22/2014	4	35	1	2	0	0	7	0	0			
7/22/2014	4	36	1	1	2	0	6	0	0			
7/22/2014	4	37	2	0	1	0	7	0	0	27.3	19.4	19.9
7/22/2014	4	38	2	1	0	0	7	0	0			
7/22/2014	4	39	0	0	0	0	9	1	0			
7/22/2014	4	40	1	1	2	0	6	0	0			
7/22/2014	4	41	4	0	0	0	6	0	0			
7/22/2014	4	42	2	1	0	0	6	1	0			
7/22/2014	4	43	2	1	0	0	6	1	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/22/2014	4	44	3	1	0	0	5	1	0			
7/22/2014	4	45	1	0	2	0	7	0	0			
7/22/2014	4	46	1	0	1	0	7	1	0	24.7	20.1	19.6
7/22/2014	4	47	6	0	0	0	3	1	0			
7/22/2014	4	48	4	0	0	0	6	0	0			
7/22/2014	4	49	1	2	0	0	7	0	0			
7/22/2014	4	50	1	0	2	0	6	1	0			
7/22/2014	4	51	1	0	0	0	9	0	0			
7/22/2014	4	52	0	1	0	0	5	4	0			
7/22/2014	4	53	0	0	0	0	10	0	0			
7/22/2014	4	54	3	0	0	0	6	1	0			
7/22/2014	4	55	1	1	0	0	8	0	0	26.5	19.4	20.6
7/22/2014	4	56	3	1	0	0	5	1	0			
7/22/2014	4	57	2	2	0	0	6	0	0			
7/22/2014	4	58	1	0	0	0	9	0	0			
7/22/2014	4	59	4	2	0	0	4	0	0			
7/22/2014	4	60	0	4	0	0	5	1	0			
7/22/2014	4	61	0	1	0	0	9	0	0			
7/22/2014	4	62	0	3	0	0	6	1	0			
7/22/2014	4	63	2	0	0	0	7	1	0			
7/22/2014	4	64	2	0	0	0	8	0	0	27.8	20.3	19.4
7/22/2014	4	65	0	0	0	0	10	0	0			
7/22/2014	4	66	2	0	0	0	8	0	0			
7/22/2014	4	67	4	0	0	0	5	1	0			
7/22/2014	4	68	2	2	0	0	6	0	0			
7/22/2014	4	69	3	0	0	0	5	2	0			
7/22/2014	4	70	0	2	0	0	6	2	0			
7/22/2014	4	71	1	0	0	0	8	1	0			
7/22/2014	4	72	0	1	0	0	8	1	0			
7/22/2014	4	73	5	0	0	0	5	0	0	26.9	23.9	19.9
7/22/2014	4	74	7	1	0	0	1	0	1			
7/22/2014	4	75	0	0	0	0	10	0	0			
7/22/2014	4	76	1	1	0	0	7	1	0			
7/22/2014	4	77	5	0	0	0	5	0	0			
7/22/2014	4	78	4	0	0	0	5	1	0			
7/22/2014	4	79	1	1	0	0	7	1	0			
7/22/2014	4	80	0	2	0	0	6	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/22/2014	4	81	0	0	0	0	7	3	0			
7/22/2014	4	82	0	0	0	0	9	1	0	30.8	20.2	17.1
7/22/2014	4	83	1	1	0	0	8	0	0			
7/22/2014	4	84	2	0	0	0	7	1	0			
7/22/2014	4	85	0	0	0	0	6	4	0			
7/22/2014	4	86	0	2	0	1	7	0	0			
7/22/2014	4	87	1	0	1	1	6	1	0			
7/22/2014	4	88	0	1	0	0	9	0	0			
7/22/2014	4	89	0	0	0	0	7	2	1			
7/22/2014	4	90	0	1	1	0	8	0	0			
7/22/2014	4	91	0	0	0	0	8	2	0	28.7	22.6	19.8
7/22/2014	4	92	0	0	0	0	8	2	0			
7/22/2014	4	93	0	0	0	0	6	4	0			
7/22/2014	4	94	0	0	0	0	8	1	1			
7/22/2014	4	95	2	0	0	2	3	3	0			
7/22/2014	4	96	0	0	0	0	9	1	0			
7/22/2014	4	97	1	3	0	0	6	0	0			
7/22/2014	4	98	1	1	0	0	8	0	0			
7/22/2014	4	99	2	1	0	0	5	2	0			
7/22/2014	4	100	3	1	0	2	3	1	0			
7/24/2014	5	1	1	1	0	0	7	1	0			
7/24/2014	5	2	0	5	0	0	5	0	0			
7/24/2014	5	3	0	3	0	0	7	0	0			
7/24/2014	5	4	0	5	0	0	3	2	0			
7/24/2014	5	5	0	8	1	0	0	1	0			
7/24/2014	5	6	0	6	2	0	2	0	0			
7/24/2014	5	7	0	6	0	0	0	2	2			
7/24/2014	5	8	0	3	0	0	2	4	1			
7/24/2014	5	9	0	6	0	0	4	0	0			
7/24/2014	5	10	0	4	0	0	5	1	0			
7/24/2014	5	11	0	0	0	0	10	0	0			
7/24/2014	5	12	0	1	0	0	8	1	0			
7/24/2014	5	13	0	2	0	0	6	2	0			
7/24/2014	5	14	0	7	1	0	0	2	0			
7/24/2014	5	15	0	5	0	0	4	1	0			
7/24/2014	5	16	0	5	1	0	2	2	0			
7/24/2014	5	17	0	8	0	0	2	0	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/24/2014	5	18	0	5	1	0	1	3	0			
7/24/2014	5	19	0	6	0	0	0	1	3			
7/24/2014	5	20	0	7	0	0	1	2	0			
7/24/2014	5	21	0	1	0	0	9	0	0			
7/24/2014	5	22	0	1	0	0	7	1	1			
7/24/2014	5	23	0	3	0	0	4	2	1			
7/24/2014	5	24	0	1	0	0	8	1	0			
7/24/2014	5	25	0	5	0	0	1	4	0			
7/24/2014	5	26	0	1	0	0	2	6	1			
7/24/2014	5	27	0	2	0	0	3	5	0			
7/24/2014	5	28	0	6	0	0	0	4	0			
7/24/2014	5	29	0	3	0	0	4	3	0			
7/24/2014	5	30	0	7	0	0	1	2	0			
7/24/2014	5	31	0	0	0	0	7	3	0			
7/24/2014	5	32	1	2	0	0	6	1	0			
7/24/2014	5	33	0	8	0	0	0	2	0			
7/24/2014	5	34	0	4	0	0	5	1	0			
7/24/2014	5	35	0	4	2	0	1	3	0			
7/24/2014	5	36	0	9	0	0	1	0	0			
7/24/2014	5	37	0	4	1	0	4	1	0			
7/24/2014	5	38	0	6	1	0	2	1	0			
7/24/2014	5	39	0	7	0	0	1	2	0			
7/24/2014	5	40	0	7	0	0	0	3	0			
7/24/2014	5	41	0	0	0	0	9	1	0			
7/24/2014	5	42	0	0	0	0	8	2	0			
7/24/2014	5	43	0	3	0	0	5	2	0			
7/24/2014	5	44	0	7	0	0	1	2	0			
7/24/2014	5	45	0	7	0	0	2	1	0			
7/24/2014	5	46	0	3	0	0	4	3	0			
7/24/2014	5	47	0	6	0	0	1	3	0			
7/24/2014	5	48	0	6	0	0	1	3	0			
7/24/2014	5	49	0	6	0	0	1	3	0			
7/24/2014	5	50	0	7	0	0	2	1	0			
7/24/2014	5	51	0	1	0	0	8	1	0			
7/24/2014	5	52	0	1	0	0	9	0	0			
7/24/2014	5	53	0	1	0	0	8	1	0			
7/24/2014	5	54	0	9	0	0	0	0	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/24/2014	5	55	0	9	0	0	0	1	0			
7/24/2014	5	56	0	7	0	0	2	1	0			
7/24/2014	5	57	0	4	0	0	4	2	0			
7/24/2014	5	58	0	7	0	0	0	3	0			
7/24/2014	5	59	0	7	0	0	1	2	0			
7/24/2014	5	60	0	7	0	0	1	2	0			
7/24/2014	5	61	0	2	0	0	8	0	0			
7/24/2014	5	62	0	2	0	0	7	1	0			
7/24/2014	5	63	0	3	0	0	7	0	0			
7/24/2014	5	64	0	3	0	0	2	4	1			
7/24/2014	5	65	0	9	0	0	0	1	0			
7/24/2014	5	66	0	9	0	0	0	1	0			
7/24/2014	5	67	0	8	0	0	1	0	1			
7/24/2014	5	68	0	9	0	0	0	1	0			
7/24/2014	5	69	0	5	0	0	4	1	0			
7/24/2014	5	70	0	5	0	0	3	2	0			
7/24/2014	5	71	0	0	0	0	9	1	0			
7/24/2014	5	72	0	3	0	0	7	0	0			
7/24/2014	5	73	0	9	0	0	0	1	0	49.7	29.2	22.4
7/24/2014	5	74	0	6	0	0	4	0	0			
7/24/2014	5	75	0	6	0	0	1	3	0			
7/24/2014	5	76	0	8	0	0	1	1	0			
7/24/2014	5	77	0	6	0	0	3	1	0			
7/24/2014	5	78	0	6	0	0	3	1	0			
7/24/2014	5	79	0	7	0	0	1	2	0			
7/24/2014	5	80	0	1	0	0	9	0	0			
7/24/2014	5	81	0	1	0	0	9	0	0			
7/24/2014	5	82	0	7	0	0	0	3	0	31.0	24.9	19.2
7/24/2014	5	83	0	8	0	0	2	0	0			
7/24/2014	5	84	0	8	0	0	1	1	0			
7/24/2014	5	85	0	7	0	0	2	1	0			
7/24/2014	5	86	0	7	0	0	2	1	0			
7/24/2014	5	87	0	9	0	0	0	1	0			
7/24/2014	5	88	0	9	0	0	1	0	0			
7/24/2014	5	89	0	3	0	0	2	5	0			
7/24/2014	5	90	0	7	1	0	0	2	0			
7/24/2014	5	91	0	5	0	0	5	0	0	30.1	24.8	19.8

