PLANT SPECIES DIVERSITY IN THE SAGEBRUSH STEPPE OF MONTANA

by

Timothy Fridolin Seipel

A thesis submitted in partial fulfillment
Of the requirement for the degree

of

Master of Science

In

Plant Sciences

MONTANA STATE UNIVERISTY
Bozeman, Montana

October 2006

APPROVAL

of a thesis submitted by

Timothy Fridolin Seipel

This thesis has been read by each member of the thesis committee and has been found to be satisfactory regarding content, English usage, format citations, bibliographic style and consistanancy, and is ready for submission to the Division of Graduate Education.

Matthew Lavin

Approved for the Department of Plant Science and Plant Pathology

John Sherwood

Approved for the Division of Graduate Education

Carl A. Fox

STATEMENT OF PERMISSION TO USE

In presenting this thesis in partial fulfillment of the requirements for a master's degree at Montana State University-Bozeman, I agree that the library shall make it available to borrowers under rules of the Library.

I have indicated my intention to copyright this thesis by including a copyright notice page, copying is allowable only for scholarly purposes, consistent with "fair use" as prescribed in the U.S. Copyright Law. Requests for permission for extended quotation from or reproduced of this thesis in whole or in parts may be granted only by the copyright holder.

Timothy Fridolin Seipel
October 2006

ACKNOWLEDGEMENTS

Without funding from the Montana Noxious Weed Trust Fund and the World Wildlife Fund this project would not have been possible. I would especially like to thank Dr. Matt Lavin for his patience and knowledge. I would like to thank my other committee members Dr. Bruce Maxwell and Dr. Dave Roberts for my general edification. The weed ecology group has greatly enhanced the thought that has gone into this thesis. Additionally, Cortland Barnes and Frank Dougher helped with GIS. And finally without the support and compassion of sweet beautiful Katharine Schultz, I wouldn’t be where I am today. I would also like to thank Joyce and Bernhard Seipel for exposing me to the world and instilling independence in me.

TABLE OF CONTENTS

TABLE OF CONTENTS-CONTINUED

TABLE OF CONTENTS-CONTINUED

LIST OF TABLES

LIST OF TABLES-CONTINUED

LIST OF FIGURES

LIST OF FIGURES-CONTINUED

ABSTRACT

Sagebrush (*Artemisia tridentata*) is abundant in Montana and is an obvious part of an assemblage of plant species.This community of plants; the sagebrush steppe contains a mixture of grasses, early and late season forbs and shrubs. It is found in semi-arid valleys and plains of Montana and the intermountain western United States, and has received much research attention regarding increasing livestock forage, or of wildlife's dependence on the sagebrush steppe plant communities.Yet, little information on plant species diversity exists. This thesis was undertaken to describe the plant species diversity in three intact sagebrush steppe sites in Montana. The sites were located in Gallitan and Phillips counties.

An average of 130 species was found at each site documenting the high levels of diversity that exist in local communities. Diversity measures were similar yet the dissimilarity among sites was high, this could reflect the high diversity of plant species in sagebrush steppe. Of the species recorded none had a restricted range, and this may represent a high rate of migration among local communities. Contrary to a designation as mixed grass prairie at the Phillips county site we found most species representative of the sagebrush steppe and areas of the Great Basin, and the site may be better classified as sagebrush steppe.

Introduced plant species were found at all sites. The Burke Park site located in the city of Bozeman has the greatest diversity and abundance of introduced species. The most abundant species were introduced forage grasses. Our results also found that introduced species were negatively associated with the distance to road or trail.This is consistent with other findings that implicate human population density and disturbance as determinants of introduced plant diversity. The implication that human related disturbance and transport of popagules are causes of introduced plant establishment highlights the need for prevention of widespread destruction of sagebrush steppe.

CHAPTER ONE

SAGEBRUSH STEPPE IN ECOLOGICAL LITERATURE

Introduction

The focus in this thesis on sagebrush habitats stems from the overarching question of whether the sagebrush steppe in western North America forms a metacommunity. That is, is the floristic composition of local communities of sagebrush steppe greatly influenced by the other local communities from within the same metacommunity? This could be regardless of variation in elevation, soil characteristics, or dominance of the species or subspecies of sagebrush? A metacommunity designation of the sagebrush steppe is reasonable given that many species and species groups are widespread throughout, but highly confined to this biome; for example, this includes many species of the genera *Astragalus*, *Eriogonum*, and *Penstemon*, or Brewer's sparrow and the Northern Sagegrouse (Lesica et al. 2006 and Welch 2005). Such endemicity suggests both temporal (evolutionary) and spatial (ecological) integrity of the sagebrush steppe.

Sagebrush

The genus *Artemisia* subgenus *Tridentatae* (sagebrush) comprises shrubby species endemic to western North America that are characteristic of the intermountain valleys and plains of western North America (West and Young 1988). Sagebrush species occur in both the New and Old World of the Northern hemisphere and sometimes collectively referred to as the genus *Serphidium*, which is diagnosed by ray florets absent, disk florets perfect and fertile, and the receptacle glabrous (MacAuthur 1979, MacAuthur and

Sanderson 1999). Recent molecular phylogenetic studies reveal that the New World sagebrush species are more closely related to each other than to any other *Artemisia* (i.e., monophyletic), thus provisionally validating the use of subgenus *Tridentatae* (Watson et al. 2002).

Artemisia tridentata is the most important and widespread species of the *Tridentatae*. Its five subspecies are largely separated by ecological characteristics. Wyoming big sagebrush (*A. tridentata* ssp. *wyomingensis*) occupies the most xeric sites on shallower soils (Kolb and Sperry 1999). Basin big sagebrush (*A. tridentata* ssp. *tridentata*) usually occupies valley bottoms with deep soils and has been used to identify farmland (Wambolt and Friscina 2002, Stegner 1940). Mountain big sagebrush (*A. tridentata* ssp. *vaseyana*) is found predominately in upland areas with rocky soils and higher precipitation than that of Wyoming big sagebrush habitat (West 1983). Subalpine big sagebrush (*A. tridentata* ssp. *spiciformis*) and xeric big sagebrush (*A. tridentata* ssp. *xericensis*) are more ecologically or geographically restricted and are only occasionally mentioned in literature (e.g., McArthur and Goodrich 1986; McArthur and Sanderson 1999).

Montana harbors 13 taxa of the subgenus *Tridentatae* (Wambolt and Frisina 2002), including four subspecies of *Artemisia tridentata*, two subspecies of *A. cana*, two subspecies of *A. arbuscula*, two subspecies of *A. tripartata, A longiloba, A. nova*, and *A. rigida*. In addition, 15 other taxa of *Artemisia* not included in the subgenus *Tridentatae* occur in Montana, including *Artemisia absinthium, A. annua, A. biennis, A. campestris*, *A. dracunculus*, *A. frigida, A. lindleyana, A. longifolia, A. ludoviciana, A. michauxiana*, *A. norvegica*, *A. pedatifida, A. scopulorum, A. spinescens, and A. tilesii* (Dorn 1984).

Sagebrush Steppe and Associated Habitats

Sagebrush taxa are estimated to cover 60 (Beetle 1960) to 109 million hectares (Wambolt and Frisina 2002) of rangeland in the western United States. Sagebrush steppe is estimated to cover 96.5-270 million hectares (Welch 2005), although West and Young (1988) and West (1983) estimate considerably less at 44.8 million hectares because they arbitrarily distinguish it from the Great Basin sagebrush habitat to the south. Many estimates exist for the distribution of sagebrush and sagebrush steppe but show large variation (Welch 2005). Potential vegetation maps of habitat types by Küchler (1970), Landsat estimations (Fisher et al. 1998), and distribution maps by Morris et al. (1976) and Beetle (1960) reveal that the sagebrush steppe is extensive in Montana, cover at least 13 million hectares.

Coming from the east, *Artemisia tridentata* becomes dominant in the landscape beginning in eastern Wyoming (Vale 1975) and northeast Montana (Morris et al. 1976), two points that define in part the eastern boundary of the sagebrush steppe. The heart of the sagebrush steppe is southern Idaho and northern Nevada. The western boundary is defined by the east slopes of the Sierra Nevada and Cascades (Daubenmire 1978) extending into southern areas of British Columbia, Canada. Sagebrush steppe is bordered by the Great Plains to the east, the Rocky Mountain coniferous forests to the north, the Pacific Cordilleras to the west and the Mojave and Chihuahua deserts to the south.

West and Young (1988) recognize the distinctions made by Küchler (1970) of Great Basin sagebrush and sagebrush steppe. Both are typified by the presence of *A. tridentata* (big sagebrush). Sagebrush steppe comprises cool season bunch grasses (*Agropyron, Stipa, Festuca, Koeleria, Poa*), and cool and warm season forbs. Great Basin sagebrush is considered more xeric with less grass cover having an increased representation of warm season species (West and Young 1988). However many reviews have not made this distinction and consider compositional distinctions between Great Basin sagebrush and sagebrush steppe to be dubious due to a broad overlap in plant species distributions (West and Young 1988). Management methods have even been applied equally to areas of Great Basin sagebrush and sagebrush steppe of Idaho and Wyoming (e.g., Plummer et al. 1955).

Sagebrush Steppe Habitats Types in Montana

Mueggler and Stewart's (1980) classification of rangeland in Montana recognized six habitats with sagebrush as a dominant, and these are summarized here:

1. *Artemisia arbuscula/Agropyron spicatum* is one of the driest habitat types of southwest Montana. Regardless, this habitat type contains many species widespread in other sagebrush habitats, including *Artemisia tridentata, Agropyron spicatum, Koeleria macranthra, Poa sandbergii*, and a variety of forbs including *Phlox hoodii, Opuntia polyacantha, Gutierrezia sarothrea, Artemisia frigida,* and *Linum lewisii*. This habitat type is fairly widespread elsewhere in Idaho, Nevada, and Oregon.

2. *Artemisia arbuscula/ Festuca idahoensis* is an infrequent habitat type found predominately at higher elevations. *Antennaria rosea, Agropyron spicatum, Koeleria*

macrantha, Phlox hoodii, and *Erigeron compositus* are common associates, but these are also very widespread species among many of the sagebrush habitats. Mueggler and Stewart report high species similarity with those of the same habitat classification in Oregon. Species shared in common are *Agropyron spicatum, Poa sandbergii, Phlox hoodii*, and *Phlox longifolia*. This habitat type is found elsewhere in Nevada and Oregon.

3. *Artemisia tridentata/ Agropyron spicatum* is found throughout Montana. Wyoming big sagebrush and low elevation Mountain big sagebrush are the predominant subspecies found in this habitat type. Other common associates include *Artemisia frigida, Guttierizia sarothrae, Koeleria macrantha, Poa sandbergii, Stipa comata, Stipa viridula*, *Opuntia polyacantha*, and *Bouteloua gracilis*, which are all very widespread species across the sagebrush steppe. This habitat type occurs elsewhere in British Columbia, Idaho, Nevada, Oregon, Utah, and Washington. The lack of a distinction between mountain and Wyoming sagebrush in the context of this habitat type suggests elevation may not be too strong a determinant of community composition.

4**.** *Artemisia tridentata/Festuca idahoensis* contains predominately Mountain big sagebrush. Dominate grasses include *Agropyron spicatum* and *Koeleria macrantha*, whereas common forbs and shrubs include *Geum triflorum, Artemisa frigida, Chrysothamnus spp., Geranium viscosissimum, Potentilla gracilis, Potentilla arguta, Helianthella uniflora,* and *Erigonum umbellatum*. All of these are widespread sagebrush steppe species. This habitat type is widespread and found elsewhere in Idaho, Nevada, Oregon, Utah, Washington, and Wyoming.

5. *Artemisia tridentata/Festuca scabrella* also contains *Festuca idahoensis* and *Agropyron spicatum*. Associated forbs include *Achillea millefolium, Arenaria congesta, Eriogonum umbellatum*, and *Cerastium arvense*, all of which are very widespread species in western North America. No mention is made of this habitat type occurring in states other than Montana.

6. *Artemisia tripartita/Festuca idahoensis* is localized in southwest Montana and shares a similar environment to *Artemisia tridentata/Festuca idahoensis*, as well as associated plant species. This habitat type is found also in Idaho (e.g., Seefeldt and McCoy 2003) and Washington. Grasses mentioned in this habitat classification include *Calamagrostis montanensis, Koeleria macrantha, Agropyron spicatum*, and *A. dasystachyum*. Shrubs present in this habitat type include *Chrysothamnus visidiflorus, Tertadymia canescens,* and *Artemisia tridentata*. Characteristic forbs include *Phlox hoodii, Antennaria rosea, Lupinus sericeus, Achillea millefolium, Gutierrezia sarothrea,* and *Artemisia frigida*. All of these species are very widespread in throughout western North America.

The remarkable aspect about the species that define the above habitat types is that they are all widespread in at least western North American, including variously among these habitat types. This hints at a potential metacommunity dynamic of the sagebrush steppe at least in Montana if not more broadly across the range of this biome.

Research Emphasis on the Sagebrush Steppe

Sagebrush has been extensively studied because of its prominence in the western landscape. One main focus of research includes the effect of sagebrush on hydrology and soils (Peterson 1995). However, most research focuses on the critical importance of sagebrush to wildlife (Welch 2005, Rotenberry and Wiens 1998, Wambolt 1996, Peterson 1995, Wambolt and McNeal 1987). Sagebrush communities provide both important browse and cover for big game, small mammals, and birds.

Sagebrush steppe is used extensively by native ungulates and for livestock grazing, and much research has focused on increasing forage within this biome (Vavara, Laycock, and Pieper 1994, Plummer et al. 1955, Pechanec et al. 1954). Domestic cattle do not prefer to eat big sagebrush so methods to remove and minimize sagebrush often have been undertaken in order to increase grass production. Some evidence however points to these measures as being costly and ineffective (Welch 2005, Wambolt and Watts1996, Ratzlaff and Anderson 1995) and this issue will be returned to later. Within the context of range improvement for livestock grazing, the various subspecies of big sagebrush all have been analyzed for differences in growth, water translocation capacity, and the ability to recover after fire (Welch 2005, Ryel et al 2003, West 1983).

Because sagebrush steppe commonly occupies valley bottoms of the intermountain west, large areas have been converted to farmland, plowed almost annually, and irrigated (Welch 2005, West and Young 1988). Range improvement has resulted in removal of sagebrush and the planting of non-native Eurasian grasses, such as *Agropyron cristatum* and *Bromus inermis* (Larson 2003, Weaver et al. 2001, West 1983, Plummer et al. 1955, Pechanec et al. 1954). Indeed, sagebrush control is most commonly justified by the assumption of increased grass production following sagebrush removal (Wambolt et al. 2001, Wambolt 1996, West and Young1988, Pechanec et al. 1954).

Removal of sagebrush is accomplished by a variety of methods, including railing, chaining, burning, and the application of herbicide (Welch 2005, Wambolt and Watts 1996, West 1983, Plummer et al. 1955, Pechanec et al. 1954). Yet increased grass production has not always followed removal of sagebrush (Welch 2005, Wambolt 1996, Ratzlaff and Anderson 1995). This is due, in part, to catastrophic plant disturbance that is intrinsic to these management methods and that facilitates the expansion of exotic plants (Ratzlaff 1995, Pechanec et al. 1954). Management methods involving exogenous disturbance (Larson 2003), or widespread plant mortality, often results in the establishment of exotic species. This concurs with Lozon and MacIsaac (1997), who reports 86% of exotic plants require disturbance to establish, Rew et al. (2005), who describe disturbance as an important component of introduced plant establishment in transects in Yellowstone National Park sagebrush steppe habitat, and Watts (1998), who found that tank tracks were responsible for the increase of introduced plant species in sagebrush steppe of southern Idaho.

During the late 19th and early 20th centuries, sagebrush steppe vegetation was heavily grazed, resulting in widespread native plant mortality. This facilitated the establishment and expansion of many exotic plant species across the western United States (Pickford 1932), with *Bromus tectorum* receiving much of the attention (Welch 2005, Bartlett et al 2002, Novak and Mack 2001). These heavily impacted rangelands were deemed in need of improvement (Vale 1973). This improvement ironically targeted sagebrush as undesirable and in need of eradication due to the status of sagebrush as an increaser (Welch 2005, Franklin 1989, West 1983, Plummer et al. 1955, Pechanec et al.

1954). Range improvement projects were thus undertaken to eliminate native undesirables, which only facilitated the spread of more exotic plants.In the most recent Range improvements the goal to increase grass production while removing sagebrush was accomplished with 2-4 D that killed forbs and shrubs while leaving grasses unharmed (Carson 1962).

As the result of management practices from 1850 to present, the amount of sagebrush steppe remaining in the western United States is estimated at 20%-30% (West 1998, Welch 2005) of the original distribution. Initial European settlers described a sea of sagebrush, whereas today this sea has retracted to scattered ponds (Welch 2005).

Plant Diversity in Sagebrush Steppe

In spite of the many studies focusing on the sagebrush steppe, the lack of studies on plant diversity within this biome motivates this study. Indeed, plant diversity could comprise as many as 5,000 vascular plant taxa, rivaling the plant diversity of such notable states as California (Hickman et al. 1993) and Texas (e.g., Correll 1979), as well as that of the Intermountain Region (Cronquist et al. 1972).

Despite the high levels of plant species diversity found in or endemic to the sagebrush biome, little information has been published with exception of Anderson and Inouye (2001) and Seefeldt and McCoy (2003). These studies document total plant species diversity and abundance. Otherwise, a simple enumeration of the total diversity of plant species in sagebrush dominated sites is rarely reported. For example, Welch's (2005) recent important review of sagebrush literature does not include a section on plant species diversity, even though reports on the diversity of fauna endemic to sagebrush habitats are given in separate chapters. Given that the sagebrush associated fauna (e.g., Brewer's Sparrow and the Northern Sagegrouse) rely on shrubs, grasses, and forbs within the sagebrush biome (Rotenberry and Wiens 1998), information on plant diversity might be important especially for the fragmented sagebrush steppe (Welch 2005). For example, knowledge of the plant diversity of the sagebrush steppe could facilitate the development of restoration benchmarks that consider the plant community as a management objective.

Research Questions and Objectives

Objectives of this study include an attempt to define a sagebrush steppe metacommunity by initially quantifying the relative abundance of all plant species within and among study sites. Because the various sagebrush dominated habitat types share a large proportion of species in common, modeling community composition among sagebrush dominated sites as a function of geographic distance is one way of revealing whether local communities are connected by immigration of constituent species (i.e., species belong to the same metacommunity). Relative species abundance distributions by themselves also offer a means to understand community composition (Thibault et al. 2004). They can be analyzed with neutral ecological models that allow for the estimation of parameters such as speciation and immigration rates within the metacommunity (Hubbell 2001). Isolated or peripheral local communities (e.g., sagebrush steppe from eastern Montana) are predicted to have low estimates of migration when compared to large or more centrally located local communities (e.g., sagebrush steppe from southwestern Montana). Finally, neutral ecological approaches, that do not consider individual differences and consider all individuals as equals, have strong implications for invasion biology because neutral ecology predicts that invading plant species will not have an advantage within a saturated local community (e.g., one not prone to high rates of human-induced or widespread plant mortality). Indeed, neutral ecology predicts that invading species will only have an advantage when the residents of the local plant community are mostly eliminated within a short time frame, which then opens resources and space to the first immigrants. Typically, these invaders would be those with the highest abundances in nearby local communities (e.g., these would be exotic species if the nearby local plant communities are those already impacted by humans).

Specific Questions to be Addressed in This Study:

1.) Can we support the suggestions of West and others (Welch 2005, West and Young 1988, Trimble 1989, West 1983) that sagebrush dominated local communities at mid elevations of the Intermountain West share a similar flora? This question will be addressed very by comparing the floristic data generated in this study with published floristic studies of other sagebrush steppe communities.

2.) Can information on species composition and relative abundance from different sample sites provide a preliminary expectation of plant diversity within the sagebrush steppe? For example, does our study site in eastern Montana, at the northeast edge of the sagebrush biome, show reduced diversity compared to our study site in southwestern Montana, which lies closer to the center of the sagebrush steppe metacommunity? Estimating biodiversity through relative species abundance distribution implies that such distributions are stable or non-transitory at least in the short term. Thus, relative species abundance profiles will be assessed for fluctuation over time (the span of this thesis requires that this be determined over the short term, but determining this over the longer term will be possible with the permanent plots established during this study).

3.) As more introduced plants become established within the sagebrush steppe of the western United States, could this largely be a function of disturbance, especially human-induced disturbance? If neutral ecological dynamics of plant communities have a strong influence on biodiversity and biogeography, then a prediction is that introduced plants are not necessarily prone to invade in the sagebrush steppe, where widespread plant mortality is not common (e.g., in contrast to cropland, riparian, or wetland plant communities).

We expect to be able to define a sagebrush steppe metacommunity using similarity in floristic composition over geographic distance. This study is intended to develop a preliminary expectation of plant diversity in sagebrush steppe given a defined sampling effort in a local community. By attempting to define a sagebrush steppe metacommunity, we should also be able to define what an intact or pristine sagebrush steppe (e.g., uninfluenced by human-related disturbance) should look like, both in terms of plant diversity and physiognomy (e.g., relative abundances of shrubs, perennial grasses, and early and late season forbs). This latter aspect could define the goals for community restoration if the idea is to restore sagebrush steppe local communities to previous levels of plant diversity.

Literature Cited

Anderson, J. E. and R. S. Inouye. 2001. Landscape-scale changes in plant species abundance and biodiversity of a sagebrush steppe over 45 years. Ecological Monographs 71: 531-556.

Bartlett, E., S. J. Novak, and R. N. Mack. 2002. Genetic Variation in *Bromus tectorum* (Poaceae): differentiation in the eastern United States. American Journal of Botany. 89: 602-612

Beetle, A. A. 1960. A study of sagebrush-section *Tridentatae* of *Artemisia*. Wyoming Agricultural Experiment Station. B-779.

Carson, R. L. 1962. Silent Spring. Riverside Press Cambridge. Massachusetts.

Correll, D. S. 1979. Manual of the vascular plants of Texas (Texas Research Foundation. Contributions). University of Texas at Dallas.

Cronquist, A., A. H. Holmgren, N. H. Holmgren, J. L. Reveal, and P. K. Holmgren. 1972. Intermountain Flora, Volume One: Geological and Botanical History, Plant Geography, Vascular Cryptogams, Gymnosperms, Glossary. New York Botanical Garden Press, New York. 270 pp.

Daubenmire, R. F. 1978. Plant Geography: with special reference to North America. Academic Press.

Dorn, R. D. 1984. Vascular Plants of Montana. Mountain West Publishing, Cheyenne, Wyoming.

Fisher, B. F., C. Winne, M. M. Thornton, T P. Tady, Z. Ma, M. M. Hart, and R. L. Redmond. 1998. Montana GAP Analysis, Montana Land Cover Atlas.

Franklin, P. L. 1989. Sagebrush Country Land and the American West. Alfred Knopf New York.

Hickman, J. C. 1993. The Jepson Manual: Higher Plants of California. University of California Press, Berkeley.

Hubbell, S. P. 2001. Unified Neutral Theory of Biodiversity and Biogeography. Princeton University Press

Kolb, K. J. and J. S. Sperry. Differences in drought adaptation between subspecies of sagebrush *Artemisia tridentata*. Ecology 80: 2373-2384

Küchler, A. W. 1970. Potential Natural Vegetation(scale 1:750000). In U.S. Geological Survey, *The National Atlas of the U.S.A.* Government Printing Office, Washington D.C.

Larson, D. L. 2003. Native and exotic plants: relationships to disturbance in mixed grass prairie. Plant Ecology 169: 317-333

Lesica, P., R. Yurkewycz, and E. Crone. 2006. Rare plants are common when you find them. American Journal of Botany. 93: 454-459

Lozon, J., and H. MacIsaac. 1997. Biological Invasions: are they dependent on disturbance? Environmental Reviews 5: 131-144

MacArthur, E. D. 1979. Sagebrush systematics and evolution. Pgs. 14-22. The sagebrush ecosystem: a symposium. Utah State University, Logan Utah, USA

McArthur, E. D., and S. Goodrich. 1986 Artemisia tridentata ssp. spiciformis: distribution and taxonomic placement. In E. D. McArthur and B. L. Welch [compilers], Proceedings—symposium on the biology of *Artemisia* and *Chrysothamnus*, 55–57, General Technical Report INT-200, U. S. Department of Agriculture, Forest Service, Intermountain Research Station, Ogden, UT.

McArthur, E. D., and S. C. Sanderson. 1999. Cytogeography and chromosome evolution of subgenus Tridentatae of Artemisia (Asteraceae). American Journal of Botany 86: 1754-1775.

Morris, M. S., R. G. Kelsey, D. Griggs. 1976. The geographic and ecological distribution of big sagebrush and other woody *Artemisias* in Montana. Montana Academy of Sciences 36: 56-79.

Mueggler, W. F., and W. L. Stewart. 1980. Grassland and shrubland habitat types of western Montana. Technical Report INT-66; Intermountain Forest and Range Experimental Station, Ogden, Utah.

Novak, S. J., and R. N. Mack. 2001. Tracing Introduction and spread: Genetic evidence *Bromus tectorum* (Cheatgrass). Bioscience 51: 114-122.

Pechanec, J. F., A. P. Plummer, J. H. Robertson, and A. C. Hull. 1954. Sagebrush Control on Rangelands. USDA Handbook 277. Intermountain Forest and Range Experiment Station, USDA Forest Service.

Peterson, J. G. 1995. Ecological Implications of Sagebrush Manipulation: A literature review. Wildlife Management Division, Montana Fish, Wildlife and Parks. Helena Montana.

Pickford, G. D. 1932. Influences of continual heavy grazing and promiscuous burning on spring fall range in Utah. Ecology 13: 159-171

Plummer, A. P., A. C. Hull, G. Stewart, and J. H. Robertson. 1955. Seeding Rangelands in Utah, Nevada, Southern Idaho, and Western Wyoming. USDA handbook 71. Intermountain Forest and Range Experiment Station, USDA Forest Service.

Ratzlaff, T., and J. Anderson. 1995. Vegetal recovery following wildfire in seeded and unseeded sagebrush steppe. Journal of Range Management 48: 386-391

Rotenberry, J. T., and J. A. Wiens. 1998. Foraging patch selection by shrub steppe sparrows. Ecology 7: 1160-1173

Ryel, R. J., M. M. Caldwell, A. J. Leffler, and C. K. Yoder. 2003. Rapid soil moisture recharge to depth by roots in a stand of *Artemisia tridentata*. Ecology 84: 757-764.

Seefeldt, S. S., and S. D. McCoy. 2003. Measuring plant diversity in the tall threetip sagebrush steppe: influence of previous grazing management practices. Environmental Management 32: 234–245.

Stegner, W. 1942. Mormon Country. University of Nebraska Press. Lincoln, Nebraska, USA.

Thibault, K. M., E. P. White, and S. K. Morgan Ernest. 2004. Temporal dynamics in the structure and composition of a desert rodent community. Ecology 85: 2649-2655.

Trimble, S. 1989. The Sagebrush Ocean. Univeristy of Nevada Press. Reno, Nevada

Vale, T. R. 1973. The Sagebrush Landscape of the Intermountain West. Dissertation University of California- Berkley.

Vale, T. R. 1975. Presettlement vegetation in the sagebrush-grass area of the Intermountain West. Journal of Range Management. 28: 32-36.

Vavara, M., W. A. Laycock, and R.D. Pieper [editors]. 1994. Ecological Implications of Livestock Herbivory in the West. Society for Range Management. Denver Colorado, USA.

Wambolt, C. L., and A. F. McNeal. 1987. Selection of winter foraging sites by elk and mule deer. Journal of Environmental Management. 25: 285-291.

Wambolt, C. L. 1996. Mule deer and elk foraging preference for 4 sagebrush taxa. Journal of Range Management 49: 499-503.

Wambolt, C. L., and M. J. Watts. 1996. Long term recovery of Wyoming Big Sagebrush after four treatments. Journal of Environmental Management 46: 95-102

Wambolt, C.L., K. S. Walhof, and M. R. Frisina. 2001. Recovery of big sagebrush communities after burning in south-western Montana. Journal of Environmental Management 61: 243-252.

Wambolt, C. L., and M. R. Frisina. 2002. Montana Sagebrush Guide. Montana Fish Wildlife and Parks, Bozeman, Montana. Pp. 71.

Watson, L. E., P. L. Bates, T. M. Evans, M. M. Unwin, and J. R. Estes. 2002. Molecular phylogeny of subtribe *Artemisiinae* (Asteraceae), including *Artemisia* and its allied and segregate genera. BMC Evolutionary Biology. 2: 17.

Watts, S. E. 1998. Short-term influences of tank tracks on vegetation and microphytic crusts in shrub-steppe habitat. Environmental Management. 22: 611-616

Weaver, T., D. Gustafson, and J. Lichthardt. 2001. Exotic plants in early and later seral vegetation of fifteen northern Rocky Mountain environments. Western North American Naturalist 61: 417-427.

Welch, B. L. 2005. Big Sagebrush: A Sea Fragmented into Lakes, Ponds, and Puddles General Technical Report RMRS-GTR-144. United States Department of Agriculture, Fort Collins, Colorado. Pp. 210.

West, N. E. 1998. Managing for biodiversity in rangelands, pp. 101-126, in W. Collins and C. Quelset (eds.), *Biodiversity in Agroecosystems. Advances in Agroecology 2*. CRC Press.

West, N. E., and J. A. Young. 1988. Intermountain Valleys and Lower Mountain Slopes, pp. 257-284, in M. Barbour and D. Billings, *North American Terrestrial Vegetation*. Cambridge University Press, Cambridge United Kingdom.

West, N. E. 1983. Great Basin-Colorado Plateau Sagebrush semi-desert, pp.331-349, in N. E. West, *Ecosystems of the World, Temperate Deserts and Semi-Deserts*; 5. Elsevier Scientific Publishing Company, Amsterdam, Netherlands.

West, N. E. 1983.Western Intermountain Sagebrush Steppe, pp.351-374, in N. E. West, *Ecosystems of the World, Temperate Deserts and Semi-Deserts*; 5. Elsevier Scientific Publishing Company, Amsterdam, Netherlands.

CHAPTER TWO

METHODS OF SAMPLING AND DATA COLLECTION

Botanical Nomenclature and Nativity Status

The mountain big sagebrush steppe on Burke Park harbors 219 vascular plant species (Appendix B) and the Porcupine site 212 species (Appendix D). The Wyoming big sagebrush steppe of the Charles M. Russell (CMR) National Wildlife Refuge harbors 337 species (Appendix C). The nomenclature for these vascular plant species follows *Vascular Plants of Montana* (Dorn 1984) with a few exceptions, such as the wheat grasses, where nomenclature follows Lavin and Seibert (2005). The "introduced" or "native" status for each of these sagebrush steppe species was determined from the PLANTS database (USDA, NRCS 2005). The plant diversity studies of Burke Park and the Charles M. Russell National Wildlife Refuge were facilitated by existing floristic lists from each of these two study areas. Lavin and various Bozeman residents (unpublished) have recorded species in Burke Park since 1991. Klaus Lackschewitz (unpublished) compiled a list of species for the CMR National Wildlife refuge. There was no preexisting list of plant species for the Porcupine area, although Husby (1982) listed some of the common sagebrush steppe species for the Gallatin Canyon. Voucher specimens for many of these species collected during the respective floristic studies are in accession in the Montana State University (MONT) Herbarium. From these floristic studies of Burke Park, and the CMR National Wildlife Refuge, a list was extracted of just the species potentially inhabiting the sagebrush steppe. This was done by determining what habitat (e.g. forest understory, and riparian) a species was most likely to inhabit.

Sampling Strategy

Estimation of Relative Species Abundance

The relative species abundance distribution (RSA or RAD) is also referred to as a dominance diversity or rank abundance distribution (e.g., Thibault et al. 2004; Whittaker 1965) and is required to implement Hubbell's (2001) neutral model of biodiversity. It has not been applied to studies of plant diversity in the sagebrush steppe, which is not surprising given that few studies of the sagebrush steppe even provide a simple enumeration of the total plant diversity except Anderson & Inouye (2001) and Seefelt & McCoy (2003). Temporal sampling of the RSA distribution through the season and among years can provide insights into the stability of the abundance profile and perhaps whether plant diversity is transitory or at equilibrium (e.g., Hubbell and Borda de Água 2004; Etienne and Olff 2005). Spatial sampling of the RSA distribution may reveal isolated or peripheral local communities, as inferred by less diversity compared with local communities that are more centrally located within the sagebrush steppe metacommunity (e.g., the edge effect; Latimer et al., 2005).

Neutral ecological approaches to the study of biodiversity and biogeography require a sample of numbers of individuals, typically many thousands of individuals distributed over 100 or more species. Model parameters such as the fundamental biodiversity parameter theta, Θ (the number of species produced per metacommunity generation), and immigration, m (the proportion of resident deaths in the local community that are replaced by immigrants from the metacommunity), are estimated from the number of species from a given number of individuals sampled (Hubbell 2001). Relative species abundances are then modeled with the zero sum multinomial distribution (e.g., Volkov et al. 2003: Latimer et al. 2005; Etienne et al. 2006, Chave and Jabot 2006), which assumes a random birth-death process for a trophically or taxonomically similar set of species (Hubbell 2001). The underlying dynamics generating a community relative species abundance profile is theoretically the relative contribution of resident and immigrant births that fill in the space briefly left unoccupied following a resident death. Generally the higher the probability that immigrants will replace resident deaths the greater the biodiversity, and the longer the rare tail of the RAD. This is because not only will potentially new species be added to the local community, but resident species will tend not to drift to extinction because their local abundances can be maintained or restored by immigration from the metacommunity. In the case of sagebrush steppe plant species that physically vary in size, resident death could be partial or entire (e.g. partial death of *Artemisia tridentata* could be replaced by an entire individual of *Astragalus miser*). In order to sample for individuals, we measured cover in square centimeters for each species encountered in a sampling quadrat. Such measures were taken for four reasons. First, individuals of many species produce rhizomes, form a mat or sod, or produce tillers or subterranean woody caudices. Counting individuals among such species is therefore problematic. Second, individuals of annuals, small forbs, large forb, small bunchgrass, large bunchgrasses, rhizomatous grasses, small shrubs, and large shrubs are not spatially equivalent. Partial death in a large shrub or large bunchgrass can be replaced by several to many births of annuals, rhizomatous grasses, or small forbs. Third, assigning cover measured in cm^2 still allows for the determination of numbers of individuals by using a conversion factor (e.g., Latimer et al. 2005; Harpole and Tilman 2005). The conversion factors used here are derived from measurements taken at the study sites. Large shrubs average 1500 cm^2 in canopy cover (e.g., *Artemisia cana* or *A. tridentata*). Large forbs and large bunchgrasses average 300 cm^2 in canopy cover (e.g., *Astragalus drummondii* or *Agropyron spicatum*). Large annuals average 100cm^2 in canopy cover (e.g. *Sisymbrium altissimum* or *Descurainria sophia*) and small forbs and bunchgrasses 50 cm^2 (e.g., *Phlox hoodii* or *Koeleria macranthra*). Rhizomatous and sod-forming grasses were treated the same as annual forbs and grasses in that all were assigned 1 cm^2 of cover per individual. That is, genets and ramets are equivalent to single individuals in the context of a resident death being replaced by another resident or perhaps an immigrant. Regardless, rhizomatous and sod-forming grasses were omnipresent in some plots, often highly variable in patch size, and usually difficult to estimate were one individual patch ended and another began. Fourth, recording simple presence in quadrats allows for determination of frequency. This measure of abundance was recorded how often species occurred within quadrats of each plot regardless of canopy cover. Using frequency as such may bias in favor of high abundances of small but frequent species. Similarly cover measures bias toward large yet infrequent species. It is important to determine how estimates differ when fitting diversity models to relative species abundance distributions derived by different methods.

