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6	GRASSLAND ROOT COMMUNITIES: SPECIES DISTRIBUTIONS AND HOW THEY ARE
7	LINKED TO ABOVEGROUND ABUNDANCE
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25 ABSTRACT

26 There is little comprehensive information on the distribution of root systems among coexisting 27 species, despite the expected importance of those distributions in determining the composition 28 and diversity of plant communities. This gap in knowledge is particularly acute for grasslands, 29 which possess large numbers of species with morphologically indistinguishable roots. In this 30 study we adapted a molecular method, fluorescent fragment length polymorphism, to identify 31 root fragments and determine species root distributions in two grasslands in Yellowstone 32 National Park. Aboveground biomass was measured and soil cores (2 cm diam) were collected 33 to 40 cm and 90 cm in an upland, dry grassland and a mesic, slope-bottom grassland, respectively, at peak foliar expansion. Cores were subdivided and species that occurred in each 34 10 cm interval were identified. The results indicated that the average number of species in 10 cm 35 intervals (31 cm³) throughout the sampled soil profile was 3.9 and 2.8 at a dry and a mesic 36 grassland, respectively. By contrast, average species number per 0.5 m^2 determined by the 37 38 presence of shoot material was 6.7 and 14.1 at dry and mesic sites, respectively. There was no 39 relationship between soil depth and number of species per 10 cm interval in either grassland, 40 despite the exponential decline of root biomass with soil depth at both sites. There also was no 41 relationship between root frequency (i.e., the percentage of samples in which a species occurred) 42 and soil depth for the vast majority of species at both sites. The preponderance of species were 43 distributed throughout the soil profile at both sites. Assembly analyses indicated that species 44 root occurrences were randomly assorted in all soil intervals at both sites, with the exception that F. idahoensis segregated from A. tridentata and P. spicata in 10-20 cm soil at the dry grassland. 45 46 Root frequency throughout the entire sampled soil profile was positively associated with shoot 47 biomass among species. Together these results indicated the importance of large, well

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48	proliferated root systems in establishing aboveground dominance. The findings suggest that
49	spatial belowground segregation of species probably plays a minor role in fostering resource
50	partitioning and species coexistence in these YNP grasslands.
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52	KEY WORDS: Fluorescent fragment length polymorphism, FFLP, grassland, plant competition,
53	roots, Yellowstone National Park
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71 INTRODUCTION

72 As sessile organisms, plants capture resources and interact with neighbors within the 73 aboveground (sward) and belowground (root) zones that they occupy. Knowledge of canopy 74 characteristics, including canopy size, shape, and leaf orientation and density, are relatively easy 75 to measure and have been critical to progress in understanding whole - plant light absorption 76 (Horn 1971, Weiner 1982, Johansson and Keddy 1991, Miller 1994), aboveground intra- and 77 inter-specific plant competition (Grime 1977), and plant community assembly and composition 78 (Grime 1977, Givnish 1982, Goldberg and Barton 1992). In contrast, the study of plant 79 interactions belowground largely has proceeded with little empirical information on the structure 80 of whole root communities under natural conditions. Plant ecologists have long considered resource partitioning an important requisite for plant 81 82 species coexistence (Hutchinson 1959, Tilman 1988). Compared to the single resource, light, obtained aboveground, roots acquire numerous resources from the soil, including water and as 83 84 many as 17 essential nutrients (Marschner 1995). Nutrient addition experiments have revealed 85 that coexisting species can partition belowground resources by being limited by different 86 combinations of nutrients (e.g. N, phosphorus, potassium, Harpole and Tilman 2007) and 87 differentiating the form and timing of nitrogen uptake (McKane et al. 1990, 2002). In addition, 88 and of particular interest in this study, coexisting species partition belowground resources by 89 segregating their root systems (Weaver 1919, Casper and Jackson 1997, Schenk et al. 1999). 90 However, important shortcomings are associated with methods typically used to measure 91 root distributions in the field. Excavating roots, perhaps the most common method to examine 92 root distributions, misses fine roots that are usually the most physiologically active. Other 93 studies that rely on morphological differences of roots to distinguish roots of different species in

soil samples, often collected by coring, are limited to species that can be distinguished
morphologically. Isotope methods have been used to isolate individually labeled plants from
neighbors (Baldwin et al. 1971, Baldwin and Tinker 1972, Fusseder 1983, Milchunas et al.
1992), but cannot be scaled up to isolate populations of different species in diverse communities.
As a consequence, there is no comprehensive information on the spatial properties of root
systems of whole plant communities, particularly in grasslands, which support species that

