



Genetic diversity in the *Gammarus pecos* species complex: Implications for conservation and regional biogeography in the Chihuahuan Desert

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ABSTRACT: We used allozyme electrophoresis to quantify genetic variation in nine populations of the *Gammarus pecos* species complex endemic to spring systems of the northern Chihuahuan Desert. There was significant within-population and high among-population genetic variation. Two populations exhibited heterozygote deficiencies and high proportions of polymorphic loci, which suggests the presence of cryptic species. Genetic distances among populations were negatively correlated with previously published morphological similarities, which suggests congruence between allozyme and morphological phenotypes. Cluster analysis of genetic distances showed four major groups of populations within the *G. pecos* complex. Genetic identities and fixed allelic differences support the presence of at least four distinct species: *Gammarus desperatus*, *G. pecos*, *Gammarus hyalleloides*, and one or more undescribed species. Relatively large genetic distances between populations suggest long periods of isolation and allopatric speciation. Patterns of among-population genetic variation were similar between amphipods and several groups of endemic fishes and snails, which suggests a coherence to biogeographic patterns within this region. Thus, the understanding of the genetic structure and taxonomic status of the *G. pecos* species complex provides insight into the biogeography of other aquatic organisms in the northern Chihuahuan Desert. Given the alarming rate at which desert spring systems are being altered and the unique biotic assemblages present, protection of these habitats is imperative.

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