Study Objective

The undeniable global increases in atmospheric CO$_2$ concentrations ([CO$_2$]$_{atm}$) and air temperatures are causing significant changes in plant communities (Parmesan, 2006). Consequently, plant communities currently suited for a particular site may not be locally adapted under future conditions. Studies that examine how individual species and plant communities respond to global climate changes are important to understanding where species will be locally adapted in the future.

The Prairie Heating and CO$_2$ Enrichment (PHACE) site outside of Cheyenne, WY is equipped with Free-Air CO$_2$ Enrichment (FACE) technology to supply elevated [CO$_2$]$_{atm}$ conditions to circular plots. There are also ceramic heaters 1.5m above each plot to supply increased warming. Experimental plots were exposed to a factorial design of ambient and future global climate conditions. Specifically, elevated [CO$_2$]$_{atm}$ treatments raise [CO$_2$]$_{atm}$ to 600ppm and elevated heat treatments increase temperatures +3 °C at night and +1.5 °C during day. These global change treatments mimic the climate that is expected for SE Wyoming in 100 years.

Currently, the Cimarron and Comanche National Grasslands in SE Colorado and SW Kansas exhibit this climate that SE Wyoming is proposed to experience within a century. Plant species native to this ‘southern range’ are likely to be more locally adapted to SE Wyoming’s future climate than the ‘northern range’ species that presently inhabit the area. It is predicted, therefore, that seedling establishment and growth of broad range and southern species will be higher than northern species in plots exposed to combined elevated [CO$_2$]$_{atm}$ and warming. Northern species, on the other hand, should preferentially establish and grow in plots experiencing ambient conditions. The main objective of this study is to determine whether or not the combined effects of global change treatments and species home range significantly affect the resulting plant community.

Plant Community Data

A seed mixture of twenty native species was introduced into twenty bare-ground PHACE subplots. The seed mix included species naturally found 1) across northern mixed-grass prairie and southern short-grass
steppe (broad range), 2) exclusively in northern mixed-grass prairie (northern range), and 3) exclusively in southern short-grass steppe (southern range). Data collected from these developing plant communities were used to determine how each global change treatment shaped the plant community after two growing seasons. Specifically, measurements of species density and relative canopy cover were taken during 2012 and 2013. Aboveground biomass was sampled after the second growing season in 2013.

Density data were collected by counting the number of individuals of a species within one subplot. Since each subplot was slightly more or less than one square meter, the raw species count data were divided by a plot-normalizing factor that scaled the data into individuals/m². The canopy cover percentage was measured for each species, bare ground, and litter within each subplot. Each percentage of individual species cover was then divided by the total plant canopy cover percentage in that plot. Thus, a cover value relative to total plant cover in a particular plot was formed. At the end of the two-growing season experiment, total aboveground biomass was clipped, dried, and weighed. Dry biomass weights were divided by a plot-normalizing factor to scale the data to grams biomass/m².

**Statistical Analysis Using Program R**

Three statistical analyses were run to detect whether or not the combined effects of global change treatment and plant home range significantly affected the plant density, relative cover, or biomass. First, graphical representations of response ratios were used to view the data relative to the control treatment (Figure 1).
To calculate a response ratio, the value of some treatment (e.g. northern species density in an AHN plot) is divided by the mean of the corresponding control treatment value (e.g. northern species density in an ACN plot). After dividing each value by the mean of the control treatment, the mean and standard error of the relative values can be taken of each treatment. Thus, each treatment can be accurately compared to one another, regardless of differing seeding rates between species or differing numbers of species within range categories.

Second, analysis of variance tests (ANOVA) were run to determine the variables explaining changes in plant communities with treatment and range. An ANOVA is a statistical test used to model the response variable (density, relative cover, or biomass) as a function of three possible explanatory variables. Here, explanatory variables include treatment code (global change treatment), species home range, and the interaction between treatment and range. This is called a three-way ANOVA since three explanatory variables were used.

When the result of an ANOVA returns a p-value less than 0.5, that explanatory variable significantly affects the response variable tested. For example, Figure 2 shows the results of an ANOVA run on total 2013 relative cover values. Here, range alone as well as the
interaction between global change treatment and range were both highly significant at explaining the relative cover in 2013.

**Figure 2:** ANOVA test using 2013 relative cover data. Results show a significant effect (p<0.5) of range and well as the interaction between treatment and range on species relative cover.

The final statistical tool used was a similarity percentage (SIMPER). This analysis compares two plant community types, provides information about how different the communities are, and reports what specific species are driving those differences. In this study, the comparison of two plant communities reveals the effect of a certain climate treatment. For example, comparison of the AHN treatment (heating only) to the ACN treatment (ambient control) looks at the effect of heat on the plant community.

A community data matrix is required to use the SIMPER analysis. This means that data must be organized horizontally with individual species as columns containing community data (density, cover, or biomass). One additional column with treatment code as a factor with two or more levels must be present as well. Then, the horizontal community data matrix can be run through the SIMPER function. This initial output reports all possible community comparison pairs and the three most influential species driving the differences between those two communities. For example, differences between the two communities AHN and ACN are driven by species THFI, SPCR, ARFR and SPCO (Figure 3). Together, these four species drive more than 80% of the difference between communities AHN and ACN.

**Figure 3:** 2013 Biomass SIMPER. This initial return shows the percent
contribution of the three most important species in describing the differences between two plant communities

Many other values can be extracted from the SIMPER object in addition to the basic cumulative contribution results. For example, the average and standard deviation of each species contribution to the overall dissimilarity in addition to the ratio between the two is provided. The average abundance of each species in each treatment is also reported (Figure 4).

Figure 4: Summery of the SIMPER object. In order, the columns report average contribution to overall dissimilarity, standard deviation of contribution, ratio of average to standard deviation of contribution, average abundances in each compared treatment, and cumulative contributions.

It is also useful to know the average dissimilarity between the two treatment communities being compared. Figure 5 shows that the plant communities in treatment AHN and ACN are 54.07% different from each other.

Figure 5: Looking at the overall dissimilarity between the plant communities in two treatment types.
All three of these statistical analyses help determine whether or not the combined effects of global change treatment and plant home range significantly affected plant community development. The response ratios visually show how species density, relative cover, and biomass change with range within each global change treatment. For this study, many response ratio values have such large error bars that significant differences cannot be determined visually.

The ANOVA results provide statistical p-values describing whether or not treatment, range, or the interaction between the two is significantly changing the plant community. Though a few data sets show that the interaction between global change treatment and species home range is significant, much of the data does not. In many cases, range alone is the only significant explanatory variable.

Finally, the SIMPER analysis reports many values describing the dissimilarity between two plant communities and the species driving those differences. This analysis is specifically useful in a situation where significant differences or influences do not arise after running other analyses. Though the differences between two communities or the combined effect of treatment and range may not be significant, it is beneficial to see what species are driving the differences that do exist.

**Literature Cited**