

Erratum to: Transfer RNA Gene Numbers may not be Completely Responsible for the Codon Usage Bias in Asparagine, Isoleucine, Phenylalanine, and Tyrosine in the High Expression Genes in Bacteria

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We regret to inform that the data presented in our published article (Satapathy et al. 2012) for the whole genome with respect to amino acid usage and NNC/NNU ratio is erroneous for the two bacteria *Pseudomonas aeruginosa* and *Streptomyces coelicolor* in Tables 1 and 2 of the article. The correct data under the “Whole genome” heading for the two bacteria are as follows:

In Table 1

- (i) The correct “Whole genome” data for the bacteria *P. aeruginosa* are 1859569, 3.56, 2.64, 4.17, 2.54.
- (ii) The correct “Whole genome” data for the bacteria *S. coelicolor* are 2560775, 2.65, 1.70, 2.86, 2.05.

In view of the above changes in Table 1, the amino acid usage data of these two bacteria given in the Supplementary Table 1 is no longer required and hence to be ignored.

In Table 2

- (i) The correct “Whole genome” data for the bacteria *P. aeruginosa* are 19.62, 6.06, 13.25, 3.82.

- (ii) The correct “Whole genome” data for the bacteria *S. coelicolor* are 61.99, 23.83, 46.16, 20.5.

In view of the above corrections in Table 1, what has been stated in the first paragraph of the result section in the article about the amino acid composition difference between the whole genomes and high expression genes in these two bacteria is no longer valid and hence to be ignored.

In view of the above corrections in Table 2, the NNC/NNU results for the two bacteria are in agreement with the earlier observation of Sharp et al. (2005). Hence what has been stated in the third paragraph in the discussion section of the article is no longer valid and hence to be ignored.

The changes in Tables 1 and 2 have no effect on the main findings of the analyses presented in the article. There is no change in the Title, Abstract, and Reference sections of the article.

Corrected tables with the relevant changes in the footnote are given below.

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Table 1 Usage (in %) of phenylalanine (Phe), asparagine (Asn), isoleucine (Ile) and tyrosine (Tyr) amino acids

S. no.	Strain	Group	Genome size	GC (%)	Top 100 HE genes					Whole genome				
					Total	Phe	Asn	Ile	Tyr	Total	Phe	Asn	Ile	Tyr
1	<i>S. aureus</i>	Firmicutes	2903636	32.84	33828	3.50	4.70	7.42	2.82	801462	4.48	5.69	8.59	3.93
2	<i>S. mutans</i>	Firmicutes	2030921	36.83	39508	3.60	5.06	6.85	3.26	579702	4.76	4.85	7.74	3.85
3	<i>L. monocytogenes</i>	Firmicutes	2944528	37.98	31671	3.72	4.58	6.96	3.2	870878	4.53	4.62	7.84	3.45
4	<i>H. influenzae</i>	γ Proteobacteria	1830069	38.15	25071	4.38	5.23	6.75	3.28	521077	4.48	4.88	7.11	3.14
5	<i>B. subtilis</i>	Firmicutes	4214630	43.52	32519	3.65	4.06	6.45	3.02	1228408	4.50	3.95	7.37	3.49
6	<i>L. plantarum</i>	Firmicutes	3348625	44.42	32119	3.63	4.58	6.54	3.50	920243	3.97	4.41	6.56	3.52
7	<i>E. coli</i>	γ Proteobacteria	4639675	50.00	22219	3.34	3.94	5.99	2.58	1313473	3.90	3.89	6.01	2.83
8	<i>N. europaea</i>	β Proteobacteria	2812094	50.72	22536	4.05	3.70	6.17	2.95	800071	3.92	3.58	6.39	2.84
9	<i>P. syringae</i>	γ Proteobacteria	6538260	58.34	26326	3.18	3.26	5.10	2.87	1814263	3.63	3.19	4.98	2.55
10	<i>B. longum</i>	Actinobacteria	2260266	60.13	30848	3.55	3.90	6.04	2.91	640513	3.41	3.43	5.37	2.68
11	<i>D. vulgaris</i>	δ Proteobacteria	3773159	63.28	26270	3.49	3.03	5.09	2.55	1020841	3.59	2.41	4.45	2.27
12	<i>B. japonicum</i>	α Proteobacteria	9105828	64.06	23090	3.55	3.61	5.29	2.70	2634346	3.73	2.76	5.26	2.21
13	<i>R. palustris</i>	α Proteobacteria	5467640	65.03	30075	3.91	3.96	5.46	3.20	1580833	3.64	2.58	5.26	2.22
14	<i>P. aeruginosa</i>	γ Proteobacteria	6264404	66.56	21744	3.59	3.68	5.05	2.72	1859569	3.56	2.64	4.17	2.54
15	<i>R. sphaeroides</i>	α Proteobacteria	4603060	68.79	23416	3.74	3.25	5.56	2.72	943868	3.49	2.02	4.52	1.91
16	<i>T. thermophilus</i>	Deinococcus-Thermus	2116056	69.50	23854	3.45	2.84	4.87	3.11	589163	3.77	1.55	2.67	2.87
17	<i>S. coelicolor</i>	Actinobacteria	9054847	72.00	27997	2.68	2.61	4.02	2.33	2560775	2.65	1.70	2.86	2.05

