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ERRATUM

Common variants in MODY genes increase the risk of gestational diabetes mellitus

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Unfortunately some of the footnotes in Table 1 of this article were incorrect. The corrected table is reproduced here.

Table 1 Genotype and allele distributions and corresponding odds ratios for GDM

SNP (rs number)	Genotype or allele	GDM *n* (%)	Controls *n* (%)	OR (95% CI) for GDM, additive model/ allelic effect	OR (95% CI) for GDM, recessive model	OR (95% CI) for GDM, dominant model
GCK −30G→A (rs1799884)	GG	435 (67.8)	889 (72.3)			
	GA	181 (28.2)	316 (25.7)	1.17 (0.94–1.45)		
	AA	26 (4.0)	24 (2.0)[a]	2.21 (1.26–3.90)[b]	2.12 (1.21–3.72)[d]	1.24 (1.01–1.53)[e]
	A	233 (18.1)	364 (14.8)	1.28 (1.06–1.53)[c]		
HNF1A I27L (rs1169288)	II	242 (39.4)	559 (46.1)			
	IL	298 (48.5)	508 (41.8)	1.36 (1.10–1.67)[f]		
	LL	74 (12.1)	147 (12.1)[a]	1.16 (0.85–1.60)	0.99 (0.74–1.34)	1.31 (1.08–1.60)[e]
	L	446 (36.3)	802 (33.0)	1.16 (1.001–1.34)[c]		
HNF4A (rs2144908)	GG	425 (67.8)	854 (70.1)			
	GA	167 (26.6)	316 (25.9)	1.06 (0.85–1.32)		
	AA	35 (5.6)	48 (4.0)	1.47 (0.93–2.30)	1.44 (0.92–2.25)	1.12 (0.91–1.37)
	A	237 (18.9)	412 (16.9)	1.14 (0.96–1.37)		
HNF4A (rs2425637)	GG	159 (24.7)	317 (25.8)			
	GT	310 (48.2)	617 (50.2)	1.00 (0.79–1.27)		
	TT	174 (27.1)	295 (24.0)	1.18 (0.90–1.54)	1.17 (0.94–1.46)	1.06 (0.85–1.32)
	T	658 (51.2)	1207 (49.1)	1.09 (0.95–1.24)		
HNF4A (rs1885088)	GG	412 (65.2)	791 (65.6)			
	GA	199 (31.5)	354 (29.4)	1.08 (0.87–1.33)		
	AA	21 (3.3)	60 (5.0)	0.67 (0.40–1.12)	0.66 (0.40–1.09)	1.02 (0.83–1.25)
	A	241 (19.1)	474 (19.7)	0.96 (0.81–1.14)		

[a] Differences in genotype frequencies between women with and without GDM (p=0.010 for *GCK* −30G→A and p=0.016 for *HNF1A* I27L)
[b] p=0.006 for comparison of AA genotype vs GG genotype between women with and without GDM
[c] Differences in allele frequencies between women with and without GDM (p=0.008 for *GCK* −30G→A and p=0.048 for *HNF1A* I27L)
[d] p=0.009 for comparison between women with and without GDM using a recessive model (AA vs GA+GG)
[e] Comparison between women with and without GDM using a dominant model (p=0.039 for *GCK* −30G→A and p=0.007 for *HNF1A* I27L)
[f] p=0.004 for comparison of IL genotype vs II genotype between women with and without GDM