101 The inability to identify plant roots comprehensively in grasslands has prevented the 102 resolution of basic questions about community organization. For instance, how do root zone 103 distributions and sizes vary among co-occurring species? Is root zone size related to canopy 104 size? How is root zone size associated with nutrient uptake capacity? In addition, the dearth of 105 information on the full compliment of coexisting species has stalled progress on exploring how 106 root segregation may contribute to soil resource partitioning among species.

107 Molecular identification methods have great potential for providing the necessary 108 information to address these questions. Researchers have developed the use of restriction 109 fragment length polymorphism (RFLP) analysis of plastid genes and the rDNA internal 110 transcribed spacer (ITS) region to identify root species in woodland, savanna, alpine, and 111 grassland sites (Bobowski et al. 1999, Linder et al. 2000, Brunner et al. 2001, Ridgway et al. 112 2003). Ridgway et al. (2003) also described an alternative method with the potential to be more 113 efficient than RFLP analysis. This latter technique identifies species based on direct analysis of 114 fluorescently-tagged DNA amplification products (FFLP) from the plastid tRNA-Leu (trnL) 115 gene.

116 We have examined the root community structure of two grasslands in Yellowstone 117 National Park (YNP), one upland, dry site, and a second slope-bottom, mesic site. Roots were 118 identified using FFLP analysis of species diagnostic portions of the *trn*L gene. This technique 119 allowed us to determine, for the first time that we are aware, the root distributions of the 120 preponderance of the coexisting species in grasslands under natural conditions. We addressed 121 two specific questions: (1) How segregated (horizontally and by depth) were the root systems of 122 coexisting grassland species? (2) Was aboveground biomass and the volume of soil exploited by 123 species related in these grasslands?

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125 MATERIALS AND METHODS

Field methods We examined the root distributions of co-occurring plant species at two 126 127 grasslands on the northern winter range of YNP. YNP's northern winter range, a mostly rolling grassland and shrub-grassland, is grazed by herds of elk (Cervus elaphus), bison (Bison bison), 128 129 and pronghorn (Antilocapra americana), primarily during October – April each year. The 130 climate of the northern winter range is characterized by long, cold winters and short, dry 131 summers. Thirty-year (1977 - 2007) mean annual precipitation and temperature at Mammoth 132 Hot Springs in the northwest corner of YNP were 370 mm, with 62% falling during the April -133 Sept growing season, and 4.9°C, respectively. Soils of the northern winter range were derived 134 from mostly tertiary and quaternary volcanic materials that have been glaciated several times 135 after their deposition.

Rolling topography on the northern winter range creates steep gradients of soil moisture,
organic carbon and nitrogen, and plant productivity and composition. In this study, we
contrasted root distributions of coexisting plant species in two grasslands, a relatively dry upland

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grassland situated on a large bench above Crystal Creek, and a mesic grassland located at the
base of a slope in a large shallow depression above Mammoth Hot Springs. The two sites
differed markedly in aboveground production (116 gm⁻² [CB] vs 235 gm⁻² [M]) and soil N

142 (0.23% vs 0.78%) and C (2.4% vs 10.4%) content (Frank 2007).

Shoot samples (> 1 g) of all visible plant species were collected in August, 2005, and June 143 144 and July, 2006, to provide material for molecular identification of species roots. In most cases 145 shoot material from multiple (2-5) conspecific individuals was collected to explore the 146 possibility of polymorphism within species (Appendix A). Shoot biomass was determined and 147 root cores were collected in June and July of 2006 at the dry and mesic sites, respectively, after 148 shoots had reached peak biomass in each grassland. A 3 x 4 m plot of homogeneous vegetation 149 was established at each site. Within the plot, three parallel 4 m transects spaced 1 m apart were 150 established and five, 2 cm diam root cores were collected at 1 m intervals starting at the beginning of each transect (15 cores /site). Soil was cored to 90 cm at M. At CB, large 151 152 subsurface rocks limited the depth of soil cores to 30 or 40 cm. Each core was separated into 0-5 153 cm, 5-10 cm, and, thereafter, 10 cm intervals. Care was taken to as much as possible limit roots of one interval contaminating another. Soil cores were stored at -20°C until processed for root 154 155 identification.

