

# Genetic variants of the paraoxonases (PON1 and PON2) in the Chilean population

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We estimated the frequencies of PON1 and PON2 variants (linked genes) in two hospital samples taken from the northern (San José Hospital, SJH) and eastern (Clínica Las Condes, CLC) parts of Santiago, Chile, using the polymerase chain reaction followed by restriction endonuclease digestion. The two hospital samples have different degrees of Amerindian admixture (SJH, 34.5%; CLC, 15.9%), which is reflected in the observed frequencies of the PON1\*B allele (SJH, 43.1%; CLC, 33.7%) and the PON2\*S allele (SJH, 86.3%; CLC, 77.6%); both allele frequencies are significantly different between samples. The frequencies of the combined PON1-PON2 genotypes \*A/\*B-\*C/ \*C, \*A/\*B-\*S/\*S, and \*B/\*B-\* S/\*S and of the haplotypes PON\*A,C and PON\*B,S were significantly different between the SJH and CLC groups. None of the genotype frequencies deviated significantly from those predicted by the Hardy-Weinberg equation. No linkage disequilibrium was found between the PON1 alleles and any of the PON2 alleles in e