

GENETIC VARIATION AND POPULATION STRUCTURE IN THE
ENDANGERED HOUSTON TOAD IN CONTRAST TO ITS COMMON
SYMPATRIC RELATIVE, THE COASTAL PLAIN TOAD

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ABSTRACT

I determined the number of populations, the levels of genetic diversity within and among populations, and migration/movement rates at the landscape and fine scales in the endangered Houston toad, *Bufo houstonensis* (Anura: Bufonidae) using mitochondrial sequence data and microsatellite loci. Genetic clustering analyses indicate nine populations across the range. The most divergent population was in Austin County, Texas. Genetic diversity was high across the range and within populations. I also examined population genetic structure and diversity in a common, sympatric congener, the coastal plain toad (*Bufo nebulifer*). *Bufo houstonensis* and *B. nebulifer* have comparable levels of genetic diversity, but *B. nebulifer* appears to migrate less frequently or over less distance than its endangered congener. Finally, I investigated the baseline levels of genetic admixture, or hybridization, in *B. houstonensis*. Admixture between *B. houstonensis* and two sympatric species (*B. nebulifer* and *Bufo woodhousii*) was detected. With continued habitat alteration and rising temperatures, both habitat isolation and offset breeding season have already partially broken down as isolating mechanisms and may deteriorate further; consequently, opportunities for hybridization events will increase. Conservation recommendations for *B. houstonensis* include supplementation programs to increase the number of individuals, preservation of all three habitat types (breeding/nursery, occupied, and dispersal), special attention towards the Austin County population, and involvement of the general public in conservation.