

Analysis of population structure for *Pleurodeles waltl* and *Pelobates cultripipes* in Mediterranean wetlands

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Introduction

- Comparative study done in 2017 looking at microsatellite data for *Pleurodeles waltl* (Iberian ribbed newt) and *Pelobates cultripipes* (Iberian spadefoot toad) in Madrid, Spain¹
 - P. waltl* – 411 individuals, 20 populations; 18 microsatellite loci used
 - P. cultripipes* – 302 individuals, 16 populations; 16 microsatellite loci used
- Both species are endemic and widely distributed, but fragmented¹
 - "Near Threatened" due to loss of Mediterranean wetland habitat
- Initial study used BAPS v6 to determine genetic structure¹
 - BAPS tends to overestimate the number of clusters and have less accuracy in the number of correct groupings compared to STRUCTURE³
- Objective: To determine population structure using STRUCTURE and compare results to BAPS results¹

Methods

- P. waltl*
 - 346 individuals, 2 ploidy, 17 loci
 - 10,000 burn-in, 100,000 reps.
 - K was set from 1-20 w/ 10 iterations
- P. cultripipes*
 - 240 individuals, 2 ploidy, 14 loci
 - 10,000 burn-in, 100,000 reps.
 - K was set from 1-17 w/ 10 iterations
- Analyzed using Structure Selector² and Structure Harvester → Identifies most likely populations (K) and visualize genetic clusters
- K was chosen using the Mean LnP(K)±Stddev
 - Natural log of probability of # of K
- CLUMPAK test used to determine locations of populations compared to original map¹

Results

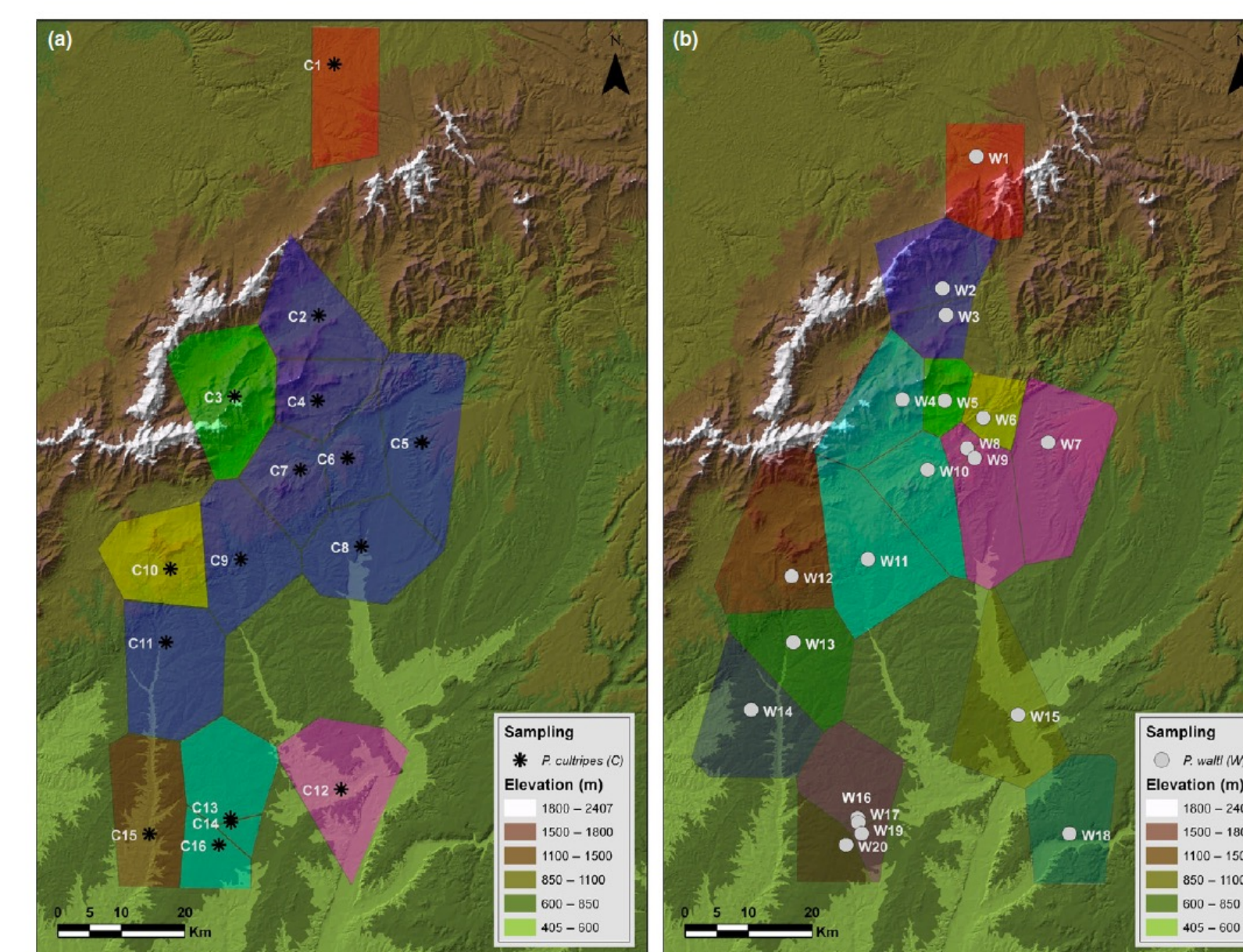


Figure 1. Sampling locations for *P. cultripipes* (a - left) and *P. waltl* (b - right). Each point indicates a sample population, and each color indicates an optimal cluster determined by BAPS. BAPS determined the optimal number of clusters for *P. cultripipes* was K=7 and for *P. waltl*, K=13. Figure adapted from Gutiérrez-Rodríguez et al. (2017).