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/24/2014	5	92	0	6	0	0	3	1	0			
7/24/2014	5	93	0	7	0	0	1	2	0			
7/24/2014	5	94	0	7	0	0	1	2	0			
7/24/2014	5	95	0	9	0	0	1	0	0			
7/24/2014	5	96	0	6	0	0	2	2	0			
7/24/2014	5	97	0	9	0	0	0	1	0			
7/24/2014	5	98	0	7	0	0	0	3	0			
7/24/2014	5	99	0	6	1	0	1	2	0			
7/24/2014	5	100	0	6	2	0	0	2	0			
7/23/2014	6	1	7	0	0	0	3	0	0			
7/23/2014	6	2	3	1	0	1	5	0	0			
7/23/2014	6	3	3	0	0	2	5	0	0			
7/23/2014	6	4	3	0	0	0	6	1	0			
7/23/2014	6	5	7	0	0	2	1	0	0			
7/23/2014	6	6	7	0	0	0	3	0	0			
7/23/2014	6	7	5	0	0	1	4	0	0			
7/23/2014	6	8	7	0	0	1	2	0	0			
7/23/2014	6	9	5	0	0	0	5	0	0			
7/23/2014	6	10	7	0	0	0	2	1	0	26.7	13.9	8.2
7/23/2014	6	11	3	1	0	1	5	0	0			
7/23/2014	6	12	1	0	0	1	6	1	1			
7/23/2014	6	13	6	0	0	0	4	0	0			
7/23/2014	6	14	1	0	0	0	8	0	1			
7/23/2014	6	15	6	0	0	2	2	0	0			
7/23/2014	6	16	4	0	0	0	6	0	0			
7/23/2014	6	17	3	0	0	0	6	1	0			
7/23/2014	6	18	4	0	0	1	3	2	0			
7/23/2014	6	19	8	0	0	0	2	0	0			
7/23/2014	6	20	4	0	0	1	5	0	0			
7/23/2014	6	21	4	0	0	0	6	0	0			
7/23/2014	6	22	5	0	0	0	3	2	0			
7/23/2014	6	23	4	0	0	0	6	0	0			
7/23/2014	6	24	5	0	0	0	5	0	0			
7/23/2014	6	25	6	0	0	1	2	1	0			
7/23/2014	6	26	5	0	0	1	4	0	0			
7/23/2014	6	27	7	0	0	1	2	0	0			
7/23/2014	6	28	6	0	0	0	4	0	0	37.3	16.6	12.7

