Genetic Connectivity in a Montane Salamander (*Pseudoeurycea leprosa*)

Emily Brink, Galen Burrell, Nicki Felger, Emmanuel Green
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PURDUE UNIVERSITY FORT WAYNE
Department of Biology

Introduction

- Salamander migration is restricted in montane habitats.
- Populations become isolated spatially and genetically.
- Velo-Antón et al. (2013) used microsatellites to investigate genetic structure between populations
- Using STRUCTURE analysis, they found 7 distinct genetic clusters in 23 sampled populations
- Considerable population admixture in two regions of the study area:
  - Central populations
  - Eastern populations

Objective

- Compare two methods of assessing genetic variation
  - STRUCTURE
  - Discriminant Analysis of Principle Components (DAPC)
- Does our DAPC analysis support/refute author conclusions?

Methods

- 351 individuals sampled from 23 localities – 9 microsatellites amplified and analyzed
- DAPC generated using *Adegenet* package in Rstudio
- Calculated DAPC for 7 clusters (same as original paper)
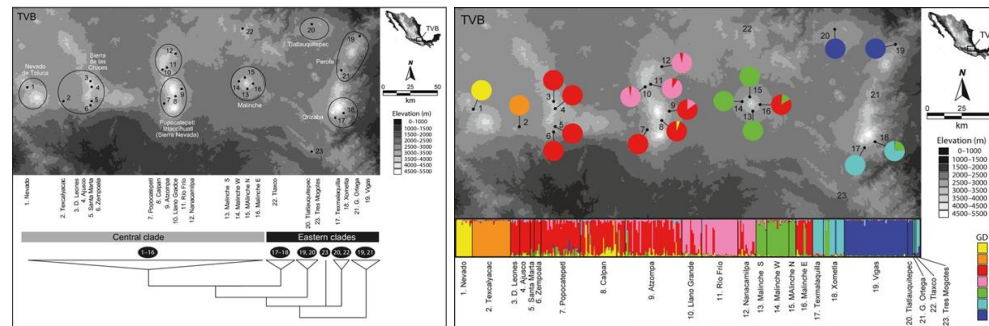
Synthesis of Results from Research Studies

Fig 1: Two maps describing salamander populations sampled in mountains of central Mexico
Results of Bayesian phylogeny (left) and STRUCTURE analysis (right) by Velo-Antón et al. (2013).

Fig 2: Results of DAPC (right) using K=7 clusters provides evidence for four distinct genetic groups. Distance between clusters indicates genetic differentiation.
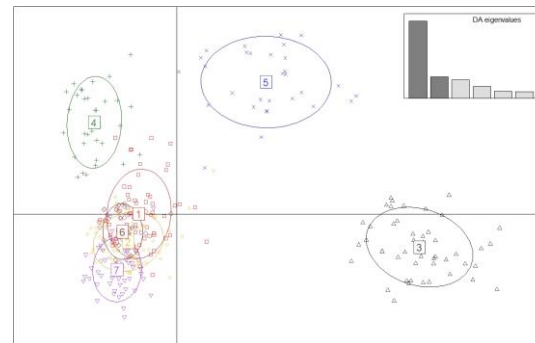
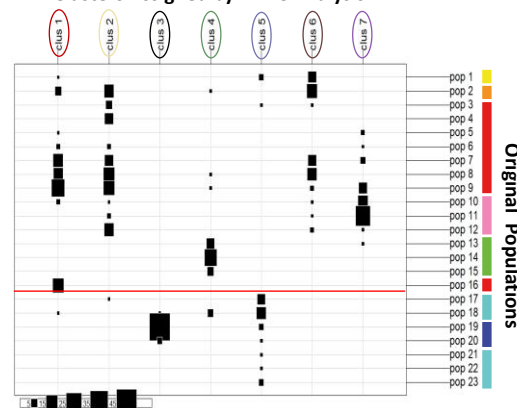**Clusters Assigned by DAPC Analysis**

Fig 3: Table displaying assignment of individuals from sampled populations to DAPC clusters (left).
Original populations are color coded relative to their assignment in STRUCTURE.
Red line indicates central/eastern division.

Conclusions

- Our analysis agrees with findings in original paper
- Based on DAPC, 4 genetically differentiated groups (Fig. 2)
  - Central and eastern groups in different clusters
- Significant admixture within central and eastern groups also predicted by DAPC (Fig. 3)
- DAPC suggested 9 clusters as the optimum number for the data – reveals more diversity in eastern populations
- STRUCTURE discerned greater diversity within central populations
- More sampling in these populations would give greater detail on genetic structure
- Future spatial PCA analysis – need individual GPS data

Acknowledgements

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Literature Cited

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