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Meat metabolomic pathway of Nellore and crossbred Angus x Nellore cattle (#640)

Juan F. M. Gomez[1], Daniel S. Antonelo[2], Nara Cônsolo[1], Mariane Beline[1], Bruna Pavan[1], Camilla Souza[1], Rodrigo S. Goulart[1], Luiz Colnago[3], Saulo L. Silva[1]

[1] University of Sao Paulo, Faculty of Animal Science and Food Engineering, Pirassununga, Brazil; [2] University of Sao Paulo, Faculty of Medicine Veterinary and Animal Science, Pirassununga, Brazil; [3] Embrapa Instrumentation, Department of Chemistry, São Carlos, Brazil

Introduction

Metabolomics is known as the comprehensive analysis of the whole metabolome, which refers to the full complement of small molecule metabolites in a cell, tissue or organism, under a given set of conditions (Patty et al., 2012). Pathway analysis can be performed using metabolites data, which allows for much more complete and in-depth analysis into meat metabolism and therefore can be used to investigate differences between breeds. Therefore, this study was carried out to evaluate the meat metabolites pathway of Nellore and crossbred Angus x Nellore cattle.

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, one 2.5 cm thick sample of longissimus muscle was collected (between 12th and 13th ribs) and posteriorly was aged (0 to 4 °C) during 7 d for evaluating meat metabolites. A total of 0.5 g of each sample was used and processed according to Beckonert et al. (2007). One dimensional proton nuclear magnetic resonance (1D ^{1}H-NMR) was used for metabolite profiling. The 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. The 1D ^{1}H-NMR spectra were processed, and metabolites were quantified using the Chenomx NMR Suite Professional 7.7 software (Chenomx Inc., Edmonton, Canada). Metabolites quantification were imported to web-based tool MetaboAnalyst 2.0, data were normalized by Pareto scaling and the Principal component analysis (PCA) was performed. For metabolic pathway, the pathway library used was *Bos taurus* was performed, with a global test and relative betweenness centrality as algorithms.

Results

Thirty-one metabolites were identified in meat of Nellore and crossbred Angus x Nellore cattle, among which the acetate, acetyl carnitine, alanine, anserine, carnosine, choline, creatinine, glucose, glutamate, glycerate, glycine, IMP, isoleucine, methionine, and succinate differed ($P < 0.10$) between breeds (Table 1). The principal component scores plot (PC 1 39.6% and PC 2 11.7%) of the metabolite concentrations (Figure 1) shows a discrete overlap between breeds, suggesting few differences between them.

The main metabolic pathways involving the breed differentiation were glutamine and glutamate metabolism; valine, leucine and isoleucine biosynthesis; and glutathione metabolism (Figure 2), which may be due to the amounts of glycine, glutamate and isoleucine present in meat, allowing a clear differentiation between breeds.

The glutamate is closely related with glutamine metabolism and, in association with glycine, are substrates for glutathione synthesis, in addition to participating in the glutathione metabolism (Wang et al., 2013). In this sense, increasing glutamate content also increase glutamine content, amino acid that plays in regulating the skeletal muscle mass by regulating protein metabolism (Xi et al., 2011). Glutamate content is correlated with the increase in glycolytic muscle fibers in beef cattle and the increase in oxidative muscle fibers in porcine (Cornet and Bousset, 1999).

Additionally, leucine is correlated with valine and isoleucine biosynthesis pathway and can be correlated with differences on growth patterns between breeds since it has a fundamental role for the initiation of anabolic processes in the muscle, including myofibrillar protein synthesis (Churchward-Venne et al., 2012).

Conclusion

In conclusion, the glutamine and glutamate metabolism, valine, leucine and isoleucine biosynthesis, and glutathione metabolism are the most important pathways to differentiate meat from Nellore and crossbred Angus x Nellore cattle.

Notes

Metabolite	Concentration (µmol/g meat)
Lactate	50
Creatine	**22.0**
Carnosine	**10.9**
Glucose	**3.51**
Glycerate	**2.31**
Glycerol	2.25
Glutamine	1.91
Carnitine	1.75
Alanine	**1.53**
Betaine	1.02
Glycine	**0.99**
Methionine	**0.97**
Choline	**0.89**
Acetyl carnitine	**0.79**
Inosine monophosphate	**0.76**
Threonine	0.66
ATP	0.62
Creatinine	0.61
Anserine	**0.60**
Adenine	0.50
Inosine	0.47
Glutamate	**0.39**
Fucose	0.33
NADH	0.29
Valine	0.27
β-alanine	0.16
Isoleucine	**0.15**
Acetate	**0.14**
Fumarate	0.11
Proline	0.10
Succinate	**0.05**

