Artykuł przeglądowy *Review*

Genetic progress and health implications in swine breeding

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Summary

Directional selection aimed at improving productive traits in pigs has caused limitations in adaptive mechanisms, affecting also, to some extent, the health of these animals. The article shows some health problems in swine, being a consequence of directional selection. It also refers to results obtained in studies within molecular genetics, cytogenetics and immunogenetics, showing an improvement in genotypes, and to some methods for prevention and control of several dysfunctions connected with some infectious diseases in pigs.

Keywords: pig, genetics, dyschondroplasis, stress, viral and bacterial infections

The first pig was domesticated thousands of years ago, but the greatest rate of genetic changes in swine breeding received emphasis in the 20th century, especially in the 1950s. Initially, the selection index included daily gains, feed conversion rate (FCR), meat content (lean percentage and meat quality) in a carcass and backfat thickness.

As a result of selection, based on several swine generations, strengthening of production parameters in certain breeds was obtained, and new lines, found especially useful for cross-breeding of pigs destined for production on a commercial scale, resulted.

The reports on Dutch Landrace breed show that over a period of 60 years (1930-1990) daily gains increased from 500 g/day to 840 g/day, whereas feed conversion rate (FCR) decreased from 3.5 kg to 2.8 kg and almost a two-fold decrease (from 45 mm to 24 mm) in backfat thickness was observed (23).

Since the 1990s, cytogenetics and molecular genetics as well as advanced statistical methods have been commonly applied in pig breeding. Improvements in molecular genetics provided new tools for testing the presence of gene mutations responsible for major phenotypic variation of quantitative traits and genes responsible for animal resistance/susceptibility to diseases. At the same time, the classical selection index was replaced by Blup-animal model methodology (BLUP – Best Linear Unbiased Prediction), both for production and reproduction traits, based on animal model (49). The improvement was aimed at genotypes and creation of new breeding lines, with regard to production traits. In addition to the production traits, also others connected with reproduction performance (a litter size, mortality index of piglets, length of sow's life) and resistance to stress and diseases were taken into consideration.

The data in literature show that an improvement of production traits often corresponds with detrimental effects on animal health, resulting from physiological imbalance in pigs of high genetic potential. They are manifested in a low-efficient thermoregulation mechanism, labile cardiovascular system, reduced vasculature of the lungs, development of the alimentary tract and the osseous system as well as retarded growth of these animals. Selection directed towards an improvement of production traits has resulted in a situation where the level of these traits approached the margins of physiological potential in these animals. This effect is clearly seen in a weakened immune response of pigs to infectious diseases and stress, and also reduced quality of pork.

The selection of pigs aimed at a rapid growth of body mass ratio has resulted in large disproportions between body mass and the strength of legs and heart efficiency. Today, pigs are more susceptible to a sudden „cardiac" death, since their heart is too small in relation to the body mass. For comparison, the mass of the heart of a wild pig accounts for 0.38% of body mass, while that of the Landrace breed accounts for 0.21% (5). Genetic progress has also resulted in a weakened immune response due to vaccination (32, 47).

Selection towards the improvement of prolificacy in pigs (litter size) has resulted in some detrimental effects connected with the number of mummified foetuses and piglets born alive (18).

Legs and lameness

Dyschondroplasia, e.g. osteochondrosis and osteoarthrosis (degenerative joint disease) are genetically conditioned diseases affecting the legs of pigs. The incidence of these diseases is greater in breeds and lines exhibiting fast body gain and hypertrophy of some muscles (e.g. ham) at a relatively low feed intake (13, 41).

At an early stage, arthrosis is manifested in a degeneration of the articular cartilage caused by metabolic disorders, and at later stages, mainly in joint overload, injuries, posture faults or changes due to osteochondrosis. Arthrosis affects mainly the following joints: knee, cubital and brachium (11). Both *osteoarthrosis and arthrosis* have a genetic background (12, 44, 51). Pigs of the Landrace breed are especially prone to these diseases, since at least one of the lesions occurs in 100% of Landrace pigs (13). Selection conducted in Norway for ten years did not decrease the incidence of these diseases (10). The results of the studies show that these genetic disorders in swine are primarily dependent on boars (45).

In the etiology of dyschodnroplasia, hard floor with no litter is likely to affect a young skeleton of pigs. A sudden pressure of muscles on the cartilage results in disorders affecting pig growth (39, 40).