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/23/2014	6	29	2	0	0	0	7	1	0			
7/23/2014	6	30	2	0	0	1	7	0	0			
7/23/2014	6	31	5	0	0	0	5	0	0			
7/23/2014	6	32	4	0	0	0	6	0	0			
7/23/2014	6	33	5	0	0	0	4	1	0			
7/23/2014	6	34	3	0	0	0	6	1	0			
7/23/2014	6	35	8	0	0	0	2	0	0			
7/23/2014	6	36	4	0	0	0	6	0	0			
7/23/2014	6	37	4	0	0	0	5	0	1			
7/23/2014	6	38	4	0	0	1	5	0	0			
7/23/2014	6	39	5	0	0	1	4	0	0			
7/23/2014	6	40	1	0	0	2	7	0	0			
7/23/2014	6	41	0	0	0	0	10	0	0			
7/23/2014	6	42	2	0	0	0	8	0	0			
7/23/2014	6	43	4	0	0	0	5	1	0			
7/23/2014	6	44	5	0	0	0	5	0	0			
7/23/2014	6	45	5	0	0	0	5	0	0			
7/23/2014	6	46	3	0	0	0	5	2	0	26.9	16.5	12.6
7/23/2014	6	47	1	0	0	0	9	0	0			
7/23/2014	6	48	5	0	0	0	5	0	0			
7/23/2014	6	49	5	0	0	1	4	0	0			
7/23/2014	6	50	4	0	0	1	4	0	1			
7/23/2014	6	51	1	1	0	0	8	0	0			
7/23/2014	6	52	3	2	0	0	5	0	0			
7/23/2014	6	53	1	0	0	2	7	0	0			
7/23/2014	6	54	3	0	0	1	6	0	0			
7/23/2014	6	55	3	0	0	1	4	2	0			
7/23/2014	6	56	7	0	0	0	3	0	0			
7/23/2014	6	57	8	0	0	0	2	0	0			
7/23/2014	6	58	3	0	0	0	7	0	0			
7/23/2014	6	59	8	0	0	0	2	0	0			
7/23/2014	6	60	5	0	0	0	5	0	0			
7/23/2014	6	61	2	0	0	1	6	1	0			
7/23/2014	6	62	5	0	0	0	4	1	0			
7/23/2014	6	63	1	0	0	1	8	0	0			
7/23/2014	6	64	5	0	0	0	4	0	1	29.1	16.5	14.7
7/23/2014	6	65	7	0	0	1	2	0	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/23/2014	6	66	2	0	0	0	7	1	0			
7/23/2014	6	67	3	0	0	1	6	0	0			
7/23/2014	6	68	6	0	0	0	4	0	0			
7/23/2014	6	69	6	0	0	2	2	0	0			
7/23/2014	6	70	3	1	0	1	3	2	0			
7/23/2014	6	71	4	0	0	0	5	1	0			
7/23/2014	6	72	3	0	0	1	6	0	0			
7/23/2014	6	73	4	0	0	0	6	0	0			
7/23/2014	6	74	5	0	0	0	5	0	0			
7/23/2014	6	75	3	0	0	1	6	0	0			
7/23/2014	6	76	4	0	0	0	5	1	0			
7/23/2014	6	77	3	0	0	1	5	0	1			
7/23/2014	6	78	5	0	0	0	5	0	0			
7/23/2014	6	79	4	1	0	0	5	0	0			
7/23/2014	6	80	4	0	0	1	4	1	0			
7/23/2014	6	81	3	0	0	0	7	0	0			
7/23/2014	6	82	3	0	0	0	6	1	0	25.6	15.4	10.9
7/23/2014	6	83	1	0	0	0	9	0	0			
7/23/2014	6	84	3	0	0	1	6	0	0			
7/23/2014	6	85	4	0	0	6	0	0	0			
7/23/2014	6	86	3	0	0	0	7	0	0			
7/23/2014	6	87	2	0	0	0	8	0	0			
7/23/2014	6	88	1	0	0	0	9	0	0			
7/23/2014	6	89	1	0	0	0	9	0	0			
7/23/2014	6	90	1	0	0	0	9	0	0			
7/23/2014	6	91	3	0	0	0	7	0	0			
7/23/2014	6	92	0	0	0	1	9	0	0			
7/23/2014	6	93	1	0	0	0	9	0	0			
7/23/2014	6	94	1	0	0	0	9	0	0			
7/23/2014	6	95	4	0	0	0	6	0	0			
7/23/2014	6	96	6	0	0	4	0	0	0			
7/23/2014	6	97	7	0	0	0	3	0	0			
7/23/2014	6	98	0	0	0	0	8	2	0			
7/23/2014	6	99	5	0	0	1	4	0	0			
7/23/2014	6	100	7	0	0	1	0	2	0			
7/21/2014	1	1	1	0	0	0	9	0	0			
7/21/2014	1	2	6	0	0	0	3	1	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/21/2014	1	3	3	0	0	0	7	0	0			
7/21/2014	1	4	5	4	0	0	0	0	1			
7/21/2014	1	5	5	0	0	0	5	0	0			
7/21/2014	1	6	3	0	0	1	6	0	0			
7/21/2014	1	7	3	0	0	0	5	2	0			
7/21/2014	1	8	0	0	0	0	10	0	0			
7/21/2014	1	9	6	0	0	0	4	0	0			
7/21/2014	1	10	2	0	0	0	8	0	0	8.1	9.7	15.3
7/21/2014	1	11	3	0	0	0	7	0	0			
7/21/2014	1	12	5	0	0	0	4	1	0			
7/21/2014	1	13	5	0	0	0	5	0	0			
7/21/2014	1	14	3	0	0	0	6	1	0			
7/21/2014	1	15	3	0	0	0	6	0	1			
7/21/2014	1	16	2	0	0	0	7	0	1			
7/21/2014	1	17	1	0	0	0	7	1	1			
7/21/2014	1	18	1	0	0	0	8	0	1			
7/21/2014	1	19	5	0	0	0	3	2	0	8.3	7.9	12.00
7/21/2014	1	20	0	0	0	0	10	0	0			
7/21/2014	1	21	5	0	0	0	5	0	0			
