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Erratum

Intron Length and Codon Usage

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Re: J Mol Evol (2001) 52:2–5. The corrected version of Table 1 appears below.

Table 1. Coefficients of Spearman rank correlation between the frequency of optimal codons (FOP) and effective number of codons (ENC) and the within-gene average internal intron length and ratio of intervening to coding sequence lengths (IVS/CDS)

Organism	Number of genes analyzed	GC3s% of CDS mean CV, %	Frequency of optimal codons (FOP)		Effective number of codons (ENC)	
			Avg. intron length	IVS/CDS	Avg. intron length	IVS/CDS
Saccharomyces cerevisiae	224	39.0	0.61	0.69	−0.59	−0.72
(baker's yeast)		17.1	($<10^{-4}$)	($<10^{-4}$)	($<10^{-4}$)	($<10^{-4}$)
Schizosaccharomyces	2,309	30.8	—	—	−0.13	−0.10
pombe (fission yeast)		14.9			($<10^{-4}$)	($<10^{-4}$)
Emericella nidulans (mold)	203	59.9	0.18	0.44	−0.09	−0.30
		12.6	(<0.02)	($<10^{-4}$)	(<0.3)	($<10^{-4}$)
Neurospora crassa (fungus)	133	70.6	0.15	0.36	−0.14	−0.35
		12.0	(<0.1)	($<10^{-4}$)	(<0.2)	($<10^{-3}$)
Candida albicans	34	26.1	—	—	−0.77	−0.60
(pathogenic yeast)		31.7			($<10^{-4}$)	($<10^{-3}$)
Dictyostelium discoideum	138	15.7	0.35	0.15	−0.01	−0.27
(cellular slime mold)		44.5	($<10^{-4}$)	(<0.1)	(<0.7)	($<10^{-3}$)
Tetrahymena thermophila	22	40.0	—	—	−0.62	−0.59
(ciliate)		39.7			(<0.01)	(<0.01)
Chlamydomonas reinhardtii	83	86.2			−0.16	0.06
(unicellular plant)		5.0			(<0.2)	(<0.6)
Caenorhabditis elegans	14,673	37.6	−0.03	−0.07	0.12	0.14
(nematode)		23.0	($<10^{-3}$)	($<10^{-4}$)	($<10^{-4}$)	($<10^{-4}$)
Xenopus laevis	54	50.3			0.23	0.11
(clawed frog)		16.1			(<0.1)	(<0.5)
Gallus gallus	158	67.5	—	—	0.34	0.30
(chicken)		24.6			($<10^{-4}$)	($<10^{-3}$)
Mus musculus	981	62.2	—	—	0.07	0.15
(mouse)		17.2			(<0.03)	($<10^{-4}$)
Rattus norvegicus	348	62.7			0.17	0.26
(rat)		17.9			(<0.01)	($<10^{-4}$)
Homo sapiens	2,543	64.0	—	—	0.25	0.27
(human)		24.7			($<10^{-4}$)	($<10^{-4}$)
Arabidopsis thaliana	21,238	40.0	—	—	0.16	0.05
(thale cress)		15.3			($<10^{-4}$)	(<0.12)
Zea mays	91	76.6	—	—	0.26	0.55
(corn)		23.4			(<0.02)	($<10^{-4}$)

Significance levels are shown in parentheses; the empty cells are because optimal codons are not known for the corresponding species. Sequences were extracted from GenBank (only the complete ones). Genes were checked for duplicates on the ground of gene names. The intron/exon boundaries were taken from annotations.

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