

Ruminal microbiota is associated with feed efficiency phenotype of fattening bulls fed high-concentrate diets*S. Costa-Roura*^A, *D. Villalba*^{A,D}, *M. Blanco*^{B,C}, *I. Casasús*^{B,C}, *J. Balcells*^A and *A. R. Seradj*^A^A Departament de Ciència Animal, Universitat de Lleida, Av. Alcalde Rovira Roure 191, 25198, Lleida, Spain^B Unidad de Producción y Sanidad Animal. Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA). Avda. Montañana 930, 50059, Zaragoza, Spain.^C Instituto Agroalimentario de Aragón – IA2 (CITA-Universidad de Zaragoza), Zaragoza, Spain.^D Corresponding author. Email: daniel.villalba@udl.cat**Supplementary material***Supplementary Table 1* Animals classified into four categories of feed efficiency according to their random regression coefficients for average daily gain (ADG) and metabolic weight (MW) obtained in the residual feed intake model.

Feed efficiency category	Description	Animals	Sampled animals ^A	Random regression coefficients	
				mean (standard error)	
				ADG	MW
i	Low-efficiency in ADG and low-efficiency in MW	100	13	+0.22 (0.026) ^a	+0.012 (0.001) ^a
ii	Low-efficiency in ADG and high-efficiency in MW	108	12	+0.33 (0.027) ^b	-0.015 (0.001) ^b
iii	High-efficiency in ADG and low-efficiency in MW	85	11	-0.25 (0.024) ^c	+0.12 (0.001) ^a
iv	High-efficiency in ADG and	94	12 ^B	-0.26 (0.025) ^c	-0.014 (0.001) ^b

high-efficiency in
MW

^{a-c} Mean values within a column with unlike superscript letters differ ($P < 0.05$).

^A Feces and ruminal fluid samples were obtained and animals were subjected to further apparent digestibility, ruminal fermentation and microbiota characterisation.

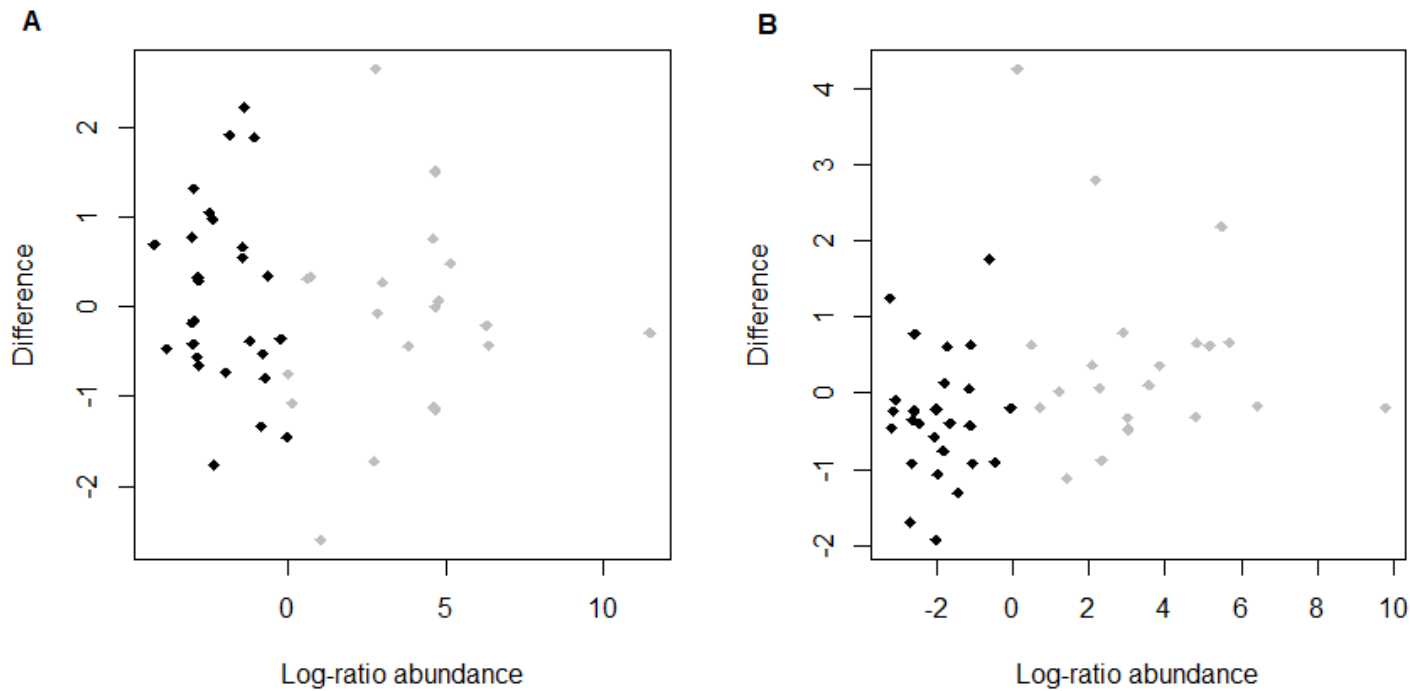
^B One animal in the category iv was excluded from the trial due to a respiratory illness.

