

THE ROLE OF ADH1B IN ALCOHOL CONSUMPTION AND STROKE SUSCEPTIBILITY

Paulos-Pinheiro S^{a,b}; Coelho JI^{a,b}; Albergaria I^a, MSc; Gaspar G^a, MSc; Ferro JM^{c,d}, MD, PhD; Vicente AM^{a,b,e}, PhD



^aDepartamento Promoção da Saúde e Prevenção de Doenças Não Transmissíveis, Instituto Nacional de Saúde Dr. Ricardo Jorge (INSA), Lisbon, Portugal; ^bInstituto Gulbenkian de Ciência, Oeiras, Portugal; ^cInstituto de Medicina Molecular, Faculdade de Medicina da Universidade de Lisboa, Lisbon, Portugal ; ^dServiço de Neurologia, Hospital de Santa Maria, Lisbon, Portugal; ^eCenter for Biodiversity, Functional & Integrative Genomics (BIOFIG), Lisbon, Portugal

INTRODUCTION

While heavy episodic drinking has been shown to be harmful to the heart, moderate alcohol consumption is thought to be protective against cardiovascular disease, through the regulation of rising HDL cholesterol levels.¹ The cardio-protective effect of alcohol is now not thought to vary by beverage type. In fact, evidence for an additional cardio-protective effect of antioxidant polyphenols in red wine is weak.²⁻³ The study of genetics variants of the alcohol dehydrogenase (ADH) and aldehyde dehydrogenase (ALDH) genes involved in alcohol metabolism is important to understand the patterns of drinking habits and its effects in stroke susceptibility. The enzyme alcohol dehydrogenase (ADH), which oxidizes alcohol to acetaldehyde, has proven to play an important role in alcohol metabolism. Seven genes encoding ADH are found in a tight cluster on chromosome 4 and some are polymorphic in white European populations.⁴ More active variants of ADH cause higher concentrations of acetaldehyde in the body following alcohol consumption and are therefore protective against drinking. Functional variants in both ADH1B and ADH1C have been associated with alcohol consumption or alcohol dependence.⁵⁻⁹ The ADH1B variant (rs1229984) has emerged as the most strongly associated with alcohol phenotypes and is therefore the most suitable instrument for Mendelian randomization studies in Europeans.⁶ The A allele has an allele frequency of approximately 2-5% in Europeans and plays a protective role against heavy drinking because it confers an higher alcohol metabolic rate and consequent accumulation of toxic acetaldehyde.¹⁰⁻¹¹

We genotyped SNP rs1229984 using a TaqMan Drug Metabolism Genotyping Assay in 569 stroke patients with extended clinical and lifestyle information and in 433 controls with matching clinical and lifestyle information (Table 1). Case-control analysis was performed in SPSS (v20.0) and p-values and odds ratio were calculated using Pearson's *chi*-squared test. The interpretation of the results allowed to determine the effect of the genetic variant on stroke susceptibility.

METHODS

All genotyping plates contained quality control samples: no-template controls, HapMap individuals and duplicated samples within and across genotyping plates.

Table 1 – Characterization of the studied population

	• •													
Characteristic	Controls	Patients	Р											
ge and Gender														
Age, mean±SD (years)	64.0±5.5	51.6±8.9	<10-4*											

Hence we analyzed if a possible association of the SNP rs1229984 with stroke susceptibility is mediated by the patterns of alcohol consumption.

RESULTS

The SNP met quality control criteria and was further evaluated.

Genotyping results are shown in Table 2. AA and AG genotypes were taken together for further analysis to enable a better statistical analysis. Association analysis between each two variables was performed and its results are shown in Table 3. On the associations analysis with significant results (genotype-stroke and alcohol consumption-stroke) we tested whether the third variable (alcohol consumption and genotype, respectively) was modifying the observed effect. As Tables 4 and 5 illustrate alcohol consumption modifies the association genotype-stroke (P=0.008) with excessive alcohol consumption playing the largest effect on this modification (P=0.034). Genotype also modifies the association alcohol consumption-stroke (P<10⁻⁴).