Transect Layout

Given that we want to characterize plant diversity within the sagebrush steppe, we positioned transects within intact vegetation as much as possible (Figs. 2.1-2.3). This may have biased the results but we justified this by the goal of quantifying diversity in sagebrush steppe. Indications of intact cover included a diversity of shrubs (e.g., not purely *Artemisia tridentata*), perennial grasses, and early- and late-season forbs. These indicators of intact sagebrush steppe vegetation might be provisional, but all observations reveal that sagebrush steppe greatly impacted by human-related activity (e.g., heavy livestock grazing, construction, heavy foot or vehicle traffic, etc.) lose diversity in all of these categories, especially shrub and late-season forb diversity. Such observations have been corroborated by Bob Skinner and Dan Harrell, biologists on the Charles M. Russell National Wildlife Refuge, who observe that overgrazing first takes out late-season forb diversity, then shrub diversity, then early season forb diversity, and finally perennial grass diversity (Skinner observes that disturbed sites are recolonized by these same plant groups in the reverse order).

Permanent plots were established in both Burke Park and the Charles M Russell Wildlife Refuge study areas. Each plot measured 10 by 50 m, or 5 m along each side of a 50 m transect tape. Two quadrat frames, each 0.5 by 0.5 m, were laid out side by side resulting in a total quadrate size of 1.0 by 0.5 m, the longer length running perpendicular to the 50 m transect. Blue road whiskers anchored with 6-12 in. spikes marked the ends of each transect and the corners of each quadrat.

With respect to quadrat size, Daubenmire frames (0.2 by 0.5 m) were too small to capture the larger-scale diversity, and frames larger than 1.0 by 0.5 m would have rendered the estimation of cover for each species too time consuming. Species occurring within a plot but not in any of the constituent quadrats were scored as present, similar to the nested sampling of Stohlgren et al. (1998). One frame at a time for each pair was evaluated. The abundance of each plant species was established by visual estimation. First, a complete list of species was made for each quadrat, and then these were ordered in relative abundance. With the aid of the 0.5 by 0.5 frame that was subdivided into 650 cm^2 quarters, and a Dell Pocket Computer stylus that measured 10 cm long, the cover of each species was estimated in cm^2.

Burke Park Study Site

Location and Description

Burke Park is located within and on the east side of Bozeman, Montana, USA. The Park is approximately 16 hectares in size and comprises a long and narrow ridge top and a west-facing slope running in a north-south direction. The slope is dominated by *Pseudotsuga menzeiesii*, *Pinus flexilis*, and various shrub species of mostly the *Rosaceae* and *Caprifoliaceae*. The ridge top is representative of the mountain big sagebrush steppe found in this general upland region of Gallatin County, and has a network of community trails that are maintained to varying degrees. Trails and fences have been improved or built to protect the native vegetation, although unprotected sites still remain.

The ridge along the top of Burke Park was once a Crow Indian camp and obsidian tools are still found on the site today (Kiefer 2005). Peet’s Hill at the north end of the ridge is named for John M. Peet (1864-1933), a local grocer whose family ran a dairy here. The City of Bozeman shut down the dairy after an outbreak of typhoid fever in the Bozeman water supply that supposedly originated from the Peet’s dairy. The Burke family purchased the land from Earl Peet, John’s son, which was used as horse pasture until 1993 when the land was purchased by Bozeman and dedicated as a City Park. Burke Park is named for the Burke family, who sold the land to the City of Bozeman for a modest sum (Pohl 2002). Whatever level of livestock grazing occurred in this area was apparently not too detrimental to the vegetation or its recovery because today the Park harbors a rich flora of over 270 vascular plant species, including a diversity of shrubs, perennial grasses, and early- and late-season forbs. The park is surrounded with the urban landscapes of Bozeman and areas near the park average 800 people per square mile (NRIS 2005)

Classification

The dominant subspecies of sagebrush in the Burke Park area is *Artemisia tridenata* ssp. *vaseyana*. The vegetation along the ridge top of Burke Park can be classified following Mueggler and Stewart (1980) as the mountain big sagebrush and Idaho fescue (*Artemisia tridentata*/*Festuca idahoensis*) habitat type.

Number and Size of Plots and Quadrats

A total of 15 permanent 50 by 10 m plots were established in Burke Park with metal spikes and blue road whiskers. Fifteen quadrats were permanently established within each plot. Because much of the park occurs near trails, agricultural fields, or other heavily disturbed areas, positioning 15 plots located as far as possible from heavy disturbance resulted in a predominantly north-south orientation and arrangement of the plots (Fig. 2.1). All plots and quadrats were marked with a Garmin handheld GPS unit, and waypoints for each are reported in the appendix A.

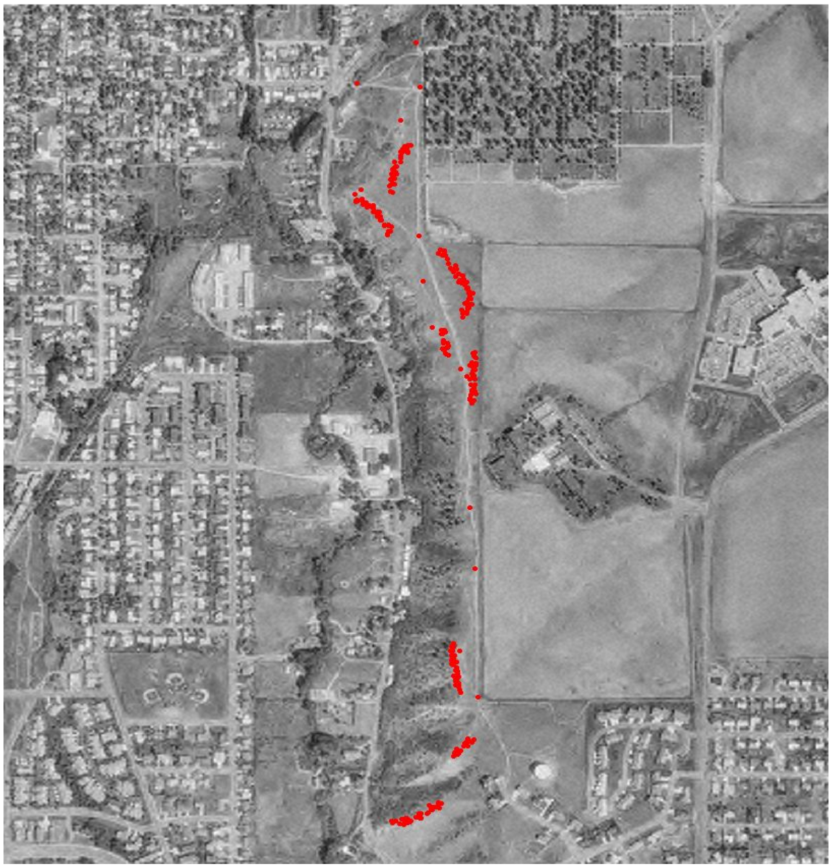

Figure 2.1. Burke Park plot locations are indicated by the contiguous red dots. Bozeman Deaconess Hospital is located far right center. Hillcrest Rest Home is located within the crop field at right of center.

Charles M Russell National Wildlife Refuge (CMR) Study Site

Location and Description

The study site is located near the northeast edge of the sagebrush biome (Beetle 1960) in southern Phillips County, Montana. It occurs in one of the most sagebrush dense areas of the State (Fisher et al. 1998) and in one of the least densely populated counties of the Montana (NRIS 2005). It has been grazed for the last 140 years by cattle and sheep, but grazing peaked before the beginning of the 20th century (Anonymous 2002). Plots were established in the area of the Reynolds Hill Road, which connects Malta, Montana, with the Fourchette Bay area of Fort Peck Reservoir, the main reservoir along the Missouri River in northcentral Montana. Preliminary inspection of this area during May 2003 revealed that the Reynolds Hill Road area between Telegraph Creek to the west and Kill Woman Creek to the east, and north to the UL Bend Wilderness area, harbored an intact stand of Wyoming sagebrush steppe that was rich in plant species.

Classification

The principal sagebrush subspecies in the CMR study area is *Artemisia tridentata* ssp. *wyomingensis* (Wambolt and Frisina 2002). According to Mueggler and Stewart (1980) the overall study site would be classified as a big sagebrush and bluebunch wheatgrass (*Artemisia tridentata/Agropyron spicatum*) habitat type. This habitat type is widely distributed geographically throughout much of Montana.

Number and Size of Plots and Quadrats

A total of 24 plots were permanently established throughout the region of the Reynolds Hill road area (Fig. 2.2). The number of plots is greater here than in Burke Park simply because the area of sagebrush steppe was larger in size. As a consequence, each plot was sampled with just 10 quadrats. Plots and transects were geographically marked with a Garmin handheld GPS unit, and the resulting waypoints are reported in Appendix A2. Plots are located on land of the Bureau of Land Management, National Wildlife Refuge, and private holdings of the American Prairie Foundation.

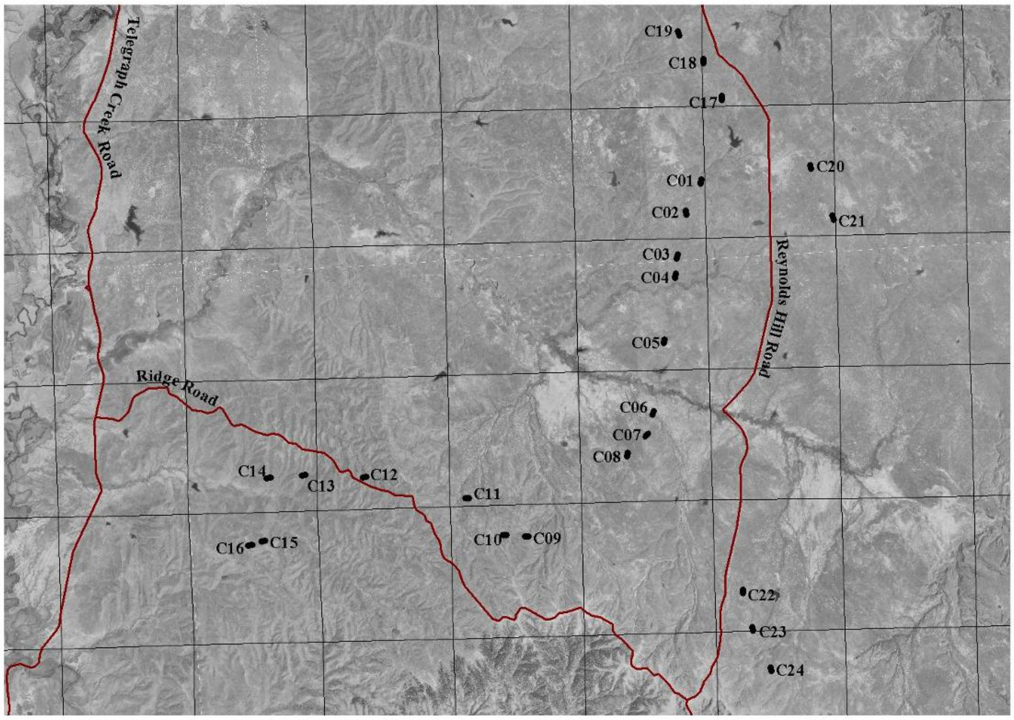

Figure 2.2. CMR plot locations are indicated by the black dots. The edge of the Missouri Breaks country can be seen at the very bottom center. The Reynold’s Hill road is bisected in this photograph by the west flowing Box Elder Creek, which joins south flowing Telegraph Creek.

Porcupine Creek in the Gallatin River Drainage

Location and Description

This study site is located in southwest Montana on south facing aspects above the Gallatin River near the mouth of Porcupine creek. It is located in upper elevation reaches of the sagebrush steppe. Some of the area was part of exclosures set up by the Montana Fish Wildlife and Parks (Kurt Alt personal communication 2004) but the whole area is generally intact with dense stands of mountain big sagebrush and Idaho fescue.

Classification

The site is dominated by *Artemisia tridentata* spp. *vaseyana*. The habitat classification according Mueggler and Stewart (1980) is big sagebrush and Idaho fescue (*Artemisia tridentata/Festuca idahoensis*), which is the same as the classification for Burke Park except that the Porcupine study site is in the *Geranium viscosissimum* phase.

Number and Size of Plots and Quadrats

A total of 23 plots each with 10 quadrats were established but not permanently marked. We recorded only frequency (presence-absence) within each quadrat. This study site was included in order to compare species diversity among study sites given similar sampling efforts. Sampling frequency with presence absence per quadrat proved more expedient and may have most elegantly captured relative species abundance for the sake of modeling the zero sum multinomial.

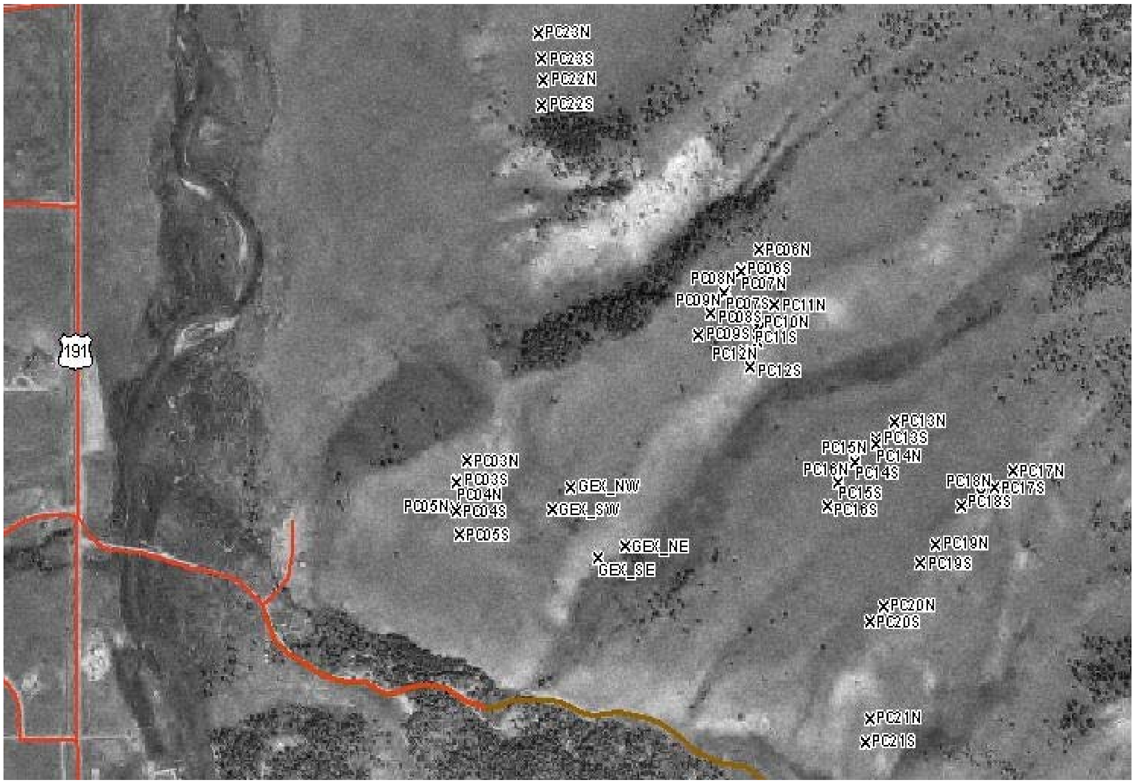

Figure 2.3. Porcupine plot locations are indicated by endpoints of transects. Two plots are located within the wildlife exclosure, which is located near the center of this photo where the symbos "GEX" (Gallatin Exclosure) mark the corners of this exclosure. The turn from highway 191 to the Big Sky access road is just off the top left of the photo.

Climate

Climate data for each study site are available (Western Regional Climate Center 2006) within approximately 20 km of each site. The observation sites include Telegraph Creek (248161) for the CMR site, Gallatin Gateway 26S (243368) for the Porcupine site, and Bozeman Montana State University (241044) for Burke Park. The Porcupine study site has the lowest mean annual temperature of 3.8 C°. Burke Park and the CMR sites have values of 6.16 C° for Burke Park, and 6.33 C° for the CMR site. The CMR site receives the lowest amount of average yearly precipitation, 307 mm. Porcupine is intermediate receiving 347 mm, and Burke Park receives 477 mm.

Temporal Sampling

The Burke Park plots were established in June of 2004, and sampled during June, July, and August of that year, and again in June and August of 2005. The CMR plots were established during June 2005 and sampled in June and August of that year, and again in June and August of 2006. The Porcupine site was sampled once during June of 2006.

Data Analysis

Relative species abundance data were analyzed with a variety of methods implemented in the R statistical package 2.1.1 (R Development Core Team 2005). Diversity indexes were calculated with the packages LabDSV (Roberts 2006) and Vegan (Oksanen et al. 2005) community ecology packages. Code for modeling the zero sum multinomial was provided by Latimer (2005), as well as by Chave and Jabot (2006). R code developed during this study is provided in Appendix F. The regression analysis preformed employed a linear model using standard packages in R 2.1.1 and a normal distribution.

Literature Cited

Anderson, J. E., and R. S. Inouye. 2001. Landscape-scale changes in plant species abundance and biodiversity of a sagebrush steppe over 45 years. Ecological Monographs 71: 531-556.

Anonymous. 2002. Charles M Russell National Wildlife Refuge 2002 Annual Narrative: Habitat Management. Lewistown Montana.

Beetle, A. A. 1960. A study of sagebrush-section *Tridentatae* of *Artemisia*. Wyoming Agricultural Experiment Station. B-779.

Chave, J., and F. Jabot. 2006. Tatame, version 1.1. Estimation of Θ and m by maximum likelihood in the neutral model with dispersal limitation. Published by the authors, Toulouse, France. Available at http://www.edb.ups-tlse.fr/equipe1/chave/tetame.htm

Dorn, R. D. 1984. Vascular Plants of Montana. Mountain West Publishing, Cheyenne, Wyoming.

Etienne, R. S., and H. Olff. 2005. Confronting different models of community structure to species-abundance data: a Bayesian model comparison. Ecology Letters 8: 493-504

Etienne, R. S., A. M. Latimer, J. A. Silander Jr., and R. M. Cowling. 2006. Comment on "neutral ecological theory reveals isolation and rapid speciation in a biodiversity hot spot". Science 311: 610b.

Fisher, B. F., C. Winne, M. M. Thornton, T P. Tady, Z. Ma, M. M. Hart, and R. L. Redmond. 1998. Montana GAP Analysis, Montana Land Cover Atlas.

Harpole, W. S., and D. Tilman. 2006. Non-neutral patterns of species abundance in grassland communities. Ecology Letters 9: 15–23.

Hubbell, S. P. 2001. Unified Neutral Theory of Biodiversity and Biogeography. Princeton University Press.

Hubbell, S. P., and L. Borda de Água. 2004. "The Unified Neutral Theory of Biodiversity and Biogeography: Reply". Ecology 85: 3175-3178.

Husby, P. O. 1982. Effects on grazing in *Atremisia tridentata/Festuca idahoensis* habitat type. M.S. thesis, Montana State University-Bozeman

Kiefer, M. 2005. Where We Play: The stories behind our arenas, parks and playgrounds in the Gallatin Valley. Bozeman Daily Chronicle, Sunday, June 19.

Lavin, M., and C. Siebert. 2005. Grasses of Montana. Montana State University Herbarium, Bozeman, MT (gemini.oscs.montana.edu/~mlavin/herb/mtgrass.pdf).

Latimer, A. M., J. A. Silander Jr., and R. M. Cowling. 2005. Neutral Ecological Theory Reveals Isolation and Rapid Speciation in a Biodiversity Hot Spot. Science 309: 1722-1725.

Natural Resource Information System (NRIS), Montana Maps. 2005. Population density 2000 census. http://nris.state.mt.us/

Mueggler, W. F., and W. L. Stewart. 1980. Grassland and shrubland habitat types of western Montana. Technical Report INT-66; Intermountain Forest and Range Experimental Station, Ogden, Utah.

Oksanen, J., R. Kindt, P. Legendre, and B. O'Hara. 2005. Vegan: community ecology package, version 1.7-84 (16 December 2005). Available at http://cc.oulu.fi/~jarioksa/.

Pohl, D. 2002. Burke Park Master Plan, Bozeman, Montana. Draft. Prepared for the Bozeman Recreation and Park Advisory Board (available at: http://www.bozeman.net/burkeparkmasterplan.html).

R Development Core Team. 2005. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Roberts, D. 2006. Laboratory for Dynamic Synthetic Vegephenonenology (LabDSV). Montana State University, Department of Ecology (available at http://ecology.msu.montana.edu/labdsv/R/)

Seefeldt, S. S., and S. D. McCoy. 2003. Measuring Plant Diversity in the Tall Threetip Sagebrush Steppe: Influence of Previous Grazing Management Practices. Environmental Management 32 (2): 234–245.

Stohlgren, T., K. Bull, and Y. Otuski. 1998. Comparison of rangeland vegetation sampling techniques in the central grasslands. Journal of Range Management 51:164-172.

Thibault, K. M., E. P. White, and S. K. Morgan Ernest. 2004. Temporal dynamics in the structure and composition of a desert rodent community. Ecology 85: 2649-2655.

USDA, NRCS. 2005. The PLANTS Database, Version 3.5 (http://plants.usda.gov). Data compiled from various sources by Mark W. Skinner. National Plant Data Center, Baton Rouge, LA 70874-4490 USA.

Volkov, I., J. R. Banavar, S. P. Hubbell, and A. Maritan. 2003. Neutral theory and relative species abundance in ecology. Nature 424: 1035-1037.

Wambolt, C. L., and M. R. Frisina. 2002. Montana Sagebrush Guide. Montana Fish Wildlife and Parks.

Western Regional Climate Center. 2006. Desert Research Institute. Reno, Nevada. http://www.wrcc.dri.edu/CLIMATEDATA.html

Whittaker, R. H. 1965. Dominance and diversity in plant communities. Science 147: 250–260.

CHAPTER THREE

PLANT DIVERSITY IN THE MONTANA SAGEBRUSH STEPPE: PART OF A LARGER METACOMMUNITY?

Introduction

Plant species diversity in the sagebrush steppe is potentially as high as any species rich biome in North America, but this aspect of the sagebrush steppe has been neglected. Welch (2005) summarized the many important aspects of the sagebrush biome, and among the chapters devoted to biodiversity, none mention anything about plant species diversity. This neglect is noteworthy given that the Intermountain Flora project (Cronquist et al. 1972), which comprises in large part the sagebrush steppe of Utah, Nevada, and adjacent California and Idaho, was implicitly undertaken because of the high levels of plant diversity occurring in this region. The authors mentioned the logical inclusion of floristically similar regions in Wyoming (e.g., the Red Desert) and elsewhere to the east of Utah, but they stated that this would have significantly increased the numbers of species to be included in the Intermountain Flora project. Apparently the magnitude of additional floristic work that would have been involved by including these more easterly distributed regions of sagebrush steppe was considered too daunting.

From a floristic perspective, not only has the plant diversity within the sagebrush steppe been neglected, but so has this biome within the state of Montana. The authors of the Intermountain Flora hardly acknowledge Montana as floristically related, even though plant species that are mostly confined to the Intermountain Region often have a northeastern-most occurrence within Montana (e.g., *Astragalus playtropis* is a classic example). In contrast, the *Flora of the Great Plains* (McGregor and Barkley 1986) readily includes the eastern half of Montana within this floristic province, even if such diagnostic species such as big bluestem (*Andropogon gerardii*), switchgrass (*Panicum virgatum*), and porcupine needlegrass (*Stipa spartea*) are very sporadic if not rare in the eastern part of the state. Additionally, Mueggler and Stewart (1980) treat the shrub and grasslands of only western Montana, thus implying that eastern Montana harbors a fundamentally different shrub and grassland vegetation.

This is a preliminary quantification of the plant diversity within the Montana sagebrush steppe using a metacommunity concept. A metacommunity is an evolutionary biogeographic unit in which member species originate, live, and eventually go extinct (Hu et al. 2006). The constituents of a metacommunity are potentially sympatric and trophically similar, and they actually or potentially compete for the same or similar resources (Hubbell 2001). A metacommunity can also be defined as an assemblage of local communities comprising many species of the same trophic level (e.g., vascular plant species) that are connected via immigration. Such metacommunities are bound in space, as in the case of the sagebrush metacommunity where physiognomically and floristically similar open shrub steppe habitats are confined to the mid elevations of the intermountain west. The sagebrush steppe is also bound in evolutionary time where local communities share a similar history of disturbance regimes, climate, and most importantly speciation and dispersal events.

The metacommunity perspective (sensu Hubbell 2001) assumes that the many vascular plant species inhabiting the sagebrush steppe are ecologically equivalent or nearly so. The death of one individual is replaced by the birth of another individual regardless of species designation. This is tenable given the high levels of plant species diversity within the sagebrush steppe, and that distance among local communities within a metacommunity and the size of the area occupied by an individual community are generally significant determinants of community similarity and species diversity (Hubbell 2001). Because plant species inhabiting the sagebrush steppe have been subjected to similar environmental selection pressures for many millennia to a million or more years, spatial and temporal variations in temperature, moisture, natural disturbance, and soil structure could be relatively inconsequential in shaping local plant community composition and diversity compared to the influences of the relative abundances of species at the metacommunity scale. This assertion is indirectly supported by Anderson & Inouye (2001), who find climatic and edaphic factors having little influence on community composition and diversity for sagebrush steppe communities. It concurs also with Pechanec et al. (1937), who documented that native forbs have the ability to survive drought with little impact.

The sagebrush ocean (Trimble 1989, Welch 2005) of the western United States is a large area of dry intermountain valleys generally typified by cold moist winters and hot dry summers. The vegetation is a mixture of shrubs, cool and warm season forbs, and grasses and is physiognomically marked by the presence of big sagebrush (*Artemisia tridentate*). The metacommunity attribution to the sagebrush ocean has been implied in western popular literature (e.g. Bailey 1869; Stegner 1940; Trimble 1989). Many species such as sage grouse, brewer's sparrow, pronghorn antelope, mule deer, and (hemi-) parasitic species of Orobanchaceae, Santalaceae, and Scrophulariaceae are obligates on sagebrush (Welch 2005). If a metacommmunity is in one sense a place where species are born, live and die, then such obligates (or endemics) demonstrate the integrity of the sagebrush metacommunity spatially and temporally.

Objectives and Methods

The objective of this study is to floristically describe the sagebrush steppe metacommunity and characterize the expected levels of plant diversity in at least the northeastern portion of this biome. To quantify and develop expectations for the sagebrush steppe we use standard diversity metrics (e.g., Simpon's Index), community similarity by distance relationships, and relative species abundance modeling, including the recent development of the zero-sum multinomial (Volkov et al. 2005; Etienne and Alonso 2005, Etienne et al. 2006; McGill 2003). Sampling of the plant species diversity in the sagebrush steppe of Montana (see Methods in Chapter 2) and relating our findings to published literature on both metacommunity theory and sagebrush vegetation has allowed us to make the case that a metacommunity probably exists for the sagebrush steppe and that it extends throughout much of Montana, including the eastern part of the state that has been traditionally referred to as "Great Plains." The various local communities of sagebrush steppe, regardless of the dominant subspecies of big sagebrush or even the species of *Artemisia* section *Tridentatae*, all share a striking similarity in the physiognomy, plant species composition and diversity, including patterns of endemism (e.g. locally common but globally rare endemics).

Results

Species Richness and Diversity

Species Richness. Within 15-24 plots (50 by 10 m) comprising 225-240 sampling quadrats (1.0 by 0.5 m) in each study site, very similar numbers of species were sampled among the Burke Park, CMR, and Porcupine study sites, and the average among sites was 130 species. However subtle differences exist in patterns of diversity among sites.

Burke Park contains 219 species that were recorded from the sagebrush steppe or ridge top area over a 15 year period (Appendix C). Sampling during June 2005, when the most diverse sample was recorded yielded 134 vascular plant species from the 15 plots whereas 118 species were recorded from just within the quadrats (Table 3.1). The numbers suggest an expected species richness given a sampling effort performed during this study (Tables 3.1-3.3).

An unpublished list of vascular plants from the CMR Refuge was expanded and refined during this project, including the partitioning of species by riparian, sagebrush steppe, and forest-breaks habitats (Appendix D). The final sagebrush steppe list contains 337 species actually or potentially occurring within the sagebrush steppe of the CMR Refuge and vicinity. Sampling the 24 plots during June of 2005 yielded 128 species from within plots and 105 species in quadrats (Table 3.2). The June 2006 sample was preceded by a moister winter thereby prompting a flush of annual species. As such, 132 species were recorded from plots and 113 from quadrats, making June 2006 the most species rich sample at the CMR study site.

Sampling the Porcupine drainage in Gallatin Canyon of southwestern Montana resulted in 125 species recorded from 23 plots and 113 species from quadrats (Table 3.3).

Table 3.1. Numbers of species recorded during the sampling of Burke Park (15 1.0 by 0.5 m quadrats per 50 by 10 m plot). The 225 quadrats equal 112.5 m^2, and the 15 plots total 7,500 m^2.

	June 2004	July 2004	August 2004	June 2005	August 2005
225 quadrats	113	110	105	118	108
15 plots	Not recorded	Not recorded	Not recorded	134	127

Table 3.2. Numbers of species recorded during the sampling of the CMR study site (10 1.0 by 0.5 m quadrats per 50 by 10 m plot). The 240 quadrats equal 120 m^2, and the 24 plots total 12,000 m^2.

	June 2005	August 2005	June 2006	August 2006
240 quadrats	102	94	113	83
24 plots	127	112	132	101

Table 3.3. Numbers of species recorded during the sampling of the Porcupine drainage study site (10 1.0 by 0.5 m quadrats per 50 by 10 m plot). The 230 quadrats equal 115 m^2, and the 23 plots total 11,500 m^2.

	June 2006
230 quadrats	113
23 plots	124

<u>Standard Diversity Measures.</u> Diversity indices from each of the three study sites show similarities but results were varied among measures. Shannon's and Simpson index ranked Burke Park highest in diversity followed by Porcupine and the CMR site. Fisher's alpha was highest for Burke Park followed by the CMR site and then Porcupine, a reverse of the intermediate results of Simpson's and Shannon's indices (Table 3.4).

Table 3.4. Standard diversity indices for each of the three study sites.

	Diversity indices		
Study site	Shannon's	Simpson's	Fisher's alpha
Burke Park	2.60	.922	24.12
CMR Refuge	2.36	.902	24.02
Porcupine Creek	2.52	.916	23.295

Species Accumulation Curves. The species accumulation curves show an asymptotic flattening for all three study sites, indicating that sampling captured most of the abundant species. Species accumulate more slowly in the CMR and Porcupine study sites but there is not a significant difference (Fig. 3.1).

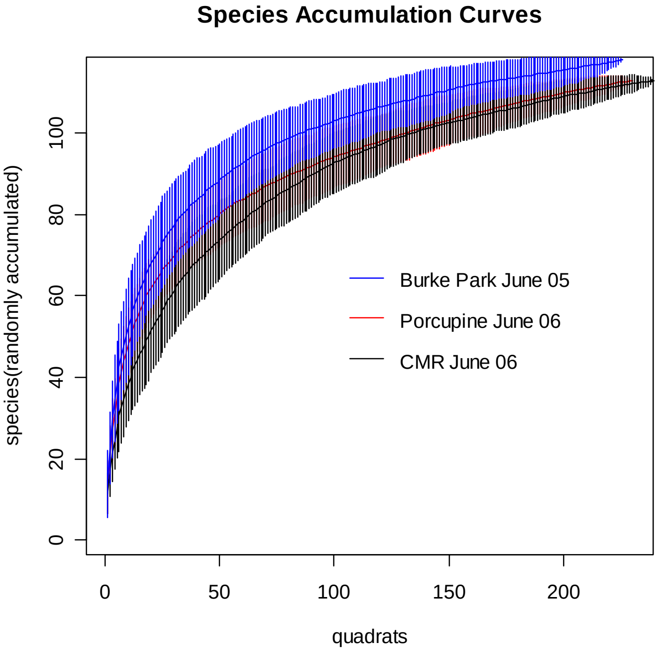

Figure 3.1. Species accumulation curves for each of the three study sites. The most diverse temporal sample is shown for each area. Shading represents 95% confidence intervals. Accumulation of species is randomized by quadrat.

Local Community Composition

Similarity of Abundant Species. The ten most abundant species (Table 3.5-3.6) in each of the three main study sites included *Artemisia tridentate* by definition, and was represented by ssp. *vaseyana* in Burke Park and Porcupine and ssp. *wyomingensis* in the CMR area. In general, the 10 most abundant species as measured in cover are similar between Burke Park and the CMR study site. Abundance data measured as frequency among sampling quadrats, however, show some notable differences among sites (Table 3.6) especially with regard to the small statured species that are widespread but with low cover (e.g., *Allium textile*, *Alyssum alyssoides*, and *Arabis nutallii*).