Table presents total number of codons and percentage of codons encoding four amino acids, phenylalanine (Phe), asparagine (Asn), isoleucine (Ile) and tyrosine (Tyr) in top 100 high expression (HE) genes as well as in the whole genome of seventeen bacteria (*Bacillus subtilis*, *Bifidobacterium longum*, *Bradyrhizobium japonicum*, *Desulfovibrio vulgaris*Hildenborough, *Escherichia coli*, *Haemophilus influenzae*, *Lactobacillus plantarum*, *Listeria monocytogenes*, *Nitrosomonas europaea*, *Pseudomonas aeruginosa*, *Pseudomonas syringae*, *Rhodobacter sphaeroides*, *Rhodopseudomonas palustris*, *Staphylococcus aureus*, *Streptococcus mutans*, *Streptomyces coelicolor*, *Thermus thermophilus*)

Table 2 Transfer RNA gene number and synonymous codon usage in phenylalanine (Phe), asparagine (Asn), isoleucine (Ile) and tyrosine (Tyr) amino acids

S. no.	Name	tRNA Gene number				Top100 HE genes ^b				Whole genome ^b			
		Phe	Asn	Ile	Tyr	Phe	Asn	Ile	Tyr	Phe	Asn	Ile	Tyr
		GAA	GTT	GAT	GTA	UUC/ UUU	AAC/ AAU	AUC/ AUU	UAC/ UAU	UUC/ UUU	AAC/ AAU	AUC/ AUU	UAC/ UAU
1	<i>S. aureus</i>	2	3	2	2	1.02	0.75	0.51	0.51	0.37	0.31	0.28	0.28
2	<i>S. mutans</i>	2	2	2	2	0.38	0.33	0.35	0.35	0.25	0.24	0.30	0.27
3	<i>L. monocytogenes</i>	2	4	3	2	1.11	1.18	0.67	0.79	0.47	0.45	0.36	0.46
4	<i>H. influenzae</i>	1	2	3	1	0.45	0.36	0.36	0.33	0.38	0.33	0.28	0.28
5	<i>B. subtilis</i>	3	4	3	2	0.78	1.36	1.06	0.81	0.46	0.77	0.73	0.53
6	<i>L. plantarum</i>	2	5	3	2	0.59	0.72	0.58	0.73	0.53	0.66	0.52	0.63
7	<i>E. coli</i>	2	4	3	3	2.42	4.54	1.99	1.88	0.74	1.24	0.83	0.76
8	<i>N. europaea</i>	1	1	1	1	0.70	0.72	0.74	0.62	0.98	0.68	1.49	0.68
9	<i>P. syringae</i>	1	2	5	1	1.38	3.03	2.30	0.94	1.81	2.36	2.25	1.80
10	<i>B. longum</i>	1	3	1	1	25.05	9.95	4.85	8.07	6.89	2.81	2.81	2.24
11	<i>D. vulgaris</i>	1	2	5	1	12.10	5.91	7.84	4.32	7.04	4.37	7.49	2.43
12	<i>B. japonicum</i>	2	2	1	1	2.55	1.77	3.12	1.51	4.70	2.21	7.16	1.15
13	<i>R. palustris</i>	1	1	2	1	12.21	4.54	10.27	2.46	6.24	2.40	8.19	1.33
14	<i>P. aeruginosa</i>	1	2	4	1	40.05	10.13	11.66	5.09	19.62	6.06	13.25	3.82
15	<i>R. sphaeroides</i>	1	1	3	0 ^a	37.09	11.06	31.50	1.86	11.96	3.63	18.90	1.12
16	<i>T. thermophilus</i>	1	1	1	1	5.65	134.40	7.30	56.15	4.68	40.06	9.30	23.38
17	<i>S. coelicolor</i>	1	2	1	1	73.90	59.83	64.41	35.22	61.99	23.83	46.16	20.5

^a No tRNA gene according the Genomic tRNA database (<http://gtmadb.ucsc.edu>)

^b The ratio between abundance values of the two synonymous codons of an amino acid in the high expression (HE) genes and in the whole genome

References

- Satapathy SS, Dutta M, Buragohain AK, Ray SK (2012) Transfer RNA gene numbers may not be completely responsible for the codon usage bias in asparagine, isoleucine, phenylalanine, and tyrosine in the high expression genes in bacteria. *J Mol Evol* 75:34–42
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