PROTEOMIC BIOMARKERS OF BEEF TENDERNESS FROM STEERS FED SORGHUM AS A SUBSTITUTE FOR MAIZE

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I. INTRODUCTION

Beef tenderness is determined during eating time and more tender meat results in repetitive purchases [1]. Dietary bioactive phytochemicals such as polyphenolic compounds can potentially be assimilated into the meat [2]. These compounds subsequently retard/inhibit enzyme activities involved in glycogen metabolism [3] and myofibrillar protein degradation thereby altering meat tenderness post-mortem [4]. Sorghum contains up to 30 g/kg dry matter (DM) tannins and it has been widely utilized in beef feedlot finisher diets to substitute maize, a more expensive energy source [5]. Studies have reported a reduction in tenderness when beef is finished with sorghum-based diets and attributed the changes to the effects of tannins on myofibrillar degradation and fat deposition [2]. However, little is known about the biochemistry of underlying processes and the major proteins involved in meat tenderness changes when finisher diets containing sorghum are fed. Thus, the current study objective was to identify proteins and biochemical pathways associated with beef tenderness from Angus steers fed graded levels of sorghum-based finisher diets.

II. MATERIALS AND METHODS

Twenty-one Angus steers were finished (90 days) with diets containing diets containing either 0 (SGD-0), 200 (SGD-200), or 400 (SGD-400) g/kg DM of sorghum grain substituting white maize grain. After 24 h post-mortem, the pH was measured with a portable handheld pH meter from the *longissimus thoracis et lumborum* (LTL) muscle which was harvested from the 9th to 13th rib, tenderness (Warner-Bratzler shear force; WBSF) determined, two-gram cubes were sampled from three loins per treatment and proteins were quantified with Bradford assay, visualized using SDS-PAGE and identified with LC-MS/MS [6]. To categorize the proteins intrinsic in beef tenderness, the identified protein gene names were compared with published literature data for tenderness [1]. The physical attributes data were analyzed using the GLIMMIX procedure of SAS.

III. RESULTS AND DISCUSSION

The inclusion of sorghum in beef finisher diets showed a linear increase ($P < 0.05$) in WBSF values which could be linked to a similar trend in dietary tannins that inhibit glycogen phosphorylase, lactate dehydrogenase and calpains thus limiting myofibril degradation [3,4]. Of the 11 differentially expressed proteins ($FDR < 0.05$), sorghum diets downregulated ($P < 0.05$) MYH1, MYH8, GYS1, HSPA8, HSP90AA1 and HSPB6 while CAPZB was upregulated ($P < 0.05$). The down-regulation of heavy chain myosin (MYH1 and MYH8) in SGD could be ascribed to the over-expression of CAPZB which provides binding sites for μ-calpain that breaks down myosin chains. The CAPZB over-expression is in turn attributable to the low calcium content of sorghum that reduces the abundance of phosphatidylinositol (4,5) bisphosphate that inhibits CAPZB activity. The downregulation of glycolytic proteins (GYS1 and PYGM) and heat shock proteins (Hsp) in sorghum diets is ascribable to the inhibitory effect of tannins [3]. Two (MYL3 and YWHAE) and 3 (HSPA9, PDIA3 and ANKRD2) tenderness-regulating proteins were uniquely expressed in SGD-200 and SGD-400, respectively. Several differentially and uniquely expressed structural proteins and glycolytic enzymes suggested that SGD could produce less tender beef which corresponded with instrumental tenderness results.

Table 1: Differentially regulated and unique proteins associated with tenderness in LTL from beef fed graded levels of sorghum

		Inclusion level (g/kg DM)			
Physical parameter		0	200	400	SEM
pH		5.7	5.9	5.8	0.04
WBSF		55.8^{b}	60.6^{ab}	65.2^{a}	2.18
Gene names	Protein names				
Differentially expressed					Mass (kDa)
MYH1	Myosin heavy chain 1	Up	Down	Down	220.8
MYH8	Myosin-8	Up	Down	Down	222.8
CAPZB	F-actin-capping protein subunit beta	Down	Down	Up	32.2
GYS1	Glycogen synthase	Up	Down	Down	76.5
PEBP1	Phosphatidylethanolamine-binding protein 1	Down	Up	Up	21.0
PYGM	Alpha-1,4 glucan phosphorylase	Up	Up	Down	97.3
PYGM	Glycogen phosphorylase, (Myophosphorylase)	Up	Up	Down	97.3
PARP6	Polymerase & Pyruvate kinase	Up	Up	Down	102.5
HSPA8	Heat shock protein family A (Hsp70) member 8	Up	Down	Down	72.3
HSP90AA1	Heat shock protein 90 alpha family class A member 1	Up	Down	Down	89.1
HSPB6	Heat shock protein	Up	Down	Down	17.5
Uniquely expressed					
RABGGTA	Geranylgeranyl transferase type-2 subunit alpha	Unique			64.9
HSPA5	Heat shock protein 70 family protein 5	Unique			72.4
APOBEC2	mRNA cytosine deaminase 2	Unique			26.0
MYL3	Myosin light chain 3		Unique		27.2
YWHAE	14-3-3 protein epsilon (14-3-3E)		Unique		29.2
HSPA9	Heat shock 70 kDa protein 9			Unique	71.2
PDIA3	protein disulfide-isomerase			Unique	51.9
ANKRD2	Ankyrin repeat domain 2			Unique	39.3

WBSF: Warner-Bratzler shear force; SEM: Standard error of means; Means within a row with different superscripts ($^{a\text{–}b}$) are different ($P < 0.05$).

IV. CONCLUSIONS

Overall, differentially and uniquely expressed proteins suggested that diets containing sorghum up to 400 g/kg yield beef of less desirable tenderness.

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