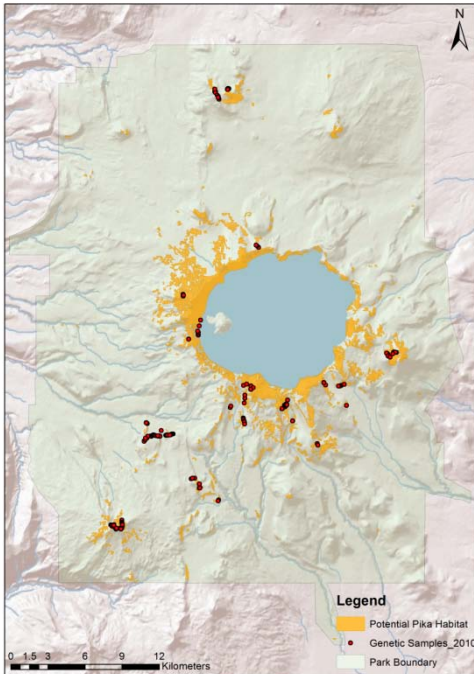




"Pikas in Peril" Research Project

Objective 2:

Habitat-specific models of connectivity and gene flow



Map of Crater Lake National Park showing potential pika habitat and locations where genetic samples were collected in 2010.

Objective 2

- Use high-resolution population genetic data to develop models of **connectivity** and **gene flow** among **fragmented populations** of the American pika in five NPS units representing different habitat types and regions
- Use these models to test how distance and landscape features affect movement and gene flow between habitat patches
- Use these findings to assess isolation of existing pika populations on NPS lands and determine **metapopulation structure** (interaction between populations)

Background

Understanding the habitat requirements of a species is a key step in species conservation. For species such as pikas that live in small areas of isolated habitat, understanding movement between patches is also very important. Pikas live in **talus** slopes and **lava** flows that are often widely scattered and separated by unsuitable habitat. Studies indicate they can move among nearby habitat patches, but how far they can move over different types of terrain is uncertain. Such movements may be very important for maintaining genetic diversity of small populations or for recolonizing areas where pikas die out. In combination with research on the distribution and habitat requirements of pikas in 8 national parks (*see Objective 1 brief*), the Pikas in Peril research team is conducting **landscape genetic** studies to understand movement and gene flow (interbreeding) among pikas in different habitat patches in 5 of those parks. From those studies, we will be able to infer how distance and habitat type affect pika movements among habitat patches. This knowledge will be an important component of understanding how pikas may respond to rapid climate change.

Parks included in Objective 2

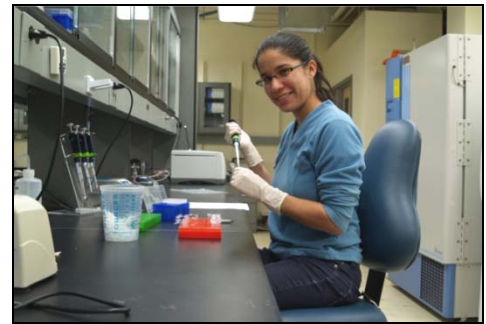
- Crater Lake National Park
- Craters of the Moon National Monument and Preserve
- Grand Teton National Park
- Lassen Volcanic National Park
- Rocky Mountain National Park



DNA for genetic analyses is extracted from pika fecal pellets. Researchers collect samples both from randomly-selected sites and by locating pikas and their haypiles within larger patches of habitat. Photos from left to right: fecal pellets; collecting pellets in the field; American pika calling.

Study design and methods

Trained field crews conducted pika surveys at over 600 sites across the 8 parks during June-October of 2010 (dates varied according to park phenology). A similar survey effort is planned for 2011. Sites are selected randomly using a spatially-balanced sampling design. At each site surveyed to determine if pikas are present, crews search for relatively fresh piles of pika droppings (ideally no more than a few weeks old). Droppings are collected in paper envelopes and returned to the laboratory at Oregon State University for DNA extraction and analysis. Team members also conduct “targeted” sampling of large patches of habitat across each study area so that population and individual-based analyses of genetic similarity can be conducted. Once DNA is extracted in the laboratory, we use pika-specific genetic markers called **microsatellites** to examine how genetically different pikas are within and between habitat patches in each park.



Above: A researcher working with DNA from fecal pellets.

Connectivity modeling with genetic data

Once lab analyses are completed, we will generate GIS-based models of landscape “resistance” based on different habitat models. Each GIS model will characterize potential **connectivity** among pika habitat patches in different ways, based on how slope, terrain type, vegetation, and distance could affect pika movements. We will test these models by determining which model best explains genetic differences among individuals and groups. Once the best connectivity model has been identified, we will use that model to predict connectivity among the patches of habitat where pikas are currently found within each park. Those models will also be used to explore scenarios of habitat change (Project objective #3). Finally, we will test whether genetic diversity of pika groups varies as a function of habitat quality and connectivity within each park, and whether genetic diversity varies strongly among the parks and/or regions. Park managers will be able to use this information to identify pika habitat patches/populations that are at higher risk of extinction, or conversely, that provide critical linkages for maintaining connectivity and diversity in across broad areas of each park. This information will also guide planning for proactive habitat management to ensure that critical areas for pika habitat or dispersal will be protected.

Key references

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These handouts were created to provide a brief description of the 3 objectives of the National Park Service Climate Change Response Program funded “Pikas in Peril” research project. For more details regarding the project and why we are studying pikas, please refer to the overall project resource brief and/or the website listed at the bottom of the page. **Terms in bold** are also defined in a **glossary** (see link).

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