At 0, 2, and 4 m distances along each transect, shoot biomass was estimated in a 0.5 m² (0.71 x 0.71m) quadrat using the canopy intercept method that related biomass to the number of times a species was contacted by a pin passed through the canopy at a fixed angle (Frank and McNaughton 1990). We recorded contacts with 50 randomly placed pins per 0.5 m² quadrat. The root cores were removed from the center of each quadrat after shoot biomass was sampled.

Molecular methods To identify roots, we first generated a library of the tRNA-Leu (*trnL*) gene

163 sequences from each species present at our field sites. Next, we identified a subregion within the

164 *trnL* intron that we could use to identify species via the fluorescent fragment length

165 polymorphism (FFLP) method of Ridgway et al. (2003). Note that this procedure identified the

166 presence of species in root samples, not the abundance of species in those samples. Detailed

167 molecular methods are provided in Appendix A.

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169 <u>Statistical methods</u> The frequency that a species was found in soil core samples was used as a 170 measure of the volume of soil that was occupied by that species. Linear and quadratic functions 171 were used to explore the relationship between root frequency and soil depth for each species at 172 each site. Relationships between overall root frequency and shoot biomass among species also 173 were explored with linear and quadratic functions. A quadratic term was added only if it was 174 found to explain an additional significant ($\alpha = 0.05$) amount of the variation in the dependent 175 variable. Variables were log-transformed to achieve homoscedasticity. 176 Analysis of species segregation patterns for canopy co-occurrence data and root cores

Analysis of species segregation patterns for canopy co-occurrence data and root cores 177 across the soil rooting depth gradient was performed using the approach of Sanders et al. (2003). 178 which calculated a standardized 'C-score' that represented the degree to which species co-179 occurred more or less often than expected by chance. The quasi-swap algorithm is a method of 180 matrix randomization that preserves row (sample richness) and column (species abundance) 181 totals with minimum bias compared to other swap algorithms (Miklós and Podani 2004). A 182 value between +/-1.96 standard deviations does not reject the null hypothesis that a community 183 is randomly assembled (P<0.05), while a value above 1.96 indicates a significant negative 184 species association (i.e., segregation). Standardized C-scores were calculated for each root depth

- strata and canopy data separately using the 'quasi-swap' algorithm with 500 permutations in the
 VEGAN statistical package (Oksanen et al. 2007) for R version 2.6.
- 187
- 188 RESULTS

Effectiveness of using *trnL* to identify roots. At the dry site, all 19 species for which leaf tissue had been sampled for *trnL* analysis possessed unique fragment lengths, with the exception of two shrub species, *T. canescens* and *C. viscidiflous*, which could not be discriminated from one another (257 bp, Appendix A). An unidentified fragment of 280 bp was detected in 8 of the 76 root samples. This fragment may represent a species that was active early in the spring and was not detected aboveground when leaf tissue was sampled for *trnL* analysis, or may represent a

polymorphism at the *trn*L region for another species. This fragment was not included in any ofthe statistical analyses.

At the mesic grassland, the fragment length for each of the 23 species for which leaf
material had been collected was unique, except in the case of three species pairs; *A. adscendens*and *S. multiradiata* (261 bp), *C. arvense* and *E. laevigatum* (269 bp), and *P. pratense* and *P. pratensis* (376 bp) (Appendix A). Members of each species pair, consequently, could not be
distinguished from one another.

Species richness The average number of species per 10 cm core interval (31 cm³, 0-5 and 5-10 samples were pooled for this analysis) varied 3.5 - 5.7 species among depths at the dry site and 2.1 - 4.3 species at the mesic site (Table 1). The average number of species per 31 cm^3 volume of soil across all depths was 3.9 and 2.8 at dry and mesic sites , respectively. There was a maximum eight species found in a 0-5 cm core (15.5 cm^3) at the dry site and a maximum 7 species found in 10-20 cm and 60-70 cm cores at the mesic site. No roots were found in one 50-

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208 60 cm core from the mesic site; however for most intervals at both sites the most species-209 depauperate soil volume was occupied by a single species (Table 1). Because the members of 210 certain pairs of species at each site could not be discriminated from one another, maximum, 211 average, and minimum values for the sites are probably conservative. For example, at the mesic site, where derived belowground species richness values were likely most conservative, 261 bp, 212 213 269 bp, and 376 bp fragments, each which could represent two species in a sample, were found 214 in 31%, 28%, and 38% of the soil core samples, repectively (Appendix B). At the dry site, the 215 257 bp fragment that could not distinguish a pair of species was found in 64% of the root 216 samples (Appendix B). As a comparison to the root species richness values, the mean (+ SE) number of species per 0.5 m^2 determined by shoot material was 6.7 (+0.5) and 14.1 (+0.6) at the 217 218 dry and mesic sites, respectively.

