

Effectiveness of applying different methods of molecular genetics in swine selection (A review)

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Abstract

The rapid development of molecular genetics in the last two decades, primarily related to the technological breakthrough in the field of genome sequencing of higher organisms, has made it possible to apply new models of work. The term (MAS – Marker Assisted Selection) was first introduced in the literature in 1986 (Tautz, D., 1986; Jung, Y., 1989; Spötter, A., 2001; Rothschild, M., 2003). Marker selection uses a DNA marker to increase the efficiency of selection work, which is based on the identification of a series of nucleotides (markers) for the studied selection trait. This approach is widely used in breeding programs as a methodological technique for intensifying the selection process (Varshney, R. et al., 2005; Nanuwong, N. and Bodhisuwan, W., 2014). A necessary condition for (MAS) is the presence of a molecular marker. Such a marker can be any fragment of DNA that is used to detect polymorphisms and is closely related to the gene responsible for the manifestation of the trait (Rothschild, M., 2007).

Key words: MAS, genetic markers, swine, selection

Ефективност от прилагане на различни методи от молекулярната генетика за селекция на свинете (Обзор)

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Резюме

Бързото развитие на молекулярната генетика през последните две десетилетия, свързано преди всичко с технологичния пробив в областта на секвенирането на генома на висшите организми, даде възможност да се приложат в практиката нови модели на работа. Терминът (MAS – Marker Assisted Selection) за пръв път е въведен в литературата през 1986 година (Tautz, D., 1986; Jung, Y., 1989; Spötter, A., 2001; Rothschild, M., 2003). Маркерната селекция използва ДНК маркер за повишаване ефективността на селекционната работа, който се основава на идентифицирането на поредица от нуклеотиди (маркери) за изследвания селекционен признак. Този подход е широко използван в селекционните програми като методологична техника за интензификация на селекционния процес (Varshney, R. et al., 2005; Nanuwong, N. and Bodhisuwan, W., 2014). Необходимо условие за (MAS) се явява наличието на молекулярен

маркер. Такъв маркер може да бъде всеки фрагмент на ДНК, който се използва за откриване на полиморфизми и е в тясна връзка с гена, който отговаря за проявлението на дадения признак (Rothschild, M., 2007).

Ключови думи: MAS, генетични маркери, свине, селекция

The selection of farm animals is carried out by selecting specific animals who have the highest qualities. The scale and complexity of the selection, the size of the population in traditional breeding programs require new approaches to which it applies (MAS). Selection by molecular markers has great potential for increasing the efficiency and accuracy of the breeding process in pigs. Several types of molecular genetic markers are known, which arise as a result of different DNA mutations: replacement mutations (single nucleotide substitutions SNP), displacements (insertions or deletions) and errors in replication of tandem DNA repeats.

Genetic markers

There are several dozen molecular markers today. In most cases, genotypes are determined using microsatellites (SSR – Simple Sequence Repeats), which are found in large quantities in the genome and are characterized by the presence of polymorphisms. Microsatellites are repetitive sections of DNA 2–6 bp long. Different alleles are characterized by a large number of repetitions. These tags have several names STMS (Sequence Tagged Microsatellite Site), STR (Short Tandem Repeat), SSR (Simple Sequence Repeat). Microsatellites are used to determine the degree of heterozygosity in small populations, breeds and for early prediction of productivity (Zinovieva, N. A., 2008; Glazko, V. I. et al., 2009). They are widely used in animal selection, for the construction of genetic maps (Rohrer, G. et al., 1996), the search for quantitative traits (QTL) associated with productive (fattening and slaughter) (De Koning, D. J. et al., 1999; Kim, S. et al., 2019) and reproductive traits of animals (Wilkie, P. J. et al., 1999; Rosendo, A. et al., 2012). Marker selection also serves to assess genetic variation

in the population (Putnová, L. et al., 2019) and to determine its structure (Swart, H. et al., 2010). To date, there are over 15,581 quantitative characteristics (QTL) in pigs related to meat qualities (<https://www.animalgenome.org/cgi-bin/QTLdb/index>, April 01, 2019). The swine genome study was used to establish the relationship between single nucleotide polymorphisms (SNPs) and economically important traits (McCarthy, M. I. et al., 2008; Yang, H. et al., 2015). The predominant number of studies with swine are related to the influence of genetic factors on meat productivity (Baby et al., 2014; Casiro et al., 2017; Gonzalez-Prendes et al., 2017; Hwang et al., 2017).

Single nucleotide polymorphisms (SNPs)

In order to more accurately assess the genetic potential of farm animals directly at the genotype level, studies are being conducted to identify informational nucleotide polymorphisms (SNPs) and to develop systems for DNA analysis of genes that affect the expression of economically useful traits (Zinovieva, N. A., 2008; Fan, B. et al., 2009). According to the generally accepted definition, SNPs are single nucleotide positions in nuclear DNA for which different sequence variants (alleles) with an allelic frequency of at least 1% can be found in the population. The causes of these substitutions may be spontaneous mutations or the influence of mutagens. A difference in the sequence of even one nucleotide pair can lead to a different manifestation of the trait. SNPs are characterized by a high frequency in the genome and a low number of mutations per generation. This distinguishes SNPs from microsatellites in terms of their ability to be used for population genetic analysis. In this regard, automatic identification methods have been developed for SNP (Linville, R., 2001).

