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How pasture-based systems may influence beef muscle characteristics

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Introduction

Beef production systems at pasture are promoted to improve animal welfare and beef quality. However, the respective effects of animal mobility and grass feeding are unknown.

This study aimed to compare the influence of the nature of the diet and physical activity on the muscle characteristics of 30-month- old Charolais steers. An other aim was to identify muscle gene expression in pasture-based systems.

Material et methods

Four groups of 6 steers were fed either cut grass or maize-silage diets indoors from weaning to slaughter, with or without 1 hour of walking per day during the last summer; one group of 6 steers was fed on grass at pasture.

Activities of glycolytic (Lactate dehydrogenase [LDH], phosphofructokinase, [PFK]) and oxidative (Isocitrate dehydrogenase [ICDH], citrate synthase [CS], hydroxyacyl-CoA dehydrogenase [HAD]) muscle enzymes were assessed in the *rectus abdominis* (RA) and *semitendinosus* (ST) muscles.

A transcriptomic analysis was performed to compare gene expression profiling in RA and ST between the extreme groups, “maize diet without any mobility” and “grass at pasture“ (pools of mRNA from 6 animals ; 4 pools; 8 macroarrays/pool) .

Results

➢ Biochemical study

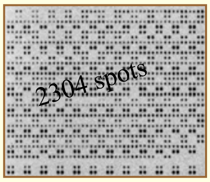
Activities of oxidative enzymes were higher and activity of LDH was lower ($P<0.05$) in the muscles from grass-fed steers, especially for ICDH in RA ($P<0.01$) and for HAD in ST ($P<0.01$) (Table 1). Activities of CS and HAD were higher in the muscles from steers with a high daily mobility.

Table 1. *Influence of the feeding regimen and mobility on metabolic enzymes activities*

	Feeding regimen (F)		**Mobility (M)**		**Effects**
	Grass (n=18)	**Maize (n=12)**	**Walking + Pasture (n=18)**	**reduced (n=12)**	
RA muscle					
PFK	18.5 ± 6.0	18.6 ± 4.9	17.2 ± 5.5	20.5 ± 5.2	
LDH	713 ± 96	667 ± 65	696 ± 98	693 ± 72	
CS	5.5 ± 0.7	5.2 ± 0.8	**5.7 ± 0.7**	**4.9 ± 0.5**	M**
ICDH	**1.5 ± 0.3**	**1.2 ± 0.2**	**1.5 ± 0.3**	**1.2 ± 0.3**	F**, M**
HAD	**2.1 ± 0.3**	**2.0 ± 0.2**	**2.2 ± 0.3**	**1.9 ± 0.2**	F^t, M**
ST muscle					
PFK	28.3 ± 7.9	27.4 ± 7.8	27.9 ± 7.8	28.0 ± 7.9	
LDH	1002 ± 96	980 ± 83	985 ± 91	1005 ± 91	
CS	4.8 ± 0.6	4.5 ± 0.9	**4.9 ± 0.8**	**4.3 ± 0.6**	M*
ICDH	1.0 ± 0.2	1.0 ± 0.3	1.0 ± 0.3	1.0 ± 0.2	
HAD	**1.7 ± 0.3**	**1.4 ± 0.3**	**1.7 ± 0.4**	**1.3 ± 0.2**	F**, M***

➢ Transcriptomic study

ANOVA showed that the muscle type has an important effect on gene expression. Interestingly, the production system had a lesser effect on relevant-gene expression. Table 2 shows examples of most variable genes in response to the production system. They correspond mainly to metabolic and contractile genes and to unknown genes (31%).

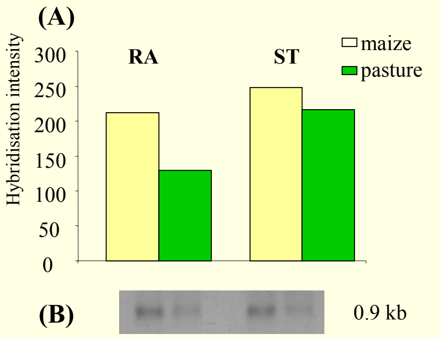


637 muscle cDNAs (400 genes) spotted in duplicate onto 8x12 cm Nylon membranes with 882 embryo and 377 mammary gland cDNA fragments and controls.

Table 2. *Examples of genes with a highly significant differential expression according to the muscle type or to the production system*

Muscle type (ST vs RA) $p<0.0001$	**Production system (Maize *vs* Pasture) $p<0.001$**
Myosin Heavy Chain 2x	Selenoprotein W
Carbonic Anhydrase III	Creatin kinase M
NADH deshydrogenase 6	Troponin T slow
GAPDH	Myosin Heavy Chain 2x
ATPases Serca1 et Serca2	LIM protein
Tropomyosin 2	Unknown genes
Aldolase a	

Under-expression of Selenoprotein W in pasture- *vs* maize-fed RA muscles (A) was confirmed by Northern-Blot (B).



Conclusions

Muscle-specific changes and enzyme-specific adaptations were observed in response to changes in diet or physical activity. Some genes are differentially expressed in pasture- *vs* maize-fed RA muscle.

Selenoprotein W could be considered as a new indicator of grass feeding. However, whether variation of its expression is linked to changes in the feeding regimen or to the mobility is still questioned.