219 There was no significant relationship between average, maximum, or minimum number of species per soil 0-10 cm interval (0-5 cm and 5-10 cm samples were combined) with soil depth 220 221 (P > 0.10) for either grassland. However, because the wet weight of the root samples declined 222 exponentially with depth (P < 0.008 for both sites, Fig. 1), we found a positive relationship 223 between the number of species to wet root weight (SP#/RT WT) with root depth (RD) for the 224 two grasslands combined (there was no significant difference in the functions between sites), described by the linear relationship log SP#/RT WT = $0.96(\log RD) - 2.3$ (r² = 0.79, P < 225 226 0.0001), where "log" denoted common logarithms.

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<u>Species root distributions</u> Fifteen of the 19 species that were collected around the plot at the dry
site for *trnL* analysis were found in the root samples, and 13 of those 15 species occurred
aboveground within the quadrats sampled for shoot biomass (Appendix B). Roots of the

231 remaining two species presumably grew from stems located outside the quadrats. The frequency 232 that species were present in root samples across all depth intervals (0-40 cm) at the dry site 233 ranged from 1% for A. cernuum and A. frigida to 73% for P. sandbergii (Appendix B). Root 234 frequency was unrelated to soil depth for any species at the dry site, with the exception of P. 235 sandbergii, whose root frequency declined linearly with depth (Fig. 2). Thirteen of the 15 236 species for which roots appeared in cores at the dry site were present in the deepest soil interval 237 (30-40 cm); the two remaining species were rare belowground and only found in one soil sample 238 each (Appendix B).

239 At the mesic site, all 19 species and species pairs identified with trnL fragments were found 240 aboveground or belowground (Appendix B). There were five unidentified species in the shoot biomass quadrats that represented 8% of the total shoot biomass present at the mesic site. Those 241 242 five species were not identified to species at the time of sampling and tissue was not collected for 243 later identification or for trnL analysis. There were no "unknown" fragments detected in root 244 samples that did not correspond to a characterized species or species pair. Therefore, the roots of 245 each of the five unknown species either, by chance, were not represented in the core samples or 246 the fragment size of the unknown species was the same as another fragment-identified species. 247 Percent root frequency across all depths (0-90 cm) at the mesic site ranged from 0% for 248 three species (*Potentilla anserina*, *Senecio sp.*, *Viola adunca*) rarely sampled aboveground to 249 38% for the species pair Phleum pratense/ Poa pratensis, which together were abundant 250 aboveground (Appendix B). Three species, or species pairs, varied significantly with depth: 1) 251 the pair, Circium arvense/ Equisetum laevigatum, was unimodally related to depth, with root 252 frequency peaking approximately 40-50 cm, (2) Fragaria virginiana was negatively, linearly 253 related to depth, and (3) Trifolium repens was positively related to soil depth (Fig 3). Thirteen of

254 the 16 species whose roots were identified in samples were detected at the deepest sampled depth

(80-90 cm); two of the remaining three species (Sisvrinchium angustifolium, Taraxacum 255

256 officinale) were found as deep as 70 - 80 cm and the third species (*Iris missouriensis*) was very

- 257 rare and found in only one soil sample (Appendix B).
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259 Relationship between root frequency and shoot biomass Log-transformed shoot biomass was 260 positively related to log-transformed root frequency (calculated for the entire sampled soil 261 profile) in both grasslands. At the dry site, the relationship was linear (Fig. 4a). The slope of the 262 $\log - \log$ relationship did not differ from unity (P = 0.71), indicating that the relationship 263 between the untransformed variables did not depart from linearity. The seven most common species that produced $> 1.2 \text{ gm}^2$ of shoot material had the seven highest root frequencies (> 264 265 20%). At the mesic site, there was an increasing quadratic relationship between log shoot biomass and log root frequency (Fig. 4b). 266