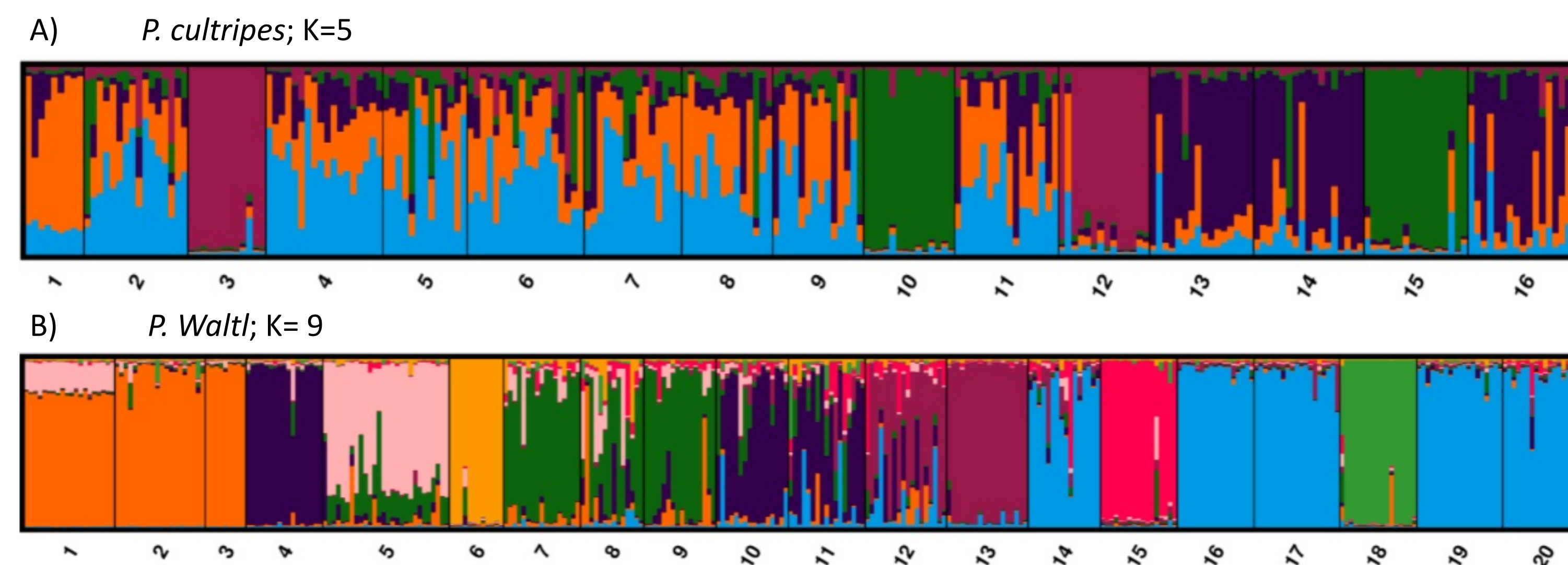


Figure 2. (A) Assignment of *P. cultripipes* to genetic clusters conformed by STRUCTURE with hypothesis K=5. (B) Assignment of *P. waltl* to genetic clusters conformed by STRUCTURE with hypothesis K=9. Each individual is represented by a vertical bar and numerical groupings refer to the geographic sites from which the individuals were sampled. Colors of genetic clusters in Fig 2 are unrelated to colors appearing in Fig 1.

- STRUCTURE identifies K=5 as the best supported hypothesis for *P. cultripipes*, as opposed to the original authors' hypothesized K value of 7.
- STRUCTURE identifies K=9 as the best supported hypothesis for *P. waltl*, as opposed to the original authors' hypothesized K value of 13.

Discussion

- BAPS treats number of populations as an unknown parameter³
- BAPS estimates the correct number of cluster for F_{ST} (total genetic variance) greater than 0.03³
- STRUCTURE estimates the correct number of clusters for F_{ST} as low as 0.01³
- STRUCTURE does not require geographic information for analysis
- Of the sampled individuals, it appears that there are 5 genetically distinct populations of *P. cultripipes* and 9 genetically distinct populations of *P. waltl*
- The original authors overestimated the number of populations for each species with hypothesized K values of 7 and 13, respectively¹.
- The STRUCTURE algorithm allows for more admixture than BAPS, providing more accurate results. BAPS tends to overestimate K values.³
- Study is limited by the absence of BAPS output included in the supplemental info of the original authors.

Literature Cited

- ¹Gutiérrez-Rodríguez, J., Gonçalves, J., Civantos, E., & Martínez-Solano, I. (2017). Comparative landscape genetics of pond-breeding amphibians in Mediterranean temporal wetlands: The positive role of structural heterogeneity in promoting gene flow. *Molecular ecology*, 26(20), 5407-5420.
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- ³Rodríguez-Ramilo, S.T., Toro, M.A. & Fernández, J. Assessing population genetic structure via the maximisation of genetic distance. *Genet Sel Evol* 41, 49 (2009). <https://doi.org/10.1186/1297-9686-41-49>
- Pritchard, J. K., Wen, X., and Daniel Falush. (2010). Documentation for structure software: Version 2.3. Unpublished manuscript. Department of Statistics, University of Oxford.