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ERRATUM

Common SNPs in *LEP* and *LEPR* associated with birth weight and type 2 diabetes-related metabolic risk factors in twins

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Owing to a typesetting error in Tables 1 and 2 of the above paper some cells and the background of some text in the legend are gray, while they should have been white.

The correct tables are reproduced below.

The typesetters would like to apologize for this error.

Table 1 Phenotypic characteristics of MZ and DZ twins by gender

Characteristic	*MZ*			*DZ*		
	Men	*Women*	P-*value*	*Men*	*Women*	P-*value*
n	179	217		107	125	
Birth weight (g)	2540 ± 443	2456 ± 488	0.11	2690 ± 446	2572 ± 474	0.002
Gestational age (weeks)[a]	36.9 ± 2.2	36.8 ± 2.6	0.98	37.4 ± 2.2	37.5 ± 2.3	0.82
Age (years)[a]	25.0 ± 4.6	24.8 ± 4.7	0.68	25.5 ± 4.7	25.6 ± 4.6	0.88
Body height (cm)	178.0 ± 5.9	165.3 ± 6.5	<0.0001	178.5 ± 6.7	166.5 ± 6.5	<0.0001
Body mass (kg)	69.3 ± 9.1	60.2 ± 9.9	<0.0001	70.1 ± 10.1	60.7 ± 10.0	<0.0001
BMI (kg/m^2)[b]	21.7 ± 1.1	21.8 ± 1.2	0.78	21.9 ± 1.1	21.7 ± 1.1	0.84
Fat mass (kg)[b]	11.3 ± 1.5	16.7 ± 1.3	<0.0001	12.2 ± 1.5	16.6 ± 1.3	<0.0001
Lean body mass (kg)	57.0 ± 6.2	42.8 ± 5.2	<0.0001	57.0 ± 6.5	43.5 ± 5.9	<0.0001
S4SF (mm)[b]	34.9 ± 1.5	56.2 ± 1.4	<0.0001	34.2 ± 1.5	52.2 ± 1.4	<0.0001
WHR (%)	82.9 ± 5.3	73.2 ± 4.5	<0.0001	82.6 ± 5.1	72.3 ± 4.2	<0.0001
IGFBP-1 (ng ml^{-1})[b]	10.9 ± 1.8	16.3 ± 2.0	<0.0001	12.2 ± 1.8	19.1 ± 2.3	<0.0001
Fasting insulin (pmol l^{-1})[b]	32.5 ± 1.5	37.8 ± 1.6	0.005	31.6 ± 1.6	40.6 ± 1.5	<0.0001
Fasting glucose (mmol l^{-1})	5.0 ± 0.4	4.6 ± 0.4	<0.0001	4.8 ± 0.4	4.6 ± 0.4	<0.0001
Leptin (ng ml^{-1})[b]	1.6 ± 3.1	11.8 ± 2.1	<0.0001	1.6 ± 2.8	11.4 ± 1.9	<0.0001
Total cholesterol (mmol l^{-1})	4.8 ± 1.0	5.1 ± 0.8	0.003	5.0 ± 1.1	5.2 ± 1.0	0.08
LDL cholesterol (mmol l^{-1})	3.0 ± 0.9	2.9 ± 0.8	0.43	3.1 ± 1.0	2.9 ± 0.8	0.03
HDL cholesterol (mmol l^{-1})	1.4 ± 0.3	1.8 ± 0.4	<0.0001	1.4 ± 0.4	1.9 ± 0.4	<0.0001
Triacylglycerol (mmol l^{-1})[b]	0.8 ± 1.5	0.9 ± 1.5	0.04	0.9 ± 1.5	0.9 ± 1.5	0.81
NEFA (mmol l^{-1})	0.5 ± 0.2	0.7 ± 0.2	<0.0001	0.5 ± 0.2	0.7 ± 0.2	<0.0001

Abbreviations: BMI, body mass index; DZ, dizygotic; HDL, high-density lipoprotein; LDL, low-density lipoprotein; WHR, waist-to-hip ratio; IGFBP1, insulin-like growth factor protein 1; MZ, monozygotic; n, number of individuals; NEFA, non-esterified fatty acids; S4SF, sum of four skinfolds; WHR, waist-to-hip ratio. Data are expressed as mean ± s.d. [a]*P*-value calculated using standard linear regression, because convergence criteria could not be met in the random intercept model. [b]Geometric mean ± s.d.

Table 2 Significant associations between the SNPs in the *LEPR* and the *LEP* gene and the metabolic risk factors for type 2 diabetes; adjusted for significant covariates

Gene (SNP)	*Trait*[a]	*Genotype*			P_G	P_A	P_D	P_R
LEPR (K109R)		KK	KR	RR				
	n (n_{MZ}/n_{DZ})[b]	354 (240/114)	194 (116/78)	46 (30/16)				
	Birth weight[c]	2511 (2465–2557)	2575 (2516–2635)	2726 (2606–2845)	0.003	**0.001**	0.01	0.003
LEPR (Q223R)		QQ	QR	RR				
	n (n_{MZ}/n_{DZ})[b]	189 (126/63)	295 (185/110)	98 (66/32)				
	Birth weight[d]	2492 (2431–2554)	2545 (2495–2595)	2655 (2571–2740)	0.009	**0.003**	0.04	0.006
LEP (19G>A)		GG	GA	AA				
	n (n_{MZ}/n_{DZ})[b]	216 (131/85)	265 (181/84)	82 (53/29)				
	HDL cholesterol[d]	1.59 (1.53–1.65)	1.64 (1.59–1.69)	1.49 (1.40–1.58)	0.02	0.35	0.64	**0.01**

Abbreviations: HDL, high-density lipoprotein; *n*, total number of individuals; n_{DZ}, number of DZ individuals; n_{MZ}, number of MZ individuals; P_A, *P*-value additive model; P_D, *P*-value dominant model; P_G, *P*-value general association model; P_R, *P*-value recessive model; SNP, single nucleotide polymorphism. Data are expressed as least squares mean (95% CI). The lowest *P*-value is shown in boldface type. See also Supplementary Tables 3, 4 and 5 for the means (95% CI) per genotype group and the mode of inheritance (additive, dominant and recessive) of the associations that were considered nonsignificant. [a]The units of the phenotypic characteristics are presented in Table 1. [b]Total number of individuals differ from the number reported in Table 1 because of missing values for the genotype, dependent variable or the covariates. [c]Adjusted for gender, gestational age and chorion type. [d]Adjusted for gender and WHR.