Burke Park and the Porcupine drainage are similar in that the ten most abundant species at the Porcupine site were all sampled at Burke Park (Tables 3.6, Appendix B-D). Burke Park differs from Porcupine in the introduced grasses, the most abundant of which is *Poa pratensis*. Introduced grass species were sampled to much less degree at Porcupine, even though these grasses occur in the area (e.g. *Poa pratensis, Phleum pratense*, and *Bromus inermis*). The bunchgrass *Agropyron spicatum* was ranked in the 10 most abundant species in each of the Burke Park and CMR study sites, but merely sampled in Porcupine. Of the 10 most abundant and frequent species in the CMR (Tables 3.5 and 3.6), *Bouteloua gracilis* and *Selaginella densa* were not sampled in Burke Park and Porcupine Creek (although *Selaginella densa* is common in the Gallatin Canyon). The Porcupine site and Burke Park lie in close proximity within the Gallatin Valley, and have a moister and cooler climate than the CMR site, explaining the absence of *Bouteloua gracilis* (a C4 grass). Of the ten most abundant species in Burke Park that were not sampled in the CMR, two species, *Allysum alyssoides* and *Bromus inermis*, are introduced. *Poa pratensis*, the most abundant species at Burke Park, was sampled in one plot at the CMR study site during June 2006, but is otherwise common in and around human influenced areas such as stock ponds.

Table 3.5. Species ranking within the 10 most abundant during any of the early and late summer sampling efforts (abundance measured as cm^2 cover).

Burke Park	CMR study site
Poa pratensis	*Artemisia tridentata wyomingensis*
Festuca idahoensis	*Selaginella densa*
Agropyron dasystachyum	*Agropyron dasystachyum*
Lupinus argenteus	*Bouteloua gracilis*
Artemisia cana	*Koeleria macrantha*
Aster falcatus	*Stipa comata*
Achillea millefolium	*Stipa viridula*
Agropyron spicatum	*Poa secunda*
Artemisia tridentata vaseyana	*Agropyron spicatum*
Bromus inermis	*Vicia Americana*
Stipa viridula	*Opuntia polyacantha*
	Artemisia frigida

Table 3.6. Species ranking within the 10 most abundant during the various early and late summer sampling efforts (abundance measured as frequency).

Burke Park	CMR study site	Porcupine Creek
Poa pratensis	*Agropyron dasystachyum*	*Festuca idahoensis*
Achillea millefolium	*Artemisia tridentata wyomingensis*	*Achillea millefolium*
Agropyron dasystachyum	*Bouteloua gracilis*	*Lupinus argenteus*
Aster falcatus	*Poa secunda*	*Artemisia tridentata vaseyana*
Lupinus argenteus	*Koeleria macrantha*	*Arenaria congesta*
Tragopogon dubius	*Selaginella densa*	*Taraxacum officinale*
Festuca idahoensis	*Artemisia frigida*	*Agropyron dasystachyum*
Artemisia cana	*Vicia Americana*	*Stipa richardsonii*
Commandra umbellatum	*Agropyron spicatum*	*Koeleria macrantha*
Melilotus officinales	*Phlox hoodii*	*Erigeron caespitosus*
Phlox longifolia	*Stipa comata*	
Allysum alyssoides	*Allium textile*	
	Carex stenophyllum	

Other abundant species at Burke Park that are not found in the CMR study site are *Festuca idahoensis, Lupinus argenteus* and *Phlox longifolia*. Of the 234 species that were recorded among quadrats from all three study sites, 28 were found at all three sites, 42 were shared between Burke Park and the CMR study site, 57 species were recorded in both Burke Park and the Porcupine site and, 34 species were shared in common at the CMR and Porcupine sites. The remaining 73 species or only 34% were unique to only one of the study sites in this project.

Geographic Distance and Dissimilarity. Burke Park and the Porcupine drainage are of a similar mountain big sagebrush habitat, and are less dissimilar to each other than either is to the CMR study site (Table 3.7). Although this is to be expected, what is particularly notable is how relatively dissimilar all three study sites are too each other (Table 3.7), and that this dissimilarity can be described as a function of geographic distance among study sites (Fig. 3.2)

Table 3.7. Jaccard's dissimilarity (lower left) and geographic distance in km (upper right) between the three study sites. Dissimilarity values were obtained from just those species sampled from plots in each of the study sites.

	Burke Park	CMR	Porcupine Creek
Burke Park	0	324.7	53.4
CMR	0.8454672	0	372.8
Porcupine Creek	0.7111951	0.8763094	0

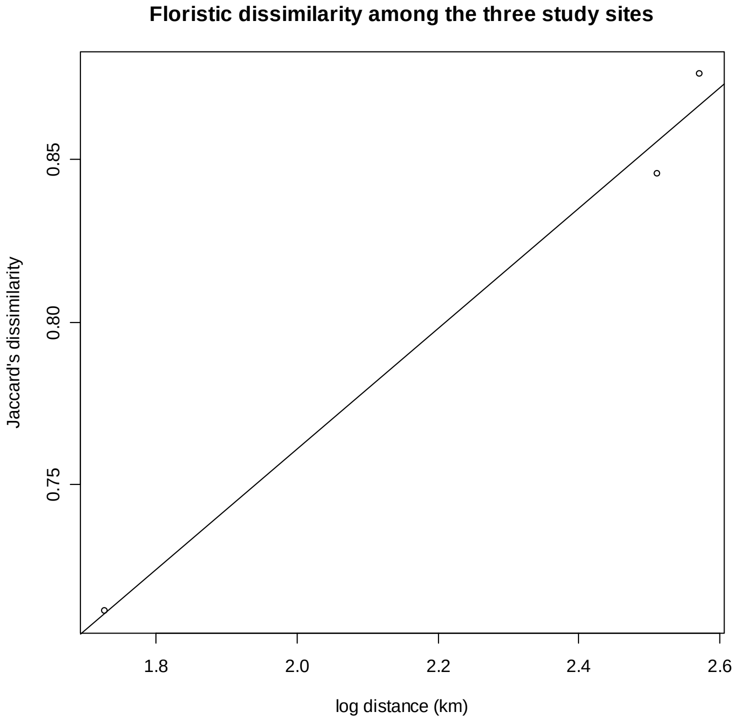

Figure. 3.2. The relationship between floristic dissimilarity and geographic distance between Burke Park, CMR, and Porcupine Creek study sites (taken from data presented in Table 00). Jaccard's dissimilarity was measured using only species sampled within plots at each study site. The slope of the line is 0.0805 (p=.0718), but the adjusted R^2= 0.9746.

In order to expand on the barely significant relationship detected above between geographic distance and community dissimilarity among the three study sites, full species lists for Burke Park, the CMR, and Porcupine Creek were compared to floristic lists of species taken from various sagebrush-steppe-dominated regions in the western United States (Culver 1994). Plant species inhabiting the sagebrush steppe were extracted from these lists (e.g., riparian, forest, and alpine plants were excluded) before comparisons were made. The positive relationship between geographic distance and community dissimilarity is illustrated with both a regression (Fig. 3.3) and cluster analysis (Fig. 3.4).

The most distant sites are floristically most dissimilar. If floristic composition serves as a proxy for community composition, then geographic proximity of local communities may well be a strong determinant in their shared community similarity. For example, the cluster of the Yellowstone, Windriver, southeast Absoroka, and Centennial Valley floristic sites (Fig. 3.4) may be as much a function of their geographic proximity as any shared ecology.

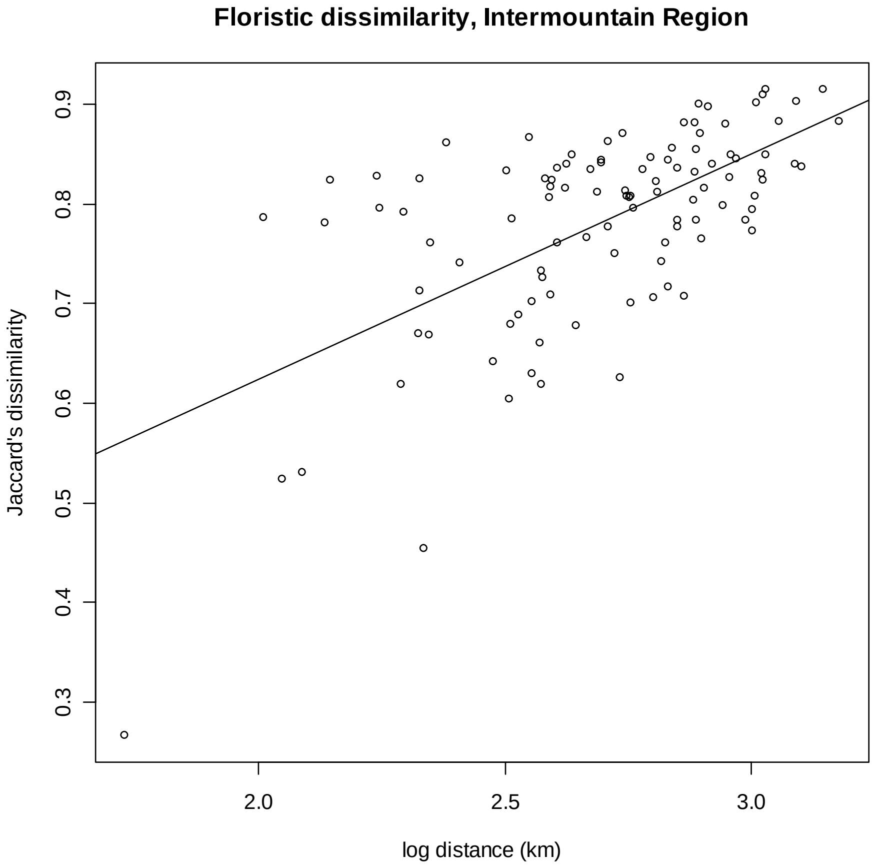

Figure 3.3. Jaccard’s dissimilarity by distance. As distance increases dissimilarity increases. The slope of the line is 0.2261 (p=1.718e-12), and the adjusted R^2=0.3847.

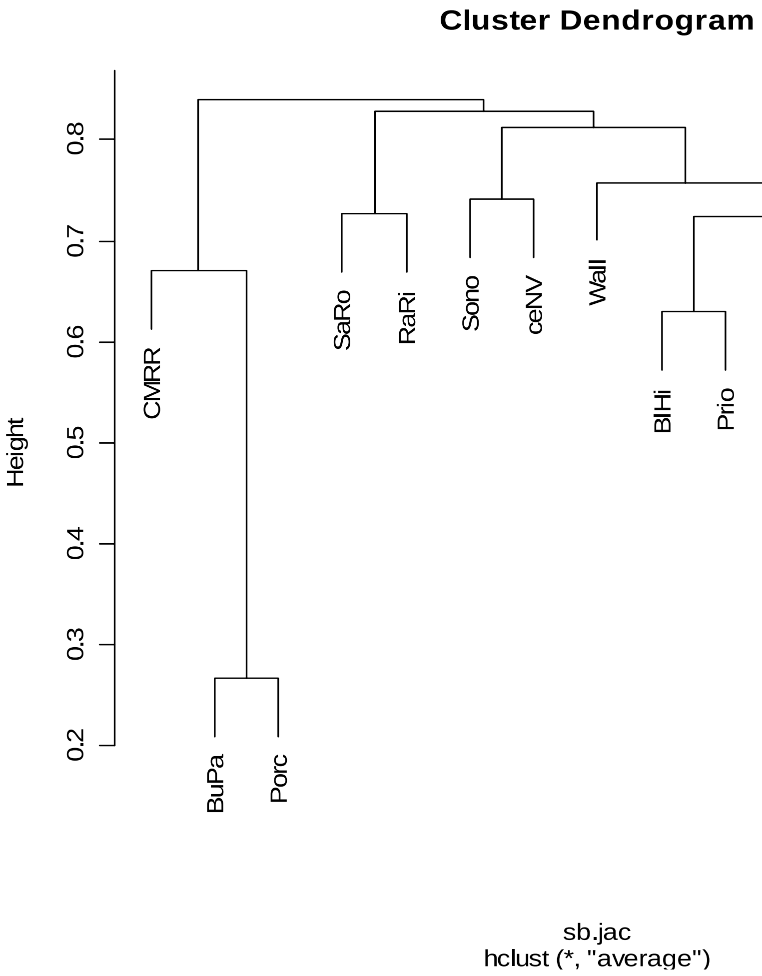

Figure 3.4. Cluster analysis of the three study sites (Burke Park, CMR, and Porcupine Creek) and selected study sites (taken from Culver 1994) for which a list of plant species inhabiting the sagebrush steppe have been extracted. Area abbreviations: BlHi = Black Hills (South Dakota, Montana, Wyoming), BuPa = Burke Park (Montana), CMRR = CMR National Wildlife Refuge (Montana), ceNV = central Nevada, CeVa = Centennial Valley (Montana), nwCO = Flat Iron region (Colorado), Prio = Prior Mts. (Montana), RaRi = Raft River Range (Utah), SaRo = Santa Rosa Range (Nevada), seAb = southeastern Absoroka Mts. (Wyoming), Sono = Sonora Pass region of the east slope Sierra Nevada (California), Wall = Wallowa Mts. (Washington), WiRi = Wind River Range (Wyoming), YeSt = Yellowstone National Park (Wyoming, Montana, Idaho).

Physiognomy of the Sagebrush Steppe Metacommunity

Grass, forb, shrub, bare ground, and litter cover were estimated for Burke Park and the CMR study sites (Tables 3.8-3.9). At Burke Park grasses dominated with an average cover of 45%. The three most abundant species were *Poa pratensis*, *Festuca idahoensis,* and *Agropyron dasystachyum*, which for example provided 38% of the total grass cover in June 2005. Shrubs had the least cover with an overall average of less than 11%, which was consistent within and among years. The dominant shrubs were *Artemisia tridentata ssp. vaseyana* and *A. cana*. Forbs were intermediate between grasses and shrubs and were the most variable in cover within a growing season, changing 10% from June to August.

Table 3.8. Composition of plant, litter, and bare ground cover at Burke Park (in % cover).

Growth habit	June 04	July 04	August 04	June 05	August 05
Grass	40.3	45.4	46.2	46.9	46.6
Forb	27.5	25.5	17.6	27.8	16.6
Shrub	10.6	11.5	11.4	10.5	11.0
Bare ground	8.0	6.6	6.4	6.2	6.1
Litter	13.4	11.0	18.4	8.6	19.7

The vegetation at the CMR study site averaged 16% shrub cover, and is primarily *Artemisia tridentata* subsp. *wyomingensis* (Table 3.9). Perennial grass cover dominated the CMR study site with *Bouteloua gracilis* and *Agropyron dasystachyum* being the most two abundant species. Shrubs had the least cover at around 16% of the total despite the visual dominance in the landscape. The forb cover was dominated by *Selaginella densa*, such that if excluded would render a forb cover of less than 6% during the June surveys, which is less than that of the shrubs. This underscores the dominance of shrubs and grasses at the CMR study site.

Table 3.9. Composition of plant, litter, and bare ground cover at the CMR study site (in % cover). The values in parentheses represent cover if *Selaginella densa* is removed from the forb category.

Growth Habit	June 05	August 05	June 06	August 06
Grass	25.0	24.7	25.7	17.8
Forb	17.9 (4.7)	16.5 (2.9)	19.9 (5.4)	16.1(1.9)
Shrub	15.7	16.1	16.3	15.8
Bare ground	21.6	21.6	19.9	20.2
Litter	19.8	21.1	18.2	30.1

Despite the dominance in cover of shrubs and grasses at the Burke Park and CMR study sites, most species were forbs (Table 3.10). The diversity of forbs is high despite the low amount of cover. Indeed an average of 100 species of forbs was sampled at each study site.

Table 3.10. Number of grass, forb and, shrub species found at Burke Park and CMR during the most diverse sample.

Growth Habit	Burke Park	CMR Site
Grass	17	23
Forb	103	96
Shrubs	13	13

Within Season Diversity

There is a change from early to late season forbs in both study areas even though some species persist throughout the growing season. Early season forbs and grasses (Appendix E1-E2) put on biomass and flower during the early growing season. They lose biomass or become absent by mid to late summer. Most early season forbs come from the families of Apiaceae, Liliaceae, Boraginaceae, Ranunculaceae, Violaceae and especially Brassicaceae. Late season forbs (Appendix E) are present during the June sample, but attain peak biomass late in the growing season (late July, August, and September). Late season forbs increase in abundance relative to the early season sample and are represented mostly by the *Asteraceae* and *Chenopodiaceae* (the latter more so in the CMR study area), and to some degree the Fabaceae. The late season is less diverse due to the loss of early season forbs (Figs. 3.5-3.6). Late season forbs (e.g. *Solidago missouriensis*, *Liatris punctata*, and *Aster falcatus*) increase in relative cover rank, whereas early season forbs decrease in abundance and rank. The shift in the relative species abundance curve in Burke Park from June to August is due primarily to a reduction in forbs, which comprise 25% of the cover during early season. The CMR site showed little temporal change in the RSA curve during 2005 but a larger difference in 2006. This is the result of a flush of early season annuals (i.e. *Phacelia linearis*, *Euphorbia spathulata*, and *Descuranaina richardsonii*) that responded to an increase in winter precipitation. The moist winter of 2005-2006 was followed by a hot summer, which caused a rapid curing of vegetation by mid summer. The result was a large shift in the within-season relative species abundance curve (Fig. 3.6).

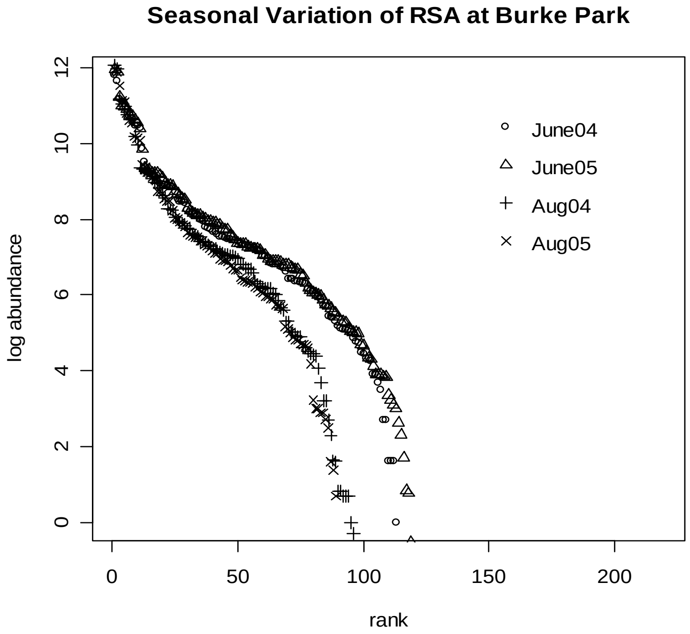

Figure 3.5. Temporal variation associated with seasonal sampling at Burke Park.

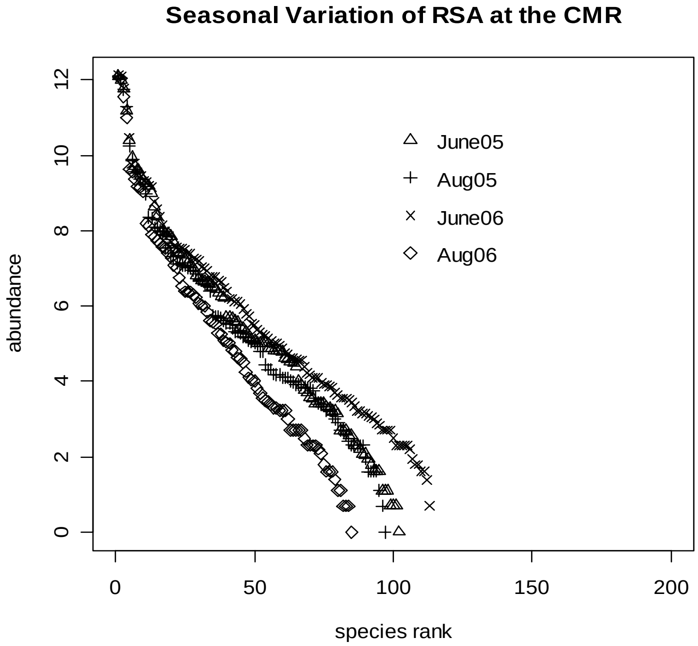

Figure 3.6. Temporal variation associated with seasonal sampling in the CMR area.

All the sites sampled of sagebrush steppe contained a diverse mixture of shrubs (e.g. *Artemisia tridenata, Chrysothamnus visidiflorus, C.nauseous, Krascheninnikovia lanata, Rosa woodsii*), grasses (e.g. *Agropyron daystachymum, A. spicatum, Bouteloua gracilis, Festuca idahoensis, and Koleria macrantha,*) and early (e.g. *Astragalus* sp., *Lomatium* sp., *Penstemon* sp., and *Phlox* sp.) and late season forbs (e.g. *Dalea* sp. *Liatrus punctata*, *Orthocarpus lutens*, and *Solidago missouriensis*). All sites contained a mixture of species representing all growth habits but the diversity in terms of species richness was greatest for the forbs.

Neutral Theory of Biodiversity and Parameter Estimation

We tried multiple ways of collecting abundance data in order to most efficiently estimate the parameters of the zero sum multinomial (Fig 3.7-3.8). The method of collecting abundance in the form of cover in cm^2 inflated the number of individuals for a given sampling effort (i.e. a total of 10^5-10^6 such "cm^2" individuals were sampled). These sample sizes were too large for expedient parameter estimation and available computer programs bogged down. Multiplying such large samples sizes by a factor such as 0.01 and then rounding up to the nearest integer resulted in a relative species abundance profile with a very long rare tail. The second method of individuals using a conversion factor (Chap. 2) inflated the relative abundance of rhizomatous grasses, which were scored as a single individual per 1 cm^2. The third method involving frequency among sample quadrats was the simplest and least time consuming in terms of data collection and parameter estimation.

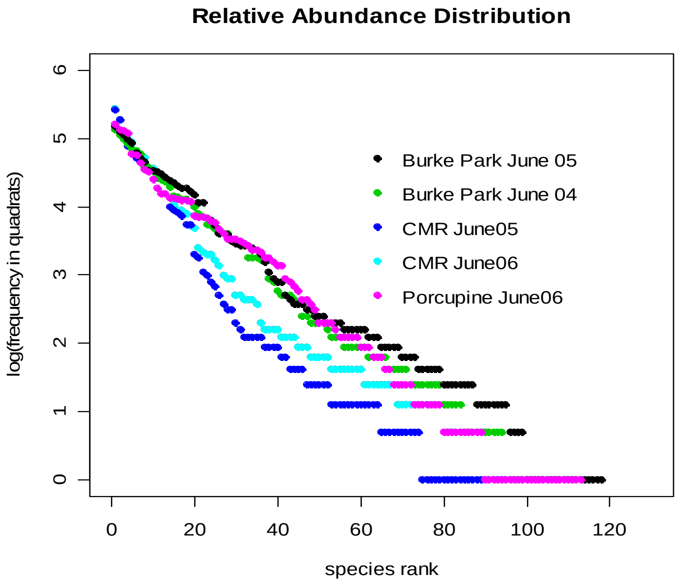

Figure 3.7. Relative species abundance distributions for Burke Park, CMR and Porcupine study sites using frequency in quadrats as a measure of abundance.

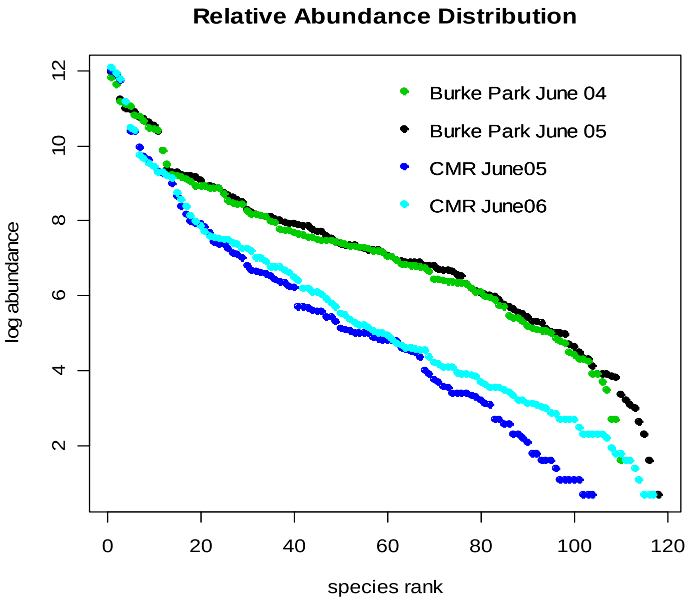

Figure 3.8. Relative abundance distribution in June 2005 for the Burke Park and CMR study sites using cm^2 cover as a measure of abundance.

In Burke Park, CMR, and Porcupine study sites, the frequency distributions (Fig 3.7) were best fit with the zero sum multinomial (Tables 3.11-3.13) with all fits having the lowest AIC values. The best fits for the zero sum multinomial had dual optima for all study sites. The highest (least negative) likelihood score occurred twice meaning the model had two points of best fit for the parameters. The fittings of the parameters and the parameter estimates are generally robust especially for theta despite using different methods to determine relative species abundance and show consistently that theta at Burke Park is highest (Tables 3.11-3.13). The theta estimates, which show convergence for theta among sites of 23-30, are reasonable considering the estimates of theta using altered foliar cover abundance measure show convergence of theta as being 18-34, similar to the range of 23-30 for the selected optimum (Table 3.14).The migration parameter showed little convergence at either one or two optima. Theta estimates correspond to migration estimates that are greatest for the CMR site (.89), intermediate Porcupine (.46) and lowest at Burke Park (.27). The high, variable and, unrealistic results of theta correspond to different estimates of migration, and are ordered differently when compared among sites. Porcupine has the highest (.137), almost identical is Burke Park (.136) and the lowest migration the CMR site (.0091). The migration parameter also showed no convergence in using the foliar abundance data, and is often unimportant to the model (Table 3.14). Therefore the best optima are those of the lowest theta estimate (Tables 3.11-3.13).

Table 3.11. Rank Abundance Distribution models fit for the Burke Park frequency data (the poisson family was used for all models except the ZSM, which is designed for count data). In all cases, the number of species is 118 and the total abundance is3189. ZSM parameter estimates were made with the program Tatame (Chave et al. 2006).

Model	Parameter 1	Parameter 2	Parameter 3	AIC value
ZSM 1st optimum	Θ=29.62	m=0.2672		248.26
ZSM 2nd optimum	Θ=132.7	m=0.0136		247.98
Mandelbrot	2.4286e+13	-7.0		520.45
Preemption	0.04814			545.88
Lognormal	3.0	1.0		835.42
Veiled.LN	3.0	1.0	1.0	837.97
Zipf	0.12895	-1.0	110.00	1474.73

Table 3.12. Relative Abundance Distribution models fit for the CMR study site using frequency data (the poisson family was used for all models except the ZSM which is designated for count data). In all cases the number of species is 113 and total abundance is 2630. ZSM parameter estimates were made with the program Tetame (Chave et al. 2006).

Model	Parameter 1	Parameter 2	Parameter 3	AIC value
ZSM 1st optimum	Θ=24.54	m=0.8899		221.2
ZSM 2nd optimum	Θ=2.149 E38	m=0.0091		221.3
Mandelbrot	25843.0	-3.7	29.3	465.0
Preemption	0.1			626.4
Lognormal	2.1	1.5		756.5
Veiled.LN	2.1	1.5	1.0	758.5
Zipf	0.2	-1.0		1214.4

Table 3.13. Relative Abundance Distribution models fit for the Porcupine study site using frequency data (the poisson family was used for all models except the ZSM which is designated for count data). In all cases the number of species is 113 and total abundance is 2955. ZSM parameter estimates were made with the program Tetame (Chave et al. 2006).

Model	Parameter 1	Parameter 2	Parameter 3	AIC value
ZSM 1st optimum	Θ=23.94	m=0.4564		239.7
ZSM 2nd optimum	Θ=111.9137	m=0.0137		236.0
Preemption	0.0501			516.5
Lognormal	2.0	1.0		753.0
Veiled.LN	2.0	1.0	1.0	755.0
Zipf	0.13526	-1.0		1336.2
Mandelbrot	5.5555e+26	12.0	199.00	512.2

Table 3.14. Estimates of theta and m for Burke Park and the CMR sites derived from R code developed by Andrew Latimer (Latimer et al. 2005) and using different methods of estimating the number of individuals. This included multiplying cm^2 cover of each species by a factor of 0.001, or converting cm^2 to number of individuals by dividing by average size (reported in Chapter 2 for the various growth forms).

Data set	Number of individuals	Theta	M
BP	311915	24.34	0.99
BP	311915	34.33	Na
BP	10040.78	18.37	0.2
BP	10040.78	14.05	0
CMR	1558	25.4	0.99
CMR	1558	23.82	Na
CMR	7351.89	8.26	0
CMR	7351.89	9.7018	0.99

Discussion

Species Richness and Diversity

The three study sites all have similar numbers of species recorded in plots and in quadrats. A total of 134 maximum species were recored from15 plots (7,500 m^2) at Burke Park, 132 maximum species from 24 plots (12,000 m^2) at the CMR study site, and 124 species from 23 plots (11,500 m^2) at the Porcupine study site. These numbers are similar to those of Anderson and Inouye (2001) who recorded 108 species from a long term basin big sagebrush study area of east-central Idaho, where they censused 92 plots each 15.24 by 4.57 m (6,408 m^2 total). They are also similar to those of Seefeldt and McCoy (2003), who recorded 84 species from a three-tip sagebrush (Artemisia tripartita) habitat in eastern Idaho using twelve 20 by 50 m modified Whittacker plots (12,000 m^2) spread among four treatments combined from grazing and fire.

Our study sites have been largely undisturbed since about 1950, according to the historical information on these areas. Currently, Burke Park receives the most disturbance via herbicide drift from adajacant barley fields, and human and dog traffic. The CMR site receives the most cattle grazing and Porcupine the most native ungulate grazing. Otherwise these areas have escaped large scale conversion to cropland or “improved range” and could thus represent an expectation of plant species diversity in a local community within the sagebrush steppe metacommunity.

The differences among the three study sites in the diversity measures are minor. Simpson’s and Shannon’s are based on richness and dominance; the steeper the slope of the relative species abundance curve the lower the diversity index (He and Hu 2005).

When comparing the CMR and Porcupine study sites, the decline in abundance at the CMR site is steeper despite it being more species rich than the Porcupine site. This accounts for the lower diversity measure at the CMR compared to the Porcupine study site. Fisher's alpha, in contrast, is affected by richness, which includes the length of the rare tail of the species abundance curve. This is the reason that the CMR has a higher diversity measure here than that of the Porcupine study site. The differences are trivial and may be explained by the geographic position of the CMR study site within the sagebrush steppe. That is, the CMR study site lies towards the northeastern edge of the sagebrush biome and the steep slopes of the relative abundance curve may reflect its distance from the metacommunity (e.g., the edge effect described in Latimer et al. 2005). Regardless, the similarity in diversity measures among the three study sites could reflect a floristic homogenization and an expectation of diversity for a sampling effort of 110 to 120 m^2 in the sagebrush steppe metacommunity.

Relative species abundance and the zero sum multinomial

The CMR area may be one of the most isolated in the sagebrush steppe metacommunity and could be of recent origin. Strong and Hills (2003) document a northward expansion of plant species following the retreat of the glaciers and climate warming. Expansion of the sagebrush steppe northeastward through Montana could have coincided with this general migration. Although Strong and Hills refer to mixed grass prairie, they report increased amounts of *Artemisia* and *Chenopodaceae* pollen, genera essentially diagnostic of the sagebrush steppe. All of the vascular plant species in the CMR region are very widespread in at least western North America and none are endemic or have a restricted range. This contrasts to other areas of the sagebrush steppe where endemics or species with narrow ranges commonly occur (Cronquist 1977; Culver 1994; Lesica et al. 2006).

The Porcupine site lies at the upper distribution of sagebrush where the sagebrush steppe metacommunity meets the montane forests. The habitat here is fragmented and confined to south facing slopes. Similarly Burke Park represents a fragment of the sagebrush steppe that was likely surrounded by riparian wetland or shrubby vegetation prior to urban development in the Bozeman area. The CMR regions lies toward the northeastern edge of the sagebrush metacommunity and could thus be equally as isolated. Regardless, diversity measures, including estimates of theta derived from the zero sum multinomial with point estimates all in the range of 24-30, as well as immigration estimates (point estimates ranging 0.27-0.89) strongly suggest that these areas are not isolated. Indeed, the similarity of diversity estimates could be due to a homogenizing effect of the high immigration rates. The high beta diversity in contrast could simply be due to the very high plant species diversity of the sagebrush metacommunity.

In putting the plant species diversity of sagebrush steppe into broader context, the theta estimates are relatively high compared to the many examples illustrated in Hubbell (2001). In comparison to some of the most species-rich metacommunities such as tropical humid forests or the Cape Floristic Province (e.g., Latimer et al. 2005, Ettienne et al. 2006), theta estimates for the sagebrush steppe are low. However, they compare well with other biodiverse regions, such as the season dry tropical forests (e.g. the Guancaste of

Costa Rica- see Hubbell 2001), which are well known for their vascular plant species diversity (Pennington et al. 2000).

Local Community Composition

Community composition in general is very similar among the three study sites, as is exemplified by the shared abundance of species such as *Artemisa tridentata*, *Agropyron dasystachyum*, and *Astragalus drummondii*. Indeed, none of the plant species in our study sites are highly localized geographically, and likely all of them are common throughout the sagebrush steppe (e.g. Anderson & Inouye 2001, Tisdale et al. 1965, Daubenmire 1978, West 1983, Jensen et al. 1988). Of the plant species recorded from our study sites 22% were common to all three study sites. These numbers may seem low, but they should be viewed in the context that there is probably a naturally high turnover in plant species diversity within the sagebrush biome (e.g., a high beta diversity), as is indicated by the relationship of geographic distance and community dissimilarity.

