

Salamander Dichotomous Key

- 1 a Hind limbs absent *Siren intermedia*
b Hind limbs present Go to 2
- 2 a External gills present in adults *Necturus maculosus*
b External gills absent in adults Go to 3
- 3 a Large size (over 7 cm long in Figure 1) Go to 4
b Small size (under 7 cm long in Figure 1) Go to 5
- 4 a Body background black, large white spots variable in size completely covering body and tail *Ambystoma tigrinum*
b Body background black, small round white spots in a row along each side from eye to tip of tail *Ambystoma maculatum*
- 5 a Body background black with white spots Go to 6
b Body background light color with dark spots and/or lines on body Go to 7
- 6 a Small white spots on black background in a row along each side from head to tip of tail *Ambystoma jeffersonianum*
b Small white spots scattered throughout a black background from head to tip of tail *Plethodon glutinosus*
- 7 a Large irregular white spots on a black background extending from head to tip of tail *Ambystoma opacum*
b No large irregular black spots on a light background Go to 8
- 8 a Round spots scattered along back and sides of body, tail flattened like a tadpole *Triturus viridescens*
b Without round spots and tail not flattened like a tadpole Go to 9
- 9 a Two dark lines bordering a broad light middorsal stripe with a narrow median dark line extending from the head onto the tail *Eurycea bislineata*
b Without two dark lines running the length of the body Go to 10
- 10 a A light stripe running the length of the body and bordered by dark pigment extending downward on the sides *Plethodon cinereus*
b A light stripe extending the length of the body without dark pigment on the sides *Hemidactylum scutatum*



Salamander Speciation Lab Answer Guide

Liyong Dong



Salamander Speciation Lab Answer Guide:

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Abstracts ,1959 **Salamanders** Ashley W. Seifert, Joshua D. Currie, 2022-10-22 This volume provides a comprehensive reference for researchers aiming to bring new techniques and approaches to their scientific research using urodeles. Chapters are authored by leaders in the field and meant to guide readers through laboratory colony husbandry, traditional molecular techniques, experimental manipulation and surgeries, bioinformatics and genomics, transgenics and lineage tracing, and physiological and organismal techniques. In addition to laboratory methods, this volume highlights techniques developed for field studies and work with wild caught animals. Written in the successful *Methods in Molecular Biology* series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step by step, readily reproducible protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and state of the art, *Methods in Salamander Research* aims to be a practical guide for researchers interested in deploying new methodologies in their lab or in the field. **Salamanders in Regeneration Research** Anoop Kumar, András Simon, 2016-10-05 This detailed volume focuses on best practices and conditions for maintaining the most commonly used salamander species in the laboratory. *Salamanders in Regeneration Research: Methods and Protocols* guides readers through experimental manipulations in vivo and in vitro, respectively. With methods on targeting a wide variety of structures ranging from the limb to the heart and to the brain, and methods for studying genetically modified organisms and tools for mining in the genomic databases. Written in the highly successful *Methods in Molecular Biology* series format, chapters include introduction to their respective topics, lists of the necessary materials and reagents, step by step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and up to date, *Salamanders in Regeneration Research: Methods and Protocols* provides a comprehensive collection of methods. **The Dividing Link** Thomas James Devitt, 2010 Plethodontid salamanders of the *Ensatina eschscholtzii* complex have received special attention from evolutionary biologists because they represent one of the very few examples of a ring species, a case where two reproductively isolated forms are connected by a chain of intergrading populations surrounding a central geographic barrier. *Ensatina* has become a textbook example of speciation, yet there still remain fundamental gaps in our knowledge of this fascinating system. In this study, consisting of three components, I extend previous work on the *Ensatina* complex in new directions. In Chapter 1, I conducted a fine scale genetic analysis of a hybrid zone between the geographically terminal forms of the ring, using Bayesian methods for hybrid identification and classification in combination with mathematical cline analyses. F1s and pure parentals dominated the sample. Cline widths were concordant and narrow with respect to dispersal, but there is cytonuclear discordance both in

