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THE EFFECT OF THE MC4R GENOTYPE ON BOAR ODOR AND FATTENING PRODUCTIVITY IN IMMUNOLOGICALLY CASTRATED AND UNCASTRATED GILTS

ВПЛИВ ГЕНОТИПУ MC4R НА ЗАПАХ КНУРА ТА ВІДГОДІВЕЛЬНУ ПРОДУКТИВНІСТЬ У ІМУННОЛОГІЧНО-КАСТРОВАНИХ ТА НЕКАСТРОВАНИХ СВИНОК

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An aspect of the need to study polymorphic variants of the MC4R (c.1426 A > G) gene is the study of methods to reduce boar odor in light of the prohibition of surgical castration of gilts. Genetic selection to reduce boar odor may be a long-term alternative. It is proved that the marker MC4R (p. Asp298Asn) can be used to reduce the level of boar odor in the fat of uncastrated boars [1, p. 1688–1697; 2, p. 934–943]. In pigs, the asp298Asn polymorphism of the melanocortin-4 receptor (c.1426 A > G) affects an important economic feature – the growth rate [1, p. 1688–1697; 2, p. 934–943]. In Ukraine, this study is being conducted for the first time, so it is of great importance for the well-being of pig product lines and the population as a whole, sale of live livestock of transboundary breeds of pigs and as finished products on the European market [3, p. 113–121]. In this regard, the purpose of our study was to determine the effect of the polymorphism of the MC4R gene on the growth rate in combination with the smell of boar in immunologically castrated and uncastrated gilts (Large White × Landrace) × Maxgro. Two groups of gilts were selected for the study: 1.control (uncastrated) – (n = 20) and 2.experimental (immune-logically castrated) – (n = 20). Genotyping of gilts was carried out in the laboratory of the genetics of the Institute of Pig Breeding and AIP of the NAAS. The polymorphism of the studied MC4R gene (c. 1426 A > G) was determined by PCR-RFLP analysis.

Deoxyribonucleic acid was extracted from swine ear tissue samples using DNA digestion using a proteinase K followed by organic extraction and DNA precipitation. Deoxyribonucleic acid was amplified using PCR performed in a total volume of 20 μL with of the 0.25 μL of each primer MC4R: 298R-5-TACCCTGACCATCTTGATTG; 298F-5`-ATAGCAACA GATGATCTCTTTG; 1.0 μL $MgCl_2$, 1.25 μL of dNTP, 1X reaction buffer NH_2SO_4, 0.5 μL of Taq DNA polymerase (Thermo Scientific), ultrapure sterile water – 5.0 μL and the final volume of the template DNA 10.5 μL. Polymerase chain reaction conditions were 94 ºC–3min.; 31 cycle:

94 ºC–25 min.; 64 ºC–26 sec.; 72 ºC–40 sec., 72 ºC–2 min. Amplicons were digested in a total volume of 30 µL with 10 units of restriction endonuclease TaqI (Thermo Scientific) for 3 h at 65 °C. Deoxyribonucleic acid fragments were separated on a 2 % agarose gel.

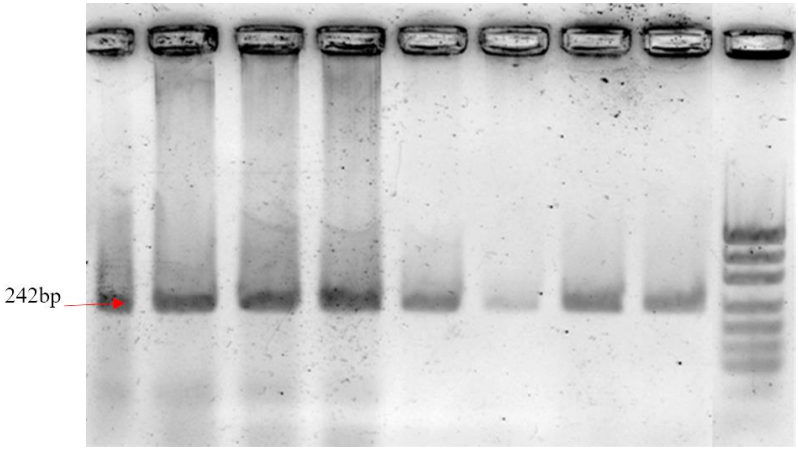

Fig. 1. Electrotrophoregram of DNA amplificiation to MC4R locus in 2 % agarose gel. Molecular mass marker pUC19 DNA/MspI

Enzymatic digestion was performed in a final volume of 15 µL, including 5 µL (~ 0.1–0.5 µg of DNA) of the PCR product, 0.2 µL of Taq I, endonuclease (Thermo Fisher Scientific™) and 2.8 µL Buffer 10X, together with nuclease-free water to reach final volume 7.0 µL. Samples were incubated at 65 °C, time – 1 hour 50 minutes for MC4R (TaqI). Electrophoretic separation of DNA fragments was carried out in 8 % polyacrylamide gel in 1xTBE buffer, at current strength (5 V/cm) gel length. Visualization of restriction products was carried out by dyeing bromide ethidium and viewing on the transilluminator in UV light. Result of electrophoregram fragments (Figure 2): track – 3,8,20 genotype $MC4R^{AG}$ (70 pb); track – 1, 2, 6, 7, 12, 17 genotype $MC4R^{AA}$ (220 pb); track – 4, 5, 9, 10, 11, 13, 14, 15, 16, 18, 19 genotype $MC4R^{GG}$ (150 pb).

