

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

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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>.

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Table 2 PCR primers used in this study

Target taxon and specific strain tested	Primer set	Primer sequences	T _m ^a	E ^b	Amplicon T _m ^c
<i>Butyrivibrio fibrisolvens</i> H17c	ButFib2F	ACCGCATAAGCGCACGGA	62	1.98	74
	ButFib2R	CGGGTCCATCTTGTACCGATAAAT	61		
<i>Eubacterium ruminantium</i> GA195	EubRum2F	CTCCCGAGACTGAGGAAGCTTG	61	1.97	80
	EubRum2R	GTCCATCTCACACCACCGGA	60		
<i>Fibrobacter succinogenes</i> S85	FibSuc3F	GCGGGTAGCAAACAGGATTAGA	59	1.93	77
	FibSuc3R	CCCCCGACACCCAGTAT	59		
<i>Megasphaera elsdenii</i> T81	MegEls2F	AGATGGGGACAACAGCTGGA	59	1.97	79
	MegEls2R	CGAAAGCTCCGAAGAGCCT	58		
<i>Prevotella brevis</i> GA33	PreBre1F	GGTTTCCTTGAGTGTATTCGACGTC	61	1.98	82
	PreBre1R	CTTTCGCTTGGCCGCTG	60		
<i>Prevotella bryantii</i> B ₁₄	PreBry2F	AGCGCAGGCCGTTTGG	61	1.95	83
	PreBry2R	GCTTCCTGTGCACTCAAGTCTGAC	61		
<i>Prevotella ruminicola</i> 23	PreRum1F	GAAAGTCGGATTAATGCTCTATGTTG	58	1.93	71
	PreRum1R	CATCCTATAGCGGTAAACCTTTGG	59		
<i>Ruminobacter amylophilus</i> H18	RumAmy2F	CTGGGGAGCTGCCTGAATG	60	1.96	82
	RumAmy2R	GCATCTGAATGCGACTGGTTG	60		
<i>Ruminococcus albus</i> 7	RumAlb3F	TGTTAACAGAGGGAAGCAAAGCA	60	1.85	75
	RumAlb3R	TGCAGCCTACAATCCGAATAA	59		
<i>Ruminococcus flavefaciens</i> FD-1	RumFla3F	TGGCGGACGGGTGAGTAA	60	1.79	78
	RumFla3R	TTACCATCCGTTTCCAGAAGCT	60		
<i>Selenomonas ruminantium</i> D	SelRum2F	CAATAAGCATTCCGCCTGGG	61	1.95	82
	SelRum2R	TTCACTCAATGTCAAGCCCTGG	61		
<i>Streptococcus bovis</i> JB1	StrBov2F	TTCTAGAGATAGGAAGTTTCTTCGG	59	1.95	82
	StrBov2R	ATGATGGCAACTAACAATAGGGGT	59		
<i>Succinivibrio dextrinosolvens</i> 22b	SucDex1F	CGTCAGCTCGTGTCTGAGAGA	60	1.95	80
	SucDex1R	CCCCTGGCAACAAAAGG	60		
Domain Bacteria ^d	BAC338F	ACTCCTACGGGAGGCAG	52	1.92-	f
	BAC805R	GACTACCAGGGTATCTAATCC	48		
Genus <i>Prevotella</i> ^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 T_m values calculated using Primer Express software (Applied Biosystems, Foster City, CA). T_m 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 T_m 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 T_m values varied among species. Five strains were tested, which included *Butyrivibrio fibrisolvens* (T_m=82°C), *Eubacterium ruminantium* (T_m=83°C), *Fibrobacter succinogenes* (T_m=85°C), *Ruminococcus flavefaciens* (T_m=83°C), and *Streptococcus bovis* (T_m=82°C).

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