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268 Aboveground and belowground species associations Plant species were associated randomly 269 aboveground and belowground at the dry site, except for a statistically significant amount of 270 species segregation that occurred in the 10-20 cm soil interval (Fig. 5). Correlation analyses 271 examining the presence and absence of all species pairs at that interval revealed significant 272 negative associations of F. idahoensis with A. tridentata and P. spicata. (P < 0.002 for both). P. 273 spicata and A. tridentata were found in six and nine of the 10, 0 - 40 cm cores in which F. 274 idahoensis roots were identified. Consequently the negative relationship between F. idahoensis 275 and A. tridentata, in particular, was not a result of the two species having been horizontally 276 separated in the sampling plot. A re-analysis of species association patterns for 10-20 cm

277samples without *F. idahoensis* resulted in the remaining species being randomly associated,278indicating that the distribution of *F. idahoensis* roots was responsible for the significant279segregation signature for roots in 10 - 20 cm soil in the original analysis. At the mesic site, plant

- 280 species were randomly associated aboveground and at each soil depth interval (Fig. 5)
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282 DISCUSSION

283 Root segregation The role of resource partitioning in promoting the diversity of plant 284 communities has been a long-term topic of great interest to plant ecologists (Hutchinson 1959, 285 Schoener 1974, Berendse 1979, Chesson 1994). Results from a number of studies indicate that 286 species spatially differentiate their root systems, which is considered a prominent mechanism used by coexisting species to partition soil resources (Casper and Jackson 1997, Schenk et al. 287 288 1999). However, most of these root investigations have been hampered by important limitations of the standard methods that are usually used to measure root distributions. Excavating roots, for 289 290 instance, results in the loss of fine roots, which often are the most physiologically active roots. 291 Other studies that rely on visually discriminating roots of different species are limited to the 292 proportionally few co-existing species that can be morphologically distinguished (Vogt et al. 293 1989, Harper et al. 1991, Casper and Jackson 1997, Schenk et al. 1999). Moreover, we are 294 unaware of any root study that has included a random null model to explore spatial co-295 occurrence.

In this study we used a molecular method to identify root fragments picked from soil cores in order to determine the distribution of the roots of plant species in two YNP grasslands. Results suggest that root segregation played a relatively minor role in resource partitioning among the great majority of the species in these grasslands. Roots picked from 31 cm³ soil volumes (10 cm

300 intervals) usually included mixed species. An average of 3.9 and 2.8 species, with maximum 301 numbers of 8 and 7 species, were found at dry and mesic sites, respectively. Analysis of 302 belowground community assembly (Fig. 5) revealed random sorting among species at each soil 303 depth at dry and mesic sites, with the exception of a statistically significant segregation signal 304 among species occurring at the 10-20 cm soil interval at the dry grassland. Further analysis 305 indicated that the segregation signature for that interval was due to F. idahoensis spatially 306 differentiating its roots from A. tridentata, a shrub, and P. spicata, a grass. The segregation of 307 two common grasses, F. idahoensis and P. spicata, that have similar mid-season aboveground 308 production pulses is consistent with results of McKane et al. (1990), who found belowground 309 spatial differentiation between two dominant grasses that possessed similar phenologies in an 310 old-field community.

311 There also was limited support for species segregating according to depth in both YNP 312 grasslands. We found that the root frequencies of a single species (*Poa sandbergii*) at the dry 313 grassland (Fig. 2) and two species (F. virginiana, T. repens) and a species pair (C. arvense/E. 314 *laevigatum*) at the mesic grassland (Fig. 3) were related to soil depth. However, root frequency 315 was unassociated with depth for the great majority of the species in both grasslands. There also 316 was no relationship between species number and soil depth, even though root biomass declined 317 exponentially with depth. Finally, the preponderance of species was found throughout the entire 318 soil profile that was sampled at each site, indicating that the vast majority of species exploited all 319 soil depths.

