

SUPPLEMENTAL MATERIAL

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Associations of cholesteryl ester transfer protein (CETP) gene variants with pituitary adenoma (doi: 10.5507/bp.2019.016)

Table 1. Frequencies of genotypes and alleles in PA and control groups.

Genotype, allele		Pituitary adenoma group (n = 142)	Control group (n = 753)	P
rs5882	G/G, n (%)	12 (8.5)	75 (10)	0.578
	G/A, n (%)	76 (53.5)	330 (43.8)	0.033
	A/A, n (%)	54 (38)	348 (46.2)	0.072
	G allele, n (%)	100 (35.2)	480 (31.9)	0.270
	A allele, n (%)	184 (64.8)	1026 (68.1)	0.270
rs708272	G/G, n (%)	55 (38.7)	224 (29.8)	0.034
	G/A, n (%)	59 (41.5)	397 (52.7)	0.015
	A/A, n (%)	28 (19.8)	132 (17.5)	0.532
	G allele, n (%)	169 (59.5)	845 (56.1)	0.289
	A allele, n (%)	115 (40.5)	661 (43.9)	0.289

Values in bold indicate significance after the Bonferroni correction ($P < 0.05/2$).

Table 2. Frequencies of genotypes and alleles in PA subgroups by invasiveness and in control group.

Genotype, Allele		Invasive pituitary adenoma subgroup (n = 84)	Noninvasive pituitary adenoma subgroup (n = 58)	P	Control group (n = 753)
rs5882	G/G, n (%)	6 (7.1)	6 (10.3)	0.500	75 (10)
	G/A, n (%)	43 (51.2)	33 (56.9)	0.503	330 (43.8)
	A/A, n (%)	35 (41.7)	19 (32.8) ¹	0.282	348 (46.2)
	G allele, n (%)	55 (32.7)	45 (38.8)	0.294	480 (31.9)
	A allele, n (%)	113 (67.3)	71 (61.2)		1026 (68.1)
rs708272	G/G, n (%)	34 (40.5) ²	21 (36.2)	0.608	224 (29.8)
	G/A, n (%)	34 (40.5) ³	25 (43.1)	0.755	397 (52.7)
	A/A, n (%)	16 (19)	12 (20.7)	0.809	132 (17.5)
	G allele, n (%)	102 (60.7)	67 (57.8)	0.618	845 (56.1)
	A allele, n (%)	66 (39.3)	49 (42.2)		661 (43.9)

¹ $P = 0.047$, ² $P = 0.043$, ³ $P = 0.033$. Values in bold indicate significance after the Bonferroni correction ($P < 0.05/2$).

Table 3. Binomial logistic regression analysis in patients with invasive and non-invasive PAs and in controls.

Genotype, allele				OR (95 % CI)	P	AIC
rs708272	Invasive	Dominant	G/A + A/A	0.623 (0.392 – 0.989)	0.045	543.597
		Over-dominant	G/A	0.610 (0.385 – 0.965)	0.034	542.953

Values in bold indicate significance after the Bonferroni correction ($P < 0.05/2$).

Table 4. Frequencies of genotypes and alleles in PA subgroups by activity and in control group

Genotype, allele		Active pituitary adenoma (n = 80)	Inactive pituitary adenoma (n = 62)	P	Control group (n = 753)
rs5882	G/G, n (%)	6 (7.5)	6 (9.7)	0.644	75 (10)
	G/A, n (%)	40 (50)	36 (58.1) ¹	0.339	330 (43.8)
	A/A, n (%)	34 (42.5)	20 (32.2) ²	0.212	348 (46.2)
	G allele, n (%)	52 (32.5)	48 (38.7)	0.277	480 (31.9)
	A allele, n (%)	108 (67.5)	76 (61.3)		1026 (68.1)
rs708272	G/G, n (%)	33 (41.3) ³	22 (35.5)	0.484	224 (29.8)
	G/A, n (%)	30 (37.5) ⁴	29 (46.8)	0.266	397 (52.7)
	A/A, n (%)	17 (21.3)	11 (17.7)	0.602	132 (17.5)
	G allele, n (%)	96 (60)	73 (58.9)	0.848	845 (56.1)
	A allele, n (%)	64 (40)	51 (41.1)		661 (43.9)

¹ $P=0.030$, ² $P=0.034$, ³ $P=0.034$, ⁴ $P=0.009$. Values in bold indicate significance after the Bonferroni correction ($P<0.05/2$).

Table 5. Frequencies of genotypes and alleles in PA subgroups by recurrence and in control group.

Genotype, allele		Recurrent pituitary adenoma subgroup (n = 30)	Non-recurrent pituitary adenoma subgroup (n = 112)	<i>P</i>	Control group (n = 753)
rs5882	G/G, n (%)	1 (3.3)	11 (9.8)	0.257	75 (10)
	G/A, n (%)	17 (56.7)	59 (52.7)	0.697	330 (43.8)
	A/A, n (%)	12 (40)	42 (37.5) ¹	0.802	348 (46.2)
	G allele, n (%)	19 (31.7)	81 (36.2)	0.517	480 (31.9)
	A allele, n (%)	41 (68.3)	143 (63.8)		1026 (68.1)
rs708272	G/G, n (%)	10 (33.3)	45 (40.2) ²	0.494	224 (29.8)
	G/A, n (%)	14 (46.7)	45 (40.2) ³	0.522	397 (52.7)
	A/A, n (%)	6 (20)	22 (19.6)	0.965	132 (17.5)
	G allele, n (%)	34 (56.7)	135 (60.3)	0.614	845 (56.1)
	A allele, n (%)	26 (43.3)	89 (39.7)		661 (43.9)

¹ $P=0.015$, ² $P=0.026$, ³ $P=0.013$. Values in bold indicate significance after the Bonferroni correction ($P<0.05/2$).