7/21/2014	1	22	4	0	0	0	5	1	0			
7/21/2014	1	23	7	0	0	0	3	0	0			
7/21/2014	1	24	3	0	0	0	6	1	0			
7/21/2014	1	25	2	0	0	0	6	2	0			
7/21/2014	1	26	5	0	0	0	4	1	0			
7/21/2014	1	27	3	0	0	0	7	0	0			
7/21/2014	1	28	3	0	0	0	7	0	0	8.8	8.5	14.8
7/21/2014	1	29	4	0	0	0	4	2	0			
7/21/2014	1	30	2	0	0	0	6	2	0			
7/21/2014	1	31	3	0	0	0	6	1	0			
7/21/2014	1	32	4	0	0	0	6	0	0			
7/21/2014	1	33	6	0	0	0	4	0	0			
7/21/2014	1	34	4	0	0	0	5	1	0			
7/21/2014	1	35	4	0	0	0	6	0	0			
7/21/2014	1	36	2	0	0	0	7	0	1			
7/21/2014	1	37	4	0	0	0	5	1	0	8.9	9.6	14.1
7/21/2014	1	38	3	0	0	0	5	2	0			
7/21/2014	1	39	2	0	0	0	6	1	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/21/2014	1	40	4	0	0	0	5	1	0			
7/21/2014	1	41	5	0	0	0	4	1	0			
7/21/2014	1	42	4	0	0	0	3	3	0			
7/21/2014	1	43	1	0	0	0	8	1	0			
7/21/2014	1	44	4	0	0	0	5	1	0			
7/21/2014	1	45	6	0	0	0	4	0	0			
7/21/2014	1	46	4	0	0	0	6	0	0	10.6	15.9	14.9
7/21/2014	1	47	2	0	0	0	7	1	0			
7/21/2014	1	48	2	0	0	0	8	0	0			
7/21/2014	1	49	3	0	0	0	5	2	0			
7/21/2014	1	50	2	0	0	0	8	0	0			
7/21/2014	1	51	5	0	0	0	5	0	0			
7/21/2014	1	52	1	0	0	0	9	0	0			
7/21/2014	1	53	1	0	0	0	9	0	0			
7/21/2014	1	54	3	0	0	0	4	3	0			
7/21/2014	1	55	4	0	0	0	5	1	0	12.5	15.2	15.5
7/21/2014	1	56	1	0	0	0	7	1	0			
7/21/2014	1	57	0	0	0	0	8	2	0			
7/21/2014	1	58	2	0	0	0	7	1	0			
7/21/2014	1	59	2	0	0	0	6	2	0			
7/21/2014	1	60	3	0	0	0	4	3	0			
7/21/2014	1	61	4	0	0	0	6	0	0			
7/21/2014	1	62	5	0	0	0	4	0	1			
7/21/2014	1	63	4	0	0	0	5	1	0			
7/21/2014	1	64	2	0	0	0	4	4	0	15.5	13.6	x
7/21/2014	1	65	1	0	0	0	8	1	0			
7/21/2014	1	66	3	0	0	0	5	2	0			
7/21/2014	1	67	6	0	0	0	4	0	0			
7/21/2014	1	68	2	0	0	0	5	3	0			
7/21/2014	1	69	5	0	0	0	4	1	0			
7/21/2014	1	70	4	0	0	0	4	2	0			
7/21/2014	1	71	3	0	0	0	6	1	0			
7/21/2014	1	72	4	0	0	0	4	2	0			
7/21/2014	1	73	4	0	0	0	5	1	0	14.4	15.1	12.7
7/21/2014	1	74	4	0	0	0	6	0	0			
7/21/2014	1	75	2	0	0	0	6	2	0			
7/21/2014	1	76	3	0	0	0	5	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/21/2014	1	77	5	0	0	0	5	0	0			
7/21/2014	1	78	3	0	0	0	5	2	0			
7/21/2014	1	79	5	0	0	0	4	1	0			
7/21/2014	1	80	3	0	0	0	6	0	1			
7/21/2014	1	81	4	0	0	0	5	1	0			
7/21/2014	1	82	1	0	0	0	9	0	0	14.2	16.9	16.6
7/21/2014	1	83	5	0	0	0	5	0	0			
7/21/2014	1	84	0	0	0	0	7	3	0			
7/21/2014	1	85	4	0	0	0	5	1	0			
7/21/2014	1	86	4	0	0	0	6	0	0			
7/21/2014	1	87	0	0	0	0	8	2	0			
7/21/2014	1	88	3	0	0	0	5	2	0			
7/21/2014	1	89	1	0	0	0	8	1	0			
7/21/2014	1	90	3	0	0	0	6	1	0			
7/21/2014	1	91	2	0	0	0	7	1	0	13.6	14.9	13.1
7/21/2014	1	92	3	0	0	0	6	1	0			
7/21/2014	1	93	5	0	0	0	4	1	0			
7/21/2014	1	94	3	0	0	0	6	1	0			
7/21/2014	1	95	3	0	0	0	5	2	0			
7/21/2014	1	96	2	0	0	0	6	2	0			
7/21/2014	1	97	3	0	0	0	5	2	0			
7/21/2014	1	98	4	0	0	0	5	0	1			
7/21/2014	1	99	2	0	0	0	8	0	0			
7/21/2014	1	100	1	0	0	0	8	1	0			
7/22/2014	2	1	3	0	0	0	7	0	0			
7/22/2014	2	2	1	0	0	0	7	2	0			
7/22/2014	2	3	0	0	0	0	7	3	0			
7/22/2014	2	4	0	1	0	0	4	5	0			
7/22/2014	2	5	0	0	0	0	9	1	0			
7/22/2014	2	6	0	0	0	0	9	1	0			
7/22/2014	2	7	0	1	0	0	4	5	0			
7/22/2014	2	8	0	0	0	0	7	3	0			
7/22/2014	2	9	0	1	0	0	6	3	0			
7/22/2014	2	10	1	0	0	0	8	1	0	22.6	19.4	18.3
7/22/2014	2	11	0	0	0	0	7	2	1			
7/22/2014	2	12	0	0	0	0	8	2	0			
7/22/2014	2	13	0	0	0	0	7	3	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/22/2014	2	14	0	0	0	0	8	2	0			