Some of the beta diversity among our study sites is no doubt due to at least a moisture gradient. For example, *Bouteloua gracilis* and a diversity of other warm season forbs and grasses were sampled only in the CMR study site. The CMR site is warmer and drier than Burke Park and Porcupine, but sagebrush steppe often includes warm season species that are widespread throughout at least the sagebrush steppe (West 1983). In contrast, *Festuca idahoensis* is notably absent from the CMR region, although this bunchgrass is abundant at the Burke Park and Porcupine study sites where it is expected at the wetter end of the moisture gradient (Mueggler and Stewart 1980) in montane sagebrush steppe associated with *Artemisia tridentata* subsp. *vaseyana* (Daubenmire

1978). Other species recorded in the CMR study site outside our plots, like *Sprobolos airiodes, Distichlis stricta,* and, *Atriplex confertifolia* (Appendix C), as well as inside our plots, such as *Atriplex gardneri*, *Elymus elymoides*, and *Sarcobatus vermiculatus*, and that are not found in the vicinity of the mountain big sagebrush sites like Burke Park and Porcupine Creek reflect the similarity of the CMR region to the Great Basin vegetation described by West and Young (1988).

The CMR region lies somewhat close to the Great Plains, and it is surprising that a proximity to this area has little influence on the community composition in the sagebrush dominated area. Hunt (1974), and Barker and Whitman (1988) classify the region in and around the CMR area as mixed grass or short grass prairie (Wheatgrass-Grama-Needle grass). However, few species that are confined to the Great Plains flora occur in the CMR region (e.g. *Poa arida* and *Psoralea agrophylla*). In contrast, many sagebrush steppe species (e.g. *Elymus elymoides, Agropyon spicatum, Silene oregana*) inhabit this area.

Despite the environmental conditions at the CMR study site that differ from those of the Burke Park and Porcupine area, the florsitic composition and physiognomy is much more similar to these more western sagebrush dominated sites than to the nearby Great Plains. The diversity of shrubs, perennial cool season grasses, and early and late season forbs (e.g., *Krascheninnikovia lanata*, *Elymus elymoides*, *Lesquerella ludoviciana*, and *Dalea purpurea*, respectively) is highly similar to other sagebrush steppe sites in western North America. Although the flora and vegetation of the CMR regions differs from those of the Burke Park and Porcupine study area, this difference may be due to not so much something like a moisture gradient but rather to the intrinsically high alfa and beta diversity of the sagebrush metacommunity. Afterall, many of the species sampled only from the CMR study site during our study do occur in the upper elevation sagebrush steppe regions of Gallatin County (e.g., most notably species like *Atriplex gardneri*, *Bouteloua gracilis*, *Elymus elymoides*, and *Seleginella densa*).

Physiognomy of the Sagebrush Steppe Metacommunity

The vegetation of the sagebrush steppe comprises a diversity of shrubs, perennial grasses, and cool and warm season forbs. The forbs are by far more species diverse than shrubs and perennial grasses. Of the approximately 100-130 species that can be expected within 15-24 50 by 10 m plots of an intact stand of sagebrush steppe, about 80 species should be forbs and most of these early season. Perhaps these sorts of numbers could be used as restoration benchmarks during recovery efforts of sagebrush steppe local communities, should a management objective include plant diversity as a goal. This physiognomy of the sagebrush steppe could be inherent because it is commonly reported for other sagebrush steppe sites. For example, Anderson and Inyoue (2001) report 12 shrub, 15 perennial grass, and 81 forb species from their study site in east central Idaho.

Forbs have the lowest cover yet their diversity and importance to wildlife is often underestimated (Crawford et. al 2004, Welch 2005). This component of diversity may be a critical part of the functional diversity of a sagebrush steppe. Bob Skinner (personal communication, USFWS Lewistown, Montana) reports that late season forbs are most impacted by summer grazing. These species are palatable and green when many early season forbs and grasses have become dormant, dry, and less palatable. Skinner’s studies reveal that late season forbs (particularly species of *Liatris* and *Dalea*) are preferentially grazed over grasses and shrubs. Late season forb diversity or abundance thus could be used for restoration goals or for identifying some of the least disturbed patches of sagebrush steppe.

Conclusion

The eastern and north central areas of Montana harbor a sagebrush steppe metacommunity, even if it might be evolutionarily recent compared to sagebrush steppe in the central and western portions of this biome. Plant genera with endemic species to the sagebrush steppe (Table 3.15-3.16) are well represented in our study sites, including the CMR region (e.g., *Erigeron* and *Penstemon*). However, such genera are represented by common and widespread species. That these genera show little if any endemism within Montana is in agreement with the high immigration rates estimated from fitting the zero sum multinomial to the relative species abundance data. This is especially the case in the north central region, and suggests an evolutionary recent expansion of this biome in a northeasterly direction, no doubt coinciding with retreat of the continental glaciers.

Table 3.15. Genera with two or more endemic species occuring within one of the 16 floristic sections of the Intermountain Flora as defined by Cronquist et al. (1972). Genera in boldface are represented in the sagebrush steppe of Montana by common and widespread species.

Astragalus	***Cryptantha***	***Cymopterus***	***Draba***	***Erigeron***
Eriogonum	*Gilia*	***Lesquerella***	***Lomatium***	***Oenothera***
Penstemon	***Phlox***	***Psoralea***	*Sclerocactus*	***Townsendia***

Table 3.16. Genera with one endemic species occuring within one of the 16 floristic sections of the Intermountain Flora as defined by Cronquist et al. (1972). Genera in boldface are represented in the sagebrush steppe of Montana by common and widespread species.

Agastache	***Allium***	*Aquilegia*	***Arabis***	*Arctomecon*
Arenaria	***Artemisia***	***Asclepias***	***Atriplex***	***Castilleja***
Cirsium	***Cuscuta***	*Cycladenia*	***Dalea***	*Echinocactus*
Ephedra	*Eremocrinum*	***Euphorbia***	***Festuca***	***Frasera***
Geranium	*Glaucocarpum*	*Hermidium*	*Hoffmanseggia*	***Hymenopappus***
Laphamia	***Lepidium***	***Lewisia***	***Lupinus***	***Machaeranthera***
Mentzelia	***Mimulus***	***Mirabilis***	*Parthenium*	*Pediocactus*
Physaria	*Porophyllum*	*Primula*	*Scuttellaria*	***Silene***
Sphaeralcea	***Sporobolus***	*Thelypodiopsis*	*Vanclevea*	***Viguiera***

The eastern occurrence of the sagebrush steppe within Montana could not be detected from reading most floristic and biogeographic accounts of the plants of western North America. For example, The Intermountain Flora (Cronquist 1972) draws an eastern limit with the Idaho and Utah state lines, even though the taxonomic keys of this flora work very well for identifying plant species from the sagebrush steppe of Montana, Wyoming, and Colorado. Trimble (1989) treats specifically the Great Basin Desert, although his expose of the sagebrush ocean could well apply to the sagebrush steppe of Montana, including the north central portion in the region of the CMR study site. Indeed, many vegetation maps of the western United States depict at least the eastern half of Montana as belonging to the Great Plains (e.g., Barker and Whitman 1988, Hunt 1974; Gould and Shaw 1983), even though sagebrush is common throughout this part of the state and Great Plains species such as *Andropogon gerardii*, *Panicum virgatum*, and *Stipa spartea* are absent. The abundance of antelope and other sagebrush obligate/facultative species in eastern Montana is further evidence that the open steppe of Montana should be considered more properly part of the sagebrush steppe rather than Great Plains metacommunity.

Literature Cited

Anderson, J. E., and R. S. Inouye. 2001. Landscape-scale changes in plant species abundance and biodiversity of a sagebrush steppe over 45 years. Ecological Monographs 71: 531-556.

Bailey, W.W. 1869. The Sage Brush. American Naturalist 13:356-360.

Barker, W. T., and W. C. Whitman. 1988. Vegetation of the Northern Great Plains. Rangelands. 10: 266-272.

Chave, J., D. Alonso, and R. S. Etienne. 2006. Comparing models of species abundance. Nature 441: E1-E2.

Crawford, J. A., R. A. Olsen, N. E. West, J. C. Mosley, M. A.Schroeder, R. F. Miller, M. A. Gregg, and C. S. Boyd. 2004. Synthesis- Ecology and management of sage grouse and sage grouse habitat. Journal of Range management. 57: 2-19.

Cronquist, A. A., H. Holmgren, N. H. Holmgren, and J. L. Reveal. 1977. Intermountain Flora: Vascular plants of the Intermountain West, USA Volume 1. New York Botanical Garden. Bronx, New York.

Culver, D. 1994. Floristic study of the Centennial Valley and Mountains, southwestern Montana. MS Thesis, Montana State University, Bozeman.

Daubenmire, R. F. 1978. Plant Geography: with special reference to North America. Academic Press.

Etienne, R. S., and D. Alonso. 2005. A dispersal limited sampling theory for species and alleles. Ecology Letters. 8:1147:1156.

Etienne, R. S., A. M. Latimer, J. A. Silander Jr., and R. M. Cowling. 2006. Comment on “neutral ecological theory reveals isolation and rapid speciation in a biodiversity hot spot”. Science 311: 610b.

Etienne, R. S., and H. Olff. 2005. Confronting different models of community structure to species-abundance data: a Bayesian model comparision. Ecology Letters 8: 493-504.

Gould, F. W., and R. B. Shaw. 1983. Grass Systematics. Texas A&M University Press.

He F. L., and X. S. Hu. 2005. Hubbell's fundamental biodiversity parameter and Simpson diversity index. Ecology Letters 8: 386-390.

Hu, X. S., F. L. He, and S. P. Hubbell. 2006. Neutral theory in macroecology and population genetics. Oikos 113: 548-556.

Hubbell, S. P. 2001. Unified Neutral Theory of Biodiversity and Biogeography. Princeton University Press.

Hunt, C. B. 1974. Natural Regions of the United States and Canada. W. H. Freeman, San Francisco.

Jensen, M. E., L. S. Peck, and M. V. Wilson. 1988. A sagebrush community classification for mountainous northeastern Nevada rangelands. Great Basin Naturalist. 48: 422-433.

Latimer, A. M., J. A. Silander, and R. M. Cowling. 2005 Neutral ecological theory reveals isolation and rapid speciation in biodiversity hotspot. Science 309:1722-1725.

McGill, B. 2003 A test of the unified neutral theory biodiversity. Nature 442: 881-885.

McGregor, R. L., and T. M. Barkley. 1986. Flora of the Great Plains. University Press of Kansas. Lawrence, Kansas.

McKane, A. J., D. Alonso, and R. V. Sole. 2004. Analytic solution of Hubbell's model of local community dynamics. Theoretical Population Biology 65: 67-73.

Mueggler, W. F., and W. L. Stewart. 1980. Grassland and shrubland habitat types of western Montana. Technical Report INT-66; Intermountain Forest and Range Experimental Station, Ogden, Utah.

Pechanec, J. F., G. D. Pickford, G. Stewart. 1937. Effects of the 1934 drought on Upper Snake River Plains, Idaho. Ecology 18:490-505.

Pennington R. T., Prado, D.E., and Pendry, C.A. 2000. Neotropical seasonally dry forests and Quaternary vegetation changes, Journal of Biogeography 27: 261-273.

Pueyo, S. 2006. Diversity: between neutrality and structure. Okios 112: 392-405.

Seefeldt, S. S., and S. D. McCoy. 2003. Measuring Plant Diversity in the Tall Threetip Sagebrush Steppe: Influence of Previous Grazing Management Practices. Environmental Management. 32: 234–245.

Schroeder, M. A., C. L. Aldridge, A. D. Apa, J. R. Bohne, C. E. Braun,S. D. Bunnell, J. W. Connelly, P. A. Deibert, S. C. Gardner, M. A. Hillard, G. D. Kobriger, S. M.

McAdam, C. W. McCarthy, J. J. McCarthy, D. L. Mitchell, E. V. Rickerson, and S. J. Stiver. 2004. Distribution of sage-grouse in North America. The Condor 106: 363–376.

Stegner, W. 1942. Mormon Country. University of Nebraska Press. Lincoln, Nebraska, USA.

Strong, W. L., and L. V. Hills. 2003. Post-Hypsithermal plant disjunctions in western Alberta. Canada Journal of Biogeography 30: 419-430.

Tisdale, E. W., M. Hironaka, and M. A. Fosberg. 1965. An area of pristine vegetation in Crater of the Moon National Monument, Idaho. Ecology 46: 349-352.

Trimble, S. 1989. The Sagebrush Ocean. Univeristy of Nevada Press. Reno, Nevada

Volkov, I., J. R. Banavar, S. P. Hubbell, and A. Maritan. 2003. Neutral theory and relative abundance in ecology. Nature 424: 1035-1037.

Welch, B. L. 2005. Big Sagebrush: A Sea Fragmented into Lakes, Ponds, and Puddles Gen. Tech Rep. RMRS-GTR-144. Fort Collins, CO: USDA

West, N. E. 1983. Great Basin-Colorado Plateau Sagebrush semi-desert. In West N.E., *Ecosystems of the World, Temperate Deserts and Semi-Deserts*; 5. Elsevier Scientific Publishing Company, Amsterdam, Netherlands.

West, N. E. 1983.Western Intermountain Sagebrush Steppe, pp.351-374, in N. E. West, *Ecosystems of the World, Temperate Deserts and Semi-Deserts*; 5. Elsevier Scientific Publishing Company, Amsterdam, Netherlands.

West, N. E., and J. A. Young. 1988. Intermountain Valleys and Lower Mountain Slopes, pp. 257-284, in M. Barbour and D. Billings, *North American Terrestrial Vegetation*. Cambridge University Press, Cambridge United Kingdom.

Whittaker, R. H. 1965. Dominance and diversity in plant communities. Science 147: 250–260.

CHAPTER FOUR

INTRODUCED PLANT DIVERSITY AND ABUNANCE IN SAGEBRUSH STEPPE

Introduction

Invasive species are often regarded as the largest threat to rangeland in the western United States including the State of Montana (Sheley & Petroff 1999). Much of the rangeland in Montana is sagebrush steppe, so understanding the diversity and dynamics of introduced plant species is important. However, the abundance and diversity of introduced plants are rarely considered within the context of native species diversity. For intact vegetation, introduced plants may randomly fluctuate in abundance and diversity in the same manner as do the native species. Concern over the invasiveness of introduced plants as they occur sporadically in native vegetation may be unfounded. Indeed, Elton (1958) is explicit about native plant communities being resistant to invasive plant species. Anderson and Inyoue (2001) reveal that cheatgrass, *Bromus tectorum*, the most feared of invasive species, is unable to invade intact sagebrush steppe in southeastern Idaho, USA. Daehler (2003) reviewed performance studies comparing native and exotic co-occurring populations and found that growth rates of native species nearly always equaled or exceeded those of introduced species. MacDougall and Turkington (2005) call introduced species “passengers” rather than drivers of change in degraded ecosystems.

Objectives

If introduced and native species' populations perform equally in undisturbed vegetation, what controls the relative diversity of natives and exotics in the sagebrush steppe of Montana? The objective is to consider models that do not require a competitive advantage (e.g. Crawley et al. 1999, Davis et al. 2000) for introduced species to establish and persist in a local community, this means that species are not inherently invasive. We have restricted the scope of this question to the sagebrush steppe because of the high degree of native and introduced plant diversity of this biome. Because sagebrush steppe is pervasive throughout western North America, answers to this question might be broadly applicable to invasion biology.

Neutral Ecological Approaches to the Study of Exotic Plant Diversity

Neutral ecological models (e.g., Hubbell 2001; Volkoff et al. 2004; Latimer et al. 2005) are useful for characterizing and quantifying the diversity of species-rich communities, and are theoretically amenable to communities also rich in introduced or exotic species. The theory has not been applied to the abundance and diversity of introduced plants, even though it may help explain the diversity by placing their relative abundance in the context of native diversity and abundance. This is contrary to Chase (2005) who asserts that neutral ecological models will not explain which communities are amenable to invasion because species differences must be considered.

Diversity Relationships of Native and Introduced plants

The relationships between native diversity and suseptibility to invasion has received much attention, but with little consensus (e.g., Brown and Peet 2003, Lonsdale 1999). Two relationships between native and introduced diversity are often cited. The first purports more diverse communities are resistant to invasion, thus resulting in a negative relationship of introduced and native diversity. Elton (1958) suggests more diverse ecological systems should be less prone to invasion. Tilman (1997, 1999) and Naeem (2000) base this relationship on competitive exclusion, where few open niches result in few available resources for the invaders. These studies supporting the negative relationship between introduced and native diversity are often experimental in nature, and involve removal and replacement of relatively few species.

The second reported relationship suggests that an environment supporting a high native diversity will also support greater introduced diversity. Stohlgren (2003, 1999) and Lonsdale (1999) find that more diverse plant communities harbor more introduced plant species. The positive relationship between native and introduced plant diversity is mostly supported by observational studies. Is it possible to find common ground among these contradictory findings from experimental and observational studies? We attempt this by understanding how abundance and diversity of native and introduced plant species in the sagebrush steppe relate.

Immigration of introduced plants into sagebrush steppe

Migration is enhanced by the degree of local mortality in a community, and is essentially the proportion of resident deaths replaced by immigrants from the metacommunity (Hubbell 2001). The number of available propagules has been implicated as important in the invasion of introduced plants (e.g., propagule pressure of Williamson and Fitter 1996, Lambrinos 2006). Another perhaps more important requirement of invasion is disturbance (Rew et al. 2005, Lozon and MacIsaac1997, Ratzlaff and Anderson 1995). Although disturbance often carries many implications (Picket et al. 1989), we define disturbance as a high rate of plant mortality or a high number of simultaneous resident plant deaths. Wholesale plant mortality resulting from a disturbance facilitates immigration by opening space and resources to available propagules, and is very likely not the norm in the sagebrush steppe, where plant mortality occurs at the individual or small patch level and generation times range from one year (annual forbs and grasses) to 50-100 years (sagebrush; Welch 2005). Such individual sporadic plant mortality within the sagebrush steppe doesn't facilitate exotic invasion of plants compared to the extensive plant mortality caused by human-related disturbance.

Results

Temporal Change in Diversity and Abundance

Burke Park Study Site. Sampling the Burke Park plots resulted in a June maximum of 115 species within the quadrats and 134 species within the plots (Table 3.1). Native species comprised 74.7% of the vegetative cover, whereas introduced species comprised 25.3% during June, 2004, which essentially is identical to 73.1% native and 26.9% introduced during June, 2005. Native species comprised 78.8% of the total richness and introduced species 21.2% recorded during June, 2004, which compared to

79.9% native and 20.1% introduced during June, 2005 (Table 4.1). No significant differences were detected either in the change of rank of each species or the number of introduced species per plot between June, 2004, and June, 2005 (Figs. 4.1- 4.2). And any change among the two years for the introduced abundance and richness were mirrored by those of the native species.

Table 4.1. Temporal comparisons in percent vegetative cover and taxa richness of native and introduced for Burke Park.

	June 2004	July 2004	August 2004	June 2005	August 2005
Introduced cover %	25.3	25.7	26.4	26.9	29.1
Native cover %	74.7	74.3	73.6	73.1	70.9
Introduced richness %	21.2	22.7	21.3	20.1	20.9
Native richness %	78.8	77.3	76.6	79.9	79.1

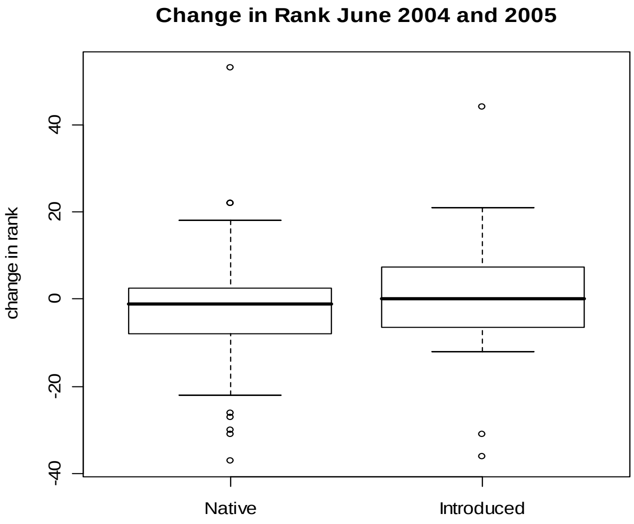

Figure 4.1. Change in rank of introduced and native species from 2004 to 2005 in Burke Park.

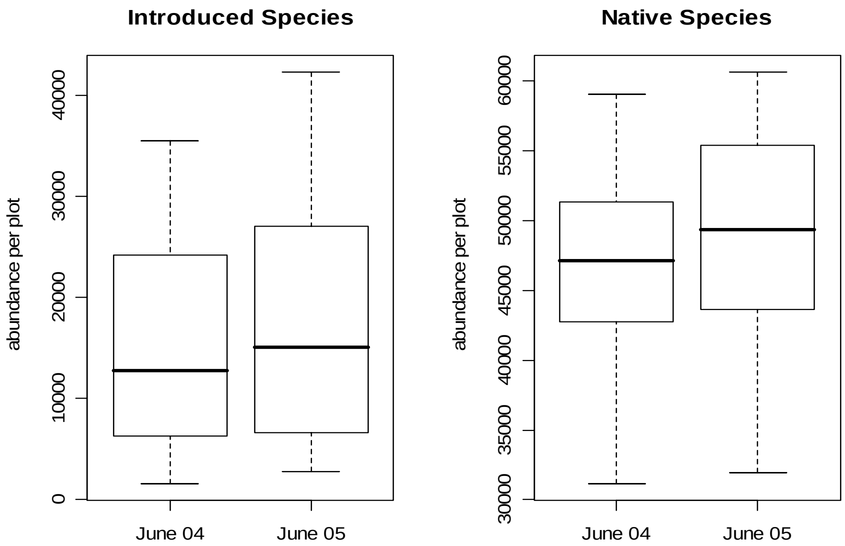

Figure 4.2. Abundance of introduced and native species per plot in June 2004 and June 2005 in Burke Park. Abundance is recorded in cm^2.

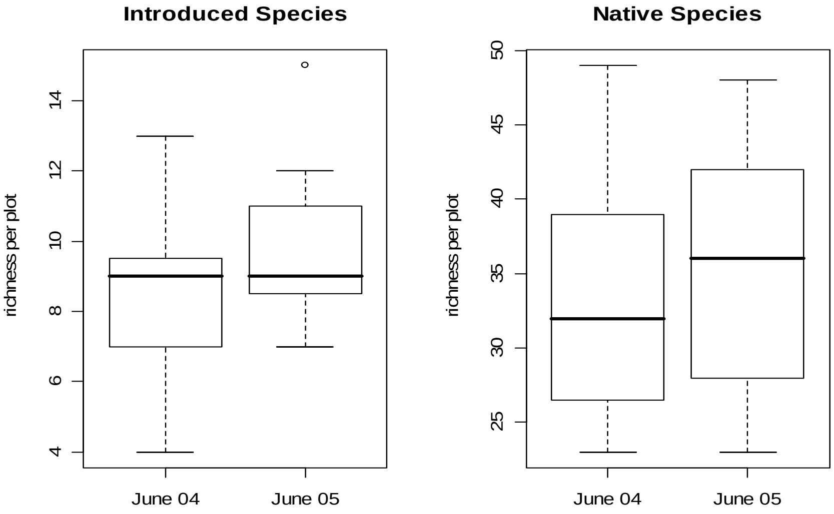

Figure 4.3 Richness of introduced and native species per plot in June 2004 and June 2005 in Burke Park.

CMR study site. During June, 2005, the 24 plots at the CMR study site included 127 recorded species (Table 3.2). Of these, 102 species were recorded within the quadrats. June 2006 was preceded by a moister winter than 2005 and yielded 132 species in plots and 113 species in quadrats. In both seasons 99% of the vegetation cover recorded was native. Of the total richness, the natives comprised approximately 93% of the all species sampled (Table 4.2). No significant relative change in abundance or rank of introduced species was detected between sampling years (Fig. 4.4-4.5). Introduced species mirrored the change in abundance of the native species, which was due to the flush of annual species during the summer of 2006 after a moist winter and spring.

Table 4.2. Temporal comparisons during peak biomass and flowering (June) in percent vegetative cover and taxa richness of native and introduced plant species at the CMR study site.

	June 2005	August 2005	June 2006	August 2006
Introduced cover %	0.9	0.1	1.0	0.1
Native cover %	99.1	99.9	99.0	99.9
Introduced richness %	6.9	3.6	6.5	2.5
Native richness %	93.1	96.4	93.5	97.5

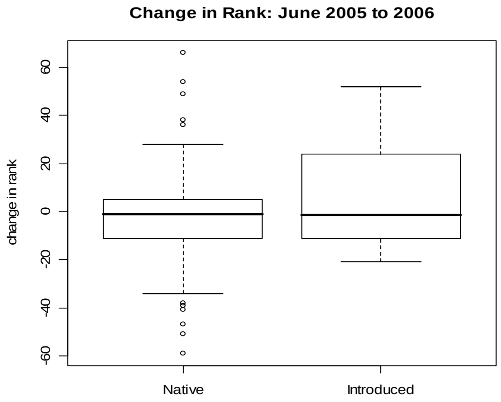

Fig. 4.4. Change in rank of introduced and native species from 2004 to 2005 in CMR study site.

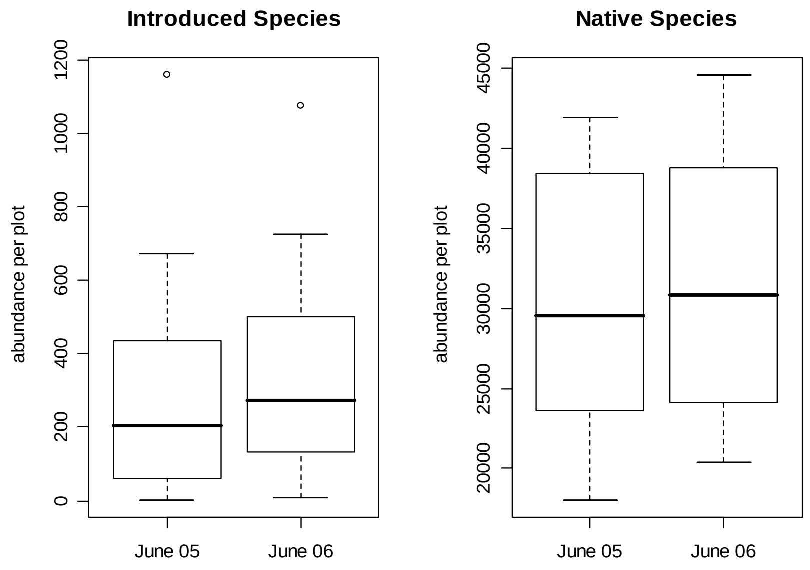

Fig. 4.5. Comparison of introduced and native plant species abundance for June 2005 and 2006 from the CMR study site.

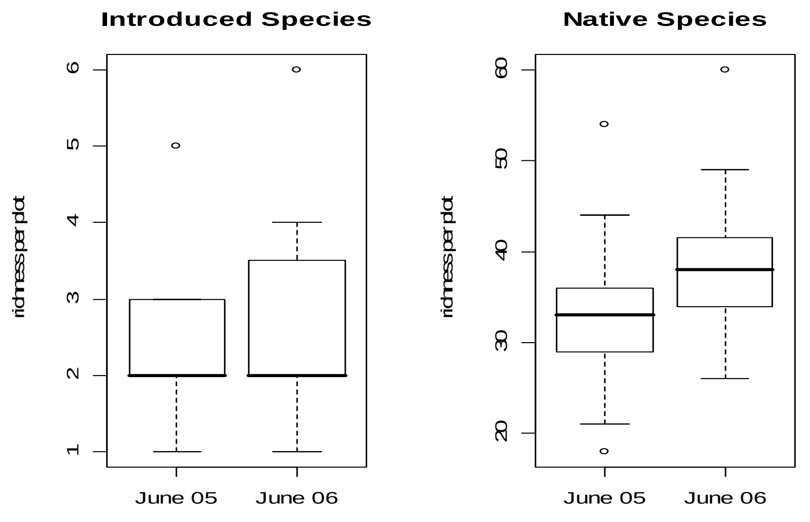

Fig. 4.6. Comparison of introduced and native plant species richness for June 2005 and 2006 from the CMR study site.

Comparing Introduced Plant Species Diversity and Abundance

From the comprehensive floristic list of each of Burke Park (Lavin et al. unpublished; and amended during this study, Appendix B) and the CMR National Wildlife Refuge (Lackchewitz unpublished; and amended during this study, Appendix C), 55 introduced species occurred in Burke Park, and another set of 55 introduced species occurred in the CMR site. During June, 2005, we sampled 27 of the 55 introduced species within the 15 plots at Burke Park (Table 4.3). The remaining introduced species were confined to trailsides and other areas of human disturbance. During June, 2005, we sampled eight introduced species in the 24 plots at the CMR (Table 4.3), revealing that the great majority of introduced species are restricted to roadsides, pastures, and other areas of human disturbance. The number of Category 1 and 2 noxious weed species, as listed by the Montana Department of Agriculture, were collectively few during the sampling of native vegetation during this project (Table 4.4). They were not the most abundant introduced species at Burke Park and were absent from the CMR study site. Burke Park harbors a greater abundance and richness of introduced plant species, as well as noxious weed species. In contrast, the CMR study site contains few introduced plant species, none of which are particularly abundant within the intact sagebrush steppe. Regardless, the CMR study site has a native flora as rich as Burke Park.

Table 4.3. Percent cover and rank of introduced species during June, 2005.

Burke Park			CMR National Wildlife Refuge		
Species	% cover	Rank	Species	% cover	Rank
Poa pratensis	15.61	1	*Taraxacum officinale*	0.7868	15
Bromus inermis	4.12	9	*Melilotus officinalis*	0.1045	33
Bromus japonicus	1.92	12	*Tragopogon dubius*	0.0180	58
Tragopogon dubius	1.14	13	*Bromus japonicus*	0.0039	78
Agropyron cristatum	1.07	15	*Camelina microcarpa*	0.0037	79
Potentilla recta	0.62	25	*Polygonum convolvulus*	0.0007	93
Melilotus officinalis	0.59	26	*Chenopodium album*	0.0004	99
Alyssum alyssoides	0.35	32	*Lactuca serriola*	0.0003	103
Bromus tectorum	0.27	40			
Centaurea maculosa	0.27	41			
Cynoglossum officinale	0.23	45			
Taraxacum officinale	0.15	54			
Phleum pretense	0.12	60			
Lonicera tatarica	0.10	63			
Medicago lupulina	0.10	66			
Cirsium arvense	0.09	68			
Thesium linophyllum	0.08	73			
Medicago sativa	0.04	81			
Lactuca serriola	0.03	85			
Dactylis glomerata	0.005	105			
Melilotus albus	0.005	107			
Camelina microcarpa	0.005	109			
Sisymbrium altissimum	0.003	111			
Descurania sophia	0.002	112			
Thlaspi arvense	0.002	113			
Lepidium campestre	0.000015	122			
Silene latifolia	0.000015	122			

Table 4.4. Category 1 and 2 Noxious Weeds (Montana Deparment of Agriculture) found within plots at both study sites.

Burke Park		CMR National Wildlife Refuge	
Species	Rank	Species	Rank
Potentilla recta	25	None	
Centaurea maculosa	41		
Cynoglossum officinales	45		
Cirsium arvense	68		

Of the introduced species sampled, Burke Park contains many perennial introduced grasses (e.g., *Poa pratensis*, *Bromus inermis*, *Phleum pretense*), early season introduced annuals (e.g., *Bromus japonicus*, *Camelina microcarpa*, *Alyssum alyssoides*), forbs (*Potentilla recta, Centaurea maculosa*) and the shrub *Lonicera tatarica*. These represent all the four growth forms of sagebrush steppe (shrubs, early and late season forbs, and grasses). The CMR study site contains predominantly early season forbs and grasses (e.g., *Bromus japonicus, Camelina microcarpa, Taraxacum officinale*). The longest living introduced species at the CMR site is *Melilotus officinales*, which is a short lived perennial. The most notable difference in the diversity of introduced plants in Burke Park and the CMR is the absence in plots of introduced forage grasses (e.g. *Agropyron cristatum, Poa pratensis, Bromus inermis*) at the CMR site.

Relative Abundance of Introduced Plant Species

The greater richness and abundance of introduced plant species in Burke Park is readily detected in the rank abundance distribution (RAD; Fig. 4.7). The difference in mean rank of introduced and native species in Burke Park is statistically insignificant (Table 4.5). The Relative abundance distribution for Burke Park has a larger spread of introduced species from the most rare to the most abundant. The introduced species in BP could be considered a representative subsample of the RAD curve representing all relative species abundance classes from most abundant to most rare, as the mean rank of the introduced species is insignificantly different from the rank of the natives.

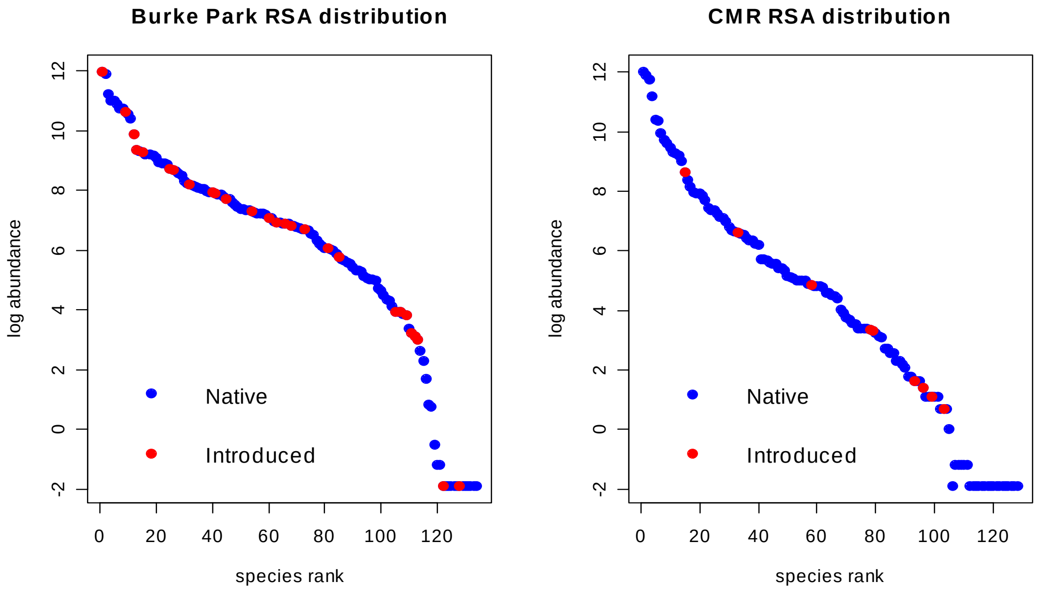

Fig. 4.7. The RAD for Burke Park and CMR study site. Introduced species are in red and native species in blue.

