

Evolution of mutation rates: phylogenomic analysis of the
photolyase/cryptochrome family.

Supplemental Material

J. Ignacio Lucas-Lledó Michael Lynch

February 13, 2009

Table 2: Maximum likelihood estimates of the nonsynonymous to synonymous substitution rates ratio (ω) for several sets of photolyase genes. Each ω estimate was obtained from a set of ‘N’ sequences that belong to the ‘Taxon’ specified by the first column (usually genus, but sometimes family) and to the type of photolyase gene specified in ‘Paralog’. When more than one estimate is available for the same genus and paralog, they have been obtained with independent sets of sequences. ‘M.P.D.’ is the maximum (synonymous) pairwise distance (substitutions per site) in that set of sequences, and ‘S.T.L.’ is the total synonymous length of the tree of those sequences (in substitutions per site, as well). Standard deviation estimates, calculated by bootstrap, are shown for ω and ‘S.T.L.’. ‘Loss’ indicates whether that paralog has been observed to be lost (L) or gained (G) in that taxon.

Taxon	Paralog	ω	S_ω	M.P.D.	S.T.L.	S_{STL}	N	loss
<i>Drosophila</i>	(6-4) photolyase	0.09914	0.01868	0.2864	0.48219	0.04369	6	
Tetraodontidae	(6-4) photolyase	0.14627	0.02430	0.5210	0.52147	0.05951	2	
<i>Aeromonas</i>	CPD class I	0.07912	0.01106	0.9868	0.98684	0.12031	2	
<i>Bacillus</i>	CPD class I	0.13524	0.02254	0.3314	0.70550	0.06629	7	G
<i>Burkholderia</i>	CPD class I	0.08841	0.02179	0.6316	0.66225	0.11009	5	
<i>Burkholderia</i>	CPD class I	0.09330	0.01563	0.6991	1.04370	0.12222	5	
<i>Corynebacterium</i>	CPD class I	0.28039	0.20196	0.0302	0.03054	0.01061	3	L
Enterobacteriaceae	CPD class I	0.16948	0.03145	0.2716	0.50005	0.04698	12	
<i>Francisella</i>	CPD class I	0.12039	0.11380	0.0380	0.03803	0.01606	2	L
<i>Legionella</i>	CPD class I	0.20669	0.04804	0.1252	0.17718	0.02869	4	
<i>Leishmania</i>	CPD class I	0.12230	0.02004	0.7123	0.71973	0.07734	3	
<i>Listeria</i>	CPD class I	0.14177	0.02767	0.3063	0.31486	0.03643	7	
<i>Neisseria</i>	CPD class I	0.33693	0.11834	0.1005	0.09780	0.01800	4	
<i>Prochlorococcus</i>	CPD class I	0.14603	0.02475	0.4507	0.68193	0.08101	5	G
<i>Prochlorococcus</i>	CPD class I	0.12685	0.03644	0.1487	0.14868	0.02509	2	G
<i>Pseudomonas</i>	CPD class I	0.07245	0.01506	0.7061	0.75423	0.09183	4	
<i>Pseudomonas</i>	CPD class I	0.06255	0.01040	0.8515	0.91290	0.08893	3	
<i>Pseudomonas</i>	CPD class I	0.05881	0.01320	0.5917	0.59170	0.06918	2	
<i>Psychrobacter</i>	CPD class I	0.18131	0.03138	0.3643	0.36431	0.04741	2	
<i>Ralstonia</i>	CPD class I	0.07453	0.01765	0.3260	0.32604	0.04209	2	L
<i>Rhodobacter</i>	CPD class I	0.12147	0.06093	0.0852	0.08523	0.02167	2	
<i>Rhodospseudomonas</i>	CPD class I	0.10959	0.01872	0.8916	0.89157	0.11195	2	
<i>Saccharomyces</i>	CPD class I	0.08617	0.01855	0.4036	0.40363	0.04902	2	
<i>Salmonella</i>	CPD class I	0.13887	0.07291	0.0555	0.05652	0.01385	3	
<i>Shewanella</i>	CPD class I	0.12117	0.03915	0.1310	0.18354	0.02498	3	L
<i>Shewanella</i>	CPD class I	0.09100	0.01160	1.0183	1.13026	0.09186	4	L
<i>Staphylococcus</i>	CPD class I	0.09624	0.01910	0.8934	0.82710	0.10708	4	L
<i>Synechococcus</i>	CPD class I	0.07042	0.01376	0.8541	0.85018	0.10843	2	
Trichocomaceae	CPD class I	0.14368	0.03133	0.2015	0.20151	0.02577	2	
<i>Trypanosoma</i>	CPD class I	0.09561	0.13497	0.0166	0.01662	0.00747	2	
<i>Vibrio</i>	CPD class I	0.13467	0.05517	0.0481	0.10393	0.02344	6	
<i>Vibrio</i>	CPD class I	0.08298	0.01912	0.4949	0.49485	0.06614	2	
<i>Xanthomonas</i>	CPD class I	0.08913	0.01235	0.9886	1.34296	0.11083	5	
<i>Yersinia</i>	CPD class I	0.09934	0.01114	1.2161	1.86003	0.14277	4	
<i>Yersinia</i>	CPD class I	0.30694	0.36318	0.0074	0.00962	0.00466	3	
Cyprinidae	CPD class II	0.14310	0.02183	0.6596	0.65964	0.06777	2	
<i>Desulfovibrio</i>	CPD class II	0.24894	0.20167	0.0254	0.02534	0.00957	2	
<i>Drosophila</i>	CPD class II	0.10001	0.01573	0.3209	0.57881	0.04555	6	
<i>Leporipoxvirus</i>	CPD class II	0.19301	0.03578	0.4549	0.45491	0.05619	2	
<i>Leptospira</i>	CPD class II	0.09289	0.01644	0.6681	0.66791	0.08293	2	
<i>Methanosarcina</i>	CPD class II	0.12464	0.02068	0.9702	0.97021	0.13052	2	
<i>Methylobacterium</i>	CPD class II	0.04541	0.02604	0.1483	0.14826	0.03175	2	
<i>Nucleopolyhedrovirus</i>	CPD class II	0.20727	0.02999	0.6661	0.66614	0.07571	2	L
<i>Oryza</i>	CPD class II	0.07453	0.01678	0.3260	0.32604	0.04026	2	
<i>Plasmodium</i>	CPD class II	0.21999	0.05239	0.1569	0.15699	0.02732	2	
<i>Plasmodium</i>	CPD class II	0.13646	0.02552	0.8451	0.84507	0.13545	2	
Tetraodontidae	CPD class II	0.12590	0.02295	0.7793	0.77930	0.11144	2	

