

[10.1071/AN20410](https://doi.org/10.1071/AN20410)

Animal Production Science

Supplementary Material

Cow–calf efficiency of beef cows grazing different herbage allowances of rangelands: hepatic mechanisms related to energy efficiency

Alberto Casal^{A,}, Mercedes Garcia-Roche^{B,C}, Adriana Cassina^C, Pablo Soca^A, and Mariana Carriquiry^B*

^ADepartamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Ruta 3 km 363, 60000 Paysandú, Uruguay.

^BDepartamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.

^CCenter for Free Radical and Biomedical Research (CEINBIO) and Departamento de Bioquímica, Facultad de Medicina, Universidad de la República, Montevideo, Uruguay.

*Correspondence to: Alberto Casal Departamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Ruta 3 km 363, 60000 Paysandú, Uruguay Email: alcas@adinet.com.uy

Table S1: Climatic conditions and cow physiological status through the year

	Summer 08/09	Fall 09	Winter 09	Spring 09	Summer/Fall 09/10
Temperature, °C	24.3	16.8	12.9	18.2	23.9
Rainfall, mm	121	180	253	561	626
Days of gestation	0-60	60–150	150–240	240–282	
Days of lactation				0–50	50–142

Table S2. Primers used for real time qPCR.

Gene¹	Accession#²		Primer sequence³	Length(bp)	Efficiency
<i>ACTB</i>	BT030480	F	CTCTTCCAGCCTTCCTTCCT	178	1.15
		R	GGGCAGTGATCTCTTTCTGC		
ATP5E	NM_001143741	F	GACATCATGGTGGCGTACTG	211	1.18
		R	CCACAGCTTCACCTTGAACA		
ATP5O	NM_174244.1	F	CCTCTCACGTCCAACCTGAT	131	1.06
		R	GCAGTGGTAACTGTGCATGG		
COX19	NM_001109966	F	CATACGGACATCCCTTTGCT	171	1.16
		R	GCTTCGGCAACTCCTTACTG		
CS	NM_001044721.1	F	AGCCAAGATACCTGTTCCT	217	0.99
		R	TGTGCTGGAAGAAACGATTG		
CYC1	NM_001038090	F	CCAGGTAGCCAAGGATGTGT	227	1.10
		R	GACCCTGAAGCTCAGGACAG		
<i>GCLC</i>	NM_001083674	F	CACAAATTGGCAGACAATGC	211	1.11
		R	GGCGACCTTCATGTTCTCAT		
<i>GPX1</i>	NM_17407	F	ACATTGAAACCCTGCTGTCC	216	1.09
		R	TCATGAGGAGCTGTGGTCTG		
<i>GPX3</i>	NM_174077	F	TGCAACCAATTTGGAAAACA	224	1.18
		R	TTCATGGGTTCCCAGAAAAG		
<i>GPX4</i>	NM_001346431.1	F	AGCCAGGGAGTAATGCAGAG	203	0.97
		R	CACACAGCCGTTCTTGTCAA		
<i>HPRT1</i>	XM_580802	F	TGGAGAAGGTGTTTATTCCTC	105	0.99
		R	CACAGAGGGCCACAATGTGA		
NDUFA4	NM_175820	F	TGCGGCTTAGCTTTTCTCTC	152	1.12
		R	GCGTGACATACAGTGCTGCT		
NDUFA13	NM_176672	F	TCGACTACAAGCGGAACCTT	233	1.11
		R	AGTTGCCTCCTCCTCCAAGT		
NDUFC1	NM_174564	F	GTTCCCGAGTGTCTCTTCA	242	1.07

