

Supplementary Table IV. Meta-analysis of genetic association for AGT-rs699, *CYP11B2*-rs1799998, *ADRB2*-rs1042713, and *ADRB2*-rs1042714

<i>AGT</i> -rs699											
Country	Model	No. publica- tion	OR	95% CI	<i>P</i> value	Model	p-hetero- geneity	I ²	Q	Tau	Egger's test <i>P</i> value
European	Allele	19	1.08	[0.96; 1.21]	0.17	Random	0.001	0.56	40.90	0.03	0.73
	Recessive	19	1.1	[0.95; 1.30]	0.19	Random	0.052	0.37	28.65	0.37	0.97
	Dominant	19	1.1	[0.95; 1.27]	0.19	Random	0.019	0.44	32.43	0.04	0.52
Japanese	Allele	8	1.23	[0.95; 1.51]	0.11	Random	0.002	0.75	28.81	0.08	0.12
	Recessive	8	1.27	[0.94; 1.71]	0.11	Random	0.001	0.79	33.50	0.79	0.05
	Dominant	8	1.28	[0.93; 1.74]	0.11	Fixed	0.64	0	5.12	0.00	0.74
East Asian	Allele	10	1.15	[0.98; 1.36]	0.07	Random	0.0004	0.70	30.46	0.04	0.27
	Recessive	10	1.23	[0.98; 1.54]	0.06	Random	0	0.78	42.69	0.79	0.36
	Dominant	10	0.98	[0.77; 1.23]	0.87	Fixed	0.13	0.34	13.73	0.08	0.092
Southern Han Chinese	Allele	5	1.04	[0.88; 1.23]	0.09	Fixed	0.54	0	3.68	0.00	0.50
	Recessive	5	1.09	[0.90; 1.32]	0.59	Fixed	0.45	0	2.19	0.00	0.05
	Dominant	5	0.85	[0.50; 1.44]	0.36	Fixed	0.70	0	4.83	0.08	0.10
Southern Indian	Allele	4	1.10	[0.97; 1.24]	0.56	Fixed	0.30	0.17	1.20	0.00	0.28
	Recessive	4	1.12	[0.94; 1.32]	0.19	Fixed	9.17	0.39	1.29	0.02	0.62
	Dominant	4	1.14	[0.88; 1.38]	0.37	Fixed	0.84	0	0.84	0.00	0.57
Northern + Southern Indian	Allele	6	1.37	[1.03; 1.82]	0.03*	Random	0.0001	0.90	50.53	0.12	0.11
	Recessive	6	1.61	[0.98; 2.67]	0.06	Random	0.0001	0.92	64.80	0.361	0.76
	Dominant	6	1.45	[1.09; 1.91]	0.009*	Random	0.0086	0.68	15.46	0.08	0.15
Middle Eastern	Allele	3	1.06	[0.63; 1.77]	0.82	Random	0.0078	0.79	9.70	0.16	0.0008
	Recessive	3	1.38	[0.31; 6.17]	0.67	Random	0.0001	0.9024	20.50	1.51	0.4254
	Dominant	3	1.07	[0.75; 1.53]	0.71	fixed	0.49	0	1.44	0.00	0.39
Latin American	Allele	3	1.08	[0.86; 1.36]	0.51	fixed	0.18	0.42	3.45	0.03	0.14
	Recessive	3	1.36	[0.76; 2.42]	0.30	random	0.08	0.61	5.16	0.16	0.1
	Dominant	3	1.07	[0.54; 2.1]	0.84	fixed	0.31	0.15	2.34	0.07	0.05
<i>CYP11B2</i> -rs1799998											
European	Allele	5	0.82	[0.75; 0.91]	0.00012*	Fixed	0.55	0	3.0337	0.00	0.77
	Recessive	5	0.72	[0.61; 0.85]	0.0019*	Fixed	0.18	0.37	6.319	0.0271	0.91
	Dominant	4	0.81	[0.70; 0.94]	0.008*	Fixed	0.96	0	0.2596	0.00	0.78
European**	Allele	4	0.82	[0.74; 0.90]	6.9E-05*	Fixed	0.69	0	1.4833	0.00	0.37
	Recessive	4	0.70	[0.59; 0.83]	6.38E-05*	Fixed	0.29	0.18	3.6657	0.0087	0.27
	Dominant	4	0.81	[0.70; 0.94]	0.008	Fixed	0.96	0	0.2596	0.00	0.50
Northern Han Chinese	Allele	8	1.09	[0.95; 1.21]	0.20	Random	0.003	0.67	21.4728	0.0193	0.80
	Recessive	8	1.10	[0.88; 1.39]	0.37	Random	0.03	0.52	14.7543	0.0542	0.86
	Dominant	8	1.10	[0.96; 1.26]	0.17	Random	0.01	0.58	16.9541	0.0225	0.51
Japanese	Allele	4	1.03	[0.88; 1.20]	0.64	Random	0.06	0.59	7.4048	0.0131	0.72
	Recessive	4	0.97	[0.82; 1.15]	0.76	Fixed	0.79	0	1.0642	0.000	0.75
	Dominant	4	1.08	[0.86; 1.37]	0.47	Random	0.02	0.68	9.6491	0.0354	0.63
East Asian [#]	Allele	12	1.06	[0.97; 1.16]	0.16	Random	0.0014	0.64	30.2462	0.0146	0.48

