## Naturalised grapevines collected from arid regions in Northern Chile exhibit a high level of genetic diversity

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## Abstract

Background and Aims Grapevine introduction into S outh A merica occurred after S panish colonisation during the 16th century. In C hile, some vines were established in small villages and oases along the A tacama D esert. Considering that these plants have survived harsh environmental conditions, we explored and collected naturalised vines from 18°34'LS (close to the P eruvian border) to 31°53'LS, in order to understand their genetic nature and preserve this germplasm. Methods and Results Over 150 grapevine accessions were collected and characterised using 11 Simple Sequence Repeats (SSR) markers, to determine the genetic diversity and to propose a population structuring. SSR diversity was high, with observed heterozygosity (H o = 0.87) greater than expected heterozygosity (H e = 0.70). Three discrete genetic groups were identified, which did not show any association with geographical distribution. Groups 1 (G1) and G3 had a higher level of genetic diversity and also an important level of heterozygosity. Conclusions The gene pool of naturalised grapevines from the A tacama D esert had a significant genetic diversity and exhibited an important level of heterozygote excess. Clustering of this diversity suggested that this naturalised grapevine germplasm would represent a novel source of allelic variants. Significance of the Study Naturalised and admixed genotypes are potential sources of new alleles, and are a unique source of diversity for grapevine breeding cultivars and/or rootstocks better adapted to the prospect of climate change..