Table 1 – Concentrations of metabolites identified and quantified in beef extracts (pooled sample).
Metabolite in bold differed between breeds ($P < 0.10$)

Notes

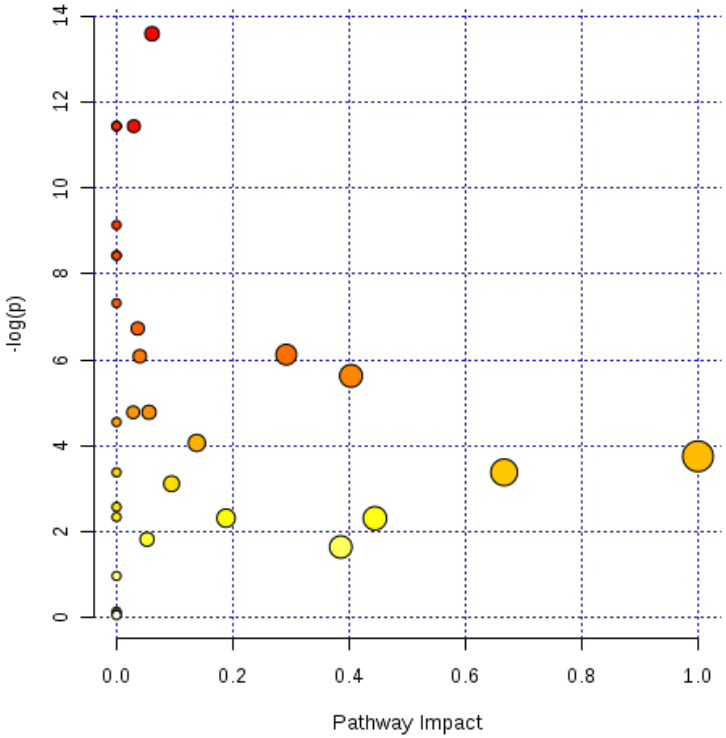

Figure 2. Pathway analysis using all the significant metabolites.
A) glutamine and glutamate metabolism; B) valine, leucine and isoleucine biosynthesis; C) glutathione metabolism.
In the scatter plot, the x-axis indicates impact on pathway whereas the y-axis indicates significant changes in a pathway, by detected metabolites. The complete pathways are identifiers for metabolites mapped in a KEGG pathway (accessible at http://www.genome.jp/kegg/pathway.html).

Notes

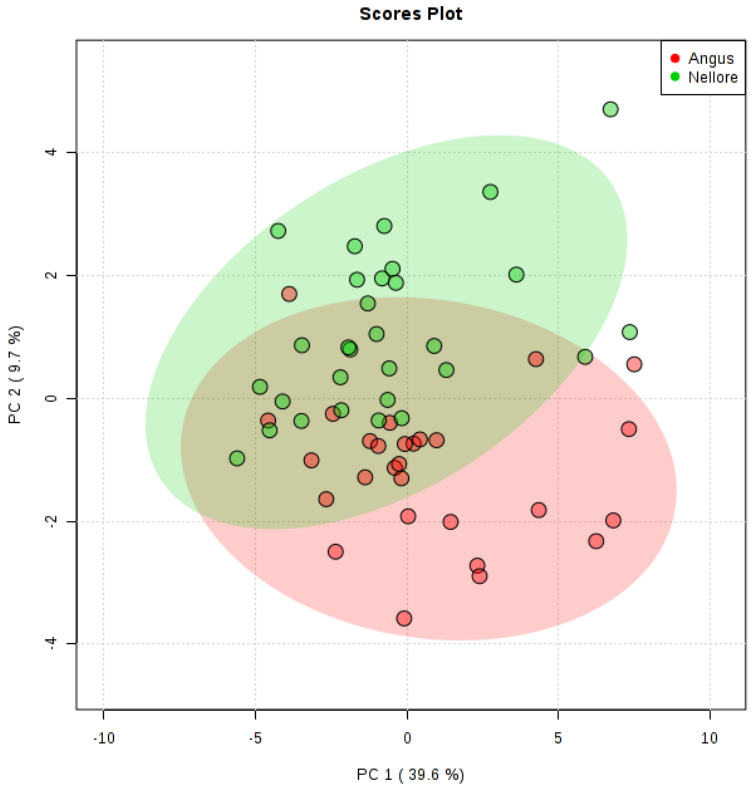

Figure 1.
Principal component scores plot of meat metabolites from Nellore and crossbred cattle

Notes