

H. Rudoman, V. Balatskyi, V. Nor. Analysis of polymorphism in Mucin 4 gene associated with animal resistance to colibacteriosis in pigs of domestic and foreign selections

Nowadays one of the most common and critical problem in pig breeding is colibacteriosis. This infectious disease has acute course and it is caused by enteropathogenic strains of bacteria *Escherichia coli*. One of the recent and effective approaches to prevent colibacteriosis is using markers of selection; it involves pig genotyping by genome loci. The chosen loci are associated with animal sensitivity to the disease and selection of animals with increased resistance by the results of genotyping. According to several researches, one of such loci is *Mucin 4 (MUC4)* gene.

MUC4 gene is located in the 13-th chromosome (SSC13q41). Mucins (*MUC*) are macromolecular glycoproteins synthesized by goblet enterocytes and play main role in protecting the intestinal epithelium from pathogens, including adhesive strains of *Escherichia coli*.

As a result of spot replacement g.1849 G>C in intron 7, structure of mucin protein encoded by gene is changing which leads to changes in the sensitivity of the intestinal mucosa to pathogenic *Escherichia coli*. G allele and respectively GG genotype determine the resistance of animals to colibacteriosis, while CC i GC genotypes are susceptible to this disease.

In Ukraine, the studies of polymorphism *MUC4* g.1849 G> C were held fragmentally and only at certain populations of Ukrainian Meat and Large White.

The aim of the work was to determine the genetic structure of pig breeds of domestic and foreign selection for *MUC4* gene and to establish the possibility of organizing marker associated selection for genetic improvement of resistance to colibacteriosis.

For research the samples of blood and hair were used from the animals of Large White of English selection, Large White of Ukrainian selection Type 1 and Type 3, Red White-Belt, Mirgorod, Poltava Meat and Landrace breeds.

DNA isolation from the samples of biomaterial were carried out using ion exchange resin Chelex-100. Genotyping was performed by PCR-RFLP by Jorgensen methods (2006) with own modifications, concerning the selection of primer annealing temperature and optimum concentration of the gel to separate the restriction fragments.

Genetic structure was determined using DNA analysis of *MUC4* locus at seven breeds and intrabreed types. Predominance of potentially beneficial G allele frequency over undesirable C allele was established in all the populations of the studied pigs. The highest frequencies of G allele were characterized for Mirgorod (0.795), Poltava Meat (0.740) and Red White-Belt (0.820) breeds.

Analysis of the distribution of genotypes showed domination of genotypes GG and GC in all analysed populations. Positive Wright fixation index and predominance of expected heterozygosity (0.484) over actual one (0.460) for Large White of Ukrainian selection Type 3 indicate the existence of moderate inbreeding and selective pressure in this herd. Other populations were characterized by a negative value of fixation index, which is indicative of an excess of heterozygotes, these breeds are in outbreeding depression.

Statically significant deviation of actual frequencies of genotypes from expected ones was identified using Hardy-Weinberg criterion for pig population of Large White of English selection and Large White of Ukrainian selection Type 1. This may indicate that these populations aren't in condition of equilibrium and about inclusion of the chosen gene to the selection process.

The valuation was performed by calculating the PIC (polymorphic information content) of the marker. Based on the calculated PIC index *MUC4* locus could be perspective to be used in marker associated selection with improving genetic resistance to colibacteriosis.

The data of *Mucin 4* gene polymorphism at Ukrainian pig populations of different origins and productive direction show the possibility of marker selection to improve the genetic resistance of animals to colibacteriosis regardless of their belonging to breed. This creates prerequisites for the establishment and implementation of the early molecular diagnosis of carriers of harmful C allele in *MUC4* gene in pig breeding.

Keywords: pigs, colibacteriosis, population, polymorphism, DNA-marker, Mucin 4 gene