The results indicating that multiple species occupied a relatively small volume of soil, the widespread random sorting of species, and the limited evidence for differentiation by depth among species in both grasslands suggests that root segregation probably played a relatively

minor role in maintaining species coexistence. Instead, differentiating the form (e.g., NH₄⁺ vs 323 324 NO_3) or timing that a nutrient is taken up (McKane et al. 1990, 2002) or differences in the 325 combinations of limiting soil resources (Harpole and Tilman 2007) may largely be responsible 326 for resource partitioning among co-occurring plant species. Of course, this study has not 327 addressed the effects of pathogens (Dobson and Crawley 1994, Mitchell 2003, Kulmatiski et al. 328 2008), herbivory (Grime 1979, Milchunas et al. 1988, Grace and Jutila 1999), and disturbance 329 (Pickett and White 1985, Picket et al. 1999), which also can be major determinants of plant 330 community composition and may have played important roles in the shoot and root community 331 properties in YNP grassland.

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<u>Shoot - root relationships</u> There has been considerable interest in factors that control the
variation in shoot vs root allocation among species and the importance of shoot vs root
competition in structuring plant communities (Cahill 1999, 2002, de Kroon et al. 2002). A
number of studies have indicated that belowground competition, in general, is stronger than
aboveground competition (Fowler 1986, Wilson 1988, Casper and Jackson 1997), in particular in
habitats primarily limited by soil resources, such as water as in the case of YNP grasslands that
were examined in this study.

Competition aboveground is generally considered to be asymmetrical because of the ability of taller plants to cast shade on their understory neighbors (Weiner 1990, Casper and Jackson 1997, de Kroon et al. 2002). Whether or not belowground competition is symmetrical or asymmetrical is still unclear. Several studies that have experimentally varied root biomass in the greenhouse and field have concluded the existence of size-symmetric root competition (Gerry and Wilson 1995, Weiner et al. 1997, Cahill and Casper 2000). However, there is evidence that

under some conditions root competition may be asymmetrical (Fransen et al. 2001). In addition, it has been proposed that asymmetrical root competition is most likely to occur in nutrient rich soils where the soil volume is completely occupied by roots and resources become available in a patchy manner as organic material is mineralized. Under such circumstances, species with more widely distributed roots may have a disproportionate competitive advantage over other species that are less proliferated throughout the soil (Fransen et al. 2001, de Kroon et al. 2002).

352 Root frequency, a measure of the soil volume occupied by a species, was positively related 353 to shoot biomass in both YNP grasslands. This indicated that the capacity of a species to 354 produce shoot biomass was associated with the volume of soil exploited by its roots. At the dry 355 site, the seven most abundant plants aboveground possessed the seven most proliferated root 356 systems, suggesting the importance of relatively extensive root systems in establishing 357 aboveground dominance. In addition, the relationship between shoot biomass and root frequency 358 at the dry grassland (Fig. 4a) indicated that the ability of a root system to support shoot biomass 359 did not vary with the volume of soil exploited by species. If one defines the competitiveness of a 360 species as the ability of that species to obtain resources, and it is further assumed that the amount 361 of shoot biomass that is supported by root system volume (i.e., frequency) is a measure of the 362 capacity of a unit of root system to supply soil resources to shoots, then competition among 363 species at the dry grassland was symmetrical; the amount of shoot biomass supported by roots 364 increased linearly as the amount of soil exploited by roots increased. In contrast, at the mesic 365 site, shoot biomass increased quadratically, at a rate greater than linear (Fig. 4b). For instance, 366 the ratio, shoot biomass : root frequency at the mesic site increased from 0.05 to 0.4, by 700%, 367 for species with 10% and 30% root frequency. The increase in the capacity of a unit root 368 distributed in the soil to supply shoot biomass as the size of a species root system increases

369 suggests that belowground competition at the mesic site was operating asymmetrically. Evidence 370 for symmetric competition at the relatively dry and infertile grassland vs asymmetric competition 371 at the relatively mesic and fertile grassland supports the notion that asymmetric competition may 372 be more common in resource-rich compared to resource-poor environments (Fransen et al. 2001, 373 de Kroon et al. 2002).

374 However, care needs to be exercised when interpreting the results of this study for several reasons. First, this study examined the presence and absence of species in soils, not their 375 376 abundance. Plant species have been found to allocate root biomass differently, some producing 377 finer roots or proliferating through the soil more diffusely than others (Eissenstat and Caldwell 378 1988). Consequently, the results do not provide information on the distribution of root biomass 379 of species. Second, we have treated all roots equivalently, even though roots will differ in 380 function, with some providing more of an anchoring function while other roots will primarily 381 function to take up resources (Robinson et al. 2002). Third, we did not measure grazing in this 382 study and therefore we do not know at our sites which species lost more aboveground biomass 383 than others to consumers and how herbivory may have influenced the distribution of roots of 384 species.

