

oversampling the small trees in the younger stands. Tree heights and diameters ranged up to 90 m and 309 cm. A total of 5,737 trees among the 32 transects were mapped and measured for height, diameter, crown height, and four crown radii. Throughout the chronosequence the stands go from being nearly completely dominated by *Pseudotsuga menziesii*, to being increasingly dominated by *Tsuga heterophylla*, and, to a lesser extent, *Thuja plicata*. The structure of the canopy goes from a simple, fairly even monolayer in the youngest stands to a very complex, highly diffuse canopy with extreme variability in both horizontal and vertical dimensions. In the older stands individuals of *Pseudotsuga* become highly complex, often with multiple, reiterated trunks, and canopy foliage spanning over 70 m. The stands with the highest component of structural complexity were aged between 500 and 700 years and retained 20.7 *Pseudotsuga*/ha. Complexity diminished in the oldest stand due to all but a single *Pseudotsuga*/ha remaining. Several parameters of structural and canopy complexity were examined and are summarized.

VANDEGRIFT, V. ELEANOR,^{1,*} HUA CHEN,¹ THOMAS R. HORTON^{1,2} and MARK E. HARMON.¹ ¹ OREGON STATE UNIVERSITY; ² SYRACUSE UNIVERSITY. **Identification of fungi decomposing woody conifer roots in Oregon using molecular methods.**

Previous studies have indicated that roots from five tree species (*Picea sitchensis*, *Tsuga heterophylla*, *Pseudotsuga menziesii*, *Pinus ponderosa*, and *Pinus contorta*) found across an environmental gradient in Oregon, decompose at different rates. These differences are not explained by moisture, temperature, or wood chemistry. We used molecular techniques to examine wood rotting fungi found in roots of these tree species and test if differences in fungal community structure might explain observed differences in decomposition. Root samples were retrieved from trees cut 5-15 years prior to sampling. Two tree species were sampled at each of three locations across Oregon. Hyphae samples were collected directly from roots, and fungi were cultured from sterile root chips. Eight hundred fifty samples have been obtained, representing 350 hyphae and 500 cultured samples. To analyze genetic diversity of the samples, Internal Transcribed Spacer - Restriction Fragment Length Polymorphism (ITS-RFLP) patterns are compared. A database of ITS-RFLP patterns obtained from sporocarps is used to match and identify the fungi from the root samples. DNA sequences and taxon specific phylogenetic sequence databases are employed to illustrate potential taxonomic relationships between remaining undescribed taxa. Multivariate analyses are used to compare differences in fungal composition between tree species. ITS-RFLP patterns indicate that there are different compositions of fungal communities compared across the five species with *P. ponderosa* and *P. contorta* having fungal communities that are most similar.

VANDER MEULEN, MICHAEL B.* and EDWARD MCCAULEY. UNIVERSITY OF CALGARY. **Generalist herbivores reduce prey community diversity in nutrient-poor systems.**

It is well known that the freshwater herbivore *Daphnia* can suppress the biomass of edible algae and that their dynamics are tightly coupled energetically. These generalist herbivores can promote the biomass and diversity of inedible algae, but few studies have tested how these herbivore dynamics affect the diversity of the edible algal community. Mechanisms, related to grazing losses and nutrient recycling, suggest that increases in grazing pressure should promote the species diversity of edible algae. We tested the hypothesis that *Daphnia* dynamics promotes the diversity of edible algal communities under conditions of either pulsed, pressed, or 'packaged' phosphorus additions (i.e. perturbations that would modify algal competition in phosphorus-limited systems). Predictions were tested in four mesocosm experiments using natural phytoplankton assemblages enclosed in situ. Each experiment lasted 40 days and documented the dynamics of phosphorus, *Daphnia*, other herbivores, and edible algal biomass and community composition in 16 replicate 700 L systems. As expected, *Daphnia* significantly suppressed edible algal biomass and increased phosphorus supplies for algae relative to controls. Contrary to expectations, increases in *Daphnia* biomass resulted in significant decreases in edible algal species diversity, but promoted diversity among major algal taxa (i.e. class level). Phosphorus additions did not influence our results. Diversity reductions due to grazing losses by *Daphnia* outweigh the effects on diversity caused by reduced algal competition.

