Erratum

Comparative Evolutionary Rates of Introns and Exons in Murine Rodents

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Re: J Mol Evol (1997) 45:125–130. There were computational errors in some of the cases listed in Table 1. Corrected values for these cases are given here (Table 1). The conclusions of the paper are unaffected. Corrected mean d in introns is 19.8 ± 0.7 SE; corrected mean d_s and d_N in exons are, respectively, 20.4 ± 1.2 and 6.4 ± 1.1 . Mean percent G + C in introns is 50.8 ± 1.2 ; in exons, mean percent G + C is 49.3 ± 0.9 at first and second

positions and 63.9 ± 1.7 at third positions. There is not a significant correlation between mean d_s and mean d_N ($r = 0.226$). However, interleukin-3 is unusual in that $d_N > d_s$, suggesting that this gene is subject to positive selection. If this gene is excluded, there is a significant positive correlation between mean d_s and mean d_N ($r = 0.508$; $P < 0.005$); we are grateful to Jianzhi Zhang for pointing this out.

Table 1. For corrected cases in mouse-rat comparisons, mean number of nucleotide substitutions per 100 sites (d_s) and per 100 nonsynonymous sites (d_N) and mean percent G + C at codon positions 1–2 (GC_{12}) and at codon position 3 (GC_3) in exons; and mean number of nucleotide substitutions per site (d) and mean percent GC (GC) in introns

Gene	#Exons	#Introns	Exons				Introns	
			d_s	d_N	GC_{12}	GC_3	d	GC
α -actin	5	5	12.3	0.0	48.5	75.1	21.7	60.8
Cytochrome <i>c</i>	1	1	14.9	0.0	46.5	50.9	20.4	46.2
Kallikrein binding protein	3	3	25.9	14.8	41.9	66.7	20.5	46.4
Metallothionein II	2	2	12.2	2.1	59.2	53.3	26.9	57.3
Nucleolin	11	10	11.2	1.9	47.9	34.4	21.3	39.2
Peripherin	8	8	25.3	1.0	47.8	69.6	19.4	58.7
Preprosomatostatin	2	1	9.8	0.0	55.1	76.5	15.4	47.4

Accession numbers are in Hughes and Yeager (1997); other cases in Table 1 from Hughes and Yeager (1997) are correct.