<i>PRDX3</i>	NM_174432.2	R	CGTGAATCCAGAGGAACTGC		
		F	CACACCAGAAAAGAGCCACA	210	1.16
		R	CTAGCCATCCATCCACACCT		
<i>PRDX5</i>	NM_174749.2	F	CCTTCTACCTCAGCCTCGAG	245	1.08
		R	CAACCTTAATCGGGGCCATG		
<i>RPL19</i>	NM_001040516.1	F	CCCCAATGAGACCAATGAAATC	156	1.14
		R	CAGCCCATCTTTGATCAGCTT		
<i>SDHA</i>	NM_174178.2	F	ACATGCAGAAGTCGATGCAG	155	1.03
		R	GGTCTCCACCAGGTCAGTGT		
<i>SDHD</i>	NM_174179.2	F	TTGGCTAGGATGGATGGAG	92	1.02
		R	ACTGAACAGAGGGGGAGGTT		
<i>SOD1</i>	NM_174615	F	AGAGGCATGTTGGAGACCTG	189	1.16
		R	CAGCGTTGCCAGTCTTTGTA		
<i>SOD2</i>	NM_201527.2	F	CAGGGACGCTTACAGATTGC	212	1.14
		R	CTGACGGTTTACTTGCTGCA		
<i>UQCRC1</i>	NM_174629.2	F	CAGTCTTCCCAGCCTACCTG	105	0.98
		R	AGCCAGATGCTCCACAAAGT		
<i>UQCRH</i>	NM_001034745	F	CTGGTGTGGCTAAGGGGATA	232	1.10
		R	GGACTCAACACAAGCAGCAA		
<i>NDUFV1</i>	Genomic DNA	F	GTTCTTCTTAGGTTCTCACGTGG	251	
		R	TGAGAATTACTGACGTGACCTCT		
<i>mt-CO1</i>	Mitochondrial DNA	F	TCTTCCCACAACACTTTCTAGGA	198	
		R	TGTCGTGGTTAAGTCTACAGTCA		

¹Genes: β -actin (*ACTB*), ATP synthase, H⁺ transporting, mitochondrial F1 complex, epsilon subunit (*ATP5E*); ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit (*ATP5O*), cytochrome c oxidase assembly factor (*COX19*); citrate syntase (*CS*), cytochrome c-1 (*CYC1*), glutamate-cysteine ligase catalytic subunit (*GCLC*), glutathione peroxidase 1 (*GPX1*), glutathione peroxidase 3 (*GPX3*), glutathione peroxidase 4 (*GPX4*), hypoxanthine phosphoribosyl transferase (*HPRT1*); NADH:ubiquinone oxidoreductase subunit A4 (*NDUFA4*), NADH:ubiquinone

oxidoreductase subunit A13 (*NDUFA13*), NADH:ubiquinone oxidoreductase subunit C1 (*NDUFC1*), peroxiredoxin 3 (*PRDX3*) and peroxiredoxin 5 (*PRDX5*), copper zinc superoxide dismutase 1, soluble (*SOD1*), manganese superoxide dismutase 2, mitochondrial (*SOD2*), ribosomal protein L19 (*RPL19*), succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (*SDHA*), succinate dehydrogenase complex, subunit D (*SDHD*), ubiquinol-cytochrome c reductase core protein I (*UQCRC1*), ubiquinol-cytochrome c reductase hinge protein (*UQCRH*). Mitochondrially encoded cytochrome c oxidase I (*mt-CO1*, mitochondrial gene) and NADH:ubiquinone oxidoreductase core subunit V1 (*NDUFV1*, nuclear gene).

²Gene bank sequences.