Supplementary Table 2 Node degree values obtained in genera networks.

Nodes	Growing period		Finishing period	
	High-efficiency	Low-efficiency	High-efficiency	Low-efficiency
Acidaminococcus	5	4	0	0
Acinetobacter	0	1	2	0
Aerococcus	4	0	0	0
Agathobacter	0	3	6	7
Allisonella	5	0	1	0
Arthrobacter	0	0	1	0
Bacteroides	3	1	0	0
Bifidobacterium	6	2	2	0
Brachybacterium	0	0	4	0
Brevibacterium	0	0	1	0
Butyrivibrio	0	2	3	10
Candidatus_Phytoplasma	3	0	0	3
Clostridium	0	1	1	2
Corynebacterium	2	0	5	3
Dialister	6	2	4	5
Dietzia	0	0	2	0
Eubacterium	8	2	1	0
Facklamia	2	0	4	0
Fibrobacter	2	1	5	8
Jeotgalicoccus	1	0	2	0
Lachnoclostridium	0	0	0	1
Lactobacillus	0	2	6	0
Megasphaera	9	0	7	9
Methanobrevibacter	5	3	0	10
Mitsuokella	8	3	6	6
Olsenella	7	6	3	0
Peptoclostridium	0	0	0	3
Prevotella	1	3	6	4
Pseudobutyrvibrio	1	2	0	5
Pseudomonas	0	2	2	0
Pseudoramibacter	5	3	8	11
Psychrobacter	4	3	0	0
Roseburia	2	0	6	6
Ruminococcus	5	2	3	5
Selenomonas	8	1	3	5
Sharpea	6	5	5	0
Staphylococcus	0	1	2	1
Treponema	5	1	3	9
Turicibacter	0	0	2	5
Weissella	1	0	0	0

Supplementary Table 3 Betweenness centrality values obtained in genera networks.

Nodes	Growing period		Finishing period	
	High-efficiency	Low-efficiency	High-efficiency	Low-efficiency
Acidaminococcus	6.3	3.0		
Acinetobacter		0.0	0.0	
Aerococcus	0.0			
Agathobacter		4.0	1.0	7.5
Allisonella	0.0		0.0	
Arthrobacter			0.0	
Bacteroides	0.0	0.0		
Bifidobacterium	2.3	2.0	4.0	
Brachybacterium			6.0	
Brevibacterium			0.0	
Butyrivibrio		0.0	0.0	5.2
Candidatus_Phytoplasma	3.0			0.5
Clostridium		0.0	0.0	1.0
Corynebacterium	0.0		9.0	0.0
Dialister	18.5	0.0	0.0	0.8
Dietzia			1.0	
Eubacterium	16.6	3.0	0.0	
Facklamia	7.0		4.0	
Fibrobacter	0.0	0.0	3.0	8.5
Jeotgalicoccus	0.0		0.0	
Lachnoclostridium				0.0
Lactobacillus		0.0	8.0	
Megasphaera	12.6		5.0	8.9
Methanobrevibacter	0.0	0.0		0.0
Mitsuokella	7.3	0.0	0.0	0.0
Olsenella	3.3	6.0	0.0	
Peptoclostridium				0.0
Prevotella	0.0	0.0	11.0	0.0
Pseudobutyrvibrio	0.0	0.0		0.9
Pseudomonas		0.0	0.0	
Pseudoramibacter	0.0	0.0	11.0	10.9
Psychrobacter	0.0	0.0		
Roseburia	0.0		6.0	2.5
Ruminococcus	0.0	0.0	0.0	0.0
Selenomonas	5.1	0.0	0.0	2.0
Sharpea	5.8	7.0	2.0	
Staphylococcus		0.0	0.0	0.0
Treponema	13.3	0.0	0.0	4.2
Turicibacter			0.0	0.0
Weissella	0.0			



Supplementary Figure 1 Graphical representation of bacterial and archaeal genera in ruminal fluid, obtained in intensively reared bulls in two periods: growing (**A**: 159 d old and 225 kg body weight) and finishing (**B**: 266 d old and 434 kg body weight). Residual feed intake was modeled to classify animals into two categories of feed efficiency: high-efficiency (HE) and low-efficiency (LE). Plots show the relationship between genera abundance and their difference in abundance between feed efficiency categories. Each point represents a different genus: black dots represent rare genera that are not significantly different between feed efficiency categories and grey dots represent abundant genera that are not significantly different between feed efficiency categories.