

CORRECTION

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Correction: Phylogeographic evidence of cognate recognition site patterns and transformation efficiency differences in *H. pylori*: theory of strain dominance

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Correction

In this published article [1], a couple of typos in Table 2 were found:

- The restriction enzymes Hpy17VII and the Hpy44II should be Hpy178II and HpyF44II instead.
- The cognate restriction site for Hpy188I, Hpy188III and HpyF2I should be TCNGA, TCNNGA, and CTRYAG, respectively.

- The subtitle 'Mean ± SD the frequency' should be followed by '/1,000 bp' instead of '/1.00 bp'
- The footnotes were misleading and are now corrected.

In addition, we apologize for the omission of following source that it should be included on the methods section as a reference:

Roberts RJ, Vincze T, Posfai J, Macelis D (2010) REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. Nucl. Acids Res. 38: D234D236.

Table 2 Mean of the observed and expected combined values of the cognate recognition sites in *H. pylori* whole genome sequences and MLS for hspAmerind and hpEurope strains

RMS	Endonuclease/ Methylase	Cognate recognition site ^a	Mean ± SD frequency/1,000 bp				O/E ratio ^b	
			Observed	Expected	Observed	Expected	MLS (N = 73)	WGS (N = 6)
Hpy166III		CCTC	2.7 + 0.41	5.49 + 0.07	2.93 + 0.02	4.50 + 0.03	0.50 ^c	0.65
Hpy178VI		GGATG	1.48 + 0.23	1.59 + 0.03	0.81 + 0.00	1.37 + 0.01	0.93	0.59
Hpy178VII		GGCC	1.24 + 0.31	1.96 + 0.05	0.98 + 0.02	1.43 + 0.02	0.63	0.68
Hpy188I		TCNGA	1.02 + 0.21	3.70 + 0.03	0.81 + 0.02	3.53 + 0.01	0.28	0.23
Hpy188III		TCNNGA	1.11 + 0.22	3.70 + 0.04	1.19 + 0.02	3.53 + 0.01	0.30	0.34
Hpy8I		GTNNAC	0.40 + 0.35	3.70 + 0.03	0.22 + 0.01	3.53 + 0.01	0.11	0.06
Hpy8II		GTSAC	0.00 + 0.00	1.56 + 0.02	0.05 + 0.00	1.37 + 0.01	0.00	0.04
Hpy8III		GWGCWC	0.07 + 0.12	0.66 + 0.01	0.19 + 0.01	0.54 + 0.00	0.10	0.36
Hpy99I		CGWCG	0.28 + 0.06	1.13 + 0.02	0.15 + 0.01	0.88 + 0.01	0.25	0.17
Hpy99III		GCGC	4.62 + 0.64	1.96 + 0.05	3.73 + 0.11	1.43 + 0.02	2.36	2.60
Hpy99IV		CCNNGG	1.62 + 0.26	1.96 + 0.05	0.70 + 0.01	1.43 + 0.03	0.83	0.49

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Table 2 Mean of the observed and expected combined values of the cognate recognition sites in *H. pylori* whole genome sequences and MLS for hspAmerind and hpEurope strains (Continued)

Hpy99VIP	GATC	5.48 + 0.44	3.70 + 0.03	3.19 + 0.04	3.53 + 0.01	1.48	0.90
Hpy99XIIP	GTAC	0.37 + 0.20	3.70 + 0.04	0.07 + 0.00	3.53 + 0.01	0.10	0.02
HpyAV	CCTTC (6/5)	0.58 + 0.12	1.58 + 0.02	0.80 + 0.02	1.37 + 0.01	0.37	0.58
HpyC1I	CCATC(4/5)	1.94 + 0.26	1.60 + 0.02	1.39 + 0.01	1.37 + 0.01	1.22	1.01
HpyCH4II	CTNAG	0.60 + 0.28	3.70 + 0.03	1.84 + 0.04	3.53 + 0.01	0.16	0.52
HpyCH4III	ACNGT	0.89 + 0.22	3.70 + 0.04	0.34 + 0.00	3.53 + 0.01	0.24	0.10
HpyCH4IV	ACGT	0.39 + 0.22	3.70 + 0.04	0.18 + 0.01	3.53 + 0.01	0.11	0.05
HpyCH4V	TGCA	3.85 + 0.75	3.70 + 0.03	3.45 + 0.03	3.53 + 0.03	1.04	0.98
HpyCI	GATATC	0.00 + 0.03	0.31 + 0.01	0.02 + 0.00	0.33 + 0.00	0.01	0.07
HpyF10VI	GCNNNNNNNGC	2.70 + 0.35	1.96 + 0.04	2.97 + 0.09	1.43 + 0.02	1.38	2.07
HpyF14I	CGCG	2.26 + 0.46	1.96 + 0.05	1.55 + 0.05	1.43 + 0.02	1.15	1.08
HpyF2I	CTRYAG	1.16 + 0.17	0.92 + 0.01	0.37 + 0.01	0.88 + 0.00	1.26	0.42
HpyF36IV	GDGCHC	0.20 + 0.21	1.22 + 0.03	0.31 + 0.01	0.93 + 0.01	0.16	0.33
HpyF44II	GGNNCC	1.21 + 0.38	1.96 + 0.05	0.44 + 0.00	1.43 + 0.02	0.62	0.31
HpyII	GAAGA	2.29 + 0.23	2.14 + 0.03	2.87 + 0.02	2.16 + 0.00	1.07	1.33
HpyIP	CATG	4.63 + 0.25	3.70 + 0.03	4.43 + 0.04	3.53 + 0.01	1.25	1.25
HpyIV	GANTC	1.70 + 0.25	3.70 + 0.04	1.66 + 0.02	3.53 + 0.01	0.46	0.47
HpyNI	CCNGG	2.04 + 0.30	1.96 + 0.05	0.87 + 0.02	1.43 + 0.02	1.04	0.61
HpyPORF1389P	GAATTC	0.01 + 0.05	0.31 + 0.01	0.11 + 0.00	0.33 + 0.00	0.03	0.32
HpyV	TCGA	0.95 + 0.25	3.70 + 0.03	0.18 + 0.00	3.53 + 0.01	0.26	0.05
HpyVIII	CCGG	1.92 + 0.30	1.96 + 0.04	1.06 + 0.02	1.43 + 0.02	0.98	0.74

^a Code of degenerate nucleotide letters: R = G or A; Y = C or T; S = G or C; W = A or T; D = not C (A or G or T); H = not G (A or C or T); N = any nucleotide.

^b O/E ratio indicates the observed/expected (O/E) ratio values. O/E ratios that are significantly (pvalue <0.05) different from unity are highlighted in **bold**.

^c Exclusively underrepresented in hp Europe MLS.

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