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Genetic variants and alcohol intake patterns in university population in Santiago of Chile

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Genetic variants involved in inefficient (*ADH1B2**2 y *ALDH2**2) or efficient (SNP6 rs1800759, *ADH4* gene) alcohol metabolism have been associated with degrees of susceptibility to alcoholism in individuals. Alcoholism susceptibility has been classified into two phenotypes: “protector phenotypes” and “risk-dependence phenotypes”, associated with inefficient and efficient alcohol genetic metabolizing variants, respectively.

Here we investigate the possible relation between genetic protective and risk-dependence variants and alcohol intake patterns according to AUDIT questionnaire designed by WHO. DNA saliva samples and data of the AUDIT questionnaire were obtained (prior approval of the ethics committee) from a sample of 210 individuals from Universidad de Chile between 18 and 25 years old.

As results, it was not possible to establish a statistic relation between protective or risk-dependence genetic variants and alcohol pattern intake. However, instead we found a higher frequency in alcohol risk-dependence allele (ji-square test = 10.33; df=2; p-value = 0.005) and risk-dependence phenotype (ji-square test= 4.33; df=1; p-value= 0.03) for *ADH4* rs1800759 marker compared to those reported in other regions of America by *1000Genomes* project.

These findings suggest that Chile would present an increased risk of alcohol dependence given by this genetic factor; data that is more relevant in individuals with alcohol consumption patterns classified as harmful or dependent. In addition, new categories of alcohol consumption (not included in the AUDIT) were identified. Finally, the lack of association between consumption patterns and genotypes for these loci is discussed.