

Project Title: Sampling western rattlesnakes and Washington ground squirrels to allow for validation of a landscape level connectivity initiative

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Partners: The Washington Wildlife Habitat Connectivity Working Group (WHCWG) is a science-based collaboration of land and resource management agencies, NGOs, universities, and Washington Treaty Tribes. The group is co-led by Washington State Departments of Fish and Wildlife (WDFW) and Transportation (WSDOT), with active participation from member organizations including The Nature Conservancy (TNC), Conservation Northwest (CNW), Washington Department of Natural Resources, U.S. Forest Service (USFS), U.S. Fish and Wildlife Service, Western Transportation Institute, and University of Washington (UW).

Project Summary: We propose to extend current work developing a validation plan for a connectivity model of Washington ground squirrels (*Urocitellus washingtoni*) and the western rattlesnake (*Crotalus oreganus*). Specifically we propose to begin sample collection to allow future genetic analysis to correlate gene flow with connectivity estimates

Need: The WHCWG recently completed a focal species connectivity assessment for the Columbia Plateau, which included many sagebrush-steppe areas. This connectivity assessment not only included mapping of key habitat areas and linkage corridors, but also a phase II initiative that assessed which core areas and linkages were most important to network connectivity, which links were most threatened by barriers, and which represent restoration opportunities. This comprehensive effort presents a guidance plan for maintaining connectivity across the Columbia Plateau and sagebrush-steppe, but as a model, requires validation to ensure we are actually representing functional connectivity. This is especially true for species that may function as linkage corridor dwellers; that is they require movement or gene flow over multiple generations to provide connectivity across a linkage corridor. Therefore, connectivity cannot be validated easily using studies of direct movement and instead multi-generational approaches such as estimation of gene flow are likely to be most effective.

Two Columbia Plateau focal species that fit this category are Washington ground squirrels (*Urocitellus washingtoni*) and the western rattlesnake (*Crotalus oreganus*). Both require sagebrush steppe and are adversely affected by agriculture and human development. Furthermore, ground squirrels may serve as an important food source for rattlesnakes and thus ground squirrel habitat may be correlated with rattlesnake gene flow. We are currently using GNLCC funding to develop a sampling design for validating the connectivity models for both these species. The sampling plan will be complete in April 2013 and will highlight specific areas to sample, with a power analysis to ensure that we will be able to detect any differences in gene flow should they occur. As part of this current effort, we will also survey potential rattlesnake den sites to confirm presence of rattlesnakes in anticipation of a genetic sampling effort.

The next necessary step is to begin sample collection for a genetic validation study. In many ways, this is the most intensive step as both species require intensive trapping or encounter survey methods to obtain a sufficient sample size. Therefore, we propose to continue our current efforts by beginning to obtain samples from Washington ground squirrels through trapping arrays and western rattlesnakes through visual encounter surveys at dens. While this initial effort will not be sufficient to collect all samples needed for the genetic validation study, the requested funding would provide important seed funding for the sampling effort. In particular, we will initially focus on known colonies to sample for ground squirrels, and select initial rattlesnake sampling areas based on both proximity to ground squirrel sampling areas as well as areas near wind energy development. This will allow us to not only understand if there are associations between ground squirrel and snake connectivity, but also begin to address the influence of wind energy development on reptile populations, an aspect that is current unknown and under-studied.

Objectives:

To sample ground squirrel and rattlesnake populations to collect tissue samples that will be used in a genetic validation study of the Columbia Plateau connectivity initiative. Samples will be collected in such a manner as to allow for an evaluation of the level of genetic connectivity across a range of predicted corridor permeability. Specifically, we will (1) sample ground squirrels in core areas to allow future evaluation of current levels of gene flow for Washington ground squirrels both within and among core habitat areas that have varying levels of predicted connectivity, (2) sample rattlesnake den sites in the vicinity of sampled ground squirrels to allow a test of the correlation of ground squirrel presence with snake gene flow; and (3) sample rattlesnake den sites at varying distances from wind energy developments to evaluate the effect of wind infrastructure on snake connectivity. There is virtually no information on the influence of wind energy development on reptile populations, and therefore this was a very uncertain parameter in the resistance surface development.

Methods:

Task 1.1: We will sample Washington ground squirrels within three habitat concentration areas (HCAs) in the vicinity of the Mansfield Plateau and Banks Lake in the northern Columbia Plateau. This area was chosen for the first sampling effort because each HCA has several known ground squirrel colonies that were observed in the past year, and predictions of linkage corridors are not uniform across the area. Ground squirrels will be caught using Sherman trap arrays within known colonies and hair will be collected from each individual to be used for genetic analysis. At each colony, we will collect samples from at least 15-20 individuals to provide sufficient power for population genetic analysis. We will attempt to sample between 6-12 colonies depending on the number of squirrels we are able to trap over a two month period.
Key personnel WDFW

Task 1.2: We will visit known rattlesnake den sites during spring emergence and fall return when snakes are concentrated at den sites. We will take a blood sample from the tail of each captured snake and paint the basal rattle so the same individual will not be sampled on multiple visits. We will sample snakes at dens that are connected by linkages that pass through known

ground squirrel colonies as well as rattlesnake linkages that do not pass through known squirrel colonies, but are otherwise similar in total resistance. *Key personnel The Orianna Society*

Task 1.3: *We will sample rattlesnake den sites (as outlined in Task 1.2) adjacent to operating wind installations (primarily in Klickitat and Columbia counties). All large wind installations are relatively recent (within the past 5–10 years), and as such would not have affected gene flow in older snakes. Therefore, at each site we will attempt to sample an even distribution of adult and juvenile/subadult snakes. If the infrastructure surrounding wind installations is reducing connectivity among rattlesnakes, we should see lower genetic similarity among juvenile rattlesnakes as compared to adults that were born before much of the wind development. Key personnel The Orianna Society*

Task 1.4: *We will develop a data management plan. This data management plan will include archiving of locality data of sampled individuals as well as plan for storing tissues collected by the project.*

Deliverables:

- Development of Data Management Plan for project (completion July 2013)
- Genetic sampling of 15–20 individuals at 6–10 ground squirrel colonies and 6–8 rattlesnake dens in the Banks Lake/Mansfield Plateau region. (completion July 2014)
- Genetic sampling of individuals at 4–7 rattlesnake dens adjacent to operating wind farms (completion May 2014).
- Final project report (completion July 2014)