METABOLOMIC ANALYSIS OF EXUDATE FROM MEAT WITH DIFFERENT LEVEL OF DRIP LOSS IN RELATIONS TO MEAT QUALITY

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I. INTRODUCTION

In the last twenty years the production and consumption of poultry meat has dramatically increased and it is expected that in the few coming years the poultry meat will become the main type of meat produced in the world. Poultry meat is willingly eaten by consumers due to its high nutritional value, high tenderness and easiness of culinary preparation. This dynamic increase of production was possible due to intensive selection for growth rate and feed conversion rate [1]. However, the results of many studies show that the quality of poultry meat has recently deteriorated by the appearance of defects such as: PSE, white stripping, wooden breast or increased drip loss [1, 3]. To explain these myopathies t modern science, for instance proteomics, has been recently applied [1, 3, 4]. The aim of the present study was to applications of metabolomics analysis of exudate from breast muscle in poultry with different level of drip loss.

II. MATERIALS AND METHODS

The research was made on the skinless breast fillets sourced from 60 broiler carcasses (7 week old male Ross broilers, approximately 2,5 kg body weight) selected form a commercial broiler processing plant. Carcasses were collected 20 min postmortem following stunning (electrical method in water bath with average value per bird 200mA and 800Hz during min. 4s - in accordance with the European Union Council Regulations (EC) No 1099/2009). Directly after removing the carcasses, the pH1 breast muscle (20 min after slaughter) was measured and identified individually carcasses were cooled by immersion method. Exactly 24 h postmortem *Pectoralis major* muscles were removed from the carcasses. After measuring pH24 muscle samples were put into plastic bags, placed in a box with ice and transported to the laboratory for further analysis. Muscle exudate was collected after 24 h of samples storage at 4^{o}C. Following muscle colour measurement the of each sample portion of 100 g of the sample was frozen for chemical analysis and the rest was used for sensory analysis. Technological quality and chemical composition of raw meat were determined by: pH24 and pH48 (WTW 340i pH meter, Weilheim, Germany), drip loss [2], colour parameters (CIE L*a*b*system; Minolta CR400, Osaka, Japan), protein content (The Kjeldahl method; FOSS Tecator 1035 Analyzer), fat content (Soxhlet and Folch extraction method), glucose and lactic acid (Accu-Chek Active glucometr, Roche, Germany). Meat sensory analysis after heat treatment with Quantitative Descriptive Analysis was evaluated (ISO 13299:2003). The metabolomics analysis was performed using Waters Acquity™ Ultra Performance LC system (Waters Corp., Milford, MA) connected to Synapt G2Si Q-TOF mass spectrometer (Waters MS Technologies, Manchester, UK) equipped with an electrospray (ESI) source (Waters, UK). Prior to UPLC-MS analysis, the extracts samples (50 µL) were diluted with prechilled methanol/ultra high purity water 1:1 (1500 µL), vortex mixed (10 min) and centrifuged at 13000 rpm for 15 min at 4 °C. The supernatants were subjected to the analysis. After analysis, the samples were divided into two groups with different natural drip loss (≤2% and >2%). The obtained data were developed using T-Student test by Statistica ver. 12.0 software (StatSoft, Inc., 2014).

III. RESULTS AND DISCUSSION

Results presented in Table 1 show that group differentiated in level of drip loss differs significantly in ultimate pH, colour parameters, glucose and glycolytic potential level, cooking yield, protein content and overall sensory quality. The metabolomics analysis of exudate indicate significant differences between groups in 11 metabolic pathways (Table 2). These pathways were related mainly to glycolysis, gluconeogenesis, adenine, adenosine and nucleotide as well as methylglyoxal degradation metabolites. The group with higher drip loss

was characterized by significantly faster glycolysis in second stage and higher level of adenosine, inosine and AMP as well as methylglycosal. Welzenbach et al. [4] in case of metabolomics analysis for drip loss explanation in pigs showed differences in 10 pathways with significant differences for sphingolipid metabolism and glycolysis/gluconeogenesis. Kuttappan et al. [1] in proteomic analysis in case of white stripping and woody breast of poultry meat myopathies revealed that glycolysis and gluconeogenesis were the major down-regulated canonical pathways in severe myopathic changes with respect to normal meat.

Table 1. Characteristics of meat quality of group with different level of drip loss

Item	Low drip loss	High drip loss	SEM	Sig. diff. p-value
pH1	6,76	6,73	0,03	0,662
pH24	6,03	5,85	0,03	0,001
Color parameters: L*	52,55	56,96	0,70	0,001
a*	-2,43	-1,97	0,10	0,023
b*	4,26	5,58	0,26	0,008
Glucose (mmol/l)	33,00	41,00	1,93	0,033
Lactate (mmol/l)	70,13	74,63	2,26	0,336
Glycolytic potential (mmol/l)	136,13	156,63	5,19	0,044
Drip loss72 (%)	1,20	2,22	0,16	0,001
Cooking yield(%)	70,35	67,21	0,53	0,001
Protein (%)	24,44	21,98	0,32	0,001
Intramuscular fat (%)	1,51	1,49	0,06	0,845
Overall sensory quality (c.u.)	7,79	7,12	0,27	0,028

Table 2. Significant differences between group in pathway analysis with XCMS Online and MUMMICHOG

Pathways	Overlap size	Pathway size	p-value
Glycolysis	6	7	0,00023
Methylglyoxal degradation I	4	4	0,00035
Gluconeogenesis	6	9	0,00039
Adenine and adenosine salvage III	4	5	0,00064
Arsenate detoxification I (glutaredoxin)	3	3	0,00098
Pyrimidine ribonucleosides degradation	3	3	0,00098
Adenine and adenosine salvage I	3	3	0,00098
Pentose phosphate pathway (non-oxidative branch)	4	6	0,00133
Methylglyoxal degradation VI	3	4	0,00279
Adenosine nucleotides degradation	4	7	0,00289
Sucrose degradation	4	8	0,00621

IV. CONCLUSION

The results showed that differences in quality of poultry meat differed in drip loss are related to differences in 11 metabolic pathways. These pathways were related mainly to glycolysis, gluconeogenesis, adenine, adenosine and nucleotide as well as methylglyoxal degradation metabolites.

REFERENCES

1. Kuttappan V.A., Bottje W., Ramnathan R., Hartson S.D., Coon C.N., Kong B.W., Owens C.M., Vazquez-Añon, Hargis B.M. (2017). Proteomic analysis reveals changes in carbohydrate and protein metabolism associated with broiler breast myopathy. Poultry Science 96: 2992-2999.
2. Prange, H., Jugert, L., Schamer, E. (1977). Untersuchungen zur Muskel-fleischqualität beim Schwein. Archiv für Experimentelle Veterinärmedizin Leipzig, 31: 235-248.
3. Schilling M.W., Suman S.P., Zhang X., Nair M.N., Desai M.A., Cai K., Ciaramella M.A., Allen P.J. (2017). Proteomic approach to characterize biochemistry of meat quality defects. Meat Science 132: 131-138.
4. Welzenbach J., Neuhoff C., Heidt H., Cinar M.U., Looft C., Schellander K., Tholen E., Groβe-Brinkhaus C. (2016). Integrative analysis of metabolomic, proteomic and genomic data to reveal functional pathways and candidate genes for drip loss in pigs. International Journal of Molecular Sciences 17: 1426.