butterflies. Butterfly communities in wet meadows showed a distinctive shift along the hydrological gradient during a drought period. These results imply that the larger Teton meadows will show more predictable (i.e., static) species-habitat associations over the long-term, but that the smaller Gallatin meadows may be an area that will exhibit the effects of global climate change faster.

MULTI-TAXA ASSESSMENT OF THE GENETIC IMPACTS OF FRAGMENTATION AND URBANIZATION IN SOUTHERN CALIFORNIA: LIZARDS (*SCELOPORUS OCCIDENTALIS*, *UTA STANSBURIANA*)

DELANEY, KATHLEEN, Robert Fisher, and Seth Riley. Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, USA (KD), U.S. Geological Survey, San Diego Field Station, San Diego, CA, USA (RF), National Park Service, Thousand Oaks, CA, USA (SR), ksemple@ucla.edu

Habitat fragmentation caused by urbanization can have significant negative effects on wildlife communities. For species with low dispersal ability and / or sensitivity to the urban matrix, there will be reduced connectivity between habitat fragments. This reduction in connectivity causes a reduction in gene flow between subpopulations which can lead to decreased genetic variability and an increased likelihood of local extinction. We examined the genetic impacts of habitat fragmentation in two lizard species (*Sceloporus occidentalis* and *Uta stansburiana*) in the Santa Monica Mountains National Recreation Area (SAMO) north of Los Angeles, California. Lizards were captured using pitfall traps in 10 small habitat fragments and 10 larger core areas. We genotyped each species at 9 microsatellite loci to obtain measures of gene flow between fragments. We also used the computer program STRUCTURE to cluster individuals according to genetic similarity. Significant FST values between fragments indicated a decrease in gene flow and loss of connectivity between fragments. In addition, our STRUCTURE results show individuals with higher genetic similarity are clustered together in populations separated by major roads. Our results reveal that both species showed a strong genetic response to habitat fragmentation. Similar results were found in Jerusalem crickets studied from the same fragments.

STATUS OF MATURE AND OLD-GROWTH FORESTS IN THE PACIFIC NORTHWEST, USA

DELLASALA, DOMINICK, James Strittholt, and Hong Jiang. World Wildlife Fund, Ashland, OR, USA (DD), Conservation Biology Institute, Corvallis, OR, USA (JT, HJ), dellasal@wwfks.org

Nearly 10 million ha of federal lands in the Pacific Northwest, USA, have been managed under the Northwest Forest Plan since 1994. The plan reduced logging levels by 80%; however, only recently are inventories on status and condition of older forests becoming available. Our objectives were to: (1) determine the areal extent of old (> 150 years) and mature (50-150 years) conifer forests using 2000 Landsat 7 ETM+ imagery, (2) examine levels of protection, and (3) determine degree of additional protection afforded to older forests if Late Successional Reserves (LSRs) and Inventoried Roadless Areas (IRAs) were fully protected. Since the time of European settlement, ~72% of the original old-growth conifer forest has been lost largely from logging and other developments. Old-growth conifer forest accounted for by protected areas (GAP 1 and 2), LSRs, and IRAs accounts for 66% of the old-growth conifer forests on public land, 51% in the region, and 14% of the amount that occurred historically. Outside of these land designations, an additional 1,240,271 ha of old growth occurs on other public land and 1,023,392 ha on private lands. Our results indicate the need to periodically monitor older forests and strengthen protections throughout the region.

RESEARCH-BASED, NON-CHEMICAL RESTORATION OF COASTAL SAGE SCRUB IN A SOUTHERN CALIFORNIAN PRESERVE

DESIMONE, SANDRA. Audubon California, Trabuco Canyon, CA, USA, sdesimone@audubon.org

Restoration of rare coastal sage scrub habitat at Audubon California's Starr Ranch Sanctuary in southern California commences year two of non-chemical control of the exotic herbaceous perennial *Cynara cardunculus*, which has invaded 251 ha of grassland stands at the 1575 ha preserve. Because analyses of aerial photoseries taken over 48 years revealed gradual coastal sage scrub colonization of grasslands, we decided to actively restore 102 ha of *C. cardunculus*–infested sites in which shrub species have begun colonization. Results from a factorial experiment established an optimum seeding rate and soil tamping technique. Restoration practices were further refined with a second experiment that showed that a combination of direct seeding and plug planting spaced over the growing season would be beneficial in our semiarid region. Exotic annual plant species require control during the restoration process. An experiment that investigated non-chemical techniques suggested that flaming and early brush cutting could control exotic annuals while natives established in early stages of restoration. Monitoring of active and passive restoration processes in a total of 18 ha over three years showed 50–60 native shrub cover in treatment areas with baseline 0–5 native cover.

NOT THE QUAKING GIANT: EVIDENCE OF SMALL CLONE SIZE IN WEST COAST ASPEN

DEWOODY, JENNIFER, Tom Rickman, Bobette Jones, and Valerie Hipkins. USDA Forest Service, PSW National Forest Genetics Lab, Placerville, CA, USA (JD, VH), USDA Forest Service, Lassen National Forest, Susanville, CA, USA (TR, BJ), jdewoody@fs.fed.us

Molecular genetic evidence of clone structure in quaking aspen (*Populus tremuloides*) disputes the conventional understanding of clone size in western North America, and presents novel challenges for the conservation of this keystone species. Aspen is capable of vegetative reproduction via suckering that can produce large clones consisting of thousands of stems covering hundreds of acres. This peculiar life history has created a mystique around aspen among the public and in the popular media, which can affect management decisions on public lands through public comments and litigation. Analysis of 871 stems of aspen systematically sampled in northeastern California using six microsatellite markers identified 432 unique clones, with a mean of 2.02 ramets sampled per clone. Number of clones per stand was significantly correlated with stand area. Genetic diversity was high in all populations, and moderate but significant genetic differentiation was observed among populations (FRT = 0.028, 95% CI 0.021 to 0.035) and among stands (FSR = 0.07, 0.049 to 0.083). These results indicate that germplasm collection and stand restoration activities should include multiple genetic individuals per stand, and should minimize the movement of germplasm among regions.