Table 4.5. Analysis of Variance Table

Burke Park, June 2005	CMR study site, June 2005
Response: rank of species in June 05	Response: rank of species in June 05
Predictor: status (Native, Introduced)	Predictor: status (Native, Introduced)
Df=1	Df=1
Sum Sq=3807	Sum Sq= 16247
Mean Sq=3807	Mean Sq=16247
F value=1.9279	F value 11.214
Pr(>F)=0.1664	Pr(>F)=0.0009042
Residuals=1975	Residuals=1449

The CMR study site has fewer introduced species sampled. In contrast to Burke Park, the rank of the introduced species at the CMR differed significantly (alpha<.05) from the natives (Fig. 4.7 Table 4.5). The introduced species were more confined to the rare tail of the CMR study site relative abundance distribution. Burke Park has a somewhat even distribution of cover classes for the introduced species, in contrast to the

CMR study site, in which the cover classes of introduced species are skewed toward the smallest cover class (Figs. 4.8).

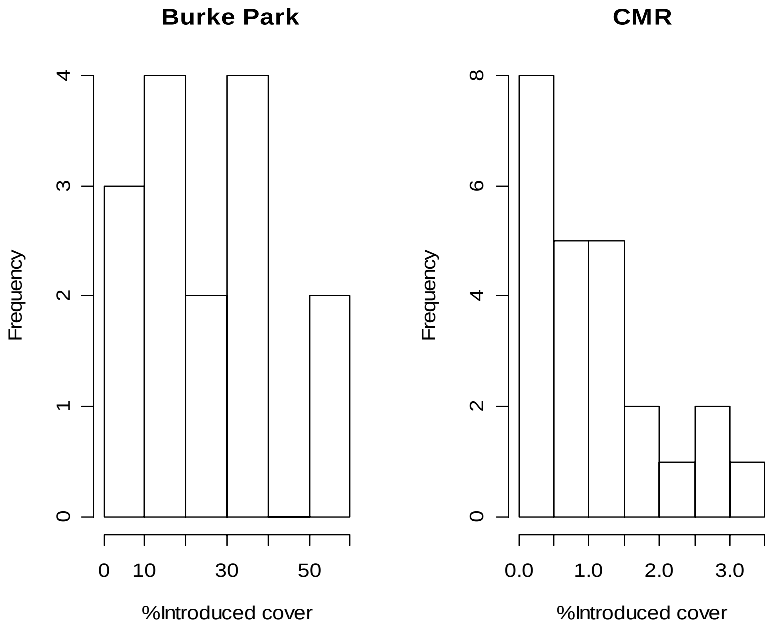

Figure 4.8. Frequency of cover classes for the introduced species between Burke Park and the CMR study site during June, 2005, which underscores the rarity of introduced plant cover in the CMR study site.

Diversity and Invasion. The sampling effort between the Burke Park and CMR study sites was equivalent, which is evidenced by 134 species sampled in the plots at Burke Park and 132 sampled at the CMR study site. Diversity indices also suggest that both study sites are approximately equivalent in species richness (Table 3.4). Fisher's alpha is nearly equivalent between the two study sites underscoring the almost identical amount of diversity among sites. Yet the diffence in the amount of introduced species richness and abundance is substantially different.

Both Burke Park and the CMR area showed significant ($p<.05$) relationships between the amount of cover of introduced species and the cover of native species when data were represented by 15 or 24 plots. Burke Park showed a strong negative relationship, whereas the CMR a positive relationship (Fig. 4.9- 4.10). In 2006 at the CMR site, introduced and native cover are not significantly related at either the quadrat or plot levels (Fig. 4.11). Burke Park retains a significant relationship in June of 2004 and 2005.

The combination of these data sets from both study sites results in an insignificant relationship between introduced and native plant diversity, which suggests diversity per se is not a determinant of invasion. The CMR area has slightly less richness and more bare ground, which might suggest there are more resources available to invading plants. This is clearly not the case, however, especially given that Burke Park with little bare ground harbors a greater richness and abundance of introduced species (Fig. 3.1 and Fig. 4.3).

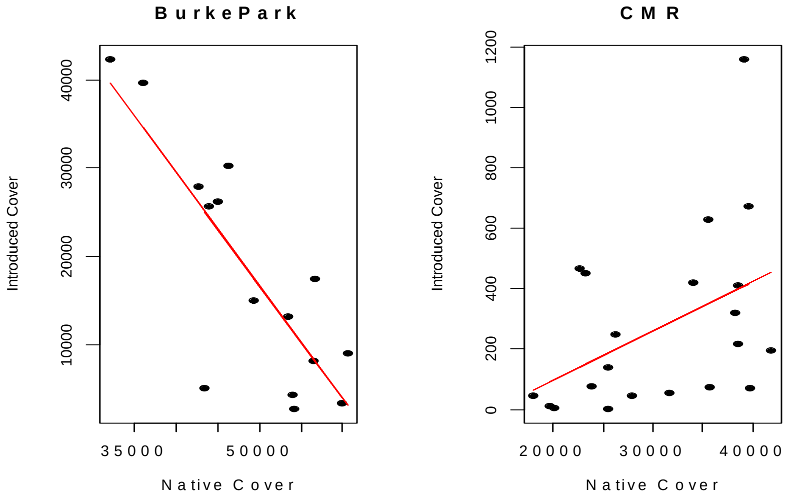

Fig. 4.9. A. Relationships of native and introduced cover at Burke Park in June of 2005. The slope is of the line is -1.074 (p=0.00159), and adjusted R^2=0.5133. B. The relationship of native and introduced cover at the CMR study site in June 2005. The slope of the line is .0148 (p=0.0457), and the adjusted R^2=0.1316.

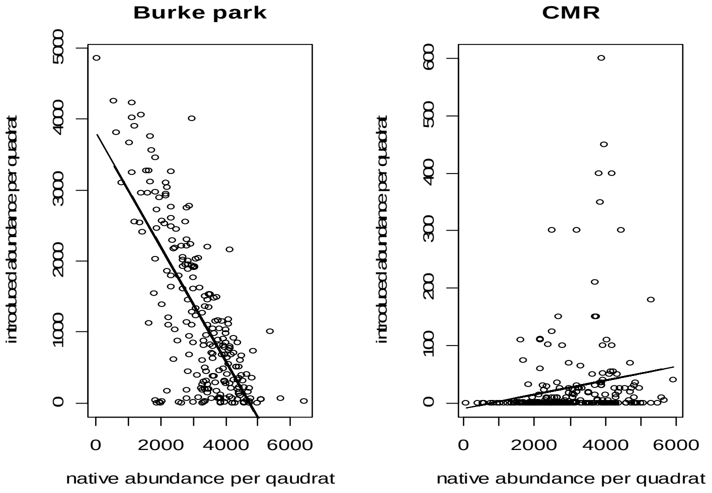

Figure 4.10. A. The relationship between native and introduced cover per quadrat at Burke Park in June, 2005. The slope of the line is 0.80 (p<2 E-16), and the adjusted R^2=0.5497). B. The relationship between native and introduced cover per quadrat at the CMR site in June 2005 (p=0.0056, m=0.012, R^2=.0279)

When data for both study areas are combined, introduced plant cover decreases significantly as a function of distance from disturbance (or source area) such as road- and trail-sides (Fig. 4.11a). Native cover was not affected by an increase in distance from disturbance (Fig. 4.11b), suggesting that native species are as likely to recolonize disturbed areas (e.g., trail and road-sides) as are introduced species. This is predicted given the abundance and richness of natives at both study sties. At all scales, distance from potential introduced plant source should be regarded as a significant predictor of introduced plant abundance within native sagebrush steppe. At the smallest scale (i.e., meters), the abundance and diversity of introduced plants decrease as distance from the source (e.g., disturbed weedy trailside) increases.

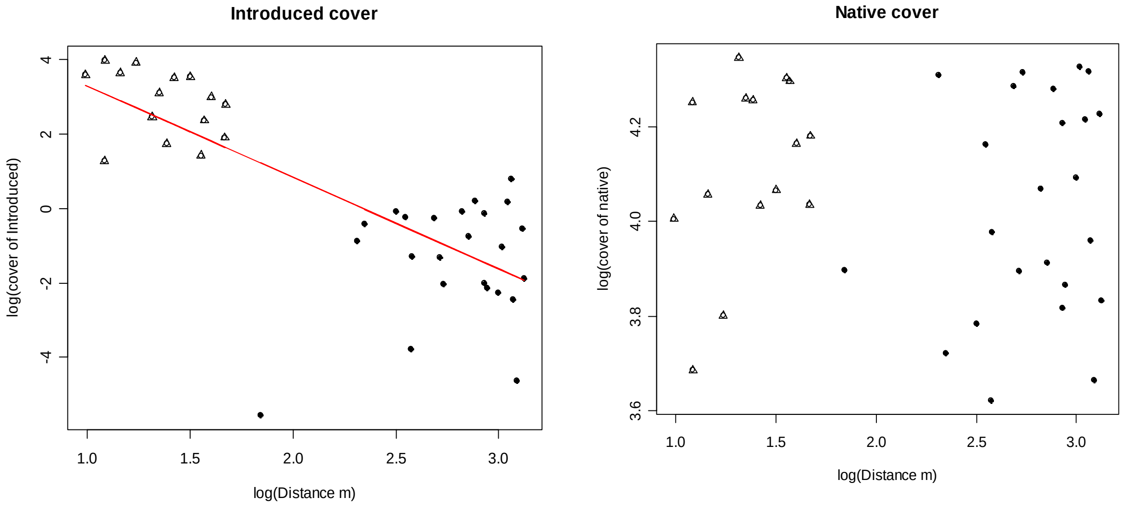

Fig. 4.11. Relationship of distance from source of introduced propagules as represented by the distance from roads or trails. A. Cover of introduced plant species. The slope is -2.45 (p=-4.4 E -8) and adjusted R^2=.0572. B. Cover of native plant species. No significant relationship between native cover and distance from road or trail (p=0.57). Triangles – Burke Park plots; closed circles – CMR plots.

Discussion

Diverstiy and Invasion

The amount of native plant diversity alone is an insignificant predictor of invasion into sagebrush steppe. The negative relationship for Burke Park suggests that diverse communities have reduced invasion potential (e.g., Tilman 1997, Elton 1958). The positive relationship at the CMR study site is consistent with Stohlgren (1999, 2003). The availability of propagules and the extent of resident death are better predictors introduced plant diversity. Human-related disturbance is a major factor of introduced plant spread throughout the sagebrush steppe of the Intermountain West (Rew et al. 2005, Welch 2005), especially the development of roads and trails. Much of the sagebrush steppe of the Intermountain West was subject to large amounts of disturbance, or wholesale (as opposed to individual or patchy) resident plant mortality (Welch 2005). The source-sink relationship is obvious by examining distance from source populations at Burke Park and CMR sites. In countering Stohlgren et al.'s (2003) conclusion that introduced plant diversity is associated with native plant diversity, Rejmanek (2003) found a strong positive relationship of introduced plant diversity with human population density and length of residency. Adding native diversity as a determinant to this model provided no additional predictive power. This suggests that although human population centers may be most dense in regions of high plant diversity (e.g., both more at southern latitudes), human activity no doubt routinely causes wholesale plant mortality and is responsible for an increase in introduced plant diversity and abundance. In terms of human population densities, Burk Park and the CMR area represent the extremes in ranges of population density in the State of Montana. The human population density around Burke Park is 800 people per square mile, whereas the area around the CMR area has 0-2 people per square mile. This explains well the observation of high diversity and abundance of introduced plants in the Burke Park study site in contrast to the CMR area as there is a readily available source from the surrounding altered landscape. Additionally, at Burke Park uncommon introduced species to Montana including *Thesium linophyllum,* captured in the plots and, *Ventenata dubia* present trailside were in the sagebrush steppe. These represent rare recent immigrants introduced into the study site.

No doubt, intact native plant cover (or any plant cover), especially in vegetation where plant mortality is not naturally extensive (e.g., as it is in a riparian or wetland setting as opposed to the sagebrush steppe), can by itself resistant exotic plant invasion. Cleland et al. (2004) reported that richness for native and introduced species is positively correlated, but also found that once introduced immigrants moved into the system, they generally increased or decreased in abundance similar to those of the natives, and that native vegetation generally reduced invasion potential. MacDougall and Turkington (2005) termed these as “passengers” in the system and found that a sufficient source of propagules is needed for introduced plants to establish in native communities.

This alternative invasion model provides a neutral explanation by not referring to species as intrinsically invasive. Invasion control in the sagebrush steppe need only involve prevention of wholesale resident plant death. In contrast to individual or patchy plant mortality that occurs naturally in the sagebrush steppe, extensive plant mortality caused by range improvement projects, plowing rangelands, sagebrush control measures, and overgrazing increases the probability of invasion especially where introduced source populations (e.g., near human population centers) are sufficient to provide propagules. This concurs with the results of the Burke Park study site that the vegetation here has resisted invasion by remaining intact, but the plant diversity at this site is greatly augmented by the surrounding extensive human activity that maintains a high diversity and abundance of introduced species.

Disturbance and Immigration

The 19th and 20th centuries brought large scale disturbance to the intermountain western United States. Tremendous overgrazing occurred on rangelands throughout the sagebrush steppe (Pickford 1932; Welch 2005; West and Young 1988). Overgrazing resulted in large scale plant mortality and a reduction in grazing capacity. To offset this reduction, Federal and State agencies undertook “range improvement” projects to increase forage. Introduced Eurasian forage grasses more tolerant to heavy grazing were planted (Plummer et al. 1955). This includes the first two most abundant introduced species in Burke Park, *Poa pratensis* and *Bromus inermis*, which are consistently some of the most abundant introduced plants in general (Weaver et al. 2001). To plant these Eurasian grasses, vegetation was removed by destructive mechanical protocols such as chaining, railing, and harrowing, with burning considered the most economical means even if it weakened the native grasses and forbs (Pechanec et al. 1954). Following the Second World War herbicide was introduced, and the application of 2-4D was undertaken over large areas with sprayers mounted to jeeps, tractors, and helicopters (Nelson et al. 1960, Carson 1962 pg. 64.). The spraying of 2-4D killed only the dicots, thus removing the shrubs and forbs and altering the physiognomic structure of the sagebrush steppe. This range stewardship resulted in large scale plant mortality and high input of exotic immigrants into the system. In contrast to the deterministic view of introduced plant species as “invaders”, much of the history of the increase in richness and abundance of introduced plant species has involved passive or neutral immigration following human destruction of resident vegetation.

Eurasian and the North American temperate deserts share a high degree of floristic similarity at the family and genus level (West 1983). It is not surprising then that nearly all the North American plant introductions into the sagebrush steppe come from the Eurasian steppe. This ecological equivalence, where species from the Eurasian steppe are “pre-adapted” to the North American steppe, is also part of the neutral perspective of introduced plant abundance and diversity. That a biogeographic asymmetry exists to invasion patterns where particularly Eurasian species invade North America and not so much in the reciprical direction (Loope 2004) could be explained by a simple island biogeographic (a.k.a. neutral) process: Eurasia is simply a huge source area compared to North America.

Conclusion

Native sagebrush steppe vegetation has the ability to resist the invasion of introduced plants, according to our preliminary findings. In spite of Burke Park being completely surrounded by the City of Bozeman and adjacent areas of intense human activity, more than 70% of the cover is native within the sagebrush-dominated sites. Much of the cover of introduced plants in Burke Park is due to one species, *Poa pratensis*, which is rarely considered an invader and which dominates the cultivated landscapes of Bozeman and vicinity.

The sagebrush steppe sites that we have studied show similar amounts of total plant species diversity and, much of the rare plant diversity in Montana occurs in the sagebrush steppe (e.g., Lesica et al. 2006). However, we find that plant diversity alone is a poor predictor of exotic plant invasion. Our findings are consistent with Rejmanek (2003), who posits that human population density and length of residency are the best predictors of introduced plant abundance and diversity. Such a view could benefit weed science. Prevention of wholesale resident death in combination with a reduction of the density of potential exotic immigrants could prevent undesirable invasions of the remaining sagebrush steppe in Montana.

Literature Cited

Anderson, J. E., and R. S. Inouye. 2001. Landscape-scale changes in plant species abundance and biodiversity of a sagebrush steppe over 45 years. Ecological Monographs 71: 531-556.

Brown, R. L., and R. K. Peet. 2003 Diversity and Invasibility of southern Appalachian Plant Communities. Ecology 84: 32-39.

Carson, R. 1962. Silent Spring. The Riverside Press Cambridge Mass. U.S.A.

Chase, J, E. 2005. Towards are really unified neutral theory for metacommunities. Functional Ecology. 19: 182-186.

Cleland, E. E., M. D. Smith, S. J. Andelman, C. Bowles, K. M. Carney, M. C. Horner-Devine, J. M. Drake, S. M. Emery, J.M. Gramling, and D. B. Vandermast. 2004. Invasion in space and time: non-native richness and relative abundance respond to inter annual variation in productivity and diversity. Ecology Letters. 10: 947-957.

Crawley, M. J., S.L. Brown, M. S. Heard, and G. R. Edwards. 1999 Invasion resistance in experimental grassland communities: species richness or species identity. Ecology Letters 2 140:148.

Daehler, C.C. 2003. Performance Comparisons of Co-Occuring Native and Alien Invasive Plants: Implictions for Conservation and Restoration. Annual Review of Ecology Evolution and Systematics. 34: 183-211.

Davis, M. A., J. P. Grime, and K. Thompson. 2000. Fluctuating resources inn plant communities: a general theory of invisibility. Ecology 88: 528-534

Elton, C.S. 1958. The ecology of invasions by plants and animals. Methuen, London, UK

Hubbell, S. P. 2001. Unified Neutral Theory of Biodiversity and Biogeography. Princeton University Press

Lambrinos, J. G. 2006. Spatially variable propagule pressure and herbivory influence invasion of chaparral shrubland by and exotic grass. Oecologia 147:327-334

Larson, D. L. 2003 Native and exotic plants: relationships to disturbance in mixed grass prairie. Plant Ecology 169: 317-333

Latimer, A. M., J. A. Silander, and R.M. Cowling. 2005 Neutral ecological theory reveals isolation and rapid speciation in biodiversity hotspot. Science 309: 1722-1725.

Lesica, P., R. Yurkewycz, and E. Crone. 2006. Rare plants are common when you find them. American Journal of Botany 93: 454-459.

Lonsdale, W. M. 1999. Global patterns of plant invasions and the concept of invasability. Ecology. 80 1522-1536.

Loope, L. 2004. The challenge of effectively addressing the threat of invasive species to the National Park System. Park Science 22: 14-20.

Lozon, J., and H. MacIsaac. 1997. Biological Invasions: are they dependent on disturbance? Environmental Reviews 5: 131-144.

MacDougall, A. S., and R. T. Turkington. 2005. Are invasive species the drivers or passengers of change in degraded ecostystems? Ecology 86: 42-55.

Naeem, S., J. M. H. Knops, and D. Tilman. 2000 Plant diversity increases the resistance to invasion in the absence of covarying extrinsic factors. Okios 91: 97-108.

Nelson, D. W. and V. N. Stokes. 1960. Using Helicopters to Chemically Control Big Sagebrush and Wyethia on the Beaverhead National Forest, 1959. U.S.D.A. Report, Region 1, Missoula, MT.

Pickett, S. T., J. Kolasa, J. J.Armesto, and S. L. Collins. 1989. The ecological concept of disturbance and its expression of at various hierarchical levels. Oikos 54: 129-136

Pechanec, J. F., A. P. Plummer, J. H. Robertson, and A. C. Hull. Sagebrush Control on Rangelands. USDA Handbook 277. Intermountain Forest and Range Experiment Station, USDA Forest Service.

Pickford, G. D. 1932. Influences of continual heavy grazing and promiscuous burning on spring fall range in Utah. Ecology 13: 159-171

Plummer, A. P., A. C. Hull, G. Stewart, and J. H. Robertson. Seeding Rangelands in Utah, Nevada, Southern Idaho, and Western Wyoming. USDA handbook 71. Intermountain Forest and Range Experiment Station, USDA Forest Service.

Ratzlaff, T., and J. Anderson. 1995. Vegetal recovery following wildfire in seeded and unseeded sagebrush steppe. Journal of Range Management 48: 386-391

Rejmanek, M. 2003. The rich get richer- responses. Frontiers in Ecology 1: 122-123

Rew, L. J., B. D. Maxwell, F. L. Dougher, and R. Aspinall. 2006. Searching for a needle in a haystack: evaluating survey methods for non-indigenous plant species. Biological Invasions 8: 523-539

Sheley, R., and J. K. Petroff. 1999. Biology and Management of Noxious Rangeland Weeds. Oregon State Univeisty Press. Corvallis, Oregon.

Stohlgren, T. J., D. Binkley, G. W. Chong, L. D. Kalkhan, K. A. Bull, Y. Otsuki, G. Newmann, M. Bashkin, and Y. Son. 1999. Exotic Plants species invade hot spots of native plant diversity. Ecological Monographs 69: 25-46.

Stohlgren, T. J., D. T. Barnett, and J. T. Kartesz. 2003. The rich get richer: patterns of plant invasions in the United States. Frontiers in Ecology & Environment 1: 11-14

Tilman, D. 1997. Community invisibility: recruitment limitation and grassland biodiversity. Ecology 78: 81-92

Tillman, D. 1999. The ecological consequences of changes in Biodiversity: a search for general principles. Ecology 80: 1455-1474

Weaver, T., D. Gustafson, and J. Lichthardt. 2001. Exotic plants in early and later seral vegetation of fifteen northern Rocky Mountain environments. Western North American Naturalist 61: 417-427.

Welch, B. L. 2005. Big Sagebrush: A Sea Fragmented into Lakes, Ponds, and Puddles Gen. Tech Rep. RMRS-GTR-144. Fort Collins, CO: USDA

West, N. E., and J. A.Young. 1988. Intermountain Valleys and Lower Mountain Slopes. In Barbour & Billings, *North American Terrestrial Vegetation*. Cambridge University Press, Cambridge United Kingdom.

Williamson, M., and A. Fitter. 1996 The varying success of Invaders. Ecology 77: 1661-1666

APPENDICES

APPENDIX A

LOCATION OF PLOTS IN THIS STUDY

Table A1. Location of permanently marked quadrats at the Burke Park study site.

Name includes T1-T15 representing transects, followed by the location of the quadrat in relation to a 50 m transect line, and how many meters left or right of the transect line. All transects run generally north-south and begin on the north end.

Name	UTM coordinate	Elevation
T1-01L4	12 T 497781 5057701	1464.7
T1-06R2	12 T 497771 5057698	1505.8
T1-09L1	12 T 497775 5057694	1503.9
T1-11R4	12 T 497768 5057692	1505.1
T1-11R5	12 T 497767 5057694	1510.3
T1-15L5	12 T 497777 5057687	1500.5
T1-16R1	12 T 497768 5057687	1513.2
T1-17L4	12 T 497777 5057686	1512.3
T1-17R4	12 T 497764 5057688	1514.4
T1-26R3	12 T 497763 5057680	1511.5
T1-27R2	12 T 497763 5057678	1513.0
T1-30R1	12 T 497763 5057676	1512.5
T1-37L3	12 T 497764 5057667	1512.3
T1-41R5	12 T 497753 5057668	1510.6
T1-48L3	12 T 497757 5057659	1508.9
T2-03R4	12 T 497751 5057655	1502.7
T2-05R4	12 T 497749 5057654	1501.2
T2-12L1	12 T 497754 5057647	1507.2
T2-13L3	12 T 497756 5057644	1508.4
T2-14R5	12 T 497747 5057644	1508.7
T2-17R4	12 T 497749 5057641	1508.4
T2-22L1	12 T 497753 5057635	1510.3
T2-26R4	12 T 497746 5057633	1510.3
T2-27R2	12 T 497748 5057631	1507.5
T2-29R2	12 T 497748 5057631	1509.6
T2-33L5	12 T 497753 5057624	1511.1
T2-34R1	12 T 497748 5057624	1510.1
T2-39R2	12 T 497744 5057620	1510.8
T2-49L1	12 T 497746 5057610	1511.3
T2-50L2	12 T 497749 5057607	1511.5
T3-08R5	12 T 497683 5057590	1507.9
T3-09R1	12 T 497686 5057594	1508.4
T3-09R5	12 T 497684 5057592	1508.7

Table A1. Location of permanently marked quadrats at the Burke Park study site.

T3-14R3	12 T 497687 5057592	1505.5
T3-16L5	12 T 497694 5057596	1507.7
T3-19L2	12 T 497696 5057589	1512.0
T3-21R1	12 T 497697 5057585	1509.9
T3-23L1	12 T 497702 5057587	1506.0
T3-24L4	12 T 497702 5057588	1509.6
T3-34L2	12 T 497708 5057583	1508.9
T3-34R1	12 T 497703 5057579	1510.1
T3-37L2	12 T 497711 5057580	1511.5
T3-40L4	12 T 497715 5057577	1512.5
T3-40L5	12 T 497714 5057583	1511.8
T3-47L1	12 T 497715 5057570	1512.3
T3-50L2	12 T 497721 5057570	1512.7
T4-03L1	12 T 497718 5057570	1501.2
T4-09L5	12 T 497726 5057569	1502.4
T4-10R1	12 T 497722 5057560	1500.5
T4-14L2	12 T 497728 5057561	1502.7
T4-18R1	12 T 497728 5057554	1502.2
T4-19R1	12 T 497729 5057554	1503.1
T4-30R2	12 T 497734 5057544	1507.7
T4-31R2	12 T 497734 5057545	1507.9
T4-32R2	12 T 497735 5057543	1503.1
T4-34L5	12 T 497742 5057545	1507.2
T4-36L2	12 T 497742 5057542	1509.4
T4-41L4	12 T 497748 5057540	1505.1
T4-45R2	12 T 497742 5057532	1509.1
T4-47R2	12 T 497740 5057525	1507.5
T4-47R5	12 T 497739 5057526	1507.9
T5-01L5	12 T 497841 5057494	1524.0
T5-02R5	12 T 497830 5057487	1523.8
T5-05L3	12 T 497841 5057488	1523.1
T5-11R1	12 T 497838 5057484	1522.8
T5-13L5	12 T 497844 5057485	1523.3
T5-20L2	12 T 497848 5057476	1524.3
T5-28R1	12 T 497849 5057467	1524.3
T5-37R2	12 T 497853 5057458	1523.8
T5-38L5	12 T 497862 5057464	1523.3
T5-41L3	12 T 497862 5057461	1522.6
T5-41L4	12 T 497862 5057460	1524.5
T5-42R2	12 T 497854 5057456	1521.9
T5-45L4	12 T 497864 5057457	1522.4

Table A1. Location of permanently marked quadrats at the Burke Park study site.

T5-45R2	12 T 497858 5057453	1524.8
T5-49R3	12 T 497859 5057451	1521.6
T6-04R4	12 T 497862 5057443	1515.4
T6-08R5	12 T 497862 5057442	1517.3
T6-12L4	12 T 497874 5057444	1513.7
T6-15R4	12 T 497869 5057435	1513.0
T6-19L3	12 T 497876 5057436	1518.0
T6-20R5	12 T 497868 5057432	1513.7
T6-21R3	12 T 497872 5057430	1517.3
T6-24L4	12 T 497882 5057432	1518.0
T6-30R1	12 T 497878 5057426	1516.1
T6-37L2	12 T 497883 5057421	1517.8
T6-38R3	12 T 497882 5057418	1520.4
T6-43R2	12 T 497885 5057414	1519.7
T6-47R4	12 T 497886 5057410	1519.2
T6-49L3	12 T 497893 5057410	1519.0
T6-50R3	12 T 497889 5057408	1520.4
T7-07R1	12 T 497887 5057402	1516.6
T7-10L1	12 T 497889 5057398	1516.4
T7-10R2	12 T 497885 5057398	1515.4
T7-19L4	12 T 497890 5057388	1515.9
T7-19R2	12 T 497881 5057392	1518.0
T7-21L2	12 T 497885 5057387	1517.3
T7-22R3	12 T 497879 5057390	1516.6
T7-23L4	12 T 497883 5057384	1516.1
T7-27L5	12 T 497886 5057381	1515.9
T7-30L5	12 T 497884 5057379	1515.2
T7-38R4	12 T 497873 5057376	1513.7
T7-39R4	12 T 497874 5057374	1519.0
T7-40L3	12 T 497882 5057373	1517.1
T7-40L4	12 T 497881 5057370	1519.7
T7-42L1	12 T 497875 5057370	1518.0
T8-01L4	12 T 497842 5057336	1524.3
T8-03L5	12 T 497844 5057334	1522.1
T8-06R1	12 T 497838 5057330	1519.7
T8-07R1	12 T 497837 5057329	1522.1
T8-20R1	12 T 497840 5057316	1518.3
T8-21R1	12 T 497841 5057314	1518.3
T8-25R1	12 T 497840 5057312	1519.5
T8-27L4	12 T 497848 5057311	1520.9
T8-32L5	12 T 497849 5057306	1520.9

Table A1. Location of permanently marked quadrats at the Burke Park study site.

T8-35L1	12 T 497846 5057302	1517.8
T8-35L3	12 T 497848 5057303	1522.4
T8-37R4	12 T 497838 5057301	1521.9
T8-40R1	12 T 497842 5057296	1522.4
T8-45R3	12 T 497844 5057292	1520.0
T8-49R1	12 T 497845 5057289	1520.4
T9-02R4	12 T 497893 5057292	1525.2
T9-07R3	12 T 497894 5057287	1523.8
T9-08R2	12 T 497894 5057285	1523.8
T9-11R3	12 T 497899 5057282	1522.6
T9-22R4	12 T 497890 5057274	1523.8
T9-23L1	12 T 497898 5057271	1524.5
T9-27L2	12 T 497898 5057268	1524.0
T9-28R5	12 T 497888 5057268	1524.8
T9-29R1	12 T 497895 5057263	1523.1
T9-31R2	12 T 497893 5057264	1523.6
T9-37L1	12 T 497896 5057259	1521.2
T9-39R1	12 T 497893 5057256	1522.4
T9-45R1	12 T 497891 5057251	1523.3
T9-48L1	12 T 497894 5057248	1521.9
T9-48R1	12 T 497892 5057247	1523.1
T10-05R2	12 T 497892 5057242	1517.1
T10-06R4	12 T 497896 5057241	1514.0
T10-08R4	12 T 497887 5057240	1517.3
T10-16R3	12 T 497889 5057230	1516.1
T10-16R5	12 T 497897 5057230	1517.6
T10-23L2	12 T 497894 5057222	1515.2
T10-25R1	12 T 497891 5057219	1517.6
T10-28L1	12 T 497897 5057217	1521.4
T10-32R3	12 T 497890 5057216	1521.2
T10-35L4	12 T 497898 5057211	1522.1
T10-37R4	12 T 497889 5057210	1519.2
T10-43R3	12 T 497888 5057202	1518.8
T10-44L3	12 T 497894 5057199	1518.3
T10-44R3	12 T 497887 5057200	1521.4
T10-45R4	12 T 497887 5057200	1520.4
T11-06L3	12 T 497859 5056713	1529.6
T11-08R4	12 T 497855 5056714	1531.7
T11-17R1	12 T 497857 5056705	1535.3
T11-17R5	12 T 497852 5056705	1533.4
T11-25R1	12 T 497857 5056696	1545.9

Table A1. Location of permanently marked quadrats at the Burke Park study site.

T11-26L1	12 T 497859 5056696	1547.6
T11-27L3	12 T 497860 5056696	1534.6
T11-30R5	12 T 497854 5056696	1535.3
T11-32R2	12 T 497858 5056691	1539.4
T11-35R2	12 T 497856 5056686	1539.7
T11-35R3	12 T 497855 5056687	1538.2
T11-37L4	12 T 497863 5056684	1537.5
T11-41R1	12 T 497858 5056681	1538.5
T11-42R3	12 T 497854 5056680	1540.4
T11-44R2	12 T 497857 5056678	1538.9
T12-06L1	12 T 497862 5056667	1540.6
T12-08L3	12 T 497866 5056665	1540.6
T12-11L4	12 T 497865 5056662	1539.4
T12-15R2	12 T 497859 5056656	1535.6
T12-18L4	12 T 497867 5056655	1539.4
T12-19L1	12 T 497864 5056653	1538.9
T12-21R1	12 T 497861 5056651	1536.5
T12-23L2	12 T 497864 5056646	1537.5
T12-24L2	12 T 497863 5056650	1538.0
T12-26R2	12 T 497861 5056646	1539.4
T12-31L2	12 T 497867 5056642	1539.9
T12-35L1	12 T 497867 5056636	1540.1
T12-36R4	12 T 497861 5056638	1538.2
T12-39L3	12 T 497868 5056635	1541.1
T12-48L1	12 T 497869 5056629	1541.8
T13-01R5	12 T 497883 5056533	1546.9
T13-05L3	12 T 497891 5056526	1548.3
T13-06R2	12 T 497886 5056529	1548.8
T13-12R1	12 T 497883 5056525	1548.3
T13-14R3	12 T 497880 5056525	1549.5
T13-15L4	12 T 497883 5056518	1546.9
T13-18R3	12 T 497878 5056523	1550.5
T13-20R1	12 T 497877 5056519	1551.4
T13-33L2	12 T 497871 5056510	1550.2
T13-36R4	12 T 497864 5056513	1548.3
T13-39L3	12 T 497866 5056504	1549.3
T13-40L1	12 T 497865 5056502	1549.5
T13-40R1	12 T 497864 5056506	1547.6
T13-41L5	12 T 497867 5056504	1549.8
T13-44R2	12 T 497860 5056506	1549.0
T14-05R4	12 T 497831 5056407	1534.1

Table A1. Location of permanently marked quadrats at the Burke Park study site.

