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NMR-based metabolomics to assess metabolites correlated with beef sensory properties (#90)

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Introduction

Metabolomics is the study of biochemical processes involving metabolites, which characterize evidence of the occurrence of biochemical activity and fingerprints from specific cellular processes (Patti et al., 2012). Thus, the metabolomics analysis allows a correlation between biochemical and phenotypic changes. Changes on meat structure and chemical properties during postmortem metabolism, such as protein degradation, glycogen and purine metabolism are responsible for producing metabolites directly or indirectly correlated with sensory properties (Nishimura et al., 1988). Thus, the study of biochemical process involving metabolites to investigate beef sensory properties may reveal precursors of meat flavor and tenderness. Therefore, this study was carried out to assess metabolites correlated with beef sensory properties.

Methods

A total of 30 Nellore and 30 crossbreed Angus x Nellore cattle (363 ± 28 kg initial body weight and 24 months old) were slaughtered and, after 24-h of chilling, the left half-carcass was divided into the region between the 12th and 13th ribs, where two 2.5 cm thick samples of *Longissimus thoracis* muscle were obtained, vacuum packed individually and then were aged (0 to 4 °C) during 7 d to assess beef sensory properties and metabolites. A total of 12 sensory sessions (nine panelists per session; a total of 108 consumer panelists) were performed to evaluate the four samples (one per treatment) for overall liking, juiciness, tenderness, and flavor by a consumer acceptance test using a nine-point hedonic scale (extremely dislike – 1; extremely like – 9) (AMSA, 2015). Additionally, a total of 0.5 g of meat (from each sample) was used for metabolomics analysis and the samples were prepared according to (Beckonert et al., 2007). One dimensional proton nuclear magnetic resonance (1D ^{1}H-NMR) was used for metabolite profiling. 1D ^{1}H-NMR spectra were acquired at 300 K on a Bruker Avance 14.1 T spectrometer (Bruker Corporation, Karlsruhe, Baden-Württemberg, Germany) at 600.13 MHz for ^{1}H, using a BBO 5 mm probe. Deuterium oxide was used as a lock solvent and DSS as internal reference for ^{1}H and an internal standard for metabolite quantitation. 1D ^{1}H-NMR spectra were processed, and metabolites were quantified using the Chenomx NMR Suite Professional 7.7 software (Chenomx Inc., Edmonton, Canada). From the data obtained by the sensory panel and the quantification of the meat metabolites, Spearman correlation coefficients (PROC CORR of SAS 9.4 software) were generated to determine the metabolites correlated with beef sensory properties.

Results

A total of 31 metabolites were quantified in beef samples, in which 19 were correlated ($P < 0.10$) with beef sensory properties (Table 1). Among them, acetate, carnosine, glutamate and glutamine were positively correlated with all sensory properties. On the other hand, betaine, carnitine, creatinine, glycerol and isoleucine were negatively correlated with all sensory properties. Carnosine was medium-high correlated with overall liking (0.48; $P = 0.0001$), flavor (0.59; $P < 0.0001$) and juiciness (0.49; $P < 0.0001$), whereas betaine was medium-high correlated with tenderness (-0.50; $P < 0.0001$).

Glutamate and carnosine are generally associated with umami flavor, which stimulates the brain to pleasure excitations, characterizing it as a superior flavor to the other taste sensations (Nishimura et al., 1988). In this sense, Kim et al. (2016) observed a higher glutamate content associated with a higher flavor meat score. Likewise, Straadt et al. (2014) reported positive correlations found between carnosine and the sensory attributes. In addition, carnosine may act as antioxidant both through scavenging radicals and by metal binding (Wu et al., 2003), which could positively contribute to the oxidative stability of beef. Therefore, in this study, the most pronounced meat flavor detected by the consumer acceptance sensory test can be attribute to the combination of those amino acids.

Similar to our results, Straadt et al. (2014) also reported that betaine negatively affects the meat tenderness, while carnosine positively affects it. Betaine enhances muscle cell survival by protecting them from apoptosis (Alfieri et al., 2006). In muscle postmortem, the decrease in inactivation of the muscle cell apoptosis cascade promotes a lower activation of caspase-3, which may lead to a decrease in the myofilament degradation and consequently decrease the meat tenderization (Picard & Gagaoua, 2017). Even though postmortem tenderization probably can be ascribed to proteolysis of larger protein structures within the meat, the amount of amino acids in the meat can probably be considered as markers of proteolysis (Graham et al. 2012), which is in agreement with the fact that the individual amino acid contents were correlated with meat tenderness in this study.

Conclusion

Several amino acids contribute to changes in the meat flavor and tender

Notes

ness. Among them, betaine and carnosine are the main meat metabolites correlated with beef sensory properties. Therefore, the combination of NMR spectroscopy and sensory analysis can be coupled through a metabolomics approach to find metabolites of importance for meat quality.

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Notes

Table 1. Correlations that differ significantly between beef metabolites and sensory properties.

Metabolite	Consumer acceptance sensory test			
	Overall liking	Flavor	Tenderness	Juiciness
Acetate	0.29**	0.39***	0.22*	0.29**
Alanine	-0.27**	-0.41***		-0.27**
Anserine		0.23*		
Betaine	-0.45***	-0.31**	-0.50***	-0.45***
Carnitine	-0.26*	-0.22*	-0.25*	-0.26*
Carnosine	0.48***	0.59***	0.43***	0.49***
Creatinine	-0.29**	-0.38***	-0.25*	-0.30**
Fumarate			0.22*	
Glucose		0.25*		
Glutamate	0.33**	0.41***	0.27**	0.34**
Glutamine	0.26**	0.25**	0.23*	0.26**
Glycerol	-0.39***	-0.31**	-0.45***	-0.40***
Glycine	-0.33**	-0.46***		-0.32**
IMP	0.26**	0.34**		0.26**
Isoleucine	-0.30**	-0.34**	-0.28**	-0.30**
Methionine	-0.27**	-0.34**		-0.27**
Succinate		0.22*		

IMP = inosine monophosphate.
* $P < 0.10$.
** $P < 0.05$.
***$P < 0.01$.

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