Nevertheless this study provides novel information on species root distributions, community belowground assembly, and the linkages between belowground and aboveground allocation strategies in grassland. The results revealed a limited amount of spatial, including depth, segregation of species in YNP grassland. We also found that shoot biomass was positively related to the soil volume exploited by a species, indicating the importance of the soil occupied by a root system in establishing aboveground dominance in semi-arid grassland. These findings

- 391 suggest that the maintenance of grassland diversity in YNP is primarily a function of factors
- 392 other than the spatial segregation of species root systems.

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- Table 1. Average, maximum, and minimum number of species found in soil intervals and
- averaged across intervals. Values for 0-5 and 5-10 cm data are both pooled and left separated.

		Dry site (Crystal Bench)					Mesic site (Mammoth)						
Soil depth (cm)		Average (n)		Maximum		Minimum		Average (n)		Maximum		Minimum	
0 - 10	0 -5	5.7	4.5 (15)	8	8	3	2	4.3	3.2 (15)	7	6	2	1
(pooled)	5 - 10	(15)	3.8 (15)		6		1		2.4 (15)		4		1
10-20		3.8 (1	5)	7		1	1	2.7 (1	4)	7		1	I
20 – 30		3.8 (1	5)	7		1 3.1 (15)		5)	5		1		
30 – 40		3.5 (12	2)	7		1	Y	3.4 (15)		6		1	
40 – 50				Y				2.6 (1	5)	4		1	
50 - 60								2.6 (1	4)	5		0	
60 – 70			_					3.4 (1	5)	7		1	
70 – 80								2.7 (1	5)	5		1	
80 - 90								2.1 (1	5)	4		1	
Average													
among 10cm 3.9 intervals		7.0		1.2		2.8		5.3		0.9			

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596 FIGURE LEGEND

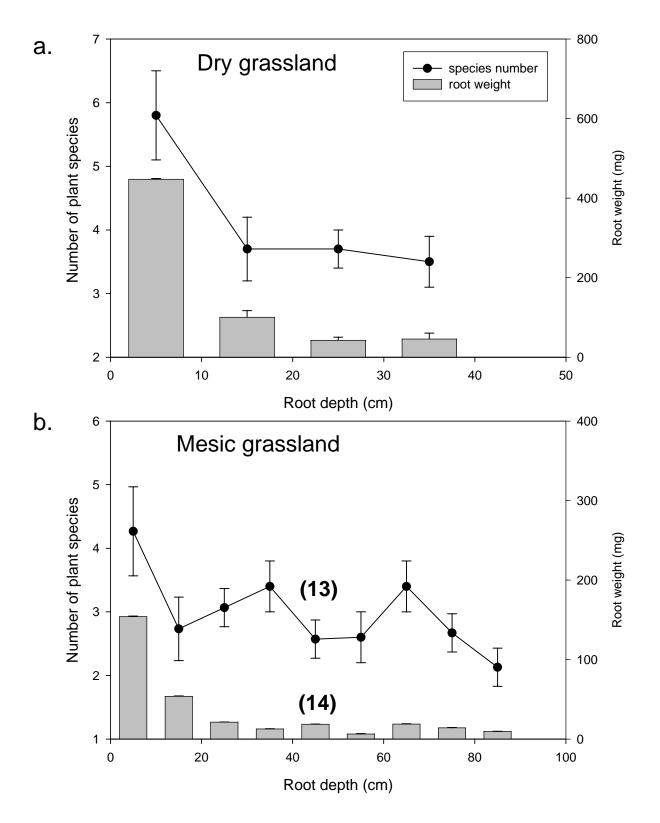
571	
598	Fig. 1. The relationships of the average number of species per root sample and wet root weight
599	with soil depth for two YNP grasslands, (a) the dry site (Crystal Bench) and (b) the mesic site
600	(Mammoth). Species number and root weight values are per 2 cm diam by 10 cm soil depth
601	increment. Sample sizes are 15, except for the 40 - 50 cm interval at the mesic grassland, which
602	is provided in parentheses (see Appendix A for explanation). Wet root weight (RW) declined
603	exponentially with soil depth for the dry site by RW = $877e^{-0.14(SD)}$ (r ² = 0.98, P < 0.008) and for
604	the mesic site by RW = $243e^{-0.09(SD)}$ (r ² = 0.94, P < 0.0001).
605	
606	Fig. 2. Relationship between root frequency (RT FREQ) and root depth (RT DEPTH) for Poa
607	sandbergii at the dry site (Crystal Bench). Root frequency is the percentage of the samples in
608	which the species was identified.
609	
610	Fig. 3. Relationships between root frequency and root depth for (a) the species pair Cirsium
611	arvense – Equisetum laevigatum and the species (b) Fragaria virginiana and (c) Trifolium
612	repens at the mesic site (Mammoth).
613	
614	Fig. 4. The relationship between common log-transformed shoot biomass and common log-
615	transformed root frequency among species at the (a) dry and (b) mesic grasslands.
616	
617	Fig. 5. Species associations aboveground and at 10 cm soil intervals belowground at the dry
618	(Crystal Bench, black) and mesic (Mammoth, grey line) grasslands. Values within dashed grey

