USGS Western Ecological Research Center
Publication Brief

Remaining Populations of Giant Gartersnake Form Five Different Genetic Clusters

The giant gartersnake (*Thamnophis gigas*) is a federally listed threatened species found only in the California Central Valley. An obligate of floodplain marshes, sloughs, and shallow lakes, its distribution has been reduced and fragmented due to human development and alteration of wetland habitat. The species is now restricted mostly to agricultural wetlands and irrigation channels.

Cryptic in behavior and relatively limited in mobility, giant gartersnakes have likely experienced genetic bottlenecks and isolation across its remaining populations. A USGS study published in *Conservation Genetics* sought to uncover such patterns in the population genetics of this species.

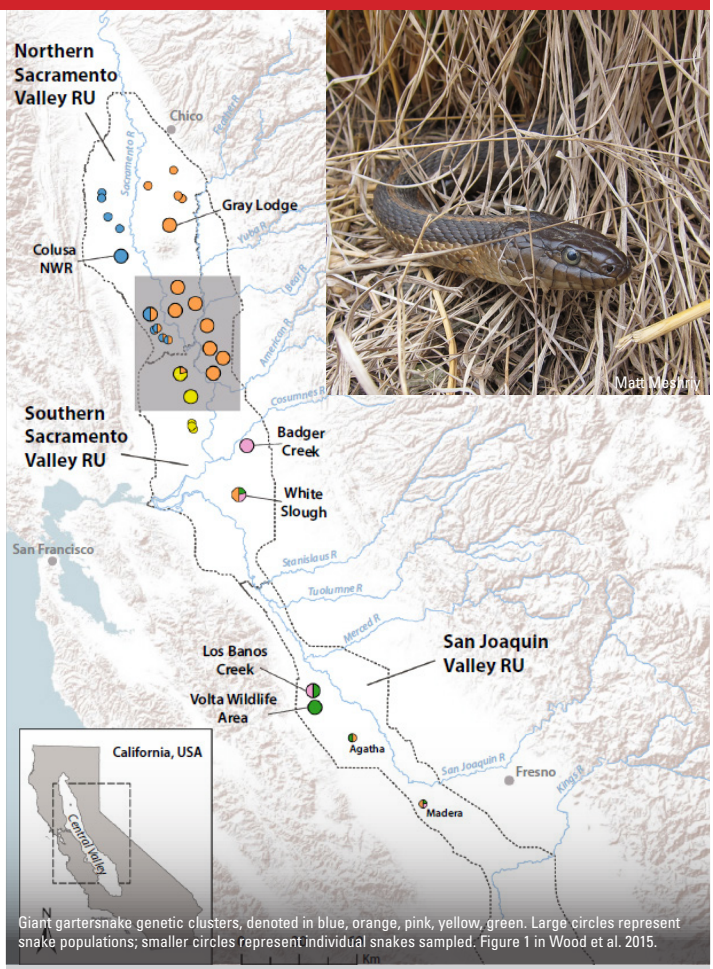
Biologists sampled a total of 477 tissues spanning the known contemporary range of the giant gartersnake. A "population" was defined by grouping together samples from snakes captured within 6 km of other snakes—given 6 km as the approximate maximum range for an individual snake.

Genetic analyses found that giant gartersnake populations fall within five genetic clusters, which tend to align with drainage basins. Populations in the northern (Sacramento Valley) drainage basins, where there is more remaining habitat, have higher genetic connectivity than populations in the southern (San Joaquin) drainage basins.

Greater genetic differences also exist among the more geographically isolated populations in the species' central and southern range. Inbreeding and population bottlenecks were detected in about half of the populations sampled, and evidence suggests the current population size presents inbreeding risks.

The study provides a first-glimpse into the population genetic health of this listed snake across its remaining range. Understanding the genetic landscape of giant gartersnakes can help managers target regions where management, land use, and water use actions can most effectively maintain genetic connectivity for the species.

This Brief Refers To:
Wood, DA, BJ Halstead, ML Casazza, EC Hansen, GD Wylie, AG Vandergast. 2015. **Defining population structure and genetic signatures of decline in the giant gartersnake (*Thamnophis gigas*): implications for conserving threatened species within highly altered landscapes.** *Conservation Genetics*. doi:10.1007/s10592-015-0720-6
http://www.werc.usgs.gov/ProductDetails.aspx?ID=5254



Giant gartersnake genetic clusters, denoted in blue, orange, pink, yellow, green. Large circles represent snake populations; smaller circles represent individual snakes sampled. Figure 1 in Wood et al. 2015.

MANAGEMENT IMPLICATIONS

- This genetic analysis identifies regions where giant gartersnake populations may be at most risk of genetic isolation, as well as regions where management actions may most efficiently encourage population connectivity.

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