A gene is a specific sequence in the DNA chain that is used to synthesize certain polypeptides or functional RNA, which subsequently determines the formation of the trait. In this way, the gene ensures hereditary transmission of the trait to the offspring. Within a population, a single gene may correspond to several different nucleotide-allele sequences. This phenomenon is called polymorphism, and such genes are polymorphic. Alleles can be dominant or recessive. Thus, the presence of a polymorphic gene is the reason for the variability in the population, which ensures the diversity of the trait within the species.

The swine genome has millions of point mutations. Using DNA markers, it is possible to determine the frequency of desired alleles for breeds and lines and, in this regard, to select animals in order to increase the concentration of desired alleles in the study population (Zinovieva, N. A., 2008; Kostyunina, O. V. and et al., 2012).

DNA markers have a number of advantages that make them important for selection:

- Allow to clearly define homozygous and heterozygous genotype;
- They are not affected by environmental conditions and have a coefficient of inheritance $h^2 = 1.0$;
- Determined regardless of age (in embryonic cells, blood samples, animal tissue);
- Can be determined for both sexes;
- The trait can be determined after slaughter.

Marker genes are suitable for assessing traits, the phenotypic manifestation of which is expressed later in life, depends on gender or its manifestation is influenced by environmental factors. Such traits are: resistance or predisposition to disease, fertility, milk production or meat productivity.

Depending on the number of genes influencing the manifestation of a given trait, they are divided into two categories:

- Main genes – a certain part of the gene can encode a product involved in a number of key processes and therefore have a very strong influence on the formation of the trait. Monogenic or monogenic traits are those which, in the case of an approximate location of a gene, make it pos-

sible to identify DNA markers located inside or in the immediate vicinity of the main gene;

- Polygenic traits (QTL locus traits). Polygenic traits include most of the economically important traits in farm animals. The manifestation of the polygenic trait is determined by different allelic variants of a number of loci scattered throughout the genome (Zinovieva, N. A., 2008).

Candidate genes

The selection of the trait we are interested in is initially based on the choice of genes that determine the biochemical processes associated with the formation of the trait. The studies are aimed at studying the polymorphism of these genes and the productive characteristics of animals carrying different alleles of this gene in their genotype. Therefore, candidate genes are genes encoding key proteins involved in trait formation. A characteristic feature of these genes is that initially the presence of allelic variants of the gene and their influence on the value of the trait are not known (Zinovieva, N. A., 2008).

According to the literature, positional and functional candidate genes differ. Positional candidate genes are located next to the quantitative trait of interest (Zinovieva, N. A., 2008). Functional candidate genes are genes whose action plays a key role in the formation of a given trait (Louveau, I., 2004). The presence of polymorphisms in these genes should be investigated in connection with the change in the trait (Linville, R., 2001). The detection of positional genes is used to identify the "muscle hypertrophy gene" (myostatin gene), which causes the double-muscling syndrome in Belgian Blue Cattle and Piedmont (Terman, A., 2005). A similar approach was used to detect the so-called "cooked ham gene" in Hampshire pigs associated with meat productivity and meat quality (Zinovieva, N. A., 2008).

There are various mechanisms for genes to influence traits. At the same time, according to many authors, marker selection is effective even in the absence of some of them, such as pleiotropy. The connection of marker genes with eco-

nomically useful traits is used in breeding with a specific population of animals to achieve economic effect (Mankowska, M., 2015).

Genetic markers can be defined as areas of DNA characterized by polymorphism for which their location on the chromosome is precisely established, but their biological function is unknown.

It should be noted that selection methods that use DNA markers are divided into two main groups: marker-assisted selection (MAS) and Genomic selection. Genomic selection (a term proposed by Hailey and Visherom in 1998) involves the simultaneous study of a large number of markers covering the entire genome. Genomic selection technology is based on the use of chips (matrices) containing information about 50–60 thousand SNPs associated with the main genes for quantitative traits. This technology has been developed in the works of a number of authors (Weisz, F. et al., 2011), who propose a methodology for analytical assessment of breeding qualities of animals with the help of a marker map covering the whole genome. Genomic selection makes it possible to determine with high accuracy the genes of each animal and the results of the manifestation of these genes when used in the breeding process.

Conclusions

The development of the method for genomic selection is based on the different interactions between QTL, their variability in different breeds, the influence of the external environment on the economically valuable traits of animals. This confirms the importance of a comprehensive study of these interactions, biological characteristics and the impact of genetic polymorphism on economically valuable traits of animals using marker selection methods. The greatest effect of (MAS) will be realized when breeding programs are adapted to make the best use of large-scale genotyping for more traits. The advantage of this complex molecular selection approach is that selection progress is achieved in a short time, unlike traditional

selection. At present, the effectiveness of pig farming will increasingly depend on the use of innovative approaches in pig farming, through the increasing use of the possibilities of molecular genetics and in particular genetic markers in the breeding process.

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