Summary of the doctoral thesis carried out by MSc Ilona Mitka, entitled:

THE ROLE OF SELECTED TRIGLYCERIDES BIOSYNTHESIS PATHWAY GENES IN FORMING PORK MEAT QUALITY AND SENSORY PARAMETERS

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Meat quality traits are moderately heritable and selection based on traditional methods is often slow and ineffective. Additional difficulty is caused by the fact, that these traits can be determined only after the slaughter of animal. In order to improve meat quality traits (including the most important parameter – intramuscular fat (IMF) content in *musculus longissimus lumborum*), marker assisted selection (MAS) seems to be more effective. In this this study particular emphasis was placed on genes that belong to the *GPAT* family. Genes that belong to the *GPAT* family are potential genetic markers for IMF content and as a result for pork quality. *GPAT* enzymes (*glycerol-3-phosphate acyltransferase enzymes*) catalyze the first step in triacylglycerols (TG) synthesis (an essential component in animal fat and IMF.

The aim of this research was to determine the association of genes: *GPAT1* and *GPAT2* with selected meat quality traits, meat texture parameters as well as fattening and slaughter traits on Polish nucleus population of pigs. The identification of polymorphisms was carried out on smaller number of animals, in all coding regions of *GPAT1* and *GPAT2* genes and also in the 3'UTR region of *GPAT1* gene, with the use of PCR-HRM method and Sanger sequencing. Estimation of alleles and genotypes frequency as well as an association analysis between selected polymorphisms of both genes with mentioned above utility traits, meat quality and meat texture parameters was performed on 948 pigs belonging to five breeds (Polish Large White, Polish Landrace, Puławska, Pietrain, Duroc) using PCR-RFLP method. Furthermore, expression of *GPAT1* and *GPAT2* genes were estimated on three tissues (*m. longissimus lumborum*, subcutaneous fat, liver) using Real-Time PCR.

The research allowed us to identify 39 mutations in *GPAT1* gene *locus*. Twelve out of them were located in coding regions, 13 in intron regions and 14 in 3'UTR region. In *GPAT2* gene only 3 mutations were identified. One out of them was located in 5'UTR region while others in intron regions. Four mutations: g.133513422C>T, g.133476803T>C, g.133476733C>T, g.48497102G>A were chosen to further stages of the research. These are mutations with probably the highest effect on the genes or proteins function. Additionally, these mutations change cutting site of restriction enzymes.

Statistical analysis showed significant association between analyzed polymorphisms and selected meat quality, meat texture parameters as well as fattening and slaughter traits. In relation to g.133513422C>T polymorphism of the *GPAT1* gene, statistical association was identified for: slaughter performance, parameters describing loin, IMF content in *m.*

longussimus lumborum, pH measurement of *m. semimembranosus* and loin muscle hardness, promoting animals with CC and CT genotypes. Further statistical analysis also showed association of the second *GPAT1* gene polymorphism (g.133476803T>C) with: loin weight, IMF content, meat colour (parameter L*) and its hardness. In this case animals with TT genotype were characterized with more favourable values for these traits. In turn, the third *GPAT1* gene polymorphism (g.133476733C>T) highly influenced the following traits: loin weight, weight of meat from primal cuts, pH measurement of *m. longissimus lumborum* and its hardness. Similarly to the first mutation, preferable values were represented by animals with CC and CT genotypes. Statistically significant differences were also shown between polymorphism in *GPAT2* gene (g.48497102G>A) and: slaughter performance, loin weight, carcass length, IMF content and *m. longissimus lumborum* hardness, promoting pigs with G allele in the genotype.

Gene expression analysis of *GPAT1* and *GPAT2* showed statistically significant differences in the mRNA level of *GPAT1* between analyzed tissues and breeds. The highest expression of *GPAT1* gene was observed in liver tissue and it was more than 28-fold higher than in *m. longissimus lumborum* and 70-fold higher than in subcutaneous fat. Furthermore, statistically significant higher *GPAT1* transcript level was observed for Duroc in comparison to other analyzed breeds. Expression of *GPAT2* gene was shown only in the liver tissues, however statistically significant differences between the analyzed breed were not demonstrated. Correlation analysis between *GPAT1* and *GPAT2* gene expression and meat quality as well as carcass parameters showed the highest association between *GPAT2* gene expression level in liver and cohesiveness and resilience of m. *longissimus lumborum* ($P \leq 0.01$).

The conducted research indicated an inability to use analyzed *GPAT1* and *GPAT2* gene polymorphisms in the selection process due to the lack of direct impact in relation to meat quality and other production traits, including meatiness and fatness. The results of the association analysis of *GPAT1* and *GPAT2* gene expression with production traits seems interesting, therefore it is recommended to continue research in this direction.

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