T14-06R1	12 T 497830 5056404	1534.1
T14-08L4	12 T 497832 5056397	1535.8
T14-12R1	12 T 497825 5056398	1535.6
T14-17R3	12 T 497820 5056399	1533.7
T14-20R5	12 T 497815 5056401	1534.9
T14-21L1	12 T 497819 5056394	1538.2
T14-21L3	12 T 497820 5056392	1537.5
T14-30L1	12 T 497812 5056388	1537.7
T14-32L3	12 T 497811 5056386	1536.5
T14-44R2	12 T 497800 5056385	1535.8
T14-45R4	12 T 497796 5056385	1534.6
T14-46R1	12 T 497798 5056382	1535.1
T14-47L4	12 T 497800 5056376	1531.0
T14-48L3	12 T 497798 5056377	1532.2
T15-02R1	12 T 497791 5056378	1537.0
T15-09L3	12 T 497782 5056371	1537.3
T15-14R1	12 T 497777 5056375	1532.9
T15-15L5	12 T 497780 5056369	1534.6
T15-17R5	12 T 497775 5056377	1531.5
T15-18L5	12 T 497776 5056368	1534.1
T15-21R2	12 T 497775 5056375	1531.0
T15-21R4	12 T 497773 5056377	1530.8
T15-23L5	12 T 497774 5056367	1531.3
T15-26R3	12 T 497769 5056373	1529.1
T15-30L5	12 T 497769 5056364	1530.8
T15-32R3	12 T 497766 5056375	1528.9
T15-35L3	12 T 497762 5056365	1528.9
T15-43R4	12 T 497754 5056371	1525.2
T15-49R4	12 T 497748 5056370	1523.3

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

Name C01-C24 refers to transects followed by meters in references to the 50 m transect and how many meters left or right of the transect line. Additionally the endpoints of the transect lines (1-24) are marked with north, south, east, and west. All east-west transects begin on the east end. North-South transects C01-C08 start on the north end. North-South transects C17-C24 start on the south end.

C0108R1	13 T 299778 5292507	822.0 m
C0109R3	13 T 299778 5292518	819.6 m
C0114L4	13 T 299783 5292511	787.9 m
C0117L2	13 T 299782 5292506	788.9 m
C0122L2	13 T 299782 5292508	789.6 m
C0122R3	13 T 299777 5292507	791.5 m
C0128L1	13 T 299780 5292500	797.1 m
C0132L1	13 T 299779 5292496	797.1 m
C0137R2	13 T 299775 5292490	788.4 m
C0150L4	13 T 299780 5292479	785.8 m
C01N	13 T 299782 5292527	861.2 m
C01S	13 T 299775 5292478	857.4 m
C0204R5	13 T 299567 5292152	812.7 m
C0213R5	13 T 299567 5292143	812.7 m
C0217R1	13 T 299574 5292139	798.5 m
C0221R5	13 T 299568 5292135	811.5 m
C0222R5	13 T 299570 5292129	811.0 m
C0223L3	13 T 299575 5292133	784.6 m
C0224L1	13 T 299576 5292130	811.2 m
C0226L3	13 T 299577 5292128	766.8 m
C0232R4	13 T 299569 5292123	802.6 m
C0233L5	13 T 299580 5292113	797.3 m
C02N	13 T 299572 5292156	813.6 m
C02S	13 T 299575 5292104	799.9 m
C0307L2	13 T 299442 5291617	783.4 m
C0312R5	13 T 299431 5291614	786.7 m
C0316R3	13 T 299433 5291612	787.0 m
C0316R4	13 T 299427 5291605	780.0 m
C0318L4	13 T 299441 5291607	780.7 m
C0321L2	13 T 299438 5291604	784.3 m
C0326L4	13 T 299439 5291599	776.1 m
C0332L3	13 T 299434 5291593	787.2 m
C0340L4	13 T 299434 5291586	782.6 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C0345L4	13 T 299432 5291581	783.4 m
C03N	13 T 299443 5291627	786.2 m
C03S	13 T 299426 5291577	781.7 m
C0407R3	13 T 299399 5291384	778.3 m
C0410R4	13 T 299398 5291382	776.9 m
C0413L3	13 T 299405 5291376	767.5 m
C0422R2	13 T 299396 5291370	775.4 m
C0423L5	13 T 299405 5291368	777.3 m
C0430R5	13 T 299391 5291362	774.5 m
C0431L1	13 T 299399 5291363	773.5 m
C0434R4	13 T 299390 5291360	776.1 m
C0440L4	13 T 299397 5291348	776.6 m
C04N	13 T 299406 5291391	776.9 m
C04S	13 T 299391 5291342	778.3 m
C0502R4	13 T 299225 5290599	769.9 m
C0513R2	13 T 299222 5290586	770.4 m
C0515R3	13 T 299220 5290586	769.9 m
C0516R5	13 T 299217 5290584	770.1 m
C0524R5	13 T 299215 5290580	770.9 m
C0526L4	13 T 299225 5290574	770.6 m
C0529R1	13 T 299216 5290575	768.2 m
C0531R5	13 T 299213 5290574	770.1 m
C0538R2	13 T 299214 5290566	770.1 m
C0542R1	13 T 299214 5290561	767.7 m
C05N	13 T 299225 5290596	769.9 m
C05S	13 T 299212 5290553	768.7 m
C0606R2	13 T 299033 5289716	769.4 m
C0607L4	13 T 299042 5289715	769.9 m
C0613R3	13 T 299032 5289712	768.5 m
C0630L4	13 T 299034 5289692	768.2 m
C0630L5	13 T 299035 5289693	768.5 m
C0632L4	13 T 299032 5289693	767.5 m
C0635R4	13 T 299024 5289691	768.0 m
C0641L4	13 T 299033 5289683	765.8 m
C0642R3	13 T 299022 5289685	767.5 m
C0644L1	13 T 299023 5289681	767.5 m
C06N	13 T 299043 5289725	771.1 m
C06S	13 T 299023 5289679	766.3 m
C0702L1	13 T 298952 5289453	768.7 m
C0707L1	13 T 298952 5289450	767.5 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C0718R4	13 T 298939 5289446	768.0 m
C0726R3	13 T 298933 5289438	771.1 m
C0727R4	13 T 298936 5289427	770.1 m
C0728R5	13 T 298930 5289435	769.7 m
C0730L4	13 T 298937 5289431	772.8 m
C0740L1	13 T 298930 5289425	771.1 m
C0747L5	13 T 298928 5289412	769.7 m
C07N	13 T 298952 5289455	773.3 m
C07S	13 T 298919 5289419	771.6 m
C0802L5	13 T 298697 5289235	780.0 m
C0805R5	13 T 298683 5289234	779.3 m
C0809L4	13 T 298692 5289228	780.2 m
C0814L2	13 T 298689 5289223	781.2 m
C0823L5	13 T 298690 5289215	782.9 m
C0824R2	13 T 298678 5289216	780.7 m
C0837R5	13 T 298674 5289205	782.4 m
C0838R3	13 T 298681 5289198	780.7 m
C0841R4	13 T 298671 5289202	781.2 m
C0849L3	13 T 298680 5289188	782.6 m
C08N	13 T 298688 5289235	781.0 m
C08S	13 T 298675 5289192	781.0 m
C0901R2	13 T 297419 5288279	805.7 m
C0902R2	13 T 297418 5288279	804.3 m
C0906L3	13 T 297410 5288276	804.5 m
C0908R1	13 T 297409 5288282	804.0 m
C0920L2	13 T 297402 5288278	804.5 m
C0929L2	13 T 297393 5288279	799.0 m
C0936R5	13 T 297387 5288289	801.1 m
C0942R3	13 T 297378 5288290	802.3 m
C0942R4	13 T 297380 5288294	800.4 m
C0946R2	13 T 297374 5288292	800.4 m
C09E	13 T 297420 5288276	805.5 m
C09W	13 T 297371 5288286	804.5 m
C1005L4	13 T 297146 5288305	793.4 m
C1010R3	13 T 297142 5288314	793.4 m
C1017R3	13 T 297134 5288315	793.0 m
C1019R3	13 T 297133 5288315	793.4 m
C1037L2	13 T 297113 5288309	794.9 m
C1040L5	13 T 297109 5288304	795.4 m
C1043R3	13 T 297107 5288314	793.9 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C1048R2	13 T 297104 5288313	793.0 m
C1049L4	13 T 297101 5288306	784.1 m
C1049R1	13 T 297102 5288314	794.6 m
C10E	13 T 297152 5288311	791.8 m
C10W	13 T 297102 5288312	791.5 m
C1105L4	13 T 296714 5288783	776.4 m
C1110R3	13 T 296709 5288794	782.9 m
C1112R4	13 T 296709 5288799	779.5 m
C1114L3	13 T 296704 5288788	777.8 m
C1114R2	13 T 296700 5288787	782.9 m
C1120R4	13 T 296698 5288794	783.8 m
C1130L5	13 T 296686 5288785	783.1 m
C1135L2	13 T 296682 5288789	785.3 m
C1140L5	13 T 296680 5288784	787.2 m
C1143R4	13 T 296676 5288798	786.7 m
C11E	13 T 296717 5288787	784.1 m
C11W	13 T 296670 5288793	786.2 m
C1204L4	13 T 295471 5289116	789.6 m
C1205R1	13 T 295471 5289122	789.4 m
C1207L4	13 T 295470 5289118	788.6 m
C1215R4	13 T 295460 5289130	788.2 m
C1219L5	13 T 295459 5289115	788.4 m
C1222L3	13 T 295456 5289116	789.8 m
C1223R5	13 T 295453 5289125	790.1 m
C1224R4	13 T 295451 5289126	788.2 m
C1235R2	13 T 295442 5289120	790.1 m
C1240L2	13 T 295437 5289110	790.3 m
C12E	13 T 295476 5289122	790.6 m
C12W	13 T 295427 5289114	792.7 m
C1303L4	13 T 294730 5289184	761.7 m
C1303R3	13 T 294729 5289194	761.2 m
C1307R4	13 T 294727 5289196	762.9 m
C1309L3	13 T 294723 5289183	763.4 m
C1318R5	13 T 294717 5289198	763.4 m
C1326L3	13 T 294709 5289184	761.0 m
C1327L3	13 T 294706 5289188	763.9 m
C1334L5	13 T 294702 5289182	762.0 m
C1338R2	13 T 294699 5289190	761.0 m
C1342R5	13 T 294694 5289196	760.5 m
C13E	13 T 294729 5289191	760.0 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C13W	13 T 294683 5289188	762.4 m
C1402L2	13 T 294298 5289177	755.5 m
C1415L5	13 T 294287 5289171	753.8 m
C1416L5	13 T 294287 5289170	754.0 m
C1419R3	13 T 294283 5289183	752.6 m
C1421L5	13 T 294280 5289172	753.8 m
C1423R2	13 T 294279 5289182	754.5 m
C1436R3	13 T 294266 5289184	753.3 m
C1439R2	13 T 294265 5289191	756.0 m
C1439R4	13 T 294261 5289185	754.5 m
C1440L2	13 T 294263 5289175	752.1 m
C14E	13 T 294300 5289179	759.3 m
C14W	13 T 294247 5289174	756.2 m
C1501L1	13 T 294190 5288413	784.1 m
C1501L5	13 T 294192 5288406	783.4 m
C1503L4	13 T 294189 5288408	783.8 m
C1503R2	13 T 294189 5288416	784.8 m
C1508L4	13 T 294184 5288411	783.8 m
C1514L3	13 T 294178 5288409	783.1 m
C1515R1	13 T 294175 5288413	782.6 m
C1533L1	13 T 294157 5288406	783.1 m
C1534L3	13 T 294159 5288405	783.8 m
C1542R3	13 T 294151 5288412	777.1 m
C15E	13 T 294186 5288413	786.5 m
C15W	13 T 294143 5288406	785.5 m
C1605L2	13 T 294022 5288367	778.5 m
C1608R2	13 T 294015 5288373	780.7 m
C1609L5	13 T 294016 5288363	781.4 m
C1623L3	13 T 294001 5288367	781.4 m
C1627L2	13 T 293996 5288369	780.5 m
C1641L1	13 T 293981 5288367	779.3 m
C1642L2	13 T 293981 5288366	777.6 m
C1645R1	13 T 293982 5288374	776.4 m
C1646L2	13 T 293977 5288371	781.9 m
C1646R1	13 T 293976 5288372	780.5 m
C16E	13 T 294030 5288369	782.4 m
C16W	13 T 293973 5288367	782.2 m
C1702L2	13 T 300091 5293487	801.6 m
C1705R1	13 T 300097 5293487	805.7 m
C1710L4	13 T 300089 5293491	805.5 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C1714R2	13 T 300098 5293493	805.2 m
C1716R3	13 T 300101 5293497	804.0 m
C1716R4	13 T 300099 5293496	805.0 m
C1724R2	13 T 300098 5293506	805.2 m
C1734R2	13 T 300100 5293516	804.5 m
C1745R5	13 T 300106 5293527	805.5 m
C1750L1	13 T 300095 5293533	803.5 m
C17N	13 T 300096 5293531	805.5 m
C17S	13 T 300096 5293484	814.1 m
C1815R2	13 T 299897 5293961	824.7 m
C1819L2	13 T 299899 5293963	823.2 m
C1829R2	13 T 299898 5293973	821.1 m
C1833L4	13 T 299891 5293976	822.8 m
C1836L2	13 T 299890 5293976	823.7 m
C1846R5	13 T 299902 5293990	824.2 m
C1847L2	13 T 299894 5293990	825.9 m
C1850L3	13 T 299892 5293992	825.9 m
C1850L5	13 T 299890 5293993	826.6 m
C18N	13 T 299897 5293997	822.5 m
C18S	13 T 299894 5293944	825.4 m
C1902R1	13 T 299634 5294315	834.1 m
C1906R3	13 T 299621 5294312	832.1 m
C1917R2	13 T 299614 5294322	832.4 m
C1920L2	13 T 299610 5294322	833.1 m
C1927R4	13 T 299618 5294330	833.1 m
C1929L3	13 T 299606 5294330	832.9 m
C1937R2	13 T 299611 5294342	832.9 m
C1939L1	13 T 299607 5294342	832.1 m
C1946R2	13 T 299611 5294348	833.3 m
C1950L1	13 T 299608 5294349	833.1 m
C19N	13 T 299608 5294351	830.0 m
C19S	13 T 299615 5294304	835.3 m
C2002L5	13 T 301132 5292579	823.7 m
C2003L1	13 T 301136 5292579	825.7 m
C2007L3	13 T 301133 5292583	824.7 m
C2014L4	13 T 301132 5292590	824.2 m
C2016R3	13 T 301142 5292593	823.7 m
C2017L5	13 T 301131 5292593	820.8 m
C2018L5	13 T 301132 5292593	824.2 m
C2021R4	13 T 301142 5292599	825.4 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C2038R3	13 T 301140 5292616	824.5 m
C2039L1	13 T 301134 5292622	823.5 m
C20N	13 T 301131 5292625	827.3 m
C20S	13 T 301137 5292576	825.7 m
C2103L4	13 T 301373 5291944	823.2 m
C2109L2	13 T 301375 5291947	822.8 m
C2113L5	13 T 301368 5291950	822.3 m
C2123L2	13 T 301369 5291964	821.6 m
C2125R1	13 T 301377 5291967	822.5 m
C2130L4	13 T 301368 5291966	822.3 m
C2133L2	13 T 301369 5291973	819.4 m
C2144L2	13 T 301366 5291982	818.7 m
C2145R3	13 T 301372 5291984	819.2 m
C2150R1	13 T 301371 5291988	818.4 m
C21N	13 T 301365 5291988	822.0 m
C21S	13 T 301380 5291941	822.0 m
C2204L4	13 T 299993 5287440	803.8 m
C2204R4	13 T 299997 5287441	804.0 m
C2210R2	13 T 300000 5287447	802.3 m
C2214R1	13 T 300000 5287448	805.2 m
C2220L4	13 T 299995 5287458	801.1 m
C2222R3	13 T 300006 5287457	803.1 m
C2225L5	13 T 299993 5287460	803.1 m
C2225R4	13 T 300006 5287458	802.3 m
C2241R4	13 T 300013 5287461	800.9 m
C2243L3	13 T 300005 5287477	802.3 m
C22N	13 T 300006 5287477	802.1 m
C22S	13 T 300000 5287436	804.0 m
C2314L3	13 T 300095 5286988	818.4 m
C2321R5	13 T 300093 5286984	819.4 m
C2323L1	13 T 300086 5286987	818.2 m
C2326L1	13 T 300084 5286989	814.8 m
C2332R4	13 T 300093 5286993	817.5 m
C2335L5	13 T 300082 5287003	815.6 m
C2347L4	13 T 300085 5287013	814.4 m
C2348L4	13 T 300085 5287012	814.1 m
C2349L1	13 T 300089 5287013	814.4 m
C2350R2	13 T 300093 5287013	812.4 m
C23N	13 T 300095 5287007	817.7 m
C23S	13 T 300095 5286963	819.4 m

Table A2. Location of permanently marked plots and qudrats at the CMR study site.

C2407L3	13 T 300288 5286465	824.0 m
C2409R1	13 T 300298 5286469	820.1 m
C2411R2	13 T 300296 5286468	821.1 m
C2411R3	13 T 300295 5286466	818.7 m
C2424R1	13 T 300294 5286479	818.4 m
C2435R3	13 T 300295 5286490	819.9 m
C2446R2	13 T 300295 5286500	815.3 m
C2447L4	13 T 300286 5286500	816.8 m
C2448L4	13 T 300287 5286502	816.0 m
C2450L2	13 T 300288 5286505	816.0 m
C24N	13 T 300290 5286502	821.3 m
C24S	13 T 300295 5286458	823.7 m

Table A3. Location of transects at the Porcupine study site. Neither transects or quadrats were permanently marked. Name contains the transect number followed by the north and south endpoints.

Name	Location	Elevation
PC03N	12 T 481118 5008244	1945 m
PC03S	12 T 481097 5008207	1938 m
PC04N	12 T 481096 5008204	1935 m
PC04S	12 T 481094 5008155	1931 m
PC05N	12 T 481096 5008150	1929 m
PC05S	12 T 481103 5008105	1919 m
PC06N	12 T 481725 5008641	1996 m
PC06S	12 T 481687 5008605	1990 m
PC07N	12 T 481687 5008601	1994 m
PC07S	12 T 481656 5008563	1990 m
PC08N	12 T 481654 5008561	1989 m
PC08S	12 T 481625 5008521	1914 m
PC09N	12 T 481623 5008521	1914 m
PC09S	12 T 481600 5008481	1972 m
PC10N	12 T 481722 5008496	1993 m
PC10S	12 T 481693 5008451	1987 m
PC11N	12 T 481758 5008537	1995 m
PC11S	12 T 481735 5008500	1990 m
PC12N	12 T 481721 5008469	1983 m
PC12S	12 T 481707 5008420	1975 m
PC13N	12 T 482006 5008317	1991 m
PC13S	12 T 481969 5008286	1988 m
PC14N	12 T 481969 5008277	1982 m
PC14S	12 T 481924 5008246	1978 m
PC15N	12 T 481925 5008243	1979 m
PC15S	12 T 481890 5008206	1974 m
PC16N	12 T 481889 5008203	1983 m
PC16S	12 T 481867 5008159	1978 m
PC17N	12 T 482252 5008225	2014 m
PC17S	12 T 482215 5008193	2007 m
PC18N	12 T 482186 5008181	2001 m
PC18S	12 T 482144 5008158	1998 m
PC19N	12 T 482093 5008088	1991 m
PC19S	12 T 482061 5008051	1985 m
PC20N	12 T 481984 5007970	1975 m
PC20S	12 T 481955 5007940	1967 m
PC21N	12 T 481956 5007759	1937 m

Table A3. Location of transects at the Porcupine study site.

PC21S	12 T 481945 5007714	1926 m
PC22N	12 T 481278 5008963	1926 m
PC22S	12 T 481274 5008914	1922 m
PC23N	12 T 481266 5009050	1928 m
PC23S	12 T 481274 5009002	1927 m

APPENDIX B

LIST OF SPECIES FROM BURKE PARK STUDY SITE

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Achillea_millefolium	F	1	N
Agoseris_glauca	F	1	N
Agropyron_albicans	G	1	N
Agropyron_cristatum	G	1	I
Agropyron_dasystachyum	G	1	N
Agropyron_intermedium	G	0	I
Agropyron_repens	G	0	I
Agropyron_spicatum	G	1	N
Allium_cernuum	F	1	N
Allium_textile	F	1	N
Alopecurus_pratensis	G	0	I
Alyssum_alyssoides	F	1	I
Alyssum_desertorum	F	0	I
Amaranthus_albus	F	0	N
Amaranthus_blitoides	F	1	I
Amaranthus_retroflexus	F	1	I
Amelanchier_alnifolia	S	1	N
Androsace_occidentalis	F	1	N
Anemone_multifida	F	1	N
Anemone_patens	F	1	N
Antennaria_microphylla	F	1	N
Antennaria_rosea	F	0	N
Apocynum_androsaemifolium	F	1	N
Arabis_drummondii	F	1	N
Arabis_glabra	F	0	N
Arabis_holboellii	F	1	N
Arabis_nuttallii	F	0	N
Arctium_minus	F	0	I
Arenaria_congesta	F	1	N
Arnica_sororia	F	1	N
Artemisia_campestris	F	1	N
Artemisia_cana	S	1	N
Artemisia_dracunculus	F	0	N
Artemisia_frigida	F	1	N
Artemisia_ludoviciana	F	1	N
Artemisia_tridentata_vaseyana	S	1	N
Asclepias_viridiflora	F	1	N

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Asperugo_procumbens	F	0	I
Aster_ascendens	F	1	N
Aster_falcatus	F	1	N
Aster_hesperius	F	0	N
Astragalus_adsurgens	F	1	N
Astragalus_agrestis	F	1	N
Astragalus_crassicarpus	F	1	N
Astragalus_drummondii	F	1	N
Astragalus_gilviflorus	F	1	N
Astragalus_miser	F	1	N
Atriplex_patula	F	0	N
Balsamorhiza_sagittata	F	1	N
Berteroa_incana	F	0	I
Besseya_wyomingensis	F	1	N
Bromus_carinatus	G	0	N
Bromus_inermis	G	1	I
Bromus_japonicus	G	1	I
Bromus_tectorum	G	1	I
Camelina_microcarpa	F	1	I
Campanula_rotundifolia	F	1	N
Capsella_bursa-pastoris	F	1	I
Caragana_arborescens	S	0	I
Cardaria_draba	F	0	I
Carduus_nutans	F	0	I
Carex_praegracilis	G	0	N
Carex_stenophylla	G	1	N
Centaurea_maculosa	F	1	I
Cerastium_arvense	F	1	N
Chenopodium_watsonii	F	1	N
Cirsium_arvense	F	1	I
Cirsium_undulatum	F	1	N
Cirsium_vulgare	F	0	I
Clematis_hirsutissimus	F	0	N
Clematis_ligusticifolia	V	0	N
Collinsia_parviflora	F	0	N
Collomia_linearis	F	1	N
Commandra_umbellata	F	1	N
Convolvulus_arvensis	F	0	I

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Cotoneaster_lucidus	S	1	N
Crataegus_douglasii	S	0	N
Crepis_occidentalis	F	1	N
Cryptantha_celosioides	F	0	N
Cynoglossum_officinale	F	1	I
Dactylis_glomerata	G	1	I
Danthonia_unispicata	G	1	N
Delphinium_bicolor	F	0	N
Descurania_sophia	F	1	I
Disporum_trachycarpum	F	1	N
Dodecatheon_conjugens	F	0	N
Draba_nemorosa	F	1	N
Echinops_ruthenicus	F	0	I
Elymus_canadensis	G	0	N
Epilobium_angustifolium	F	0	N
Epilobium_paniculatum	F	1	N
Erigeron_caespitosus	F	1	N
Erigeron_pumilus	F	0	N
Erigeron_subtrinervis	F	0	N
Erysimum_asperum	F	1	N
Euphorbia_esula	F	0	I
Festuca_idahoensis	G	1	N
Fritillaria_atropurpurea	F	1	N
Fritillaria_pudica	F	1	N
Gaillardia_aristata	F	1	N
Galium_aparine	F	1	N
Galium_boreale	F	1	N
Gaura_coccinea	F	1	N
Geranium_viscosissimum	F	0	N
Geum_triflorum	F	1	N
Glycyrrhiza_lepidota	F	1	N
Grindelia_squarrosa	F	1	N
Gutierrezia_sarothrae	F	1	N
Hedysarum_boreale	F	0	N
Helianthella_uniflora	F	1	N
Helianthus_annus	F	1	N
Helianthus_rigidus	F	0	N
Heterotheca_villosa	F	1	N

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Hordeum_jubatum	G	0	N
Iris_missouriensis	F	1	N
Juncus_balticus	G	0	N
Juniperus_communis	S	1	N
Juniperus_horizontalis	S	1	N
Juniperus_scopulorum	S	1	N
Kochia_scoparia	F	0	I
Koeleria_macrantha	G	1	N
Lactuca_serriola	F	1	I
Lappula_redowskii	F	0	N
Lepidium_campestre	F	1	I
Liatrus_punctata	F	1	N
Linum_lewisii	F	1	N
Lithospermum_arvense	F	1	N
Lithospermum_ruderale	F	1	N
Lomatium_dissectum	F	0	N
Lomatium_macrocarpum	F	1	N
Lomatium_triternatum	F	1	N
Lonicera_tatarica	S	1	I
Lotus_corniculatus	F	0	I
Lupinus_argenteus	F	1	N
Lupinus_sericeus	F	0	N
Lygodesmia_juncea	F	1	N
Mahonia_repens	F	1	N
Malva_neglecta	F	0	I
Medicago_lupulina	F	1	I
Medicago_sativa	F	1	I
Melica_spectabilis	G	1	N
Melilotus_albus	F	1	I
Melilotus_officinalis	F	1	I
Mertensia_oblongifolia	F	1	N
Microseris_nutans	F	1	N
Microsteris_gracilis	F	1	N
Monarda_fistulosa	F	0	N
Musineon_divaricatum	F	1	N
Oenothera_cespitosa	F	0	N
Orobanche_fasiculata	F	0	N
Orthocarpus_luteus	F	1	N

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Oryzopsis_hymenoides	F	1	N
Oxytropis_besseyi	F	1	N
Oxytropis_lagopus	F	0	N
Oxytropis_sericea	F	0	N
Panicum_capillare	G	1	N
Penstemon_eriantherus	F	1	N
Penstemon_nitidus	F	1	N
Penstemon_procerus	F	1	N
Phacelia_linearis	F	0	N
Phleum_pratense	F	1	I
Phlox_hoodii	F	1	N
Phlox_longifolia	F	1	N
Physocarpus_malvaceus	S	1	N
Pinus_flexilis	S	1	N
Plantago_major	F	0	N
Poa_bulbosa	G	0	I
Poa_compressa	G	1	N
Poa_cusickii	G	1	N
Poa_fendleriana	G	0	N
Poa_pratensis	G	1	I
Poa_secunda	G	1	N
Polygonum_achoreum	F	0	N
Polygonum_aviculare	F	0	I
Polygonum_douglasii	F	1	N
Populus_angustifolius	S	0	N
Potentilla_glandulosa	F	0	N
Potentilla_gracilis	F	0	N
Potentilla_hippiana	F	1	N
Potentilla_recta	F	1	I
Prunus_virginiana	S	1	N
Ranunculus_glaberimus	F	0	N
Rhus_trilobata	S	0	N
Rosa_woodsii	S	1	N
Rumex_crispus	F	0	N
Sedum_stenopetalum	F	1	N
Senecio_canus	F	1	N
Senecio_integerrimus	F	1	N
Silene_latifolia	F	1	I

Table B1. Species recorded in the sagebrush steppe habitat of Burke Park

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Sisymbrium_altissimum	F	1	I
Smilacina_racemosa	F	0	N
Smilacina_stellata	F	0	N
Solanum_dulcamara	v	0	I
Solidago_missouriensis	F	1	N
Solidago_multiradiata	F	1	N
Solidago_rigida	F	1	N
Sphaeralcea_coccinea	F	1	N
Stipa_comata	G	1	N
Stipa_viridula	G	1	N
Symphoricarpos_occidentalis	S	1	N
Syringa_vulgaris	S	0	I
Taraxacum_officinale	F	1	I
Tetradymia_canescens	S	1	N
Thesium_linophyllum	F	1	I
Thlaspi_arvense	F	1	I
Thlaspi_montanum	F	1	N
Townsendia_parryi	F	1	N
Toxicodendron_rydbergii	S	1	N
Tragopogon_dubius	F	1	I
Trifolium_hybridum	F	0	I
Trifolium_pratense	F	1	I
Trifolium_repens	F	0	I
Triteleia_grandiflora	F	0	N
Ventenata_dubia	G	0	I
Verbena_bracteata	F	0	N
Veronica_biloba	F	0	I
Vicia_americana	F	1	N
Viola_nuttallii	F	1	N
Zigadenus_venenosus	F	1	N

APPENDIX C

LIST OF SPECIES FROM THE CMR SAMPLE SITE

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Achillea_millefolium	F	1	N
Agoseris_glauca	F	1	N
Agropyron_cristatum	G	0	I
Agropyron_dasystachyum	G	1	N
Agropyron_intermedium	G	0	I
Agropyron_smithii	G	0	N
Agropyron_spicatum	G	1	N
Agropyron_trachycaulum	G	0	N
Allium_textile	F	1	N
Alyssum_desertorum	F	0	I
Amaranthus_albus	F	0	N
Amaranthus_arenicola	F	0	N
Amaranthus_blitoides	F	0	I
Amaranthus_retroflexus	F	0	I
Andropogon_scoparius	G	1	N
Androsace_occidentalis	F	1	N
Anemone_cylindrica	F	0	N
Anemone_multifilda	F	0	N
Anemone_patens	F	1	N
Antennaria_dimorpha	F	1	N
Antennaria_parvifolia	F	0	N
Antennaria_rosea	F	1	N
Apocynum_cannabinum	F	0	N
Arabis_hirsuta	F	1	N
Arabis_holboellii	F	1	N
Aristida_purpurea	G	1	N
Arnica_sororia	F	1	N
Artemisia_absinthium	F	0	I
Artemisia_campestris	F	0	N
Artemisia_cana	S	1	N
Artemisia_dracunculus	F	0	N
Artemisia_frigida	F	1	N
Artemisia_longifolia	S	1	N
Artemisia_ludoviciana	F	1	N
Artemisia_tridentata_wyomingensis	S	1	N
Asclepias_verticillata	F	0	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Aster_brachyactis	F	0	N
Aster_falcatus	F	1	N
Aster_laevis	F	0	N
Aster_pansus	F	1	N
Astragalus_adsurgens	F	1	N
Astragalus_agrestis	F	1	N
Astragalus_bisulcatus	F	1	N
Astragalus_canadensis	F	0	N
Astragalus_crassicarpus	F	1	N
Astragalus_drummondii	F	1	N
Astragalus_flexuosus	F	1	N
Astragalus_geyeri	F	0	N
Astragalus_gilviflorus	F	1	N
Astragalus_gracilis	F	0	N
Astragalus_kentrophyta	F	0	N
Astragalus_lentiginosus	F	0	N
Astragalus_lotiflorus	F	0	N
Astragalus_missouriensis	F	1	N
Astragalus_pectinatus	F	0	N
Astragalus_purshii	F	1	N
Astragalus_racemosus	F	0	N
Astragalus_spatulatus	F	0	N
Atriplex_argentea	S	1	N
Atriplex_canescens	S	0	N
Atriplex_confertifolia	S	0	N
Atriplex_gardneri	S	1	N
Atriplex_patula	F	0	N
Atriplex_powellii	F	0	N
Atriplex_rosea	F	1	N
Atriplex_suckleyi	F	0	N
Avena_sativa	G	0	I
Besseya_wyomingensis	F	0	N
Bouteloua_gracilis	G	1	N
Brickellia_eupatoroides	F	0	N
Bromus_carinatus	G	0	N
Bromus_commutatus	G	0	I

