

Summary crude odds ratios (ORs) and 95% Confidence Intervals (95% CI) for two additive models for variants of the substrate metabolism pathway genes (*CYP1A1*, *CYP1A2*, *CYP1B1*, *CYP2C9*, *CYP2E1*, *GSTA1*, *GSTM1*, *GSTP1*, *GSTT1*, *NAT1*, *NAT2*, *NQO1*)

Gene	Variant	rs number	Cases vs. controls (number of samples)	ADDITIVE MODEL: var/wt VS. wt/wt						ADDITIVE MODEL: var/var VS. wt/wt					
				N	Effect size		Heterogeneity		Power	N	Effect size		Heterogeneity		Power
					OR (95% CI)	P value	I ² (95% CI)	P value			OR (95% CI)	P value	I ² (95% CI)	P value	
Substrate metabolism															
CYP1A1	2454A>G	rs1048943	10274 vs. 11978 (13*§)	13	1.28 (1.01, 1.63)	0.05	85 (77, 91)	<0.0005	1.00	12	1.47 (1.17, 1.85)	0.001	3 (0, 60)	0.41	0.93
CYP1A1	3698T>C	rs4646903	4897 vs. 6559 (7)	7	0.94 (0.86, 1.04)	0.23	0 (0, 71)	0.63	0.27	7	0.84 (0.56, 1.27)	0.42	54 (0, 80)	0.04	0.38
CYP1A2	163C>A	rs762551	3051 vs. 5326 (9)	9	1.13 (0.95, 1.34)	0.18	63 (25, 82)	0.005	0.75	9	1.07 (0.92, 1.26)	0.40	42 (0, 73)	0.09	0.16
CYP1B1	4326C>G	rs1056836	8514 vs. 9721 (6*)	6	0.99 (0.92, 1.06)	0.69	0 (0, 75)	0.62	0.06	6	0.98 (0.90, 1.07)	0.70	0 (0, 77)	0.36	0.08
CYP2C9	430C>T	rs1799853	5134 vs. 6164 (6*)	6	0.93 (0.85, 1.02)	0.13	21 (0, 65)	0.28	0.34	6	1.29 (0.99, 1.70)	0.06	0 (0, 75)	0.66	0.46
CYP2C9	1057A>C	rs1057910	5379 vs. 6531 (6*)	6	1.08 (0.83, 1.40)	0.57	73 (33, 88)	0.002	0.26	4	0.68 (0.37, 1.26)	0.22	11 (0, 86)	0.34	0.23
CYP2E1	1053C>T	rs2031920	4456 vs. 5077 (8§)	8	0.93 (0.83, 1.05)	0.23	0 (0, 68)	0.45	0.27	8	1.23 (0.92, 1.63)	0.16	35 (0, 71)	0.15	0.34
CYP2E1	1293G>C	rs3813867	3424 vs. 4686 (7)	7	1.17 (0.92, 1.48)	0.21	53 (0, 80)	0.05	0.61	6	1.83 (0.94, 3.57)	0.08	0 (0, 75)	0.8	0.55
GSTA1	GSTA1*B allele ¹		1648 vs. 2039 (4)	4	1.03 (0.89, 1.19)			>0.05		4	1.09 (0.90, 1.32)			>0.05	
GSTM1	Null variant	n/a	18845 vs. 26663 (43)	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
GSTP1	Ile105Val	rs1695	9267 vs. 12902 (22*)	22	1.05 (0.99, 1.12)	0.11	0 (0, 46)	0.46	0.38	22	0.95 (0.86, 1.05)	0.32	36 (0, 62)	0.05	0.17
GSTP1	Ala114Val	rs1138272	5183 vs. 5457 (6*§)	6	1.02 (0.91, 1.13)	0.77	0 (0, 75)	1.00	0.07	6	0.87 (0.55, 1.37)	0.55	12 (0, 78)	0.34	0.09
GSTT1	Null variant	n/a	13410 vs. 20455 (35)	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
NAT1	slow/rapid	n/a	4791 vs. 6628 (15)	7	0.80 (0.68, 0.93)	0.003	38 (0, 74)	0.14	0.86	7	0.98 (0.79, 1.22)	0.97	0 (0, 71)	0.97	0.06
NAT2	slow/rapid	n/a	12908 vs. 16483 (26)	15	1.01 (0.83, 1.22)	0.94	81 (70, 88)	<0.0005	0.06	15	0.95 (0.76, 1.20)	0.68	64 (37, 79)	<0.0005	0.17
NQO1	Pro187Ser (C609T)	rs1800566	5084 vs. 5932 (8)	8	1.14 (0.96, 1.35)	0.12	64 (22, 83)	0.008	0.89	8	1.10 (0.76, 1.59)	0.63	56 (2, 80)	0.03	0.19
* Includes unpublished data from SOCCS															
§ Includes unpublished data from Ontario															
¹ Ekonomopoulos 2010															

