

CORRECTION

doi: 10.1136/ard.2004.025767corr1

Single nucleotide polymorphisms in the gene encoding the major histocompatibility complex class II transactivator

(CIITA) in systemic lupus erythematosus (Koizumi K, Okamoto H, Iikuni N, Nakamura T, Kawamoto M, Momohara S, Ichikawa N, Furuya T, Kotake S, Taniguchi A, Yamanaka H, Kamatani N. *Ann Rheum Dis* 2005;**64**:947–50.)

The authors have provided a new figure to replace figure 1 of this article. The figure is reproduced below.

Corrections printed in the journal also appear on the *Annals* website <http://www.annrheumdis.com> and are linked to the original publication

A

Promoter III	Coding sequence				
nt No -155 (III) A→G	nt No 1614 (C1) C→G	nt No 2509 (C2) G→A	nt No 2536 (C2) T→G	nt No 2791 (C3) G→A	

Allele frequency

Total	G 368 (92.0%)	C 128 (32.0%)	G 278 (69.5%)	T 128 (32.0%)	G 138 (34.5%)
	A 32 (8.0%)	G 272 (68.0%)	A 122 (30.5%)	G 272 (68.0%)	A 262 (65.5%)
SLE	G 192 (96.0%)	C 62 (31.0%)	G 136 (68.0%)	T 62 (31.0%)	G 70 (35.0%)
	A 8 (4.0%)	G 138 (69.0%)	A 64 (32.0%)	G 138 (69.0%)	A 130 (65.0%)
HD	G 176 (88.0%)	C 66 (33.0%)	G 142 (71.0%)	T 66 (33.0%)	G 68 (34.0%)
	A 24 (12.0%)	G 134 (67.0%)	A 58 (29.0%)	G 134 (67.0%)	A 132 (66.0%)
Patarroyo <i>et al</i> ¹⁰					
	G 37%	C 35%	G 81%	T 29%	G 35%
	A 63%	G 65%	A 19%	G 71%	A 65%

B

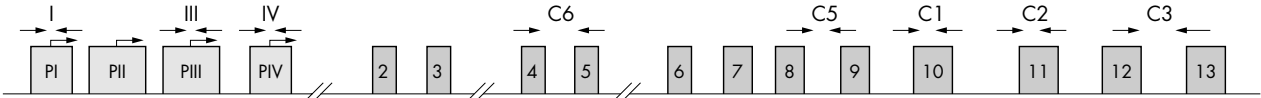


Figure 1 SNPs in *MHC2TA* pIII and coding region. (A) Genomic DNA was isolated from peripheral blood mononuclear cells, and PCR and direct sequencing were performed with eight oligonucleotide primer sets for genomic analysis of SNPs (arrows). (B) *MHC2TA* promoter elements and exon organisation. Arrows on the box represent upstream regulatory sequences for each promoter. Promoter pI is used primarily by dendritic cells, pIII by B cells, and pIV for IFN γ -inducible CIITA expression by non-professional APCs.