

Feeding level regulates the expression of some genes involved with programmed cell death and remodeling in goat and sheep mammary tissue

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SUPPLEMENTARY FILE

Supplementary Table S1. Primers used for real-time qPCR and the mean PCR efficiency for each gene as calculated by LinRegPCR software (Ramakers et al., 2003)

Gene	Protein	PCR Efficiency	Forward primer 5'-3'	Reverse primer 5'-3'
<i>STAT3</i>	signal transducer and activator of transcription 3	0.92	CGCAATTAGGCAGAGCAACTG	CCCTGTATCAGAGACCATCCCA
<i>CASPASE8</i>	caspase-8	0.95	CCACATCCAGCCTGATTGCTA	GTCTGCTCATGGCTAAGGAGAG
<i>BAX</i>	bcl-2-like protein 4	0.93	CGCCCTTTTCTACTTTGCCAG	ATGATGGTCCTGATCAACTCGG
<i>CTSB</i>	cathepsin B	0.91	TGCATTTCCCACCTCTGTCTG	TTGTGTCCAGCCTTCCAAGTG
<i>BECN1</i>	beclin-1	0.86	GAAAGGCGAGACACGTTTTTG	CTCCTGTGTCTTCAATTTTGCC
<i>MMP2</i>	matrix metalloproteinase 2	0.82	TCCATGATGGAGAGGCTGACA	AGCCCGTCTTTGCCATCAA
<i>MMP9</i>	matrix metalloproteinase 9	0.92	TGCAACGTGGACATCTTCGA	TCCCAGCCTTGAAGAAATGC
<i>RPS9</i>	ribosomal protein S9	1.000	TTCGAAGGTAATGCCCTGTTG	TTCATCTTGCCCTCGTCCA
<i>UXT</i>	ubiquitously expressed transcript	0.98	TCATTGAGCGACTCCAGGAAG'	CAGCCCAAATCCACTTGCAT

Supplementary Table S2. Mean relative transcript accumulation of genes in goat and sheep mammary tissue. Values are overall means for the three dietary treatments (FL70, FL100, FL130) and overall means for the two sampling times (30th and 60th experimental day). The units in the Table are arbitrary.

	Dietary Treatments (T)				Sampling Time (S)			Effects		
	FL70	FL100	FL130	SEM	30 days	60 days	SEM	T	S	TxS
<i>Goats</i>										
<i>STAT3</i>	0.14 ^a	0.17 ^b	0.22 ^c	0.014	0.18	0.18	0.010	**	NS	*
<i>CASPASE8</i>	0.02 ^a	0.02 ^a	0.04 ^b	0.002	0.03	0.03	0.002	*	NS	NS
<i>BAX</i>	0.02 ^a	0.02 ^{ab}	0.03	0.003	0.02	0.03	0.002	*	NS	NS
<i>CTSB</i>	0.71	0.80	0.82	0.084	0.75	0.80	0.066	NS	NS	NS
<i>BECN1</i>	0.16 ^a	0.19 ^b	0.21 ^b	0.011	0.17	0.20	0.008	*	**	*
<i>MMP2</i>	0.37	0.34	0.22	0.071	0.27	0.34	0.049	NS	NS	NS
<i>MMP9</i>	0.02	0.03	0.02	0.007	0.03	0.02	0.005	NS	NS	NS
<i>Ewes</i>										
<i>STAT3</i>	0.22	0.22	0.20	0.018	0.23	0.19	0.013	NS	*	NS
<i>CASPASE 8</i>	0.07 ^a	0.10 ^b	0.09 ^{ab}	0.006	0.10	0.08	0.005	*	**	*
<i>BAX</i>	0.05	0.06	0.05	0.006	0.05	0.05	0.003	NS	NS	**
<i>CTSB</i>	0.82	0.80	1.02	0.095	0.92	0.84	0.068	NS	NS	NS
<i>BECN1</i>	0.27 ^a	0.40 ^b	0.32 ^a	0.024	0.37	0.29	0.019	*	*	**
<i>MMP2</i>	0.15 ^{ab}	0.13 ^a	0.22 ^b	0.033	0.13	0.20	0.020	*	*	*
<i>MMP9</i>	0.003	0.001	0.001	0.001	0.002	0.001	0.005	NS	NS	NS

Means with different superscript (a, b,) in each row (between dietary treatments) for each gene differ significantly ($P \leq 0.05$)

* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.00$, NS=Non significant