VANDERVELDE, THEA,^{1,*} LISA A. SHIPLEY,¹ KATE R. SEARLE,² N. THOMSON. HOBBS² and BRUCE A. WUNDER.³ ¹ Department of Natural Resources, Washington State University; ² Natural Resource Ecology Laboratory, Colorado State University; ³ Department of Biology, Colorado State University. **Gain functions for blue duikers in small patches: Does plant geometry matter?**

Foraging by herbivores is often characterized by periods of movement interrupted by pauses for feeding. We define small patches as the area where animals feed during these pauses. Marginal value theory has been widely applied to predict residence time of herbivores in small patches. However, this application depends on the function that relates cumulative energy gains to patch residence time. In particular, this function must be smoothly decelerating. We conducted experiments to examine the strength of evidence for linear, stepped, and decelerating non-linear models representing the cumulative gain of dry matter by blue duikers as a function of their residence time in small patches. In particular, we asked the question: 'How does the geometric arrangement of plant biomass in small patches affect the support for alternative gain functions?' We offered a constant biomass of fresh alfalfa to experimental animals in small patches while varying the number of plants composing that biomass. The strength of evidence for non-linear models was greatest for small patches composed of a few, large plants, while support for stepped and linear models was greatest for patches composed of many small plants. The mechanism causing deceleration in non-linear and stepped models appeared to result from decreases in bite mass cropped as patch biomass was depleted. We conclude that plant geometry will affect the ability of marginal value models to portray herbivore decisions on patch residence time.

VANIER, CHERYL H.* and DANIEL B. THOMPSON. University of Nevada Las Vegas, Las Vegas, NV. **Phenotypic selection in a disturbance-related novel environment.**

Sudden and severe ecological disturbances create biotic and abiotic changes to a plant's environment which could alter selection in populations surviving in the soil as seeds. Natural selection in four native Mojave Desert annual (*Amsinckia tessellata*) populations was estimated to determine the impacts of fire on character evolution. The populations were in a stable (>100 years) perennial shrub community until recently when fires in 1993 and 1995 burned two populations. Burning creates a novel but benign environment, allowing higher adult biomass (average 0.096 g. in unburned (n=273) vs. 0.314 g. in burned (n=373)) and individual reproductive output (2.5 seeds/plant in unburned (n=669) vs. 8.35 in burned (n=898)). We hypothesized that taller, earlier maturing plants would be favored in unburned sites, whereas highly branched, late maturing plants would be favored in the burned environment based on temperature and soil moisture studies relating to desert annuals and perennials. Selective surfaces were approximated using a path model. Selection for many phenotypic characters in terms of viable seed output differed between disturbed and undisturbed populations. However, selection for other characters differed within disturbed and undisturbed replicates, indicating a smaller scale of spatial heterogeneity is predominately determining selection for some characters. The response to selection of ecological traits after a severe disturbance in the desert will be a combination of selection operating on both small and large scales.

VEECH, JOSEPH A.* Miami University, Oxford, Ohio. **The random placement model as a null model of four well-known biogeographic patterns.**

The random placement model specifies the probability that a given species occurs on a given island (or habitat patch) based on the relative area of the island and the abundance of that species on all islands. In effect, the model describes the random distribution of individuals. Since its introduction more than 20 years ago, the random placement model has mostly been used in the analysis of species-area relationships. However, it can also be used to derive the species presence/absence matrix, the fundamental unit in the analysis of ecological patterns such as the nestedness of species subsets and species co-occurrence. In addition, the random placement model can aid in analyses of the distribution-abundance relationship and the relationship between local and regional species richness. I discuss the ways



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