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Country	Model	No. publica- tion	OR	95% CI	<i>P</i> value	Model	p-hetero- geneity	I ²	Q	Tau	Egger's test <i>P</i> value
Indian***	Recessive	12	1.05	[0.98; 1.23]	0.12	Random	0.098	0.37	17.3484	0.0239	0.92
	Dominant	12	1.09	[0.97; 1.23]	0.47	Random	0.0043	0.60	27.2137	0.0211	0.29
	Allele	5	1.11	[0.79; 1.56]	0.52	Random	0.0001	0.88	33.8259	0.128	0.08
	Recessive	5	1.28	[0.82; 2.00]	0.26	Random	0.001	0.68	12.787	0.1626	0.01
	Dominant	5	1.02	[0.64; 1.60]	0.92	Random	0.0001	0.87	32.3344	0.2319	0.29
<i>ADRB2</i> -rs1042713											
European	Allele	11	0.98	[0.89; 1.07]	0.66	fixed	0.25	0.20	12.5137	0.0057	0.37
	Recessive	11	1.03	[0.91; 1.16]	0.68	fixed	0.68	0	7.5252	0.000	0.49
	Dominant	11	0.90	[0.76; 1.06]	0.21	fixed	0.38	0.05	10.617	0.0053	0.63
East Asian#	Allele	4	1.26	[1.05; 1.51]	0.01*	random	0.05	0.61	7.7442	0.019	0.13
	Recessive	4	1.36	[1.01; 1.83]	0.04*	random	0.07	0.58	7.0598	0.0484	0.46
	Dominant	4	1.34	[0.99; 1.83]	0.06	random	0.02	0.68	9.3567	0.0607	0.32
African American	Allele	3	0.84	[0.68; 1.05]	0.12	fixed	0.56	0	1.159	0.00	0.71
	Recessive	3	0.95	[0.67; 1.35]	0.76	fixed	0.13	0.51	4.1099	0.118	0.52
	Dominant	3	0.68	[0.48; 0.97]	0.03*	fixed	0.84	0	0.3391	0.00	0.02
<i>ADRB2</i> -rs1042714											
European	Allele	7	0.95	[0.86; 1.05]	0.29	Fixed	0.96	0	1.4441	0.00	0.44
	Recessive	7	0.97	[0.81; 1.15]	0.70	Fixed	0.87	0	0.7174	0.002	0.66
	Dominant	7	0.91	[0.79; 1.05]	0.21	Fixed	0.99	0	2.489	0.00	0.24
Northern Han Chinese	Allele	3	1.01	[0.50; 2.04]	0.98	random	0.0003	0.88	16.2104	0.3139	0.79
	Recessive	3	0.91	[0.43; 1.88]	0.79	Fixed	0.23	0.33	2.9654	0.2415	0.53
	Dominant	3	0.98	[0.42; 2.29]	0.96	random	0.0001	0.90	20.1412	0.4751	0.87
East Asian#	Allele	5	1.00	[0.68; 1.48]	0.99	random	0.0004	0.80	20.3579	0.1425	0.41
	Recessive	5	0.90	[0.50; 1.62]	0.73	Fixed	0.41	0	23.5379	0.1987	0.133
	Dominant	5	0.98	[0.63; 1.54]	0.94	random	0.0001	0.83	3.9445	0.00	0.56

*Significantly associated with HT, **exclude one study (Bengraet *al*²⁶ 2002) due to unusual genotyping frequencies; #East Asian: Northern Han Chinese and Japan; ***Indian: Eastern, Northern and Southern Indian. I², index of heterogeneity
- *AGT*-rs699: allele model (G vs. A), recessive model (GG vs. GA + AA) and dominant model (GG + GA vs. AA)
- *CYP11B2*-rs1799998: allele model (G vs. A), recessive model (GG vs. GA + AA) and dominant model (GG + GA vs. AA)
- *ADRB2*-rs1042713: allele model (G vs. A), recessive model (GG vs. GA + AA) and dominant model (GG + GA vs. AA)