³F = foreword; R = reverse

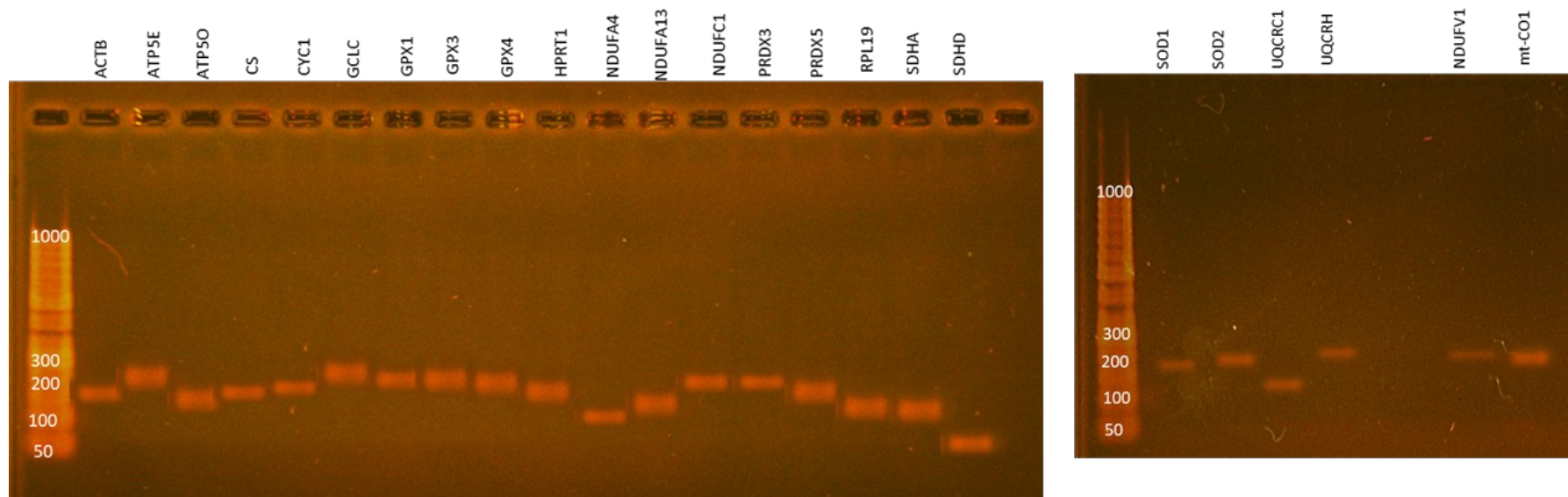


Figure S1: Primer product size as estimated by 1% agarose gel separation. Genes: β -actin (ACTB), ATP synthase, H⁺ transporting, mitochondrial F1 complex, epsilon subunit (ATP5E); ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit (ATP5O), cytochrome c oxidase assembly factor (COX19); citrate synthase (CS), cytochrome c-1 (CYC1), glutamate-cysteine ligase catalytic subunit (GCLC), glutathione peroxidase 1 (GPX1), glutathione peroxidase 3 (GPX3), glutathione peroxidase 4 (GPX4), hypoxanthine phosphoribosyl transferase (HPRT1); NADH:ubiquinone oxidoreductase subunit A4 (NDUFA4), NADH:ubiquinone oxidoreductase subunit A13 (NDUFA13), NADH:ubiquinone oxidoreductase subunit C1 (NDUFC1), peroxiredoxin 3 (PRDX3) and peroxiredoxin 5 (PRDX5), copper zinc superoxide dismutase 1, soluble (SOD1), manganese superoxide dismutase 2, mitochondrial (SOD2), ribosomal protein L19 (RPL19), succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (SDHA), succinate dehydrogenase complex, subunit D (SDHD), ubiquinol-cytochrome c reductase core protein I (UQCRC1), ubiquinol-cytochrome c reductase hinge protein (UQCRH). Mitochondrially encoded cytochrome c oxidase I (*mt-CO1*, mitochondrial gene) and NADH:ubiquinone oxidoreductase core subunit V1 (NDUFV1, nuclear gene).

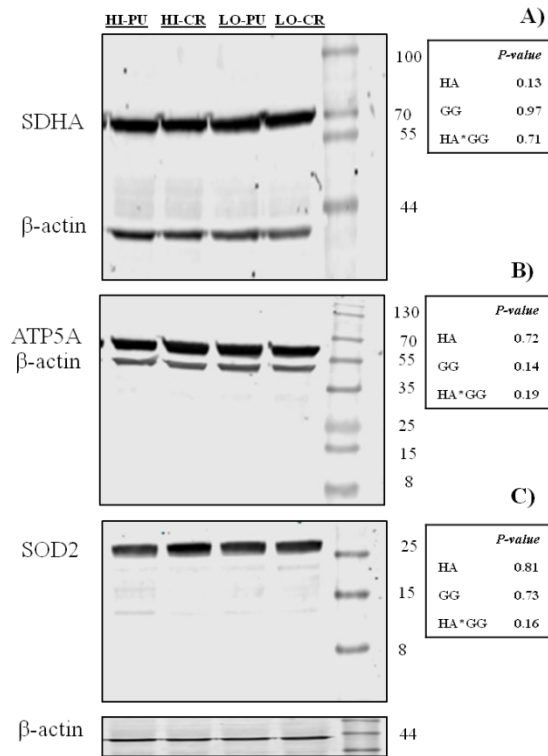


Figure S2: Representative western blot analysis of succinate dehydrogenase complex, subunit A (SDHA; **A**), ATP synthase F1 subunit alpha (ATP5A; **B**) and manganese superoxide dismutase (SOD2; **C**) antibody in liver of purebred and crossbred beef cows grazing high and low in average herbage allowances (2 vs. 4 kg dry matter/kg of body weight of annual mean, respectively) of native pastures: High-crossbred cows (HI-CR); High-purebred cows (HI-PU); Low-crossbred cows (LO-CR); Low-purebred cows (LO-PU). [n = 32, 8 cows per treatment]. A quantity of 30 µg of proteins were loaded and separated by SDS-PAGE. Immunoblotting was performed with a polyclonal antibody that recognized SDHA, ATP5A and SOD2. Data were normalized with β-actin density and normalized values were expressed as a percentage relative to the HI-CR group (Control). **CG: Cow genotype; HA*CG: HA and CG interaction.**