Appl Microbiol Biotechnol (2009) 83:987–988
DOI 10.1007/s00253-009-2033-5

ERRATUM

Dominance of *Prevotella* and low abundance of classical ruminal bacterial species in the bovine rumen revealed by relative quantification real-time PCR

David M. Stevenson · Paul J. Weimer

Published online: 29 May 2009

Erratum to: Appl Microbiol Biotechnol
DOI 10.1007/s00253-006-0802-y

This article unfortunately contained a mistake. The strain designations of two species, *Prevotella brevis* and *Prevotella bryantii*, were inadvertently reversed in Table 2. The names and sequences of the corresponding species-specific primers were not in error. The corrected table appears below.

The online version of the original article can be found at http://dx.doi.org/10.1007/s00253-006-0802-y.

D. M. Stevenson · P. J. Weimer
Agricultural Research Service, U.S. Department of Agriculture,
United States Dairy Forage Research Center,
Madison, WI 53706, USA

P. J. Weimer (✉)
Department of Bacteriology, University of Wisconsin-Madison,
Madison, WI 53706, USA
e-mail: pjweimer@wisc.edu

Table 2 PCR primers used in this study

Target taxon and specific strain tested	Primer set	Primer sequences	Tm[a]	E [b]	Amplicon Tm [c]
Butyrivibrio fibrisolvens H17c	ButFib2F	ACCGCATAAGCGCACGGA	62	1.98	74
	ButFib2R	CGGGTCCATCTTGTACCGATAAAT	61		
Eubacterium ruminantium GA195	EubRum2F	CTCCCGAGACTGAGGAAGCTTG	61	1.97	80
	EubRum2R	GTCCATCTCACACCACCGGA	60		
Fibrobacter succinogenes S85	FibSuc3F	GCGGGTAGCAAACAGGATTAGA	59	1.93	77
	FibSuc3R	CCCCCGGACACCCAGTAT	59		
Megasphaera elsdenii T81	MegEls2F	AGATGGGGACAACAGCTGGA	59	1.97	79
	MegEls2R	CGAAAGCTCCGAAGAGCCT	58		
Prevotella brevis GA33	PreBre1F	GGTTTCCTTGAGTGTATTCGACGTC	61	1.98	82
	PreBre1R	CTTTCGCTTGGCCGCTG	60		
Prevotella bryantii $B_1$4	PreBry2F	AGCGCAGGCCGTTTGG	61	1.95	83
	PreBry2R	GCTTCCTGTGCACTCAAGTCTGAC	61		
Prevotella ruminicola 23	PreRum1F	GAAAGTCGGATTAATGCTCTATGTTG	58	1.93	71
	PreRum1R	CATCCTATAGCGGTAAACCTTTGG	59		
Ruminobacter amylophilus H18	RumAmy2F	CTGGGGAGCTGCCTGAATG	60	1.96	82
	RumAmy2R	GCATCTGAATGCGACTGGTTG	60		
Ruminococcus albus 7	RumAlb3F	TGTTAACAGAGGGAAGCAAAGCA	60	1.85	75
	RumAlb3R	TGCAGCCTACAATCCGAACTAA	59		
Ruminococcus flavefaciens FD-1	RumFla3F	TGGCGGACGGGTGAGTAA	60	1.79	78
	RumFla3R	TTACCATCCGTTTCCAGAAGCT	60		
Selenomonas ruminantium D	SelRum2F	CAATAAGCATTCCGCCTGGG	61	1.95	82
	SelRum2R	TTCACTCAATGTCAAGCCCTGG	61		
Streptococcus bovis JB1	StrBov2F	TTCCTAGAGATAGGAAGTTTCTTCGG	59	1.95	82
	StrBov2R	ATGATGGCAACTAACAATAGGGGT	59		
Succinivibrio dextrinosolvens 22b	SucDex1F	CGTCAGCTCGTGTCGTGAGA	60	1.95	80
	SucDex1R	CCCGCTGGCAACAAAGG	60		
Domain Bacteria [d]	BAC338F	ACTCCTACGGGAGGCAG	52	1.92-	[f]
	BAC805R	GACTACCAGGGTATCTAATCC	48	2.01[e]	
Genus *Prevotella* [g]	PreGen4F	GGTTCTGAGAGGAAGGTCCCC	60	1.92	83
	PreGen4R	TCCTGCACGCTACTTGGCTG	61		

All primers were designed for this study except for BAC338F and BAC805R, which were designed by Yu et al. (2005).

[a] Tm values calculated using Primer Express software (Applied Biosystems, Foster City, CA). Tm varied among species

[b] *E* represents the efficiency calculated from an amplification of a dilution series of target DNA as described in the text. For the domain-level eubacterial primer, the indicated range spans the efficiencies determined against all of the indicated genus (*Prevotella*) or species level taxa listed. An efficiency of 2.0 is equivalent to 100% of theoretical amplification per PCR cycle.

[c] Amplicon Tm calculated from the dissociation protocol run on the resultant amplicon generated with the selected primer against the pure species indicated.

[d] Domain-level primers.

[e] Efficiency values varied among species within this range.

[f] Tm values varied among species. Five strains were tested, which included *Butyrivibrio fibrisolvens* (Tm=82°C), *Eubacterium ruminantium* (Tm=83°C), *Fibrobacter succinogenes* (Tm=85°C), *Ruminococcus flavefaciens* (Tm=83°C), and *Streptococcus bovis* (Tm=82°C).

[g] Genus-level primers. *P. brevis* GA33 was used as test strain.