Analysis of the growth rate was carried out according to the results of control cultivation up to 100 kg according to the following indicators: age of reaching live weight 100 kg (AGE100); fattening duration, days; average daily growth, g (ADG).

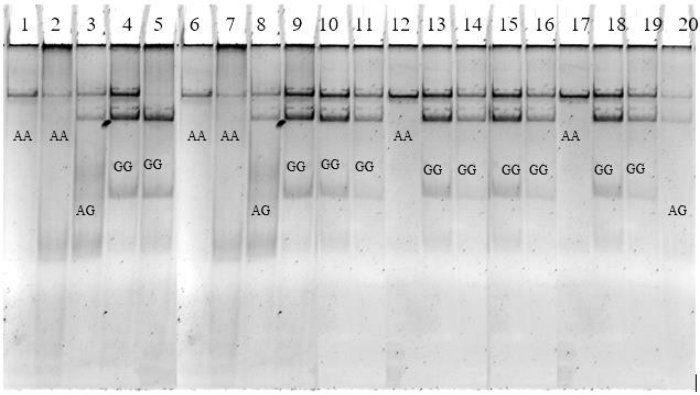

Fig. 2. Electrophoregram of restriction products Taq I locus DNA MC4R (c.1426 A>G) in 8 % PAAG. Molecular mass marker pBR322/MspI. Size of DNA fragments in (bp) major allele MC4R c.1426G (150+70); DNA fragment size in (bp) of the MC4R c.1426A minor allele (220).

Table 1

Results of fattening indicators of herds of pigs (Large White × Landrace) × Maxgro progenotyped by locus MC4R (c.1426 A > G)

Locus genotypes	Uncastrated gilts	ADG, g	AGE 100kg/day	Immuno-castrated gilts	ADG, g	AGE 100kg/day
MC4R^{AA}	5	0.928	144	6	0.966	144
MC4R^{GG}	5	0.778	152	2	0.735	167
MC4R^{AG}	10	0.858	149	12	0.924	145

Uncastrated gilts with the MC4R^{AA} genotype at the age of 144 days reached a live weight of 100 kg (ADG = 0.928 g/144 days). Immunologically castrated gilts with MC4R^{AA} genotype with a difference of ADG 0.38 g (ADG = 0.966 g/144 days). Gilts of the 1st group with the MC4R^{GG} genotype with an average daily increase of 0.778 g (159 days) 8 days earlier reached a live weight of 100 kg compared to the 2nd group (167 days) (ADG = 0.735 g/167 days). 1st group of crossbred gilts with the MC4R^{GG} genotype with an AGE100 – 15 days index (ADG = 0.778 g/152 days).

The results show that pigs with the $MC4R^{AA}$ genotype (ADG = 0.947 g/144) and $MC4R^{AG}$ (ADG = 0.891 g/147 days) have a higher average daily increase in the amount. An overall score (ADG = 0.756g/160) in immunologically castrated and uncastrated gilts with $MC4R^{GG}$ genotype lag behind by 14 days in terms of growth rate compared to gilts with $MC4R^{AA}$ and $MC4R^{AG}$ genotype. It turns out that the results of genotyping of the MC4R DNA marker will manifest themselves in different ways. Probably, it depends on the intra-breed type, lineage, maternal and paternal basis, and linear hybridization of pigs. Thus, it is possible to determine which alleles and genotypes in general will be defined as desirable in marker breeding of hybrid pigs. It was found that animals with the $MC4R^{GG}$ genotype are vulnerable to lesions and are also characterized by a lower growth rate from animals with the $MC4R^{AA}$ genotype therefore, the desired genotypic trait would be descendants polymorphic in the $MC4R^{AG}$ genotype, sorted by gender and allelic state, this will give balance in behavior, concentration of stingray and indole at an optimal level, which will positively affect the level of growth and indicators of target productivity. We evaluated the possible use of the c.1426 A > G polymorphism as a molecular marker for genetic selection towards lower boar odor levels in immunologically castrated and uncastrated pigs (Large White × Landrace) × Maxgro. This study shows that the Asp298Asn polymorphism of the MC4R gene is correlated

concentrations of androstenone, skatole, and indole in pigs. The results have implications for the continued study of the solution of the issue at the molecular genetic level in the pork industry.

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