Genetic structure in remnant populations of an endangered cyprinodontid fish, Orestias ascotanensis, endemic to the Ascotán salt pan of the Altiplano

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The impact of recent habitat fragmentation on population genetic diversity and structure has often been studied, mainly related to anthropogenic causes; however its long-term effect has been much less evaluated. In this study we analyzed the genetic variability of Orestias ascotanensis, a fish endemic to the Ascotán salt pan of Chile. This species, which formed a single and large population during the last wet period that ended 10,000 years ago, is currently represented by small populations inhabiting freshwater springs on the eastern border of the salt pan. Therefore, this species represents a unique model to evaluate the consequences of a drastic habitat fragmentation process that initiated thousands of years ago. Analysis of the control region of the mitochondrial DNA revealed high genetic diversity (haplotipic diversity ranged between 0. 78 and 0. 94) and marked differences among populations (?ST = 0. 46). Estimated effective population sizes greatly surpassed the real sizes, parti