

Genetic variation within and between four chromosomal races of *Liolaemus monticola* in Chile

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Allozyme variability was assessed within and between 18 samples of four chromosomal races of the *Liolaemus monticola* complex: "Southern, $2n=34$ ", "Northern, $2n=38-40$ ", "Multiple Fission, $2n=42-44$ " and "Northern modified 1, $2n=38-40$ ". This is an endemic montane Chilean lizard characterized by extensive chromosomal polytypy. The population genetic structure was studied by means of allozyme electrophoresis of 20 presumptive loci. Population heterogeneity analysis carried out by the estimation of Weir and Cockerham's F-statistic (?), demonstrated substantial genetic differentiation among populations. The u-statistic, genetic distance data and multivariate analyses show that genetic variation is distributed into geographically coherent population groups in accordance with three of the four chromosome races. The greatest differentiation occurs between all populations of the "Southern, $2n=34$ " race and a second group that includes all populations from the "Northern, $2n=38-40$ " plus "Northern mod