7/22/2014	2	15	1	1	0	0	6	2	0			
7/22/2014	2	16	0	1	1	0	5	3	0			
7/22/2014	2	17	0	0	0	0	7	3	0			
7/22/2014	2	18	0	1	0	0	9	0	0			
7/22/2014	2	19	1	0	0	0	5	4	0	22.7	18.5	16.5
7/22/2014	2	20	0	2	0	0	3	5	0			
7/22/2014	2	21	1	2	1	0	6	0	0			
7/22/2014	2	22	0	0	0	0	8	2	0			
7/22/2014	2	23	0	1	0	0	7	2	0			
7/22/2014	2	24	1	0	0	0	8	1	0			
7/22/2014	2	25	0	2	0	0	5	3	0			
7/22/2014	2	26	0	3	1	0	5	1	0			
7/22/2014	2	27	0	0	0	0	9	1	0			
7/22/2014	2	28	1	1	1	0	6	1	0	23.6	18.4	16.6
7/22/2014	2	29	0	2	1	0	6	1	0			
7/22/2014	2	30	0	0	0	0	6	4	0			
7/23/2014	2	31	1	0	0	0	8	1	0			
7/23/2014	2	32	0	1	1	0	7	1	0			
7/23/2014	2	33	1	2	0	0	6	0	1			
7/23/2014	2	34	0	5	1	0	4	0	0			
7/23/2014	2	35	1	2	1	0	5	1	0			
7/23/2014	2	36	0	0	1	0	8	1	0			
7/23/2014	2	37	1	3	0	0	5	1	0	25.3	17.8	x
7/23/2014	2	38	0	2	1	7	0	0	0			
7/23/2014	2	39	1	2	2	0	3	2	0			
7/23/2014	2	40	1	0	1	0	5	3	0			
7/23/2014	2	41	1	2	1	0	4	2	0			
7/23/2014	2	42	0	1	1	0	5	3	0			
7/23/2014	2	43	1	1	0	0	5	3	0			
7/23/2014	2	44	1	1	0	0	7	1	0			
7/23/2014	2	45	0	2	1	0	6	1	0			
7/23/2014	2	46	0	2	0	0	6	2	0	29.8	18.1	17.6
7/23/2014	2	47	0	0	0	0	9	1	0			
7/23/2014	2	48	2	0	0	0	7	1	0			
7/23/2014	2	49	0	0	0	0	7	3	0			
7/23/2014	2	50	0	3	0	0	5	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/23/2014	2	51	0	3	0	0	5	2	0			
7/23/2014	2	52	0	3	0	0	6	1	0			
7/23/2014	2	53	3	0	0	0	7	0	0			
7/23/2014	2	54	0	1	0	0	3	6	0			
7/23/2014	2	55	0	1	1	0	6	2	0	28.6	18.0	17.0
7/23/2014	2	56	0	1	2	0	4	3	0			
7/23/2014	2	57	1	0	0	0	8	1	0			
7/23/2014	2	58	1	0	0	0	7	2	0			
7/23/2014	2	59	0	3	0	0	6	1	0			
7/23/2014	2	60	1	2	0	0	5	2	0			
7/23/2014	2	61	1	1	2	0	4	2	0			
7/23/2014	2	62	4	1	0	0	4	1	0			
7/23/2014	2	63	0	2	0	0	7	1	0			
7/23/2014	2	64	2	2	0	0	3	3	0	27.3	21.7	x
7/23/2014	2	65	0	0	0	0	8	1	1			
7/23/2014	2	66	1	3	0	0	5	1	0			
7/23/2014	2	67	0	1	0	0	7	2	0			
7/23/2014	2	68	2	0	1	0	5	2	0			
7/23/2014	2	69	1	0	0	0	5	4	0			
7/23/2014	2	70	1	3	0	0	6	0	0			
7/23/2014	2	71	0	2	0	0	8	0	0			
7/23/2014	2	72	0	0	2	0	4	4	0			
7/23/2014	2	73	1	4	0	0	5	0	0	24.5	20.2	18.0
7/23/2014	2	74	1	3	0	0	5	1	0			
7/23/2014	2	75	0	2	0	0	6	2	0			
7/23/2014	2	76	3	1	0	0	6	0	0			
7/23/2014	2	77	0	2	0	0	7	1	0			
7/23/2014	2	78	1	1	0	0	7	1	0			
7/23/2014	2	79	2	1	0	0	6	1	0			
7/23/2014	2	80	2	0	0	0	5	3	0			
7/23/2014	2	81	0	0	1	0	8	0	1			
7/23/2014	2	82	0	3	0	0	7	0	0	25.0	16.3	13.7
7/23/2014	2	83	0	1	0	0	6	3	0			
7/23/2014	2	84	1	1	0	0	7	1	0			
7/23/2014	2	85	2	2	0	0	5	1	0			
7/23/2014	2	86	3	2	0	0	3	2	0			
7/23/2014	2	87	0	3	0	0	5	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/23/2014	2	88	1	2	0	0	4	3	0			
7/23/2014	2	89	1	1	1	0	6	1	0			
7/23/2014	2	90	0	2	0	0	6	2	0			
7/23/2014	2	91	1	0	0	0	8	1	0	25.6	18.9	16.5
7/23/2014	2	92	1	0	0	0	8	1	0			
7/23/2014	2	93	0	1	0	0	8	1	0			
7/23/2014	2	94	3	0	0	0	6	1	0			
7/23/2014	2	95	0	3	0	0	6	1	0			
7/23/2014	2	96	3	1	0	0	2	4	0			
7/23/2014	2	97	0	2	0	0	6	2	0			
7/23/2014	2	98	2	1	0	0	7	0	0			
7/23/2014	2	99	0	2	0	0	7	1	0			
7/23/2014	2	100	1	1	0	0	5	3	0			
7/23/2014	3	1	0	0	0	0	10	0	0			
7/23/2014	3	2	0	2	0	0	7	1	0			
7/23/2014	3	3	0	2	0	0	7	1	0			
7/23/2014	3	4	0	2	0	0	7	1	0			
7/23/2014	3	5	0	2	0	0	7	1	0			
7/23/2014	3	6	0	2	0	0	7	0	1			
