

Meta-Analyses of the Effect of *CYP1A1* and *CYP2D6* Polymorphisms on the Risk of Head and Neck Squamous Cell Carcinoma

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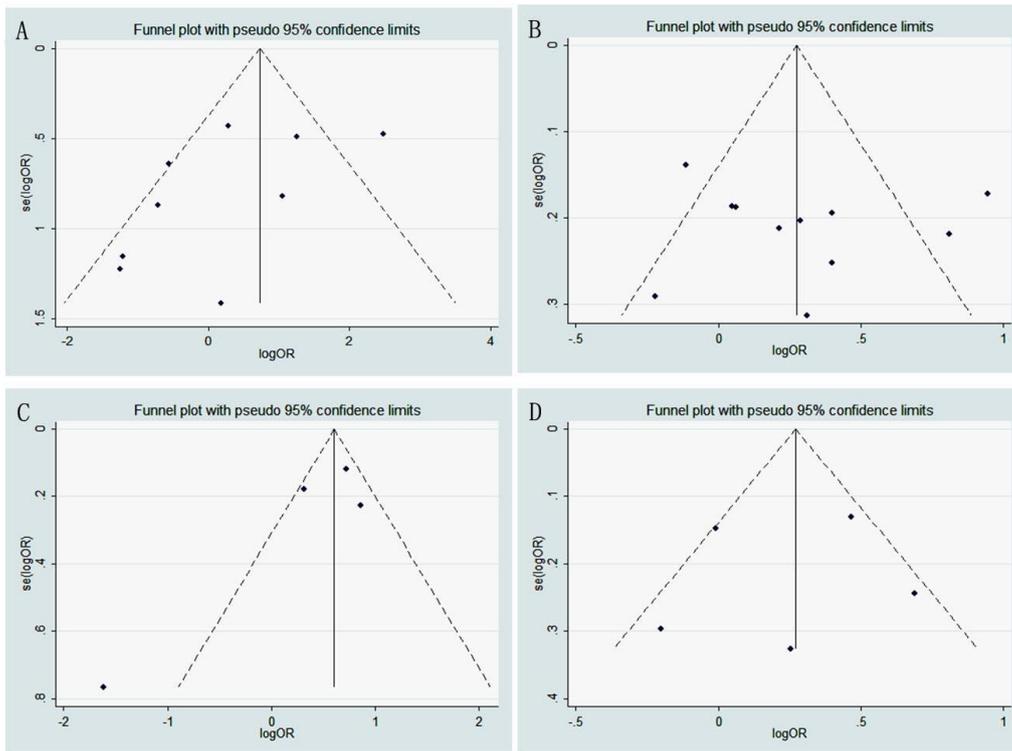
Sub-group studies	Genetic model	Cases/Control	Test of association		Test of heterogeneity		
			OR (95% CI)	<i>p</i>	<i>p</i> _Q	<i>p</i>	<i>I</i> ²
Overall	m1m1 vs m2m2	2790/3167	1.536 (0.775–3.044)	0.218	29.75	0.000	69.7
	m1m1 vs m1m2	2790/3167	1.26 (1.030–1.542)	0.007	25.9	0.025	57.5
	recessive model	2790/3167	1.316 (1.065–1.625)	0.011	30.5	0.001	63.8
	dominant model	2790/3167	1.453 (0.774–2.729)	0.245	26.84	0.001	66.5
	allele	2790/3167	1.302 (1.067–1.589)	0.009	38.74	0.000	71.6
Asian	m1m1 vs m2m2	1369/1842	2.107 (0.910–6.384)	0.036	7.26	0.202	31.1
	m1m1 vs m1m2	1369/1842	1.333 (1.009–1.889)	0.005	16.76	0.166	70.2
	recessive model	1369/1842	1.616 (1.081–2.017)	0.046	16.30	0.006	69.3
	dominant model	1369/1842	1.612 (0.589–4.412)	0.019	4.77	0.444	0.00
	allele	1369/1842	1.440 (1.326–2.348)	0.048	12.5	0.028	60.0
Non-Asian	m1m1 vs m2m2	1421/1325	0.987 (0.38–2.559)	0.835	3.31	0.192	39.5
	m1m1 vs m1m2	1421/1325	1.227 (0.927–1.624)	0.152	8.82	0.152	54.6
	recessive model	1421/1325	1.164 (0.974–1.393)	0.096	8.03	0.09	50.2
	dominant model	1421/1325	0.958 (0.37–2.479)	0.93	3.43	0.18	41.6
	allele	1421/1325	1.131 (0.962–1.330)	0.135	6.40	0.171	37.5