Summary crude odds ratios (ORs) and 95% Confidence Intervals (95% CI) for a recessive and a dominant model for variants of the substrate metabolism pathway genes (*CYP1A1*, *CYP1A2*, *CYP1B1*, *CYP2C9*, *CYP2E1*, *GSTA1*, *GSTM1*, *GSTP1*, *GSTT1*, *NAT1*, *NAT2*, *NQO1*)

Gene	Variant	rs number	Cases vs. controls (number of samples)	RECESSIVE MODEL: var/var VS. wt/wt & wt/var						DOMINANT MODEL: wt/var & var/var VS. wt/wt					
				N	Effect size		Heterogeneity		Power	N	Effect size		Heterogeneity		Power
					OR (95% CI)	P value	I ² (95% CI)	P value			OR (95% CI)	P value	I ² (95% CI)	P value	
Substrate metabolism															
CYP1A1	2454A>G	rs1048943	10274 vs. 11978 (13*§)	12	1.50 (1.19, 1.87)	<0.0005	0 (0, 58)	0.74	0.76	13	1.32 (1.05, 1.65)	0.02	85 (76, 91)	<0.0005	1.00
CYP1A1	3698T>C	rs4646903	4897 vs. 6559 (7)	7	0.90 (0.73, 1.11)	0.33	51 (0, 79)	0.06	0.15	7	0.94 (0.86, 1.03)	0.15	0 (0, 71)	0.47	0.33
CYP1A2	163C>A	rs762551	3051 vs. 5326 (9)	9	1.01 (0.87, 1.16)	0.92	5 (0, 66)	0.4	0.05	9	1.12 (0.94, 1.33)	0.20	68 (35, 84)	0.002	0.70
CYP1B1	4326C>G	rs1056836	8514 vs. 9721 (6*)	6	0.99 (0.93, 1.07)	0.88	0 (0, 72)	0.21	0.06	6	0.99 (0.92, 1.05)	0.65	0 (0, 75)	0.66	0.06
CYP2C9	430C>T	rs1799853	5134 vs. 6164 (6*)	6	1.31 (1.00, 1.72)	0.05	0 (0, 75)	0.65	0.56	6	0.96 (0.88, 1.05)	0.33	22 (0, 66)	0.27	0.16
CYP2C9	1057A>C	rs1057910	5379 vs. 6531 (6*)	4	0.68 (0.36, 1.26)	0.22	12 (0, 87)	0.33	0.2	6	1.07 (0.83, 1.38)	0.62	73 (38, 88)	0.002	0.22
CYP2E1	1053C>T	rs2031920	4456 vs. 5077 (8§)	8	1.24 (0.93, 1.63)	0.14	33 (0, 70)	0.17	0.26	8	0.96 (0.86, 1.07)	0.45	0 (0, 68)	0.5	0.13
CYP2E1	1293G>C	rs3813867	3424 vs. 4686 (7)	6	1.69 (0.87, 3.27)	0.12	0 (0, 75)	0.79	0.47	7	1.19 (0.93, 1.53)	0.18	58 (4, 82)	0.03	0.78
GSTA1	GSTA1*B allele ¹		1648 vs. 2039 (4)	4	1.17 (0.87, 1.58)			<0.05		4	1.04 (0.91, 1.20)			>0.05	
GSTM1	Null variant	n/a	18845 vs. 26663 (43)	n/a	n/a	n/a	n/a	n/a	n/a	43	1.07 (1.01, 1.13)	0.02	38 (10, 57)	0.007	0.94
GSTP1	Ile105Val	rs1695	9267 vs. 12902 (22*)	22	0.93 (0.84, 1.03)	0.15	33 (0, 60)	0.07	0.29	22	1.03 (0.97, 1.09)	0.35	9 (0, 44)	0.34	0.19
GSTP1	Ala114Val	rs1138272	5183 vs. 5457 (6*§)	6	0.87 (0.55, 1.37)	0.55	12 (0, 78)	0.34	0.09	6	1.01 (0.91, 1.12)	0.87	0 (0, 75)	0.99	0.05
GSTT1	Null variant	n/a	13410 vs. 20455 (35)	n/a	n/a	n/a	n/a	n/a	n/a	35	1.18 (1.07, 1.31)	0.002	71 (59, 79)	<0.0005	1.00
NAT1	slow/rapid	n/a	4791 vs. 6628 (15)	7	1.05 (0.86, 1.27)	0.66	0 (0, 71)	0.93	0.12	15	0.97 (0.86, 1.11)	0.69	51 (12, 73)	0.01	0.13
NAT2	slow/rapid	n/a	12908 vs. 16483 (26)	15	0.94 (0.80, 1.10)	0.45	44 (0, 70)	0.03	0.38	26	1.04 (0.92, 1.17)	0.56	78 (69, 85)	<0.0005	0.38
NQO1	Pro187Ser (C609T)	rs1800566	5084 vs. 5932 (8)	8	1.05 (0.74, 1.49)	0.78	51 (0, 78)	0.05	0.08	8	1.14 (0.96, 1.36)	0.13	68 (32, 85)	0.003	0.92
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