terms of introgression and the geographic position of mitochondrial versus nuclear clines. Nearly all hybrids possess mitochondrial DNA from one parental type, *klauberi*, suggesting isolation is asymmetrical. Selection against hybrids is inferred to be strong (2–1%), but whether this selection is endogenous (genetically based) or exogenous (environmentally based) remains to be tested. In Chapter 2, I investigated the role of late Quaternary climate change on phylogeographic patterns within the Large blotched *Ensatina* *Ensatina eschscholtzii klauberi*. Intersecting species distribution models constructed under current climatic conditions as well as two different historical time periods (Last Glacial Maximum 21 ka and mid Holocene 6 ka) predicted stable refugial areas where the species may have persisted throughout climatic fluctuations. Significant phylogeographic structure exists, but geographic structuring of genetic variation by refugia was not supported. Results suggest that populations in putative refugia have not been isolated for very long or that gene flow may have masked any earlier periods of divergence in allopatry. In Chapter 3, I conducted a multilocus phylogeographic analysis of the entire *Ensatina eschscholtzii* complex to reexamine previous phylogenetic hypotheses based on mitochondrial DNA alone. A concatenation approach was used in addition to newer methods that model the relationship between the species tree and the gene trees embedded within them. The concatenated tree was similar to previous mitochondrial trees, identifying well-supported coastal and inland clades and recovering *oregonensis* and *platensis* as paraphyletic. The concatenated tree was not well resolved at the base. Basal relationships recovered by the species tree were well resolved, but most relationships were not well supported compared to the concatenated tree. Results are generally consistent with previous efforts based on mtDNA but provide further resolution to the *Ensatina* phylogeny while highlighting the difficult nature of inferring species trees from samples of closely related populations that are experiencing gene flow.

Speciation, Phylogeography, and Gene Flow in Giant Salamanders (Dicamptodon). Craig A. Steele, 2006. Giant salamanders of the genus *Dicamptodon* occur in the Pacific Northwest of North America. The variety of geographic distributions and life history traits displayed among this genus provide opportunities to test hypotheses concerning regional biogeography, effects of Pleistocene glaciation, comparative phylogeography, and patterns of gene flow. A genus-level phylogeny was constructed to test competing biogeographic hypotheses concerning the disjunct distribution of the Idaho giant salamander *D. aterrimus* and a Pleistocene speciation hypothesis for the Cope's giant salamander *D. copei*. Results indicate speciation and distribution of *D. aterrimus* is attributable to the orogeny of the Cascade Mountains rather than recent inland dispersal, and that *D. copei* is distantly related to other coastal species and likely originated much earlier than the Pleistocene. Patterns of intraspecific variation were examined for the widespread Pacific giant salamander *D. tenebrosus*, and hypotheses concerning the location and number of Pleistocene refugia were tested. Results indicate that *D. tenebrosus* was restricted to two Pleistocene refugia: one in the Columbia River valley and another in the Klamath-Siskiyou Mountains, and has recently expanded northward from these refugia into its current distribution. Phylogeographic patterns for *D. copei* were compared to that of the codistributed Van Dyke's salamander

Plethodon vandykei Results reveal that sympatric populations displayed identical phylogeographic topologies suggesting shared evolutionary histories but topologies were ultimately incongruent due to several highly divergent allopatric populations of *D. copei* Comparative patterns of genetic population structure were examined for sympatric populations of *D. tenebrosus* and *D. copei* Results indicate that the metamorphosing species *D. tenebrosus* displayed a lack of population structure while the non metamorphosing species *D. copei* displayed a larger degree of population structure These results help explain the phylogeographic patterns presented for each species The large distribution and post glacial expansion by *D. tenebrosus* was facilitated by its high dispersal ability while the low dispersal ability of *D. copei* lead to a small and fragmented geographic range and greater phylogeographic structure within its range These results suggest that understanding life history variation on a local scale can lead to a better understanding of the mechanistic underpinnings of species distributions in general

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