HNSCC, head and neck squamous cell carcinoma; OR, odds ratio; 95% CI, 95% confidence interval; ^a*p* value of the comparison of ORs; ^b*p* value of Q-test for heterogeneity test

Supplemental Table 2 Stratified analysis of the *CYP2D6* polymorphism and HNSCC

Sub-grouped studies	Genetic model	Test of association <i>CYP2D6*4</i>			Test of heterogeneity <i>CYP2D6*4</i>			Test of association <i>CYP2D6*10</i>			Test of heterogeneity <i>CYP2D6*10</i>		
		OR (95% CI)	<i>p</i> ^a	<i>p</i> ^b	<i>I</i> ²	OR (95% CI)	<i>p</i> ^a	<i>p</i> ^b	<i>I</i> ²				
Overall	wt/wt vs wt/mt	1.25 (0.891–1.752)	0.197	0.064	54.9	1.384 (0.660–2.902)	0.390	0.001	82.8				
	wt/wt vs mt/mt	1.775 (1.165–2.703)	0.008	0.328	13.5	2.491 (1.763–3.518)	0.000	0.436	0.0				
	recessive model	1.305 (0.916–1.858)	0.14	0.029	62.9	1.531 (0.811–2.892)	0.189	0.001	81.8				
	dominant model	1.641 (1.085–2.510)	0.017	0.519	0.0	2.021 (1.441–2.833)	0.000	0.317	15.1				
Asian	allele	1.29 (0.949–1.754)	0.023	0.105	64.8	1.592 (1.009–2.512)	0.046	0.004	77.2				
	wt/wt vs wt/mt	1.644 (1.087–2.487)	0.019	0.198	39.6	0.659 (0.660–2.902)	0.379	0.799	0.0				
	wt/wt vs mt/mt	2.677 (1.165–2.703)	0.001	0.753	0.0	2.542 (1.712–3.775)	0.000	0.709	0.0				
	recessive model	1.761 (1.248–2.484)	0.001	0.245	25.9	2.485 (1.903–3.245)	0.000	0.691	0.0				
Non-Asian	dominant model	2.336 (1.319–4.137)	0.004	0.949	0.0	1.932 (1.316–2.835)	0.001	0.708	0.0				
	allele	1.675 (1.337–2.099)	0.000	0.419	0.0	2.122 (1.722–2.615)	0.000	0.574	0.0				
	wt/wt vs wt/mt	0.987 (0.38–2.559)	0.978	0.192	0.192	2.456 (1.809–3.335)	0.000	0.194	40.6				
	wt/wt vs mt/mt	1.057 (0.562–1.989)	0.864	0.993	0.0	2.307 (1.763–4.684)	0.021	0.102	62.6				
	recessive model	0.976 (0.734–1.299)	0.870	0.458	0.0	0.617 (0.136–2.786)	0.530	0.052	73.5				
	dominant model	0.958 (0.37–2.479)	0.81	0.976	0.0	2.417 (1.205–4.848)	0.013	0.099	63.3				
	allele	0.994 (0.782–1.263)	0.962	0.590	0.0	0.603 (0.091–4.000)	0.6	0.013	83.7				

HNSCC, head and neck squamous cell carcinoma; OR, odds ratio; 95% CI, 95% confidence interval; ^a*P* value of the comparison of ORs; ^b*p* value of Q-test for heterogeneity test.



Supplemental Figure1.

Begg's funnel plot for publication bias test. A: *CYP1A1* m1m1 vs m1m2. B: *CYP1A1* allel model. C: *CYP2D6*4* allel model. D: *CYP2D6*10* allel model. Each point represents a separate study for the indicated association. Logor represents natural logarithm of OR. Horizontal line represents the mean effects size.