

Corrigendum

Microbial ecosystem and methanogenesis in ruminants – CORRIGENDUM

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In Table 2 of the article by Morgavi *et al.* (2010), presented in *Animal*, some errors were inadvertently given in the 'Fibre digestibility' and 'Acetate/propionate' columns. The correct version of Table 2 is shown below. The authors apologise for any confusion caused.

Table 2 Effect of several additives on methane production, microbial populations, fibre digestibility and acetate/propionate ratio in rumen incubations *in vitro*^a

Additive	CH ₄	Methanogens	Rfl	Ral	Fsu	Fungi	Protozoa	Fibre digestibility	Acetate/propionate	Reference
BCM	−90%*	−100%*	−48%*		+68%*	+30%	No effect	No effect	Decreased	(Goel <i>et al.</i> , 2009)
BCM 2	−90%*	−100%*	−66%*		+8%	+62%*	No effect	No effect	Decreased	(Goel <i>et al.</i> , 2009)
BES	−86%**	−90%**	No effect		+50%**	−60%**			Decreased	(Guo <i>et al.</i> , 2007)
Saponins	−8%**	No effect	No effect		+41%**	−79%**	−50%*		Decreased	(Guo <i>et al.</i> , 2008)
Saponins		−16%*	−80%	−90%	No effect	−70%*	−50%	−25%*	Decreased	(Wina <i>et al.</i> , 2005)
Saponins	−6%	−78%	+30%		+40%	−40%	−39%	No effect	No effect	(Goel <i>et al.</i> , 2008)

Rfl = *Ruminococcus flavefaciens*; Ral = *Ruminococcus albus*; Fsu = *Fibrobacter succinogenes*; BCM = bromochloromethane; BES = bromoethanesulfonate.

^aAll the additives were added to batch mixed cultures *in vitro* except BCM 2 that was added to continuous cultures.

Cellulolytic bacterial species, methanogens and fungi were estimated by quantification of their *rrs* gene by relative quantitative PCR, except in the work of Wina *et al.* (2005) in which they were estimated by quantification of 16S RNA using dot blots, and in Guo *et al.* (2008), in which methanogens were estimated by PCR quantification of the *mcrA* gene.

Protozoa were quantified by cell counting or by *rrs* gene PCR quantification (only in Guo *et al.*, 2008).

*, ** Indicate significant differences ($P < 0.05$ and $P < 0.01$, respectively) as reported in the original reference.

Reference

Morgavi DP, Forano E, Martin C and Newbold CJ 2010. Microbial ecosystem and methanogenesis in ruminants. *Animal* 4, 1024–1036. doi:10.1017/S1751731110000546.