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Bromus_inermis	G	1	I
Bromus_japonicus	G	1	I
Bromus_pumpellianus	G	0	N
Bromus_tectorum	G	0	I
Calamagrostis_montanensis	G	1	N
Calamovilfa_longifolia	G	1	N
Calochortus_nuttallii	F	1	N
Calylophus_serrulatus	F	0	N
Calystegia_sepium	F	0	N
Camelina_microcarpa	F	1	I
Campanula_rotundifolia	F	0	N
Caragana_arborescens	S	0	I
Cardaria_draba	F	0	I
Carex_douglasii	G	0	N
Carex_filifolia	G	1	N
Carex_hoodii	G	0	N
Carex_pensylvanica	G	0	N
Carex_rossii_Boott.	G	0	N
Carex_stenophylla	G	1	N
Carex_xerantica	G	0	N
Castilleja_sessiliflora	F	0	N
Centaurea_maculosa	F	0	I
Centaurea_repens	F	0	I
Cerastium_arvense	F	1	N
Cerastium_nutans	F	0	N
Chaenactis_douglasii	F	0	N
Chenopodium_album	F	1	I
Chenopodium_atrovirens	F	0	N
Chenopodium_desiccatum	F	0	N
Chenopodium_leptophyllum	F	1	N
Chenopodium_pratericola	F	1	N
Chenopodium_subglabrum	F	0	N
Chorispora_tenella	F	0	I
Chrysothamnus_nauseosus_graveolens	S	0	N
Chrysothamnus_nauseosus_nauseosus	S	1	N
Chrysothamnus_viscidiflorus	S	0	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Cirsium_arvense	F	0	I
Cirsium_undulatum	F	0	N
Cirsium_vulgare	F	0	I
Cleome_serrulata	F	0	N
Collinsia_parviflora	F	0	N
Collomia_linearis	F	1	N
Comandra_umbellata	F	1	N
Conringia_orientalis	F	1	I
Convolvulus_arvensis	F	0	I
Conyza_canadensis	F	0	N
Coryphantha_missouriensis	F	1	N
Coryphantha_vivipara	F	1	N
Crepis_atribarba	F	0	N
Crepis_occidentalis	F	1	N
Cryptantha_celosioides	F	0	N
Cryptantha_minima	F	0	N
Cryptantha_spiculifera	F	0	N
Cymopterus_acaulis	F	1	N
Dalea_candida	F	1	N
Dalea_purpurea	F	1	N
Danthonia_unispicata	G	0	N
Delphinium_bicolor	F	0	N
Descurainia_richardsonii	F	1	N
Distichlis_stricta	G	1	N
Draba_albertina	F	1	N
Draba_nemorosa	F	0	N
Draba_reptans	F	1	N
Dracocephalum_parviflorum	F	0	N
Dyssodia_papposa	F	0	N
Echinacea_angustifolia	F	0	N
Elymus_canadensis	G	0	N
Elymus_elymoides	G	1	N
Epilobium_paniculautm	F	1	N
Eragrostis_cilianensis	G	0	I
Eragrostis_pectinacea	G	0	N
Erigeron_caespitosus	F	0	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Erigeron_compositus	F	0	N
Erigeron_corymbosus	F	0	N
Erigeron_ochroleucus	F	1	N
Erigeron_pumilus	F	0	N
Erigeron_strigosus	F	0	N
Eriogonum_annuum	F	0	N
Eriogonum_cernuum	F	0	N
Eriogonum_flavum	F	0	N
Eriogonum_pauciflorum	F	1	N
Erysimum_asperum	F	1	N
Erysimum_inconspicuum	F	1	N
Euphorbia_esula	F	0	I
Euphorbia_glyptosperma	F	0	N
Euphorbia_robusta	F	0	N
Euphorbia_serpyllifolia	F	0	N
Euphorbia_spathulata	F	1	N
Festuca_octoflora	G	1	N
Filago_arvensis	F	1	N
Fritillaria_pudica	F	0	N
Gaillardia_aristata	F	0	N
Gaura_coccinea	F	1	N
Geum_triflorum	F	0	N
Glycyrrhiza_lepidota	F	1	N
Grindelia_squarrosa	F	1	N
Gutierrezia_sarothrae	F	1	N
Haplopappus_acaulis	F	0	N
Hedemoa_drummondii	F	0	N
Hedemoa_hispidum	F	1	N
Helianthus_annuus	F	1	N
Helianthus_maximiliani	F	0	N
Helianthus_petiolaris	F	1	N
Heterotheca_villosa	F	0	N
Hordeum_jubatum	G	0	N
Hymenopappus_polycephalus	F	0	N
Hymenoxys_richardsonii	F	1	N
Iva_axillaris	F	1	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Iva_xanthifolia	F	0	N
Juniperus_communis	S	0	N
Juniperus_horizontalis	S	0	N
Juniperus_scopulorum	S	0	N
Juniperus_scopulorum_x_horizontalis	S	1	N
Kochia_scoparia	F	0	I
Koeleria_cristata	G	1	N
Krascheninnikovia_lanata	S	1	N
Lactuca_serriola	F	1	I
Lappula_redowskii	F	1	N
Lepidium_densiflorum	F	1	N
Lepidium_perfoliatum	F	0	I
Lesquerella_alpina	F	1	N
Lesquerella_ludoviciana	F	1	N
Liatris_punctata	F	1	N
Linum_lewisii	F	0	N
Linum_rigidum	F	1	N
Lithospermum_incisum	F	1	N
Lomatium_foeniculaceum	F	1	N
Lupinus_argenteus	F	0	N
Lupinus_pusillus	F	1	N
Lychnis_alba	F	0	I
Lygodesmia_juncea	F	1	N
Machaeranthera_canescens	F	1	N
Machaeranthera_grindelioides	F	0	N
Machaeranthera_pinnatifida	F	1	N
Machaeranthera_tanacetifolia	F	0	N
Malva_parviflora	F	0	I
Medicago_lupulina	F	0	I
Medicago_sativa	F	0	I
Melilotus_alba	F	0	I
Melilotus_officinalis	F	1	I
Mentzelia_albicaulis	F	0	N
Mentzelia_decapetala	F	0	N
Mentzelia_laevicaulis	F	0	N
Microseris_nutans	F	1	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Microsteris_gracilis	F	1	N
Mirabilis_linearis	F	1	N
Monarda_fistulosa	F	0	N
Monolepis_nuttalliana	F	1	N
Muhlenbergia_cuspidata	G	1	N
Munroa_squarrosa	G	0	N
Musineon_divaricatum	F	1	N
Nemophila_breviflora	F	0	N
Nepeta_cataria	F	0	I
Nothocalais_cuspidata	F	0	N
Oenothera_albicaulis	F	0	N
Oenothera_biennis	F	0	N
Oenothera_cespitosa	F	0	N
Oenothera_nuttallii	F	0	N
Opuntia_fragilis	F	1	N
Opuntia_polyacantha	S	1	N
Orobanche_fasciculata	F	0	N
Orobanche_ludoviciana	F	0	N
Orthocarpus_luteus	F	1	N
Oryzopsis_hymenoides	G	0	N
Oryzopsis_micrantha	G	0	N
Oxytropis_besseyi	F	0	N
Oxytropis_lambertii	F	1	N
Oxytropis_monticola	F	0	N
Oxytropis_sericeus	F	0	N
Panicum_capillare	G	0	N
Paronychia_sessiliflora	F	0	N
Penstemon_albidus	F	1	N
Penstemon_nitidus	F	1	N
Phacelia_linearis	F	1	N
Phacelia_thermalis	F	0	N
Phleum_pratense	G	0	I
Phlox_alyssifolia	F	0	N
Phlox_hoodii	F	1	N
Picradeniopsis_oppositifolia	F	0	N
Plantago_lanceolata	F	0	I

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Plantago_major	F	0	N
Plantago_patagonica	F	1	N
Poa_ampla	G	1	N
Poa_annua	G	0	I
Poa_arida	G	1	N
Poa_bulbosa	G	0	I
Poa_compressa	G	0	I
Poa_cusickii	G	0	N
Poa_juncifolia	G	1	N
Poa_pratensis	G	1	I
Poa_secunda	G	1	N
Polanisia_trachysperma	F	0	N
Polygala_alba	F	0	N
Polygala_verticillata	F	0	N
Polygonum_aviculare	F	0	I
Polygonum_convolvulus	F	1	I
Polygonum_erectum	F	0	N
Polygonum_ramosissimum	F	1	N
Portulaca_oleracea	F	0	N
Potentilla_gracilis	F	1	N
Potentilla_hippiana	F	1	N
Potentilla_pensylvanica	F	1	N
Psoralea_argophylla	F	1	N
Psoralea_esculenta	F	1	N
Psoralea_lanceolata	F	0	N
Psoralea_tenuiflora	F	0	N
Ranunculus_glaberrimus	F	0	N
Ratibida_columnifera	F	1	N
Rhus_trilobata	S	1	N
Rosa_arkansana	S	0	N
Rosa_woodsii	S	1	N
Rumex_acetosella	F	0	I
Rumex_crispus	F	0	I
Rumex_venosus	F	0	N
Salsola_iberica	S	0	I
Sarcobatus_vermiculatus	S	1	N

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Schedonnardus_paniculatus	G	1	N
Selaginella_densa	F	1	N
Senecio_canus	F	1	N
Senecio_integerrimus	F	1	N
Setaria_viridis	G	0	I
Shepherdia_argentea	S	0	N
Silene_oregana	F	1	N
Sisymbrium_altissimum	F	0	I
Sisymbrium_loeselii	F	0	I
Smilacina_stellata	F	0	N
Solanum_rostratum	F	0	N
Solanum_triflorum	F	0	N
Solidago_missouriensis	F	1	N
Solidago_mollis	F	1	N
Solidago_rigida	F	0	N
Sphaeralcea_coccinea	F	1	N
Sporobolus_airoides	G	1	N
Sporobolus_cryptandrus	G	1	N
Stephanomeria_runcinata	F	0	N
Stipa_comata	G	1	N
Stipa_viridula	G	1	N
Suaeda_calceoliformis	S	0	N
Suaeda_moquinii	S	0	N
Symphoricarpos_albus	S	1	N
Symphoricarpos_occidentalis	S	0	N
Taraxacum_laevigatum	F	0	N
Taraxacum_officinale	F	1	I
Thermopsis_rhombifolia	F	1	N
Thlaspi_arvense	F	0	I
Townsendia_excapa	F	0	N
Townsendia_hookeri	F	0	N
Toxicodendron_rydbergii	F	0	N
Tradescantia_occidentalis	F	0	N
Tragopogon_dubius	F	1	I
Trifolium_hybridum	F	0	I
Trifolium_repens	F	0	I

Table C1. Species potentially occupying the sagebrush steppe habitat of the CMR study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Triodanis_leptocarpa	F	0	N
Triticum_aestivum	G	0	I
Verbena_bracteata	F	0	N
Vicia_americana	F	1	N
Viola_adunca	F	0	N
Viola_canadensis	F	0	N
Viola_nuttallii	F	1	N
Yucca_glauca	S	1	N
Zigadenus_venenosus	F	0	N

APPENDIX D

SPECIES LIST FROM THE PORCUPINE SITE

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Achillea_millefolium	F	1	N
Agoseris_glauca	F	1	N
Agropyron_dasystachyum	G	1	N
Agropyron_spicatum	G	1	N
Agropyron_trachycaulum	G	0	N
Allium_cernuum	F	1	N
Allium_textile	F	1	N
Alyssum_desertorum	F	1	I
Amelanchier_alnifolia	S	1	N
Androsace_occidentalis	F	1	N
Anemone_multifida	F	1	N
Anemone_patens	F	1	N
Antennaria_rosea	F	1	N
Arabis_drummondii	F	1	N
Arabis_glabra	F	1	N
Arabis_hirsuta	F	1	N
Arabis_holboellii	F	1	N
Arabis_nuttallii	F	1	N
Arenaria_congesta	F	1	N
Arenaria_sp.	F	1	N
Arnica_sororia	F	1	N
Artemisia_campestris	F	0	N
Artemisia_cana	S	0	N
Artemisia_dracunculus	F	0	N
Artemisia_frigida	F	1	N
Artemisia_ludoviciana	F	0	N
Artemisia_tridentata_vaseyana	S	1	N
Aster_ascendens	F	0	N
Aster_ericoides	F	0	N
Aster_hesperius	F	0	N
Aster_occidentalis	F	1	N
Aster_scopulorum	F	1	N
Astragalus_adsurgens	F	0	N
Astragalus_agrestis	F	1	N
Astragalus_drummondii	F	1	N
Astragalus_falcatus	F	1	I
Astragalus_flexuosus	F	0	N
Astragalus_gilviflorus	F	0	N
Astragalus_miser	F	1	N

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Astragalus_purshii	F	1	N
Balsamorhiza_sagittata	F	1	N
Beckmannia_syzigachne	F	0	N
Besseya_wyomingensis	F	1	N
Bromus_anomalus	G	1	N
Bromus_carinatus	G	1	N
Bromus_inermis	G	0	I
Bromus_japonicus	G	0	I
Calamagrostis_montanensis	G	1	N
Camelina_microcarpa	F	1	I
Campanula_rotundifolia	F	1	N
Capsella_bursa-pastoris	F	0	I
Caragana_arborescens	S	0	I
Cardus_nutans	F	0	I
Carex_filifolia	G	1	N
Carex_geyeri	G	1	N
Carex_hoodii	G	0	N
Carex_microptera	G	1	N
Carex_petasata	G	1	N
Carex_praegracilis	G	0	N
Carex_stenophylla	G	1	N
Carex_villicola	G	0	N
Castilleja_pallescens	F	1	N
Cerastium_arvense	F	1	N
Chenopodium_album	F	0	I
Chrysothamnus_nauseosus	S	1	N
Chrysothamnus_viscidflorus	S	1	N
Cirsium_arvense	F	0	I
Cirsium_flodmanii	F	1	N
Cirsium_scariosum	F	1	N
Cirsium_undulatum	F	0	N
Cirsium_vulgare	F	0	I
Clematis_hirsutissimus	F	0	N
Clematis_ligusticifolia	F	0	N
Collinsia_parviflora	F	1	N
Collomia_linearis	F	1	N
Commandra_umbellata	F	1	N
Crataegus_douglasii	S	0	N
Crepis_atribarba	F	1	N

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Crepis_occidentalis	F	1	N
Cryptantha_celosioides	F	0	N
Cymopteris_bipinnatus	F	1	N
Danthonia_intermedia	G	1	N
Danthonia_unispicata	G	1	N
Delphinium_bicolor	F	1	N
Disporum_trachycarpum	F	0	N
Dodecatheon_conjugens	F	1	N
Draba_nemorosa	F	0	N
Dracocephalum_parviflorum	F	0	N
Elymus_canadensis	G	0	N
Elymus_cinereus	G	1	N
Epilobium_angustifolium	F	0	N
Epilobium_paniculatum	F	1	N
Erigeron_caespitosus	F	1	N
Erigeron_compositus	F	1	N
Erigeron_pumilus	F	0	N
Erigeron_subtrinervis	F	1	N
Eriogonum_umbellatum	F	1	N
Erysimum_asperum	F	1	N
Erysimum_cheiranthoides	F	1	N
Erysimum_inconspicuum	F	1	N
Festuca_idahoensis	G	1	N
Fragaria_virginiana	F	1	N
Fritillaria_atropurpurea	F	0	N
Fritillaria_pudica	F	0	N
Gaillardia_aristata	F	0	N
Galium_aparine	F	0	N
Galium_boreale	F	1	N
Gaura_coccinea	F	0	N
Geranium_viscosissimum	F	1	N
Geum_triflorum	F	1	N
Glycyrrhiza_lepidota	F	0	N
Grindelia_squarrosa	F	0	N
Haplopappus_acaulis	F	1	N
Hedysarum_boreale	F	0	N
Helianthella_uniflora	F	1	N
Helianthus_annus	F	0	N
Heterotheca_villosa	F	0	N

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Heuchara_grossularicola	F	0	N
Heuchara_parviflora	F	1	N
Hordeum_jubatum	G	0	N
Iris_missouriensis	F	0	N
Juncus_balticus	G	0	N
Juniperus_communis	S	1	N
Juniperus_horizontalis	S	0	N
Juniperus_scopulorum	S	1	N
Koeleria_macrantha	G	1	N
Krascheninnikovia_lanata	S	1	N
Lactuca_serriola	F	0	I
Lappula_redowskii	F	0	N
Liatrus_punctata	F	0	N
Linum_lewisii	F	1	N
Lithospermum_arvense	F	0	N
Lithospermum_ruderale	F	1	N
Lomatium_dissectum	F	0	N
Lomatium_macrocarpum	F	1	N
Lomatium_triternatum	F	0	N
Lupinus_argenteus	F	1	N
Lupinus_sericeus	F	0	N
Lychnis_alba	F	1	I
Mahonia_repens	F	1	N
Maianthemum_racemosa	F	0	N
Maianthemum_stellata	F	0	N
Melilotus_officinalis	F	0	I
Mertensia_oblongifolia	F	1	N
Microseris_nutans	F	1	N
Microsteris_gracilis	F	1	N
Monarda_fistulosa	F	0	N
Muhlenbergia_richardsonis	G	0	N
Musineon_divaricatum	F	0	N
Oenothera_cespitosa	F	0	N
Orobacnche_fasiculata	F	1	N
Orthocarpus_luteus	F	0	N
Oxytropis_besseyi	F	0	N
Oxytropis_deflexa	F	1	N
Oxytropis_lagopus	F	1	N
Oxytropis_sericea	F	0	N

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Penstemon_cyaneus	F	0	N
Penstemon_eriantherus	F	0	N
Penstemon_nitidus	F	0	N
Penstemon_procerus	F	1	N
Penstemon_radicosus	F	1	N
Phacelia_franklanii	F	0	N
Phacelia_linearis	F	0	N
Phleum_pratense	G	1	I
Phlox_hoodii	F	1	N
Phlox_longifolia	F	0	N
Phlox_multiflora	F	1	N
Physocarpus_malvaceus	S	0	N
Poa_cusickii	G	0	N
Poa_juncifolia	G	1	N
Poa_pratensis	G	1	I
Poa_secunda	G	1	N
Polygonum_douglasii	F	1	N
Potentilla_fruticosa	F	0	N
Potentilla_glandulosa	F	1	N
Potentilla_gracilis	F	1	N
Prunus_virginiana	S	0	N
Pseudotseuga_menziesii	S	1	N
Ranunculus_glaberimus	F	0	N
Ribes_setosum	S	1	N
Ribes_aureum	S	0	N
Rosa_woodsii	S	1	N
Sedum_stenopetalum	F	1	N
Senecio_canus	F	1	N
Sencio_dimorphyllus	F	0	N
Senecio_integerrimus	F	1	N
Senecio_serra	F	0	N
Solidago_missouriensis	F	1	N
Solidago_multiradiata	F	1	N
Stipa_richardsonii	G	1	N
Stipa_viridula	G	1	N
Symphoricarpos_albus	S	0	N
Symphoricarpos_occidentalis	S	1	N
Taraxacum_officinale	F	1	N
Taraxacum_laevigatum	F	1	N

Table D1. Species recorded in the sagebrush steppe of the Porcupine study site.

Species	Growth Habit F=Forb, G=Grass and, S=Shrub	Presence/Absence 1= present in at least one sample	Nativity status N=Native, I=Introduced
Tetradymia_canescens	S	1	N
Thelypodium_paniculatum	F	1	N
Thlaspi_arvense	F	1	I
Thlaspi_montanensis	F	1	N
Townsendia_parryi	F	1	N
Tragopogon_dubius	F	1	I
Triteleia_grandiflora	F	0	N
Vicia_americana	F	0	N
Viola_adunca	F	1	N
Viola_nuttallii	F	1	N
Zigadenus_venenosus	F	1	N

APPENDIX E

EARLY AND LATE SEASON FORBS

Table E1. Early and late season forbs recorded in plots at Burke Park. Values are the change in abundance in cm^2 from June to August of both sampling years.

Late season forbs		Early season forbs	
Amaranthus_blitoides	0.15	*Achillea_millefolium*	-41381
Amaranthus_retroflexus	0.15	*Agoseris_glauca*	-980
Apocynum_androsaemifolium	1090	*Allium_cernuum*	-4103.85
Artemisia_campestris	335	*Allium_textile*	-380.3
Artemisia_ludoviciana	1511.15	*Alyssum_alyssoides*	-5691.3
Asclepias_viridiflora	0.3	*Androsace_occidentalis*	-27
Aster_ascendens	804.75	*Anemone_multifida*	-520
Aster_falcatus	25699	*Anemone_patens*	-275
Centaurea_maculosa	1453.45	*Antennaria_microphylla*	-650
Chenopodium_watsonii	0.15	*Arabis_drummondii*	-2.15
Cirsium_undulatum	0.45	*Arenaria_congesta*	-930.45
Erigeron_caespitosus	2702.3	*Arnica_sororia*	-18953.2
Grindelia_squarrosa	0.3	*Artemisia_frigida*	-339.85
Gutierrezia_sarothrae	565.3	*Astragalus_adsurgens*	-936.85
Helianthus_annus	554.15	*Astragalus_agrestis*	-865.3
Heterotheca_villosa	1148	*Astragalus_crassicarpus*	-0.15
Liatrus_punctata	3960	*Astragalus_drummondii*	-1344.7
Lygodesmia_juncea	177	*Astragalus_gilviflorus*	-1
Mahonia_repens	104.85	*Astragalus_miser*	-3600
Orthocarpus_luteus	17.3	*Balsamorhiza_sagittata*	-3324.85
Penstemon_eriantherus	11.85	*Besseya_wyomingensis*	-4529
Polygonum_douglasii	13	*Camelina_microcarpa*	-629.3
Sedum_stenopetalum	14.7	*Capsella_bursa-pastoris*	-46
Silene_latifolia	0.15	*Cerastium_arvense*	-297.7
Solidago_missouriensis	4188.15	*Cirsium_arvense*	-397.15
Sphaeralcea_coccinea	208.3	*Collomia_linearis*	-1709.6
Thesium_linophyllum	194.85	*Commandra_umbellata*	-2731
		Crepis_occidentalis	-4705.45
		Cynoglossum_officinale	-1436
		Descurania_sophia	-27.3
		Disporum_trachycarpum	-320
		Draba_nemorosa	-14
		Epilobium_paniculatum	-386
		Erysimum_asperum	-150.15
		Fritillaria_atropurpurea	-15
		Fritillaria_pudica	-5.3
		Gaillardia_aristata	-73.85
		Galium_aparine	-1173.15
		Galium_boreale	-1443
		Gaura_coccinea	-3665
		Geum_triflorum	-1009.3

Table E1. Early and late season forbs recorded in plots at Burke Park. Values are the change in abundance in cm^2 from June to August of both sampling years.

Late season forbs	Early season forbs	
	Helianthella_uniflora	-2979.85
	Lactuca_serriola	-283
	Lepidium_campestre	-0.15
	Linum_lewisii	-1023
	Lithospermum_arvense	-2252
	Lithospermum_ruderale	-481.4
	Lomatium_macrocarpum	-13001.3
	Lomatium_triternatum	-330.3
	Lupinus_argenteus	-91359
	Medicago_lupulina	-258.3
	Medicago_sativa	-199.4
	Melilotus_albus	-25
	Melilotus_officinalis	-4422.7
	Mertensia_oblongifolia	-395
	Microseris_nutans	-80.15
	Microsteris_gracilis	-1518
	Musineon_divaricatum	-1586
	Oxytropis_besseyi	-210
	Penstemon_nitidus	-120
	Phleum_pratense	-89.85
	Phlox_hoodii	-3667.15
	Phlox_longifolia	-15196
	Potentilla_hippiana	-0.15
	Potentilla_recta	-2369.85
	Senecio_canus	-383
	Senecio_integerrimus	-3160.15
	Sisymbrium_altissimum	-100.3
	Solidago_rigida	-139.85
	Taraxacum_officinale	-2877.3
	Thlaspi_arvense	-85
	Thlaspi_montanum	-0.15
	Townsendia_parryi	-190.15
	Tragopogon_dubius	-17058.9
	Vicia_americana	-11731.9
	Viola_nuttallii	-5752
	Zigadenus_venenosus	-1700.6

Table E2. Early and late season forbs recorded in plots at the CMR study site. Values are the change in abundance in cm^2 from June to August of both sampling years.

Late season forbs		Early season forbs	
Arabis_hirsuta	2.99	*Achillea_millefolium*	-237.02
Artemisia_frigida	298	*Agoseris_glauca*	-140.22
Aster_falcatus	567.04	*Allium_textile*	-5870.03
Aster_pansus	0.02	*Androsace_occidentalis*	-47.05
Astragalus_adsurgens	0.01	*Anemone_patens*	-0.01
Astragalus_bisulcatus	70.01	*Antennaria_dimorpha*	-113.2
Atriplex_rosea	0.01	*Antennaria_rosea*	-1677.18
Chenopodium_album	4.01	*Arabis_holboellii*	-17.99
Chenopodium_pratericola	43.01	*Arnica_sororia*	-0.01
Comandra_umbellata	120.01	*Astragalus_agrestis*	-1490.15
Dalea_purpurea	118.08	*Astragalus_crassicarpus*	-0.13
Epilobium_paniculautm	38.01	*Astragalus_drummondii*	-1300.01
Eriogonum_pauciflorum	0.02	*Astragalus_flexuosus*	-400
Glycyrrhiza_lepidota	35	*Astragalus_gilviflorus*	-37.98
Grindelia_squarrosa	115.01	*Astragalus_missouriensis*	-23.02
Gutierrezia_sarothrae	655.85	*Astragalus_purshii*	-177.07
Helianthus_annuus	7.98	*Calochortus_nuttallii*	-15
Iva_axillaris	10.01	*Camelina_microcarpa*	-169
Liatris_punctata	0.06	*Cerastium_arvense*	-164.03
Linum_rigidum	57.96	*Chenopodium_leptophyllum*	-14
Lithospermum_incisum	19	*Collomia_linearis*	-870.01
Machaeranthera_pinnatifida	23.01	*Conringia_orientalis*	-10
Mirabilis_linearis	30	*Crepis_occidentalis*	-332.16
Polygonum_convolvulus	4.99	*Cymopterus_acaulis*	-31.04
Polygonum_ramosissimum	8.98	*Descurainia_richardsonii*	-0.01
Potentilla_gracilis	19.99	*Descurainia_richardsonii*	-491.02
Potentilla_pensylvanica	24.81	*Draba_albertina*	-41.01
Ratibida_columnifera	3.03	*Draba_reptans*	-12
Silene_oregana	3.01	*Erigeron_ochroleucus*	-70.2
Solidago_missouriensis	1120.01	*Erysimum_asperum*	-15
		Erysimum_inconspicuum	-18.2
		Euphorbia_spathulata	-25
		Filago_arvensis	-36.05
		Gaura_coccinea	-114.99
		Hedemoa_hispidum	-19
		Hymenoxys_richardsonii	-1541.03
		Lactuca_serriola	-2.01
		Lappula_redowskii	-30.01
		Lepidium_densiflorum	-111.17
		Lesquerella_alpina	-0.02

Table E2. Early and late season forbs recorded in plots at the CMR study site. Values are the change in abundance in cm^2 from June to August of both sampling years.

Late season forbs		Early season forbs	
		Lesquerella_ludoviciana	-100.99
		Lomatium_foeniculaceum	-385
		Lupinus_pusillus	-0.02
		Lygodesmia_juncea	-15
		Machaeranthera_canescens	-0.04
		Melilotus_officinalis	-465.98
		Microseris_nutans	-0.02
		Microsteris_gracilis	-54
		Monolepis_nuttalliana	-60.01
		Musineon_divaricatum	-3631.04
		Oxytropis_lambertii	-25
		Penstemon_albidus	-143.21
		Penstemon_nitidus	-10
		Phacelia_linearis	-1999.03
		Phlox_hoodii	-10728
		Plantago_patagonica	-837.16
		Potentilla_hippiana	-0.01
		Psoralea_argophylla	-691.1
		Senecio_canus	-0.01
		Senecio_integerrimus	-0.02
		Sphaeralcea_coccinea	-283.99
		Taraxacum_officinale	-10824
		Thermopsis_rhombifolia	-71.99
		Tragopogon_dubius	-205.06
		Vicia_americana	-21231
		Viola_nuttallii	-125.03

