



Population connectivity of isolated Tillandsia lomas in the Atacama Desert of northern Chile

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In hyper arid habitats, where moisture is extremely scarce and at best only available very locally, plant populations are expected to show some degree of genetic isolation from each other. In the coastal Atacama Desert of Northern Chile, the presence of stratocumulus clouds that form below 1000 m altitude deliver regular fog to the western slopes of the coastal cordillera allowing for a band of vegetation of relatively high species diversity, while the eastern slopes descend into the hyper arid core of the Atacama Desert. However, where the fog can penetrate further inland through the presence of suitable geological corridors such as surface rivers, plant life can to a limited extent also establish at some distance away from the coast, in an otherwise totally barren environment. *Tillandsia landbeckii*, a functionally rootless air-plant in the pineapple family, completely depends on fog for water and nutrients, and is thus found only in close association with such fog corridors. Here, we investigate the genetic connectivity within and between populations of *T. landbeckii*, using Genotyping-by-Sequencing (GBS). The detection and analysis of single nucleotide polymorphisms (SNPs) is a comparatively cost-effective method providing larger data sets than alternatives such as microsatellites, and allows to investigate population structure without prior knowledge of the genome, as well as potential hybridization patterns.