Table 3: Efficiency of photolyases in the prevention of UV-induced mutations, measured as the proportion of UV-induced mutations avoided by the ectopic expression of those photolyases in irradiated cell cultures

Species	Paralog	Efficiency (%)	Reference
<i>Salmonella typhimurium</i>	Class I	90	Otoshi et al. (2000)
<i>Escherichia coli</i>	Class I	74	Tanaka et al. (2001)
<i>Monodelphis domestica</i>	Class II	72	Asahina et al. (1999)
<i>Potorous tridactylus</i>	Class II	86 ± 6	You et al. (2001)
<i>Xenopus laevis</i>	(6-4)	57	Otoshi et al. (2000)
<i>Arabidopsis thaliana</i>	(6-4)	59	Tanaka et al. (2001) ^a

^aThe measures obtained by You et al. (2001) for *A. thaliana* have been excluded. They found that, *A. thaliana* (6-4) photolyase did not prevent any UV-induced mutation, probably due to the existence of a redundant DNA-repair pathway.

References

- Asahina, H., Z.-B. Han, M. Kawanishi, T. Kato, Jr., H. Ayaki, T. Todo, T. Yagi, H. Takebe, M. Ikenaga, and S. H. Kimura. 1999. Expression of a mammalian DNA photolyase confers light-dependent repair activity and reduces mutations of UV-irradiated shuttle vectors in xeroderma pigmentosum cells. *Mutat Res* **435**:255–262.
- Otoshi, E., T. Yagi, T. Mori, T. Matsunaga, O. Nikaido, S.-T. Kim, K. Hitomi, M. Ikenaga, and T. Todo. 2000. Respective roles of cyclobutane pyrimidine dimers, (6-4)photoproducts, and minor photoproducts in ultraviolet mutagenesis of repair-deficient xeroderma pigmentosum A cells. *Cancer Res* **60**:1729–1735.
- Tanaka, M., S. Nakajima, M. Ihara, T. Matsunaga, O. Nikaido, and K. Yamamoto. 2001. Effects of photoreactivation of cyclobutane pyrimidine dimers and pyrimidine (6-4) pyrimidone photoproducts on ultraviolet mutagenesis in SOS-induced repair-deficient *Escherichia coli*. *Mutagenesis* **16**:1–6.
- You, Y.-H., D.-H. Lee, J.-H. Yoon, S. Nakajima, A. Yasui, and G. P. Pfeifer. 2001. Cyclobutane pyrimidine dimers are responsible for the vast majority of mutations induced by UVB irradiation in mammalian cells. *J Biol Chem* **276**:44688–44694.