APPENDIX F

R-CODE DEVELOPED FOR THIS STUDY

```
##Relative species abundance distribution for June
##using cm2 cover as the abundance measure
##Import CMR June vegetation matrix
x.j<-read.table("CMRjun05.txt",header=T,row.names=1)
cmr.jun.05<-t(x.j[1:337,])
cmr.jun.05<-data.frame(cmr.jun.05)
row.names(cmr.jun.05)<-names(x.j)
names(cmr.jun.05)<-row.names(x.j[1:337,])
dim(cmr.jun.05)
##and masks 0 abundant species
tmp1.j<-cmr.jun.05
mask0.j<-apply(tmp1.j,2,sum)
tmp2.j<-tmp1.j[,mask0.j>0]
##combines matrix into single abundance vector
tmp3.j<-apply(tmp2.j,2,sum)
d.j.05<-(tmp3.j)#/731033.5)*100#number is total amount of cover
recorded from xls sheet.

##Import CMR June vegetation matrix
x.j.6<-read.table("CMRjun06.txt",header=T,row.names=1)
cmr.jun.06<-t(x.j.6[1:337,])
cmr.jun.06<-data.frame(cmr.jun.06)
row.names(cmr.jun.06)<-names(x.j.6)
names(cmr.jun.06)<-row.names(x.j.6[1:337,])
dim(cmr.jun.06)
##and masks 0 abundant species
tmp1.j.6<-cmr.jun.06
mask0.j.6<-apply(tmp1.j.6,2,sum)
tmp2.j.6<-tmp1.j.6[,mask0.j.6>0]
##combines matrix into single abundance vector
tmp3.j.6<-apply(tmp2.j.6,2,sum)
d.j.06<-(tmp3.j.6)#/764580.4.5)*100#number is total amount of cover
recorded from xls sheet.

##June 2004 vegetaion matrix Burke Park
bp.june04<-read.table("BPJune04.txt",header=T)
tmp1.bp.4<-bp.june04[,1:219]
mask0.bp.4<-apply(tmp1.bp.4>0,2,sum)
tmp2.bp.4<-tmp1.bp.4[,mask0.bp.4>0]
tmp3.bp.4<-apply(tmp2.bp.4,2,sum)
d.bp.j.4<-(tmp3.bp.4)#/925850)*100


##June 2005 vegetaion matrix Burke Park
bp.june05<-read.table("BPJune05.txt",header=T)
tmp1.bp<-bp.june05[,1:219]
mask0.bp<-apply(tmp1.bp>0,2,sum)
tmp2.bp<-tmp1.bp[,mask0.bp>0]
tmp3.bp<-apply(tmp2.bp,2,sum)
d.bp.j<-(tmp3.bp)#/1004103)*100

##sorts data in order RSA curve
d.bp.j.log<-log(sort(floor(d.bp.j),decreasing=TRUE))
d.bp.j.log.4<-log(sort(d.bp.j.4,decreasing=TRUE))
```

```
##sorts data in order and plot RSA curve
d.j.05.log<-log(sort(floor(d.j.05),decreasing=TRUE))
d.j.06.log<-log(sort(floor(d.j.06),decreasing=TRUE))

############################
yrange<-range(-5,15)
xrange<-range(0,140)
#possible to add this in below. ylim=yrange,xlim=xrange,
plot(d.bp.j.log,type="p",main="Relative Abundance
Distribution",xlab="species rank",ylab="log abundance")
points(d.bp.j.log,col=1,pch=19)
points(d.bp.j.log.4,col=3,pch=19)
points(d.j.05.log,col=4,pch=19)
points(d.j.06.log,col=5,pch=19)
legend(60,11,c("Burke Park June 05"),col=1,pch=19,bty="n")
legend(60,12,c("Burke Park June 04"),col=3,pch=19,bty="n")
legend(60,10,c("CMR June05"),col=4,pch=19,bty="n")
legend(60,9,c("CMR June06"),col=5,pch=19,bty="n")
######################################
############################
##Relative species abundance using frequency also calculates
##diveristy of all sites
y<-read.table("BP.quadmat.June04.txt",header=T,row.names=1)
bp.ab.jun.04<-t(y)
bp.ab.jun.04<-data.frame(bp.ab.jun.04)
row.names(bp.ab.jun.04)<-names(y)
names(bp.ab.jun.04)<-row.names(y)
dim(bp.ab.jun.04)
bp.ab<-bp.ab.jun.04
bp.ab.jun.04[bp.ab>0]<-1
bp.f.j04<-(bp.ab.jun.04)
tmp1.bp<-bp.f.j04
mask0.bp<-apply(tmp1.bp>0,2,sum)
tmp2.bp<-tmp1.bp[,mask0.bp>0]
bp.fr.j04<-apply(tmp2.bp,2,sum)
bp.fr.j04
bp.j04.f<-sort(bp.fr.j04,decreasing=TRUE)
############################
y<-read.table("BP.quadmat.June05.txt",header=T,row.names=1)
bp.ab.jun.05<-t(y)
bp.ab.jun.05<-data.frame(bp.ab.jun.05)
row.names(bp.ab.jun.05)<-names(y)
names(bp.ab.jun.05)<-row.names(y)
dim(bp.ab.jun.05)
bp.ab<-bp.ab.jun.05
bp.ab.jun.05[bp.ab>0]<-1
bp.f.j05<-(bp.ab.jun.05)
tmp1.bp<-bp.f.j05
mask0.bp<-apply(tmp1.bp>0,2,sum)
tmp2.bp<-tmp1.bp[,mask0.bp>0]
bp.fr.j05<-apply(tmp2.bp,2,sum)
bp.fr.j05
bp.j05.f<-sort(bp.fr.j05,decreasing=TRUE)
```

```
##########CMR data sets##############
################################################################
y<-read.table("CMR.quadmat.June06.txt",header=T,row.names=1)
cmr.ab.jun.06<-t(y)
cmr.ab.jun.06<-data.frame(cmr.ab.jun.06)
row.names(cmr.ab.jun.06)<-names(y)
names(cmr.ab.jun.06)<-row.names(y)
dim(cmr.ab.jun.06)
cmr.ab<-cmr.ab.jun.06
cmr.ab.jun.06[cmr.ab>0]<-1
cmr.f.j06<-(cmr.ab.jun.06)
tmp1.cmr<-cmr.f.j06
mask0.cmr<-apply(tmp1.cmr>0,2,sum)
tmp2.cmr<-tmp1.cmr[,mask0.cmr>0]
cmr.fr.j06<-apply(tmp2.cmr,2,sum)
cmr.fr.j06
cmr.j06.f<-sort(cmr.fr.j06,decreasing=TRUE)

############################
y<-read.table("CMR.quadmat.June05.txt",header=T,row.names=1)
cmr.ab.jun.05<-t(y)
cmr.ab.jun.05<-data.frame(cmr.ab.jun.05)
row.names(cmr.ab.jun.05)<-names(y)
names(cmr.ab.jun.05)<-row.names(y)
dim(cmr.ab.jun.05)
cmr.ab<-cmr.ab.jun.05
cmr.ab.jun.05[cmr.ab>0]<-1
cmr.f.j05<-(cmr.ab.jun.05)
tmp1.cmr<-cmr.f.j05
mask0.cmr<-apply(tmp1.cmr>0,2,sum)
tmp2.cmr<-tmp1.cmr[,mask0.cmr>0]
cmr.fr.j05<-apply(tmp2.cmr,2,sum)
cmr.fr.j05
cmr.j05.f<-sort(cmr.fr.j05,decreasing=TRUE)
#############################################
#PORCUPINE
yx<-read.table("PC.quadmat.j060.txt",header=TRUE,row.names=1)
pc.f.jun.06<-t(yx)
pc.f.jun.06<-data.frame(pc.f.jun.06)
row.names(pc.f.jun.06)<-names(yx)
names(pc.f.jun.06)<-row.names(yx)
dim(pc.f.jun.06)
pc.f.j06<-pc.f.jun.06
tmp1.pc<-pc.f.j06
mask0.pc<-apply(tmp1.pc>0,2,sum)
tmp2.pc<-tmp1.pc[,mask0.pc>0]
pc.fr.j06<-apply(tmp2.pc,2,sum)
pc.fr.j06
pc.j06.f<-sort(pc.fr.j06,decreasing=TRUE)

####Frequency Relative Abundance Distribution#########
#####################################
cmr.j05.f<-log(sort(cmr.fr.j05,decreasing=TRUE))
cmr.j06.f<-log(sort(cmr.fr.j06,decreasing=TRUE))
```

```
bp.j04.f<-log(sort(bp.fr.j04,decreasing=TRUE))
bp.j05.f<-log(sort(bp.fr.j05,decreasing=TRUE))
pc.j06.f<-log(sort(pc.fr.j06,decreasing=TRUE))

yrange<-range(0,6)
xrange<-range(0,130)
#possible to add this in below. ylim=yrange,xlim=xrange,
plot(cmr.j06.f,type="p",ylim=yrange,xlim=xrange,main="Relative
Abundance Distribution",xlab="species rank",ylab="log(frequency in
quadrats)")
points(cmr.j06.f,col=5,pch=19)
points(cmr.j05.f,col=4,pch=19)
points(bp.j04.f,col=3,pch=19)
points(bp.j05.f,col=1,pch=19)
points(pc.j06.f,col=6,pch=19)

legend(60,5,c("Burke Park June 05"),col=1,pch=19,bty="n")
legend(60,4.5,c("Burke Park June 04"),col=3,pch=19,bty="n")
legend(60,4,c("CMR June05"),col=4,pch=19,bty="n")
legend(60,3.5,c("CMR June06"),col=5,pch=19,bty="n")
legend(60,3,c("Porcupine June06"),col=6,pch=19,bty="n")

cmr.j05.f
cmr.j06.f
bp.j04.f
bp.j05.f

bp.f.j04
bp.f.j05
##frequency diversity calculations quadrat
library(vegan)
mean(diversity(cmr.f.j06,index="shannon"))
mean(diversity(bp.f.j05,index="shannon"))
mean(diversity(pc.f.j06,index="shannon"))
mean(diversity(cmr.f.j06,index="simpson"))
mean(diversity(bp.f.j05,index="simpson"))
mean(diversity(pc.f.j06,index="simpson"))

plot(specaccum(pc.f.j06,method="random"),col=2,main="Species
Accumulation Curves",xlab="quadrats",ylab="species(randomly
accumulated)")
plot(specaccum(cmr.f.j06,method="random"),add=T,main="Species
Accumulation Curves")
plot(specaccum(bp.f.j05,method="random"),add=T,col=4,main="Species
Accumulation Curves",xlab="quadrats",ylab="species(randomly
accumulated)")

legend(100,70,c("Burke Park June 05"),col=4,lty=1,bty="n")
legend(100,60,c("CMR June 06"),col=1,lty=1,bty="n")
legend(100,50,c("Porcupine June 06"),col=2,lty=1,bty="n")

##fit of frequency using fuction from vegan
radfit(bp.fr.j04)
radfit(bp.fr.j05)
```

```
radfit(cmr.fr.j05)
radfit(cmr.fr.j06)
radfit(pc.fr.j06)

plot(radfit(bp.fr.j04))
plot(radfit(bp.fr.j05),main="Burke Park")
plot(radfit(cmr.fr.j05))
plot(radfit(cmr.fr.j06),main="CMR")
plot(radfit(pc.fr.j06),main="Porcupine drainage")

##vectors of abundance for fitting ZSM using Te Tame
write.table(bp.fr.j04, file="d.bp.fr.j04.txt", quote=F, row.names=T,
sep="\t")
write.table(bp.fr.j05, file="d.bp.fr.j05.txt", quote=F, row.names=T,
sep="\t")
write.table(cmr.fr.j05, file="d.cmr.fr.j05.txt", quote=F, row.names=T,
sep="\t")
write.table(cmr.fr.j06, file="d.cmr.fr.j06.txt", quote=F, row.names=T,
sep="\t")
write.table(pc.fr.j06, file="d.po.fr.j06.txt", quote=F, row.names=T,
sep="\t")
#fit of fisher’s alpha
fisherfit(bp.fr.j05)
fisherfit(cmr.fr.j06)
fisherfit(pc.fr.j06)

#####Comparisons of vegetation similarity using distance measures###
##the functions come from the ladsv and vegan libraries
##the data comes from the text file bpcmr.txt that combinded the data
sets.
##nov 16 2005

x<-read.table("BPCMR.txt",header=T,row.names=1)
veg<-t(x)
veg<-data.frame(veg)
row.names(veg)<-names(x)
names(veg)<-row.names(x)
bp.sum<-apply(veg[1:15,],2,sum)
cmr.sum<-apply(veg[16:39,],2,sum)

library(labdsv)
library(vegan)

##This will remove non-sampled species then proceed to dissimilarity
measures
##this isn't needed because functions ignore values with 0 in both rows
veg.comb<-rbind(cmr.sum,bp.sum)
tmp1<-veg.comb
mask0<-apply(tmp1>0,2,sum)
tmp2<-tmp1[,mask0>0]
veg.pres<-tmp2

vegdist(veg.pres,method="jaccard")
vegdist(veg.pres,method="bray")
```

```
cmr<-veg[16:39,]
bp<-veg[1:15,]
##fit the shannon-wiener, fisher's alpha,
mean(diversity(cmr,index="shannon"))
mean(diversity(bp,index="shannon"))

fisherfit(cmr.sum)
fisherfit(bp.sum)

#rank and abunance vectors from all sampling times
##compares changes from year to year at BP and 2005 change at CMR
bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
attach(bp.temp)
##looks at mean rank and test for difference in J05#####
mean(rankj05[status=="I"])
mean(rankj05[status=="N"])

bp.ri.j05<-(rankj05[status=="I"])
bp.rn.j05<-(rankj05[status=="N"])

rank.i.lm<-lm(rankj05~status)
anova(rank.i.lm)
##zero abundant species are within data set.
boxplot(rankj05[status=="N"],rankj05[status=="I"],names=c("Native","Int
roduced"),main="Species Rank")
###same process for A05####zero abundant present
mean(ranka05[status=="I"])
mean(ranka05[status=="N"])
rank.i.lm.a<-lm(ranka05~status)
anova(rank.i.lm.a)

###abundance ##zero abundant species present
sum(june05[status=="I"])
hist(june05[status=="I"],br=500)
mean(june05[status=="I"])
mean(june05[status=="N"])
abund.i.lm.a<-lm(june05~status)
anova(abund.i.lm.a)
sum(june05[status=="I"])+sum(june05[status=="N"])
boxplot(june05[status=="N"],june05[status=="I"],names=c("Native","Intro
duced"),main="Species abundance")

##sum june is the temporal sample added together.
mean(sumjun[status=="I"])
mean(sumjun[status=="N"])
abund.i.lm.a<-lm(sumjun~status)
anova(abund.i.lm.a)

##changes in RSA curve associated with sampling time
plot(log(sort(june04,decreasing=TRUE)),ylab="log
abundance",xlab="rank",main="Seasonal Variation of RSA at Burke Park")
points(log(sort(june05,decreasing=TRUE)),pch=2)
points(log(sort(aug05,decreasing=TRUE)),pch=3)
```

```
points(log(sort(aug04,decreasing=TRUE)),pch=4)
legend(150,11,"June04",pch=1,bty="n",cex=1.0)
legend(150,10,"June05",pch=2,bty="n",cex=1.0)
legend(150,9,"Aug04",pch=3,bty="n",cex=1.0)
legend(150,8,"Aug05",pch=4,bty="n",cex=1.0)
###################################################
##this is percent for abundance and rank change from 04 to 05
##the zero abundant species are taken out by brute force
pc.bp.j05.i<-
data.frame(june05[status=="I"]/(sum(june05[status=="I"])+sum(june05[sta
tus=="N"])))
mask0.bp<-apply(pc.bp.j05.i>0,2,sum)
p.bp<-as.vector(sort(pc.bp.j05.i[,mask0.bp>0],decreasing=T)*100)
hist(p.bp,br=100)
sort(june05)-sort(june04)
rank.change<-as.vector((rankj05)-(rankj04))
names(rank.change)<-row.names(bp.temp)
r.c<-sort(rank.change)
r.c.bp<-r.c[-c(129:211)]
########removes all zero abundant species in original data.frame
###change introduced rank
rank.change.i<-as.vector((rankj04[status=="I"])-(rankj05[status=="I"]))
r.c.i.t<-sort(rank.change.i)
r.c.i<-r.c.i.t[-c(3:31)] #commands remove zero abundant
###change native rank
rank.change.n<-as.vector((rankj04[status=="N"])-(rankj05[status=="N"]))
r.c.n.t<-sort(rank.change.n)
r.c.n<-r.c.n.t[-c(7:61)] #commands remove zero abundant
mean(r.c.n)
mean(r.c.i)
boxplot(r.c.n,r.c.i,names=c("Native","Introduced"),ylab = "change in
rank",
main="Change in Rank: June 2004 to 2005")
cbind(r.c.n,r.c.i)

###change introduced abundance
abund.change.i<-as.vector((june04[status=="I"])-(june05[status=="I"]))
a.c.i<-sort(abund.change.i)
aci<-a.c.i[-c(17:46)] #commands remove zero abundant
###change native abundance
abund.change.n<-as.vector((june04[status=="N"])-(june05[status=="N"]))
a.c.n<-sort(abund.change.n)
acn<-a.c.n[-c(73:127)] #commands remove zero abundant

boxplot(acn,aci,names=c("Native","Introduced"),ylab = "change in
abundance",
main="Change in Abundance: June 2004 to 2005")
mean(acn)
mean(aci)


detach(bp.temp)
#######################################################################
####
```

```
cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
attach(cmr.temp)
mean(rankj05[status=="I"])
mean(rankj05[status=="N"])
rank.i.lm<-lm(rankj05~status)
anova(rank.i.lm)

mean(june05[status=="I"])
mean(june05[status=="N"])
abund.i.lm.a<-lm(june05~status)
anova(abund.i.lm.a)
(sum(june05[status=="I"]>0)/(sum(june05[status=="I"]>0)+sum(june05[stat
us=="N"]>0)))*100

#RSA CMR temporal change
plot(log(sort(floor(june05),decreasing=TRUE)),pch=2,xlim=c(0,200),main=
"Seasonal Variation of RSA at the CMR",ylab="abundance",xlab="species
rank")
points(log(sort(floor(aug05),decreasing=TRUE)),pch=3)
points(log(sort(floor(june06),decreasing=TRUE)),pch=4)
points(log(sort(floor(aug06),decreasing=TRUE)),pch=5)
legend(100,11,"June05",pch=2,bty="n",cex=1.0)
legend(100,10,"Aug05",pch=3,bty="n",cex=1.0)
legend(100,9,"June06",pch=4,bty="n",cex=1.0)
legend(100,8,"Aug06",pch=5,bty="n",cex=1.0)

####################################################################
##this is percent for abundance and rank change from 05 to 06
##the zero abundant species are taken out by brute force
pc.cmr.j05.i<-
data.frame(june05[status=="I"]/(sum(june05[status=="I"])+sum(june05[sta
tus=="N"])))
mask0.cmr<-apply(pc.cmr.j05.i>0,2,sum)
p.cmr<-as.vector(sort(pc.cmr.j05.i[,mask0.cmr>0],decreasing=T)*100)
hist(p.cmr,br=100)
sort(june06)-sort(june05)
rank.change<-as.vector((rankj06)-(rankj05))
names(rank.change)<-row.names(cmr.temp)
r.c<-sort(rank.change)
r.c.cmr<-r.c[-c(87:288)]
########removes all zero abundant species in original data.frame
###change introduced rank
rank.change.i<-as.vector((rankj05[status=="I"])-(rankj06[status=="I"]))
r.c.i.t<-sort(rank.change.i)
r.c.i<-r.c.i.t[-c(4:47)] #commands remove zero abundant
###change native rank
rank.change.n<-as.vector((rankj05[status=="N"])-(rankj06[status=="N"]))
r.c.n.t<-sort(rank.change.n)
r.c.n<-r.c.n.t[-c(47:204)] #commands remove zero abundant
mean(r.c.n)
mean(r.c.i)
boxplot(r.c.n,r.c.i,names=c("Native","Introduced"),ylab = "change in
rank",
```

```
main="Change in Rank: June 2005 to 2006")
cbind(r.c.n,r.c.i)

###change introduced abundance
abund.change.i<-as.vector((june05[status=="I"])-(june06[status=="I"]))
a.c.i<-sort(abund.change.i)
aci<-a.c.i[-c(9:52)] #commands remove zero abundant
###change native abundance
abund.change.n<-as.vector((june05[status=="N"])-(june06[status=="N"]))
a.c.n<-sort(abund.change.n)
acn<-a.c.n[-c(86:245)] #commands remove zero abundant

boxplot(acn,aci,names=c("Native","Introduced"),ylab = "change in
abundance",
main="Change in Abundance: June 2005 to 2006")
mean(acn)
mean(aci)

###June 2004
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJune04.txt",header=T)
bp.june04<-data.frame(x.bp.j[,1:219])
row.names(bp.june04)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.j04.i<-bp.june04[bp.temp$status=="I"]
bp.j04.n<-bp.june04[bp.temp$status=="N"]

apply(bp.j04.i>0,1,sum)
apply(bp.j04.n>0,1,sum)
x.i.f<-sum(floor(apply(bp.j04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.j04.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100


x.i<-sum(floor(apply(bp.j04.i,2,sum)))
x.n<-sum(floor(apply(bp.j04.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

#################################################################
##July 2004
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJuly04.txt",header=T)
bp.july04<-data.frame(x.bp.j[,1:219])
row.names(bp.july04)<-seq(1:15)
library(vegan)
##ju=JULY
bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.ju04.i<-bp.july04[bp.temp$status=="I"]
bp.ju04.n<-bp.july04[bp.temp$status=="N"]
```

```
x.i<-sum(floor(apply(bp.ju04.i,2,sum)))
x.n<-sum(floor(apply(bp.ju04.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.ju04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.ju04.n>0,2,sum)))

(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
####
###August 2004
#masked zero abundant species, retained 15 rows
x.bp.a<-read.table("BPAug04.txt",header=T)
bp.aug04<-data.frame(x.bp.a[,1:219])
row.names(bp.aug04)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.a04.i<-bp.aug04[bp.temp$status=="I"]
bp.a04.n<-bp.aug04[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.a04.i,2,sum)))
x.n<-sum(floor(apply(bp.a04.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.a04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.a04.n>0,2,sum)))

(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100


########################################################################
########
##June 05
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJune05.txt",header=T)
bp.june05<-data.frame(x.bp.j[,1:219])
row.names(bp.june05)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.j05.i<-bp.june05[bp.temp$status=="I"]
bp.j05.n<-bp.june05[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.j05.i,2,sum)))
x.n<-sum(floor(apply(bp.j05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100
```

```
x.i.f<-sum(floor(apply(bp.j05.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.j05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
#########
##August 05
#masked zero abundant species, retained 15 rows
x.bp.a<-read.table("BPAug05.txt",header=T)
bp.aug05<-data.frame(x.bp.a[,1:219])
row.names(bp.aug05)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.a05.i<-bp.aug05[bp.temp$status=="I"]
bp.a05.n<-bp.aug05[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.a05.i,2,sum)))
x.n<-sum(floor(apply(bp.a05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.a05.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.a05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

###############################################################
###############################################################
##Import CMR June vegetation matrix
x.j<-read.table("CMRjun05.txt",header=T,row.names=1)
cmr.jun.05<-t(x.j[1:337,])
cmr.jun.05<-data.frame(cmr.jun.05)
row.names(cmr.jun.05)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.j05.i<-cmr.jun.05[cmr.temp$status=="I"]
cmr.j05.n<-cmr.jun.05[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.j05.i,2,sum)))
x.n<-sum(floor(apply(cmr.j05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.j05.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.j05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
#######
##Import CMR June vegetation matrix
```

```
x.j<-read.table("CMRaug05.txt",header=T,row.names=1)
cmr.aug.05<-t(x.j[1:337,])
cmr.aug.05<-data.frame(cmr.aug.05)
row.names(cmr.aug.05)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.a05.i<-cmr.aug.05[cmr.temp$status=="I"]
cmr.a05.n<-cmr.aug.05[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.a05.i,2,sum)))
x.n<-sum(floor(apply(cmr.a05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.a05.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.a05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
#######
##Import CMR June vegetation matrix
x.j<-read.table("CMRjun06.txt",header=T,row.names=1)
cmr.jun.06<-t(x.j[1:337,])
cmr.jun.06<-data.frame(cmr.jun.06)
row.names(cmr.jun.06)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.j06.i<-cmr.jun.06[cmr.temp$status=="I"]
cmr.j06.n<-cmr.jun.06[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.j06.i,2,sum)))
x.n<-sum(floor(apply(cmr.j06.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.j06.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.j06.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100


##################################################################
##Import CMR June vegetation matrix
x.j<-read.table("CMRaug06.txt",header=T,row.names=1)
cmr.aug.06<-t(x.j[1:337,])
cmr.aug.06<-data.frame(cmr.aug.06)
row.names(cmr.aug.06)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.a06.i<-cmr.aug.06[cmr.temp$status=="I"]
```

```
cmr.a06.n<-cmr.aug.06[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.a06.i,2,sum)))
x.n<-sum(floor(apply(cmr.a06.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.a06.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.a06.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100
######################################################################
#####
##looks at the relationship between I N abundance and Frequencey per
#plot
##for all samples

j04.i<-apply(bp.j04.i,1,sum)
j04.n<-apply(bp.j04.n,1,sum)

j05.i<-apply(bp.j05.i,1,sum)
j05.n<-apply(bp.j05.n,1,sum)

j04.i.f<-apply(bp.j04.i>0,1,sum)
j04.n.f<-apply(bp.j04.n>0,1,sum)

j05.i.f<-apply(bp.j05.i>0,1,sum)
j05.n.f<-apply(bp.j05.n>0,1,sum)


bp.in.lm<-lm(j04.i~j04.n)
cor(j04.n,j04.i)
plot(j04.n,j04.i,main="Burke Park",xlab="Native Cover",ylab="Introduced
Cover",pch=19)
lines(j04.n,fitted(bp.in.lm),col=2)
summary(bp.in.lm)


bp.in.lm.5<-lm(j05.i~j05.n)
cor(j05.n,j05.i)
plot(j05.n,j05.i,main="Burke Park",xlab="Native Cover",ylab="Introduced
Cover",pch=19)
lines(j05.n,fitted(bp.in.lm.5),col=2)
summary(bp.in.lm.5)
##Freq BP richness
bp.in.lm.5.f<-lm(j05.i.f~j05.n.f)
cor(j05.n.f,j05.i.f)
plot(j05.n.f,j05.i.f,main="Burke Park",xlab="Native
Richness",ylab="Introduced Richness",pch=19)
lines(j05.n.f,fitted(bp.in.lm.5.f),col=2)
summary(bp.in.lm.5.f)


par(mfrow=c(1,2))
```

```
hist((j04.i/(j04.i+j04.n))*100,xlab="%Introduced cover",main=" Burke
Park")
hist((j05.i/(j05.i+j05.n))*100,xlab="%Introduced cover",main=" Burke
Park")

hist((j04.n/(j04.i+j04.n))*100,xlab="%Native cover",main=" Burke Park")
hist((j04.n/(j05.i+j05.n))*100,xlab="%Native cover",main=" Burke Park")

par(mfrow=c(1,2))
boxplot(j04.i.f,floor(j05.i.f),names=c("June 04","June 05"),ylab="
richness per plot",main="Introduced Species")
boxplot(j04.n.f,floor(j05.n.f),names=c("June 04","June 05"),ylab="
richness per plot",main="Native Species")

par(mfrow=c(1,2))
boxplot(j04.i,j05.i,names=c("June 04","June 05"),ylab=" abundance per
plot",main="Introduced Species")
boxplot(j04.n,j05.n,names=c("June 04","June 05"),ylab=" abundance per
plot",main="Native Species")
########################################################################
####CMR#############ABUNDANCE########
j05.i<-apply(cmr.j05.i,1,sum)
j05.n<-apply(cmr.j05.n,1,sum)

apply(cmr.a05.i,1,sum)
apply(cmr.a05.n,1,sum)

j06.i<-apply(cmr.j06.i,1,sum)
j06.n<-apply(cmr.j06.n,1,sum)

apply(cmr.a06.i,1,sum)
apply(cmr.a06.n,1,sum)
##########FREQ##################
j05.i.f<-apply(cmr.j05.i>0,1,sum)
j05.n.f<-apply(cmr.j05.n>0,1,sum)

apply(cmr.a05.i>0,1,sum)
apply(cmr.a05.n>0,1,sum)

j06.i.f<-apply(cmr.j06.i>0,1,sum)
j06.n.f<-apply(cmr.j06.n>0,1,sum)

apply(cmr.j06.i>0,1,sum)
apply(cmr.j06.n>0,1,sum)


cmr.in.lm<-lm(j05.i~j05.n)
cor(j05.n,j05.i)
plot(j05.n,j05.i,main="CMR",xlab="Native Cover",ylab="Introduced
Cover",pch=19)
lines(j05.n,fitted(cmr.in.lm),col=2)
summary(cmr.in.lm)

cmr.in.lm.6<-lm(j06.i~j06.n)
```

```
cor(j06.n,j06.i)
plot(j06.n,j06.i,main="CMR",xlab="Native Cover",ylab="Introduced
Cover",pch=19)
lines(j06.n,fitted(cmr.in.lm.6),col=2)
summary(cmr.in.lm.6)

hist((j06.i/(j06.i+j06.n))*100,xlab="%Introduced cover",main=" CMR
study site")
hist((j05.i/(j05.i+j05.n))*100,xlab="%Introduced cover",main=" CMR
study site")

hist((j06.n/(j06.i+j06.n))*100,xlab="%Native cover",main=" CMR study
site")
hist((j05.n/(j05.i+j05.n))*100,xlab="%Native cover",main=" CMR study
site")

par(mfrow=c(1,2))
boxplot(j05.i.f,j06.i.f,names=c("June 05","June 06"),ylab=" richness
per plot",main="Introduced Species")
boxplot(j05.n.f,j06.n.f,names=c("June 05","June 06"),ylab=" richness
per plot",main="Native Species")

par(mfrow=c(1,2))
boxplot(j05.i,j06.i,names=c("June 05","June 06"),ylab=" abundance per
plot",main="Introduced Species")
boxplot(j05.n,j06.n,names=c("June 05","June 06"),ylab=" abundance per
plot",main="Native Species")


################
##combinded data sets from cmr and bp
bp.j04.i.p<-apply(bp.j04.i,1,sum)
bp.j04.n.p<-apply(bp.j04.n,1,sum)

bp.j05.i.p<-(apply(bp.j05.i,1,sum))
bp.j05.n.p<-(apply(bp.j05.n,1,sum))

cmr.j05.i.p<-(apply(cmr.j05.i,1,sum))
cmr.j05.n.p<-(apply(cmr.j05.n,1,sum))

cmr.j06.i.p<-(apply(cmr.j06.i,1,sum))
cmr.j06.n.p<-(apply(cmr.j06.n,1,sum))

all.n<-c(bp.j04.n.p,cmr.j06.n.p)
all.i<-c(bp.j04.i.p,cmr.j06.i.p)

all.i.n.lm<-lm(all.i~all.n)
par(mfrow=c(1,1))
plot(all.n,all.i,main="Combinded data
sets",xlab="Native",ylab="Introduced")
summary(all.i.n.lm)

##position of Introduced species in the relative species abundance
curve
```

```
par(mfrow=c(1,2))
bp.rsa.in<-read.table("BPtempsamp.txt",header=T)
attach(bp.rsa.in)
plot(rankj05,log(june05),col=4,pch=19,main="Burke Park RSA
distribution",ylab="log abundance",xlab="species rank",cex=1.2)
points(rankj05[status=="I"],log(june05[status=="I"]),col=2,pch=19,cex=1
.2)
legend(5,0,"Introduced",pch=19,col=2,bty="n",cex=1.2)
legend(5,2,"Native",pch=19,col="blue",bty="n",cex=1.2)

#####June 2004#######
par(mfrow=c(1,2))
bp.rsa.in<-read.table("BPtempsamp.txt",header=T)
attach(bp.rsa.in)
plot(rankj04,log(june04),col=4,pch=19,main="Burke Park RSA
distribution",ylab="log abundance",xlab="species rank",cex=1.2)
points(rankj04[status=="I"],log(june04[status=="I"]),col=2,pch=19,cex=1
.2)
legend(5,2,"Introduced",pch=19,col=2,bty="n",cex=1.2)
legend(5,3,"Native",pch=19,col="blue",bty="n",cex=1.2)
#########################

cmr.rsa.in<-read.table("CMRtempsamp.txt",header=T)
attach(cmr.rsa.in)
plot(rankj05,log(june05),col=4,pch=19,main="CMR RSA
distribution",ylab="log abundance",xlab="species rank",cex=1.2)
points(rankj05[status=="I"],log(june05[status=="I"]),col=2,pch=19,cex=1
.2)
legend(5,0,"Introduced",pch=19,col=2,bty="n",cex=1.2)
legend(5,2,"Native",pch=19,col="blue",bty="n",cex=1.2)

plot(rankj06,log(june06),col=4,pch=19,main="CMR RSA
distribution",ylab="log abundance",xlab="species rank",cex=1.2)
points(rankj06[status=="I"],log(june06[status=="I"]),col=2,pch=19,cex=1
.2)
legend(5,2,"Introduced",pch=19,col=2,bty="n",cex=1.2)
legend(5,3,"Native",pch=19,col="blue",bty="n",cex=1.2)

plot(bp.rsa.in$rankj05[bp.rsa.in$status=="I"],log(bp.rsa.in$june05[bp.r
sa.in$status=="I"]),main="RSA distribution of Introduced
species",xlab="rank",ylab="abundance",col=2,pch=19,cex=1.2)
points(cmr.rsa.in$rankj06[cmr.rsa.in$status=="I"],log(cmr.rsa.in$june06
[cmr.rsa.in$status=="I"]),col="blue",pch=19,cex=1.2)
legend(5,3,"Burke Park",pch=19,col=2,bty="n",cex=1.2)
legend(5,2,"CMR",pch=19,col="blue",bty="n",cex=1.2)

###Number and Abundance in percent for each temporal sample
###June 2004
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJune04.txt",header=T)
bp.june04<-data.frame(x.bp.j[,1:219])
row.names(bp.june04)<-seq(1:15)
library(vegan)
```

```
bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.j04.i<-bp.june04[bp.temp$status=="I"]
bp.j04.n<-bp.june04[bp.temp$status=="N"]

x.i.f<-sum(floor(apply(bp.j04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.j04.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100


x.i<-sum(floor(apply(bp.j04.i,2,sum)))
x.n<-sum(floor(apply(bp.j04.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

#################################################################
##July 2004
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJuly04.txt",header=T)
bp.july04<-data.frame(x.bp.j[,1:219])
row.names(bp.july04)<-seq(1:15)
library(vegan)
##ju=JULY
bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.ju04.i<-bp.july04[bp.temp$status=="I"]
bp.ju04.n<-bp.july04[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.ju04.i,2,sum)))
x.n<-sum(floor(apply(bp.ju04.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.ju04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.ju04.n>0,2,sum)))

(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

#######################################################################
####
###August 2004
#masked zero abundant species, retained 15 rows
x.bp.a<-read.table("BPAug04.txt",header=T)
bp.aug04<-data.frame(x.bp.a[,1:219])
row.names(bp.aug04)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.a04.i<-bp.aug04[bp.temp$status=="I"]
bp.a04.n<-bp.aug04[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.a04.i,2,sum)))
x.n<-sum(floor(apply(bp.a04.n,2,sum)))
(x.i/(x.n+x.i))*100
```

```
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.a04.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.a04.n>0,2,sum)))

(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
########
##June 05
#masked zero abundant species, retained 15 rows
x.bp.j<-read.table("BPJune05.txt",header=T)
bp.june05<-data.frame(x.bp.j[,1:219])
row.names(bp.june05)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.j05.i<-bp.june05[bp.temp$status=="I"]
bp.j05.n<-bp.june05[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.j05.i,2,sum)))
x.n<-sum(floor(apply(bp.j05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.j05.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.j05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

########################################################################
#########
##August 05
#masked zero abundant species, retained 15 rows
x.bp.a<-read.table("BPAug05.txt",header=T)
bp.aug05<-data.frame(x.bp.a[,1:219])
row.names(bp.aug05)<-seq(1:15)
library(vegan)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.a05.i<-bp.aug05[bp.temp$status=="I"]
bp.a05.n<-bp.aug05[bp.temp$status=="N"]

x.i<-sum(floor(apply(bp.a05.i,2,sum)))
x.n<-sum(floor(apply(bp.a05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(bp.a05.i>0,2,sum)))
x.n.f<-sum(floor(apply(bp.a05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100
```

```
##############################################################
CMR
##############################################################
##Import CMR June vegetation matrix
x.j<-read.table("CMRjun05.txt",header=T,row.names=1)
cmr.jun.05<-t(x.j[1:337,])
cmr.jun.05<-data.frame(cmr.jun.05)
row.names(cmr.jun.05)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.j05.i<-cmr.jun.05[cmr.temp$status=="I"]
cmr.j05.n<-cmr.jun.05[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.j05.i,2,sum)))
x.n<-sum(floor(apply(cmr.j05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.j05.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.j05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

#######################################################################
#######
##Import CMR Aug vegetation matrix
x.j<-read.table("CMRaug05.txt",header=T,row.names=1)
cmr.aug.05<-t(x.j[1:337,])
cmr.aug.05<-data.frame(cmr.aug.05)
row.names(cmr.aug.05)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.a05.i<-cmr.aug.05[cmr.temp$status=="I"]
cmr.a05.n<-cmr.aug.05[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.a05.i,2,sum)))
x.n<-sum(floor(apply(cmr.a05.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.a05.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.a05.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

#######################################################################
#######
##Import CMR June vegetation matrix
x.j<-read.table("CMRjun06.txt",header=T,row.names=1)
cmr.jun.06<-t(x.j[1:337,])
cmr.jun.06<-data.frame(cmr.jun.06)
row.names(cmr.jun.06)<-names(x.j)
```

```
cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.j06.i<-cmr.jun.06[cmr.temp$status=="I"]
cmr.j06.n<-cmr.jun.06[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.j06.i,2,sum)))
x.n<-sum(floor(apply(cmr.j06.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.j06.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.j06.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100


#################################################################
##Import CMR June vegetation matrix
x.j<-read.table("CMR.aug06.txt",header=T,row.names=1)
cmr.aug.06<-t(x.j[1:337,])
cmr.aug.06<-data.frame(cmr.aug.06)
row.names(cmr.aug.06)<-names(x.j)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.a06.i<-cmr.aug.06[cmr.temp$status=="I"]
cmr.a06.n<-cmr.aug.06[cmr.temp$status=="N"]

x.i<-sum(floor(apply(cmr.a06.i,2,sum)))
x.n<-sum(floor(apply(cmr.a06.n,2,sum)))
(x.i/(x.n+x.i))*100
(x.n/(x.n+x.i))*100

x.i.f<-sum(floor(apply(cmr.a06.i>0,2,sum)))
x.n.f<-sum(floor(apply(cmr.a06.n>0,2,sum)))
(x.i.f/(x.n.f+x.i.f))*100
(x.n.f/(x.n.f+x.i.f))*100

####Analysis of I and N species at the quadrat level.
######
y<-read.table("CMR.quadmat.June05.txt",header=T,row.names=1)
cmr.ab.jun.5<-t(y)
cmr.ab.jun.5<-data.frame(cmr.ab.jun.5)
row.names(cmr.ab.jun.5)<-names(y)
names(cmr.ab.jun.5)<-row.names(y)
dim(cmr.ab.jun.5)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.ab.i.5<-apply(cmr.ab.jun.5[cmr.temp$status=="I"],1,sum)
cmr.ab.n.5<-apply(cmr.ab.jun.5[cmr.temp$status=="N"],1,sum)
par(mfrow=c(1,2))
cmr.ab.in.5<-lm(cmr.ab.i.5~cmr.ab.n.5)
```

```
plot(cmr.ab.n.5,cmr.ab.i.5,ylab="introduced abundance per
quadrat",xlab="native abundance per quadrat", main="CMR")
lines(cmr.ab.n.5,fitted(cmr.ab.in.5))
summary(cmr.ab.in.5)

#####################
y<-read.table("CMR.quadmat.June06.txt",header=T,row.names=1)
cmr.ab.jun<-t(y)
cmr.ab.jun<-data.frame(cmr.ab.jun)
row.names(cmr.ab.jun)<-names(y)
names(cmr.ab.jun)<-row.names(y)
dim(cmr.ab.jun)

cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
cmr.ab.i<-apply(cmr.ab.jun[cmr.temp$status=="I"],1,sum)
cmr.ab.n<-apply(cmr.ab.jun[cmr.temp$status=="N"],1,sum)
par(mfrow=c(1,2))
cmr.ab.in<-lm(cmr.ab.i~cmr.ab.n)
plot(cmr.ab.n,cmr.ab.i,ylab="introduced abundance per
quadrat",xlab="native abundance per quadrat", main="CMR")
summary(cmr.ab.in)
###############################################################
##USES TEXT FILE OF 226 QUADRATS
x<-read.table("BP.quadmat.June05.txt",header=T,row.names=1)
bp.ab.jun.05<-t(x)
bp.ab.jun.05<-data.frame(bp.ab.jun.05)
row.names(bp.ab.jun.05)<-names(x)
names(bp.ab.jun.05)<-row.names(x)

bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
bp.ab.i<-apply(bp.ab.jun.05[bp.temp$status=="I"],1,sum)
bp.ab.n<-apply(bp.ab.jun.05[bp.temp$status=="N"],1,sum)

bp.ab.in<-lm(bp.ab.i~bp.ab.n)
plot(bp.ab.n,bp.ab.i,ylab="introduced abundance per
quadrat",xlab="native abundance per qaudrat",main="Burke park")
lines(bp.ab.n,fitted(bp.ab.in))

summary(bp.ab.in)

##this set of code looks at the rank of present natives and non-
natives.
##for the bp and cmr. and subset of data removes present species.
##BP##
bp.temp<-data.frame(read.table("bptempsamp.txt",header=T,row.names=1))
attach(bp.temp)
mean(rankj05[status=="I"])
mean(rankj05[status=="N"])
rank.i.lm<-lm(rankj05~status) # this model and anova have 0abund
species
anova(rank.i.lm)
#removes 0 abundant species manually
bp.j05.n<-sort(rankj05[status=="N"],decreasing=F)
```

```
bp.j05.i<-sort(rankj05[status=="I"],decreasing=F)
boxplot(bp.j05.n[1:108],bp.j05.i[1:28],names=c("Native","Introduced"),m
ain="BP Species Rank June 05")
detach(bp.temp)

##CMR ###
cmr.temp<-
data.frame(read.table("cmrtempsamp.txt",header=T,row.names=1))
attach(cmr.temp)
mean(rankj05[status=="I"])
mean(rankj05[status=="N"])
rank.i.lm<-lm(rankj05~status) # this model and anova have 0 abund
species
anova(rank.i.lm)
#removes 0 abundant species manually
cmr.j05.n<-sort(rankj05[status=="N"],decreasing=F)
cmr.j05.i<-sort(rankj05[status=="I"],decreasing=F)
boxplot(cmr.j05.n[1:119],cmr.j05.i[1:9],names=c("Native","Introduced"),
main="CMR Species Rank June 05")
#anova(cmr.j05.n[1:119],cmr.j05.i[1:9])
detach(cmr.temp)
```