7/23/2014	3	7	0	5	0	0	4	1	0			
7/23/2014	3	8	0	2	0	0	6	2	0			
7/23/2014	3	9	0	1	0	0	8	0	1			
7/23/2014	3	10	0	0	0	0	6	2	2	26.2	20.3	17.4
7/23/2014	3	11	0	2	0	0	7	1	0			
7/23/2014	3	12	0	2	0	0	7	0	1			
7/23/2014	3	13	0	6	0	0	4	0	0			
7/23/2014	3	14	0	0	0	0	10	0	0			
7/23/2014	3	15	0	4	0	0	5	0	1			
7/23/2014	3	16	0	2	0	0	6	1	1			
7/23/2014	3	17	0	1	0	0	6	2	1			
7/23/2014	3	18	0	4	0	0	4	2	0			
7/23/2014	3	19	0	0	0	0	7	2	1	19.7	17.8	17.7
7/23/2014	3	20	0	2	0	0	3	4	1			
7/23/2014	3	21	0	4	0	0	5	0	1			
7/23/2014	3	22	0	3	0	0	3	2	2			
7/23/2014	3	23	0	0	0	0	8	1	1			
7/23/2014	3	24	1	0	0	0	7	1	1			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/23/2014	3	25	1	3	0	0	5	1	0			
7/23/2014	3	26	0	0	0	0	6	4	0			
7/23/2014	3	27	0	1	0	0	7	1	1			
7/23/2014	3	28	0	3	0	0	6	0	1	21.7	17.1	16.3
7/23/2014	3	29	0	3	0	0	6	1	0			
7/23/2014	3	30	0	2	0	0	6	1	1			
7/23/2014	3	31	0	3	0	0	7	0	0			
7/23/2014	3	32	0	4	0	0	3	2	1			
7/23/2014	3	33	0	4	0	0	6	0	0			
7/23/2014	3	34	0	3	0	0	6	1	0			
7/23/2014	3	35	0	8	0	0	1	1	0			
7/23/2014	3	36	0	6	0	0	2	1	1			
7/23/2014	3	37	0	6	0	0	4	0	0	24.9	17.1	15.2
7/23/2014	3	38	0	6	0	0	2	1	1			
7/23/2014	3	39	1	3	0	0	4	2	0			
7/23/2014	3	40	0	1	0	0	6	2	1			
7/23/2014	3	41	0	2	0	0	6	2	0			
7/23/2014	3	42	0	0	0	0	7	1	2			
7/23/2014	3	43	0	2	0	0	7	0	1			
7/23/2014	3	44	0	5	0	0	5	0	0			
7/23/2014	3	45	0	3	0	0	5	1	1			
7/23/2014	3	46	0	4	0	0	5	1	0	22.4	23.2	20.4
7/23/2014	3	47	0	2	0	0	5	2	1			
7/23/2014	3	48	0	1	0	0	6	1	2			
7/23/2014	3	49	0	2	0	0	7	1	0			
7/23/2014	3	50	0	7	0	0	1	2	0			
7/24/2014	3	51	0	1	0	0	9	0	0			
7/24/2014	3	52	0	1	0	0	8	1	0			
7/24/2014	3	53	0	2	0	0	6	2	0			
7/24/2014	3	54	0	3	0	0	6	0	1			
7/24/2014	3	55	0	3	0	0	7	0	0	28.7	23.1	18.8
7/24/2014	3	56	0	3	0	0	4	3	0			
7/24/2014	3	57	0	1	0	0	6	3	0			
7/24/2014	3	58	0	3	0	0	6	1	0			
7/24/2014	3	59	1	1	0	0	4	4	0			
7/24/2014	3	60	0	3	0	0	3	4	0			
7/24/2014	3	61	0	1	0	0	8	1	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/24/2014	3	62	0	4	0	0	6	0	0			
7/24/2014	3	63	0	0	0	0	8	1	1			
7/24/2014	3	64	0	3	0	0	6	1	0	22.5	16.6	14.9
7/24/2014	3	65	0	0	0	0	9	1	0			
7/24/2014	3	66	0	1	0	0	5	3	1			
7/24/2014	3	67	0	2	0	0	5	3	0			
7/24/2014	3	68	0	2	0	0	8	0	0			
7/24/2014	3	69	0	0	0	0	9	1	0			
7/24/2014	3	70	0	0	0	0	6	4	0			
7/24/2014	3	71	0	0	0	0	9	0	1			
7/24/2014	3	72	0	0	0	0	8	2	0			
7/24/2014	3	73	0	0	0	0	10	0	0	19.0	16.8	15.5
7/24/2014	3	74	0	4	0	0	5	1	0			
7/24/2014	3	75	1	1	0	0	7	0	1			
7/24/2014	3	76	0	1	0	0	7	2	0			
7/24/2014	3	77	0	1	0	0	7	2	0			
7/24/2014	3	78	0	1	0	0	8	1	0			
7/24/2014	3	79	0	0	0	0	8	2	0			
7/24/2014	3	80	0	2	0	0	8	0	0			
7/24/2014	3	81	0	3	0	0	6	1	0			
7/24/2014	3	82	0	1	0	0	8	1	0	21.0	18.0	14.7
7/24/2014	3	83	0	0	0	0	10	0	0			
7/24/2014	3	84	0	1	0	0	7	1	1			
7/24/2014	3	85	0	3	0	0	7	0	0			
7/24/2014	3	86	0	2	0	0	5	3	0			
7/24/2014	3	87	0	0	0	0	7	2	1			
7/24/2014	3	88	0	2	0	0	7	1	0			
7/24/2014	3	89	0	1	0	0	7	2	0			
7/24/2014	3	90	0	2	0	0	7	1	0			
7/24/2014	3	91	0	0	0	0	10	0	0	25.0	19.5	15.6
7/24/2014	3	92	0	2	0	0	8	0	0			
7/24/2014	3	93	0	2	0	0	5	1	2			
7/24/2014	3	94	0	1	0	0	8	1	0			
7/24/2014	3	95	0	0	0	0	7	3	0			
7/24/2014	3	96	1	0	0	0	7	1	1			
7/24/2014	3	97	0	0	0	0	10	0	0			
7/24/2014	3	98	0	3	0	0	5	2	0			