- lines indicate random associations; values above 1.96 indicate a significant negative association 619
- 620 (P<0.05)
- 621



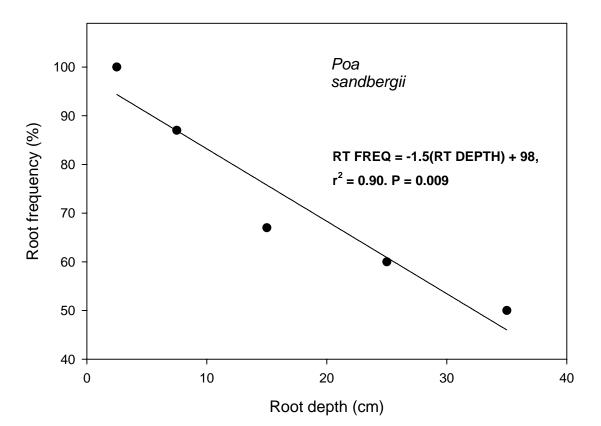
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Fig. 1



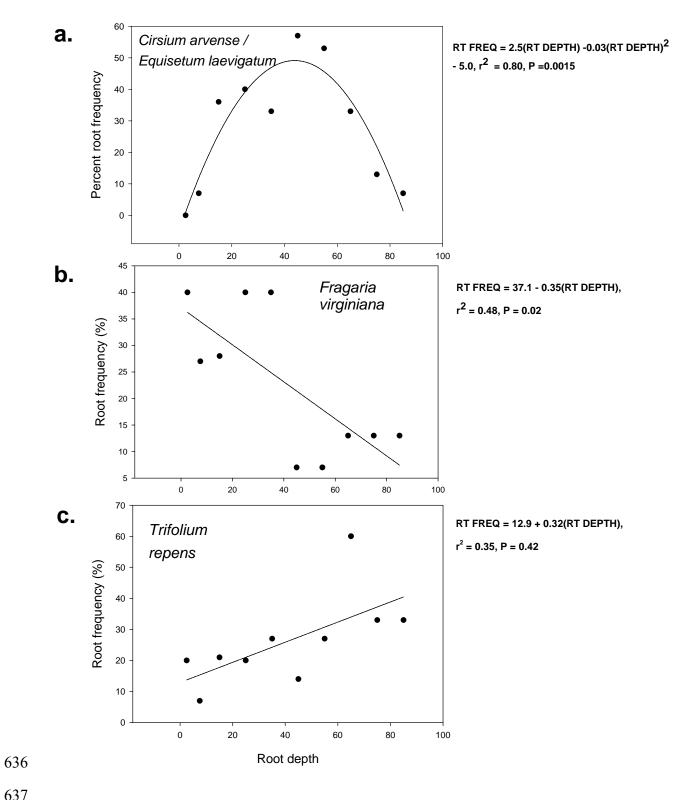
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639

100 a. Dry, upland Shoot biomass (g/m²) 10 $r^2 = 0.30, P = 0.05$ 1.0 0.1 0.01 |__ 1.0 10 100 100 Mesic, swale Shoot biomass (g/m²) 10r² = 0.83, P < 0.0001 1.0 0.1-0.01 0.1 1.0 10 100

Root frequency (%)

640

b.

641 642

Fig. 4



