

## ABSTRACT

Prairie fragmentation, the need for legume inoculants used in restoration and revegetation programs, and the importance of understanding prairie ecosystem processes, have prompted the study of native prairie rhizobial diversity. In this thesis research, a survey of the rhizobia associated with *Dalea purpurea* Vent., a native legume, was performed across nine remnants, and various site and soil variables were analyzed in order to determine which factors might affect the rhizobial distribution found. BOXA1R PCR was used to characterize rhizobial diversity, while 16S rRNA gene-sequence analysis allowed the identification of the most abundant species found. Rarefaction analysis was performed to obtain the expected genotype richness and Shannon Index per site, and compare them with site area. In addition, a canonical discriminant analysis (CDA) was used to identify which soil variables best discriminated among sites, and determine if there was any relationship with genotype distribution. Of the 1029 rhizobia analyzed, 53 clusters were found, with only four accounting for 84% of the samples. Of the four major clusters, three had a 16S rRNA gene sequence similar to *Rhizobium gallicum*, and, of these, two were ubiquitous throughout the study area. The fourth major cluster was similar to *R. etli*, the main common bean (*Phaseolus vulgaris*) microsymbiont. Site area positively correlated with genotype richness, while no clear relationship was found with soil variables. The implications of these results for prairie rhizobia biogeography and inoculant research are discussed.