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Dear Grant,

This is a brief set of thoughts and recommendations as you consider strategies for the Coyote Valley habitat plan. As you know, I have over 20 years experience working with pond-breeding amphibians in California, particularly California tiger salamander (*Ambystoma californiense*, CTS) and to a lesser extent, California red-legged frog (*Rana draytoni*, RLF).

The basic biology of both species is similar—they reside much of the year in various underground retreats, and go to ponds and pools to breed. For CTS, our work has demonstrated that adults and subadults move considerable distances from breeding sites. We have documented movements of young juveniles in their first few months of life of a kilometer, and we can statistically infer that movements of well over a mile are quite common. We also know that movements between breeding sites are common; this last observation in particular argues for the importance of landscapes that have multiple breeding and rodent-rich upland habitat, all interconnected in an intact landscape. Because the valley bottoms are all essentially destroyed for most CTS metapopulations, it is essential to protect whatever uninterrupted habitat that we can in order to ensure that the species remains on what landscapes are left.

At complete cross-purposes with this model of large, unfragmented landscapes is our recent work documenting that non-native, invasive barred tiger salamander (*A. tigrinum mavortium*) genes have been expanding throughout the central coast region CTS populations. This threat of genetic “biopollution” is documented as a major threat to CTS, and was listed as one of the key issues in the conservation of the species when the Central Distinct Population Segment was federally listed in 2004. As the attached manuscript (in press in *Ecological Applications* and due out in the next month or two) documents, non-native genes have spread from their original source of introductions in the Salinas Valley right up to your area, and it may have extended up to your actual region (lat/long data are listed in the Appendix, which I have also attached). This makes management decisions rather difficult, since the goal with the non-native genes is to **prevent gene flow**, while the goal with native CTS and RLF is to promote gene flow. Doing both on the same landscapes is clearly a huge management challenge.

My own feeling is that we need to proceed in the following way:

- 1) Determine if non-native genes have arrived in the Coyote Valley. To do so means sampling populations over several years, genotyping individuals, and determining if they are pure native or not. This really should be done for many sites, and many salamanders per site. I have permits to conduct this work, but I do not have funding for it or permission to get onto properties.

2) Based on what we learn in 1), several management schemes seem possible. These could range from eliminating one or a few sites, to simply promoting normal gene flow. However, it is very hard to know what to recommend in the absence of the genetic data.

3) Regardless of the *current* state of the populations, we also should have a very regular (yearly, in my opinion) sampling of a set of pools to determine if the genetic picture is changing, either for the better or the worse.

4) Based on 3), we should be able to implement a reasonable adaptive management scheme that reflects the current, on-the-ground status of the non-native invasion.

My lab is well equipped to do both the field and genetics work, and we are willing to do both if there are funds available. We have also proposed a long-term sampling transect that would allow us to determine movement of the genetic front over years, and I would be happy to try to include some sites from the Coyote Valley landscape in that transect. These sites are clearly most useful if they are on public land, or land with long-term conservation easements that allow relatively easy access.

OK, I hope that helps. Good luck with your workshop. If you need any of our papers on the subject, let me know.

Sincerely,

H. Bradley Shaffer  
Professor, Evolution and Ecology &  
Director, Center for Population Biology