



## Longissimus and semimembranosus muscles transcriptome comparison in pig displays marked differences

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Frédéric Herault, Annie Vincent, Olivier Dameron, Pascale Le Roy, Pierre Cherel, et al.. Longissimus and semimembranosus muscles transcriptome comparison in pig displays marked differences. 64. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2013, Nantes, France. Wageningen Academic Publishers, Annual Meeting of the European Association for Animal Production, 64, 2013, Annual Meeting of the European Association for Animal Production. hal-01210421

**HAL Id: hal-01210421**

**<https://hal.science/hal-01210421>**

Submitted on 3 Jun 2020

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**Correlation of CTSD and CTSF genes expression and economically important traits in pigs in Poland**A. Bereta<sup>1</sup>, K. Ropka-Molik<sup>2</sup>, M. Różycki<sup>1</sup>, K. Piórkowska<sup>2</sup>, M. Tyra<sup>1</sup> and R. Eckert<sup>1</sup><sup>1</sup>National Research Institute of Animal Production, Department of Animal Genetics and Breeding, Sarego 2, 31-047 Krakow, Poland, <sup>2</sup>National Research Institute of Animal Production, Laboratory of Genomics, Sarego 2, 31-047 Krakow, Poland; anna.bereta@izoo.krakow.pl

The aspartic proteinase CTSD plays a role in the proteolysis of intra- and extracellular proteins, while cysteine protease cathepsin F is involved in proteolytic processing closely related with the remodeling of the intimal extracellular matrix. The aim of our study was to evaluation of expression profile of CTSD and CTSF genes in porcine skeletal muscles (m. semimembranosus and longissimus dorsi). Furthermore, we analyzed association of expression levels and economically important traits in pig. The analysis was performed on 164 animals belonged to four pig breed: Polish Landrace (n=50) and Polish Large White (n=50), Pietrain (n=16) and Puławska (n=48). Relative quantification of mRNA abundance was performed with 7500 Real-Time PCR System using TaqMan® MGB probes labeled with FAM, VIC or NED and with endogenous controls OAZ1 and RPL27. In both analyzed tissue, the lowest CTSD gene expression was obtained for Polish Landrace and Puławska breeds ( $P < 0.05$ ). The differences in CTSF expression between pig breeds were similar: the lowest mRNA level was observed in Puławska breed and the highest in Pietrain (statistically significant in longissimus dorsi,  $P < 0.05$ ). We obtained low correlation coefficient between expression of CTSF gene in m. semimembranosus and ham weight (0.24,  $P = 0.008$ ). Also, significant correlation we obtained for CTSD transcript level in m. semimembranosus and ham weight, average backfat thickness (cm), loin eye area (cm<sup>2</sup>) and lean meat percentage (%), however correlation coefficients were low (0.15; 0.21; 0.15; and 0.19; respectively,  $P < 0.05$ ). The study was supported by the Polish Ministry of Science and Higher Education (project no. NN311349139).

**Longissimus and semimembranosus muscles transcriptome comparison in pig displays marked differences**F. Héroult<sup>1</sup>, A. Vincent<sup>1</sup>, O. Dameron<sup>2</sup>, P. Le Roy<sup>1</sup>, P. Cherel<sup>3</sup> and M. Damon<sup>1</sup><sup>1</sup>INRA, UMR1348 PEGASE, 35590 Saint-Gilles, France, <sup>2</sup>INSERM, UMR936, 35065 Rennes, France,<sup>3</sup>Hendrix-Genetics, RTC, 45808 Saint Jean de Brayes, France; frederic.herault@rennes.inra.fr

Longissimus lumborum (LM) and semimembranosus (SM) are used for different meat consumption. Both are classified as glycolytic muscles but have different myofiber composition and metabolic properties. Compare LM and SM transcriptome profiles may clarify the biological events which could explain their phenotypic differences. The 90 pigs used in this study were produced as an inter-cross between 2 commercial sire lines. Muscle samples were collected 20 minutes post-mortem, snap frozen and used for total RNA isolation. Transcriptome analysis was undertaken using a pig muscle microarray: the 15K Genmasqchip. Analyses were performed using R software. Raw data were submitted to quality filtration and normalization. Probes with the smallest expression variability were filtered out. Normalized data were analyzed using a linear model of variance taking into account fixed effects of slaughter date, sex, sire and muscle. Carcass weight was used as a covariate. Genes which were differentially expressed between muscles were clustered according to their semantic similarities. Semantic similarities were computed according to Wang's method using Gene Ontology (GO) Biological Process (BP) terms. Thus, functional characterizations of genes clusters were performed with WebGestalt using GO BP terms. A total of 3,867 genes were differentially expressed between the 2 muscles, out of which 1,729 and 2,138 were over-represented respectively in LM and in SM. A set of 1,047 differentially expressed genes with a muscle fold change ratio above 1.5 was used for functional characterization. Five clusters related to energy metabolism, cell cycle, gene expression, anatomical structure development and signal transduction/immune response were identified. These results shed light on differential transcriptome profiles between LM and SM. This variability could affect muscle development and hence meat quality.