Table 4 – Modifying effect of alcohol consumption on the association Table 5 – Modifying effect of genotype on the association alcohol

	Gender (male), n/N (%)	201/433 (46.4)	362/569 (63.6)	<10 ⁻⁴ *
roke type				
	Ischemic stroke, n/N (%)	-	451/569 (79.3)	-
	Hemorrhagic stroke, n/N (%)	-	107/569 (18.8)	-
	Unknown type of stroke, n/N (%)	-	11/569 (1.9)	-
roke Risk Factors	5			
	Hypertension (>85-140mmHg), n/N (%)	157/426 (36.9)	313/500 (62.6)	<10-4+
	Diabetes, n/N (%)	52/412 (12.6)	85/526 (16.2)	0.128^{+}
	Hypercholesterolemia, n/N (%) (cholesterol > 200mg/dl)	296/433 (68.3)	329/519 (63.4)	0.108^{+}
	Smoking, n/N (%)	120/423 (28.4)	257/557 (46.1)	<10-4+
	Drinking, n/N (%)~			<10-4+
	None	254/407 (62.4)	242/558 (43.4)	
	Moderate consumption of alcohol	82/407 (20.1)	49/558 (8.8)	
	Excessive consumption of alcohol	71/407 (17.4)	267/558 (47.8)	
) - standard dav	viation: ~Alcohol consumption was divided in three category	ries according to	the amount of alcoho	l consumed/d

SD – standard deviation; ~Alcohol consumption was divided in three categories, according to the amount of alcohol consumed/day. None: <1 beverage/day; Moderate consumption: 1 beverage/day for females and 1-2 beverages/day for males; Excessive consumption: >1 beverage/day for females and >2 beverages/day for males (Rimm & Moats, 2007); * Mann-Whitney test; ⁺ Pearson's *Chi*-squared test.

	Table 2 –	Genotyp	oing res	ults		genotype-stroke									consumption-stroke									
Stroke	Alcohol Consumption	1	Genoty	/pe	Total	Alcohol Consumption	Genoty	ре	Str Patients	oke Controls	Total	Р	OR	Genotype	Alcohol Consumptio	on	Stro Patients	oke Controls	Total	Ρ	OR			
		GG	AG	AA				N	34	40	74					Ν	34	40	74			i de la		
Patients	None	208	32	2	242	None	AA and AG	%	14.0%	15.7%	14.9%		0.85	AA and AG	None	%	52.3%	55.6%	54.0%	0.3	0.85			
	Moderate consumptic	n 43	6	0	49		66	N	208	214	422		1		Moderate consumption	Ν	6	19	25		0 32			
	Evenesivo consumptio	n 242	22	С	267		66	%	86.0%	84.3%	85.1%	0.590				%	9.2%	26.4%	18.2%					
		11 242	23	Z	207		Total	Ν	242	254	496				Excessive consumption	Ν	25	13	38		1.92			
	Total	493	61	4	558		Total	%	100.0%	100.0%	100.0%					%	38.5%	18.1%	27.7%					
	None	214	37	3	254		AA and AG	Ν	6	19	25		0.46		Total	Ν	65	72	137					
	Moderate consumptio	n 63	17	2	82			%	12.2%	23.2%	19.1%		0.40			%	100.0%	100.0%	100.0%					
Controls				-		Moderate Consumption	n GG	N	43	63	106	0.124	0.68		None Moderate consumption	N	208	214	422		1			
	Excessive consumptio	n 58	12	1				%	87.8%	76.8%	80.9%					%	42.2%	63.9%	51.0%					
	Total	335	66	6	407		Total	N	49	82	131					N	43	63	106		0.68			
	None	422	69	5	496		AA and AG	%	100.0%	100.0%	100.0%			GG	Excessive consumption	%	8.7%	18.8%	12.8%	<10-4				
	Modorato concumptio	n 106	22	С	121			N	25	13	38		0.46			IN 0/		کک 17 ک0/			4.17			
Total	woderate consumption		23	Z	101	Excessive Consumption		%	9.4%	18.3%	11.2%					70 NI	49.1%	225	30.2% 000					
	Excessive consumptio	n 300	35	3	338		GG	N N	242	58 300	0.034	4.17		Total	IN 0/		335 100.0%	020 100.0%						
	Total	828	127	10	965			%	90.6%	81.7%	88.8%					70 NI	2/2	25/	100.070					
							Total	Total N			338				None	м %	Δ 4 2 Δ3 Δ%	62.4%	51 <i>4</i> %					
							70 NI	100.0%	100.0%	100.0%		-	1		N	49	82	131						
Table 3 – Association analysis results			AA and AG	0/		/ Z 17 7%					Moderate consumption	%	8.8%	20.1%	13.6%									
		Stucko	nalia Alashalasa		currention			N	<u> </u>	225	878 [0.008		Total	Excessive consumption	N	267	71	338	<10 ⁻⁴				
		Stroke		Alconol comsumption		Total	GG	%	88.4%	82.3%	85.8%					%	47.8%	17.4%	35.0%					
Ger	notype	0.008		0.07	4			N	.558	407	965				Total	N	558	407	965			E		
St	roke	-		<10	4		Total	%	100.0%	100.0%	100.0%					%	100.0%	100.0%	100.0%					

DISCUSSION AND CONCLUSIONS

(1) In this study we did not find an association between the SNP rs1229984 and alcohol phenotype. However, further studies in larger populations are needed to confirm these