Table H.9. Data collected in 2014 for long-term climate change study (continued).

Date	PLOT #	Quadrat	POPR	Sedge	SPPE	BRIN	GR	FO	BR	% H2O(0-30)	% H2O(30-60)	% H2O(60-90)
7/24/2014	3	99	0	0	0	0	9	1	0			
7/24/2014	3	100	0	2	0	0	7	1	0			

APPENDIX I. RESEARCH PERMIT FOR CHAPTER FIVE OF THE DISSERTATION.

PERMIT WAS ISSUED BY THE NATURE CONSERVANCY

The Nature Conservancy
Protecting nature. Preserving life.™

The Nature Conservancy in Minnesota
11101 West River Parkway, Suite 200
Minneapolis, MN 55415

tel [612] 331-0750
fax [612] 331-0770

nature.org

RESEARCH PERMIT

May 21, 2014

Steven Travers
NDSU 701-231-9435 steven.travers@ndsu.edu
1340 Bolley Drive
Steven 218
Fargo, ND 58102

RE: Long term monitoring of species abundance in the tallgrass prairie of Minnesota

This Research Permit ("Permit") serves as permission for you to conduct research on the long term monitoring of species abundance in the tallgrass prairie of Minnesota , as described in the attached Permit Application (the "Research") at the following TNC Preserve: Bluestem Prairie SNA (the "Preserve"). Since Bluestem Prairie is also a Scientific and Natural Area, you will need a separate permit from the Minnesota Department of Natural Resources. Please call or e-mail Mark Cleveland, DNR Scientific and Natural Areas Management Coordinator, at 651-259-5094 or mark.cleveland@state.mn.us regarding this separate permit. The Research is subject to the following requirements:

1. **Contact stewardship staff (listed below) before entering the Preserve** to avoid conflicts with stewardship management activities such as prescribed burning.
2. If you have questions about the Preserve' management history or planned management activities (e.g. prescribed fire, weed control, mowing), please feel free to contact **Matt Mecklenburg, Land Steward at 218-498-2679.**
3. The Research must be completed by August 15, 2014. Research activities and sampling methods will be carried out as outlined in the attached Permit Application. All field markers, equipment, and other materials must be removed from the Preserve by this date.
4. Minimize the spread of invasive species while conducting the Research (Please refer to http://mipn.org/prevention.html for helpful tips and information from the Midwest Invasive Plant Network).
5. No vehicles may be driven on the Preserve.
6. Carry this letter while on the Preserve – with an attached copy of your Permit Application- and extend courtesy to other site visitors, explaining the Research when necessary.
7. You and/or your assistants are using the Preserve at your own risk. You agree to take all necessary safety precautions to protect yourself, your assistants, and other Preserve visitors. The Conservancy makes no warranties or representations concerning the suitability of the Preserve for any purpose. You hereby indemnify the Conservancy against any loss or damage arising from your presence on the Preserve.
8. Acknowledge The Nature Conservancy in any presentations or publications generated by this work.
9. Submit electronic copies of: a preliminary research summary by December 31, 2014, and a final report upon completion of your work, to jpastika@tnc.org and mcornett@tnc.org. Include maps and spatial data with your report. We would also appreciate receiving a copy of any future peer-reviewed publications that summarize work conducted on our lands – in pdf format if possible.
10. The Conservancy may terminate this Permit at any time upon two weeks written notice. In addition, if you default in performance of this Permit, whether for circumstances within or beyond your control, the Conservancy may immediately terminate this Permit by written notice to you.
11. **This Permit is not effective until you sign and date below to acknowledge your agreement with the terms and conditions set forth in this Permit.**

If you have any questions or comments about this permit, please feel free to call me at 218-727-6119.

Sincerely,

Meredith W. Cornett

Meredith Cornett
Director of Conservation Science, TNC

ec/cc: Brian Winter, Matt Mecklenburg, Marissa Ahlering, Mark Cleveland

I agree to abide by the terms and conditions set forth in this Research Permit

_Steven Travers_____ ___5/24/2014_____
Signature Date
____Steven Travers_____
Print Name

APPENDIX J. RESEARCH PERMIT FOR CHAPTER FIVE OF THE DISSERTATION. THE PERMIT WAS ISSUED BY THE DEPARTMENT OF THE NATURAL RESOURCES FOR THE SCIENTIFIC AND NATURAL AREA

STATE OF MINNESOTA
DEPARTMENT OF NATURAL RESOURCES
DIVISION OF ECOLOGICAL SERVICES
SCIENTIFIC AND NATURAL AREAS PROGRAM

SPECIAL PERMIT NUMBER: **2013-25R**

SCIENTIFIC AND NATURAL AREAS: **Bluestem Prairie Scientific and Natural Area**

DATE: May 13, 2014

By virtue of the authority conferred on me by the Commissioner of Natural Resources relative to Scientific and Natural Areas, I grant permission to:

Name of Principal Investigator: Steve Travers

North Dakota State University, Department of Biological Sciences
1340 Bolley Drive, Stevens 218, Fargo, ND 58102
Work Telephone: 701-231-9435 E-mail: Steven.travers@ndsu.edu
Experience in Research Area: Career in field ecology starting in 1990
Field Crew Members: Designated field assistants

to enter upon the above Scientific and Natural Areas (SNAs) for the purpose of **Long term monitoring of species abundance in the tallgrass prairie.**
It is understood that the above named person has a clear understanding of the purpose and long-term goal of state Scientific and Natural Areas. In keeping with this purpose, they shall always conduct their activities in a manner that is least disruptive to the on-going natural processes of these areas. Permission must be received from the SNA Program if the permitee desires or anticipates deviating from this permit. In addition, the following conditions are placed on the proposal submitted:

1. This permit must be amended to include the names of any additional personnel, volunteers or contractors before they can collect specimens under this permit.
2. All work shall be done to prevent the inadvertent transport of invasive species with adherence to DNR Operational Order # 113 and Division of Ecological Resources Op. Order 113, Divisional Guidelines.
3. State listed endangered or threatened species may only be collected under the special permit from the DNR's Division of Ecological Resources. Please contact Richard Baker, Minnesota Endangered Species Coordinator, MNDNR. He can be reached by phone (651-259-5073) or by e-mail (richard.baker@dnr.state.mn.us).
4. No motorized vehicle (other than the helicopters) may be used within the SNA boundary.
5. Trampling of vegetation shall be avoided.
6. Flags used to mark plants, plots, or other features will be removed from the site upon completion of the study.
7. Please carry this permit while on the SNA and extend courtesy to any other site visitors, explaining this research work when necessary.
8. The researchers will consult with SNA Specialist, Shelley Hedtke (Phone # 218-739-7576 ex. 262) (email shelley.hedtke@state.mn.us).
9. Please acknowledge the Minnesota DNR, Scientific and Natural Areas Program in any articles and presentations concerning this research.
10. Please submit electronically a copy of the list of specimens collected by December 31, 2014 to mark.cleveland@state.mn.us. This list should specify the disposition of all specimens and include maps, GPS points, or other information on location of the collections of each species. We would also appreciate receiving a copy of any future peer-reviewed publications that summarize work conducted on our lands – in pdf format if possible. If for any reason you do not do any work under this research permit, please notify us.

As with all SNA(s), the sites you have selected may be subject to planned management activities (e.g. brush and tree removal, prescribed burns, seed harvest, etc) during the duration of your permitted activities. Please contact the SNA Program with questions or concerns: (telephone) 651-259-5094, (e-mail) mark.cleveland@state.mn.us.

This permit is valid from the date of issuance through December 31, 2014 and may be revoked at any time to protect the resources of the SNA upon verbal or written communication. Upon request, this permit may be renewed for 2015.

By

Ann Pierce, Manager, Ecosystem Management and Protection Services Section
Division of Ecological & Water Resources
500 Lafayette Rd., Box 25
St. Paul, MN 55155-4025

This SCIENTIFIC AND NATURAL AREA was established to protect and perpetuate Minnesota's rare and unique natural resources for nature observation, education and research purposes.

Principal activities which are **UNLAWFUL** in the use of this area are listed below:

* Collecting plants, animals, rocks or fossils
* Camping, picnicking, and swimming
* Horses, dogs, and other pets
* Snowmobiles and other motorized vehicles
* Hunting, trapping, fishing and boating
* Entry into restricted areas and sanctuaries