- results. Also it would be interesting to observe whether the activity of ADH1B varies within groups of individuals sharing the same genotype, which might influence individual alcohol tolerance.
- (2) We tested whether the amount of alcohol consumed was modifying the association genotype-stroke and we observed, as expected¹², that heavy drinking increases in about four times (OR=4.17) stroke risk in the group of A allele non-carriers. On the other hand, A carriers present a decrease to about half (OR=0.46) stroke risk despite the excessive alcohol consumption, which suggests that the A allele plays a protective role on stroke susceptibility. Further studies are needed to validate the same trend in groups of individuals with lighter alcohol consumption.
- (3) We confirmed the importance of alcohol as a stroke risk factor. While moderate consumption appears to be protective (OR<1), heavy drinking is potentially harmful (OR>1), as previously mentioned.¹ However, when testing whether the genotype was modifying the association alcohol consumption-stroke, we observed a protective role of A allele, which is consistent with previous results. In fact, considering individuals with none or moderate alcohol consumption, A carriers show a decreased stroke risk when compared with non-carriers (0.85>OR_{A carriers}>0.32 *vs* 1>OR_{A non carriers}>0.68). Individuals consuming excessive amounts of alcohol, despite an increased stroke risk, have larger probability of developing an event if they are A non carriers (OR_{A carriers}=1.92 *vs* OR_{A non carriers}=4.17).

In conclusion, A allele of the SNP rs1229984 appears to be protective against stroke. However, further studies are needed to replicate these results in other populations. Because the associations analyzed are complex, functional studies including other relevant genetic variants, such as ALDH, should be performed. Physiological studies including variables such as hypertension and hypercholesterolemia would also be interesting.

ACKNOWLEDGMENTS: This work was part of a collaboration between Grupo de Neurogenética e Saúde Mental, Departamento de Provoção da Saúde e Prevenção de Doenças Não Transmissíveis, INSA, Lisboa, and Genetic Epidemiology Group, Department of Epidemiology and Public Health, University College of London, London. Samples collection was supported by fellowship PECS/T/SAU/179/95, from Fundação para a Ciência e a Tecnologia (FCT; Portugal).

REFERENCES: [1] – Kloner RA, Rezkalla SH (2007) To Drink or Not to Drink? That Is the Question. Circulation 116:1306-131; [2] – Britton A, McKee M (2000) The relation between alcohol and cardiovascular disease in Eastern Europe: explaining the paradox. J Epidemiol Community Health. 54(5):328-332; [3] – Fuchs FD, Chambless LE (2007) Is the cardioprotective effect of alcohol real?. Alcohol. 41(6):399-402; [4] – Agarwal DP (2001) Genetic polymorphisms of alcohol metabolizing enzymes. Pathol Biol. 49(9):703-709; [5] – Tolstrup JS, Nordestgaard BG, Rasmussen S, Tybjaerg-Hansen A, Gronbaek M (2008) Genetic variations in alcohol dehydrogenase, drinking habits and alcoholism. Ugeskr Laeger. 170(35):2672-2675; [6] – Macgregor S, Lind PA, Bucholz KK, Hansell NK, Madden PA, Richter MM, et al. (2009) Associations of ADH and ALDH2 gene variation with self report alcohol reactions, consumption and dependence: an integrated analysis. Hum Mol Genet. 18(3):580-93; [7] – Kuo PH, Kalsi G, Prescott CA, Hodgkinson CA, Goldman D, van den Oord EJ, et al. (2008) Association of ADH and ALDH genes with alcohol dependence (IASPSAD) sample. Alcohol dependence (IASPSAD) sample. Alcohol Clin Exp Res. 32(5):785-95; [8] – Carr LG, Foroud T, Stewart T, Castelluccio P, Edenberg HJ, Li TK (2002) Influence of ADH1B polymorphism on alcohol use and its subjective effects in a Jewish population. Am J Med Genet. 112(2):138-43; [9] – Zuccolo L, Fitz-Simon N, Gray R, Ring SM, Sayal K, Davey Smith G, et al (2009) A non-synonymous variant in ADH1B is strongly associated with prenatal alcohol use in a European sample of pregnant women. Hum Mol Genet. 18(22):4457-4466; [10] – Borras E, Coutelle C, Rosell A, Fernandez-Muixi F, Broch M, Crosas B, et al. (2000) Genetic polymorphism of alcohol dehydrogenase in europeans: the ADH2*2 allele decreases the risk for alcoholism and is associated with prenatal alcohol use in a European sample of pregnant women. Hum Mol Genet. 81(4):842-6; [12] – Ringleb PA, Bousser M-G, Ford G, Bath P, Brainin M, Caso V, et al. (20