Osteoarthrosis and arthrosis are diagnosed based on clinical, radiographic and ultrasonic pictures. If any symptoms are found in reproductive herds, culling is inevitable. These diseases are a serious problem in intensive pig breeding, focused on fast body gain and hypertrophy of some muscles, in contrast to extensive breeding systems with a higher level of welfare, where the frequency of these diseases is incomparable. In extensive breeding, the locomotor system of pigs is well-developed because the animals have more space to move around, which is favourable for the proper development of the skeletal tissue and bones. Dyschodnroplasia may, therefore, be qualified as a civilization disease resulting from an excessive exploitation of animals.

Susceptibility to infectious diseases

PRRS (porcine reproductive and respiratory syndrome) is one of dangerous infectious diseases of genetic background, found in pigs in recent years. The affected pigs are susceptible to respiratory tract infections and reduced prolificacy. The syndrome is conditioned by a mutation in the *Mx1* gene that causes an absolute loss of the ability to suppress virus propagation (e.g. influenza viruses and PRRS causative virus). The deletion allele, *Mx1*^{c}, was found to be segregating in the breeds of Landrace, Berkshire, Duroc, Hampshire, and Yucatan miniature pig (35). This mutation was found to exist at a relatively high frequency in the Landrace and Hampshire breeds (35). It has not been detected in Japanese and Meishan (Chinese) native populations. However, susceptibility to PRRS was found in pigs of Přeštice Black-Pied breed, whereas Large White breed has been reported to be resistant to this syndrome (54). The highest percentage of pigs with the two mutated alleles was detected in the Landrace breed, while in others, the homozygotes occurred rarely or have never been found (35). On the other hand, the percentage of heterozygotic pigs was very high in Landrace and Hampshire breeds, but it was markedly lower in Berkshire and Duroc breeds. Similar results have been reported by other authors (37) who found high frequency (about 30%) of mutated alleles in herds of Landrace and other common breeds, while the frequency of homozygotic individuals as regards that mutation was relatively low (3.7%). If the alleles are detected in the herd, all heterozygotic and dominant homozygotic individuals should be eliminated.

Huge losses in pigs are due to the diarrhoea of piglets caused by F4 *Escherichia coli*. Each year about 10 million piglets die all over the world because of diarrhoea (4). Susceptibility to diarrhoea depends on the presence of special receptors on the surface of the epithelium cells of the small intestine enabling growth of bacteria. The presence of the receptors is conditioned by three genes: F4ab, F4ac and F4ad (43). *Loci* F4ab and F4ac are closely linked and located very close to the *MUC4* gene. For this reason, molecular tests identifying alleles of the *MUC4* gene are used for determining the genotypes of pigs susceptible (dominant homozygotes and heterozygotes) and resistant (recessive homozygotes) to F4 *Escherichia coli* strains (20).

Piglets from sows devoid of the receptor, but having it inherited from the boar, are more prone to diarrhoea caused by *E. coli* F4, since they do not receive *E. coli* antibodies with the colostrum and milk of their mother. The hereditary F4ad receptor is not yet known, but it seems quite likely that it is also controlled by the dominating gene (6).

In Switzerland, it was found that piglet mortality due to the F4 *E. coli*-induced diarrhoea reached 22% (52). In Germany, the overall mortality of piglets caused by *E. coli* was found within the range from 1% to 8% (16). Similar mortality rates were found and reported in Poland (38). Significant differences in the susceptibility of piglets to diarrhoea caused by *E. coli* were observed between breeds (17, 54). The highest susceptibility was found in Polish Landrace, Belgian Landrace and Duroc breeds (17). The results of the studies conducted in the Czech Republic show that pigs of Large White and Přeštice Black-Pied breeds are also susceptible to F4 *E. coli* infections (54).

Oedema is a disease caused by enterotoxygenic F18 *E. coli* strains that colonise the pig small intestine. Its symptoms are: ataxia, convulsions and paralysis and diarrhoea in the period of weaning. As has been reported, adhesion of *E. coli* F18 bacteria (possessing fimbriae) depends on a *FUT1* gene, located on chromosome 6, very close to the *RYR1* gene (ryanodine receptor, responsible for malignant hyperthermia). Susceptibility to infections caused by F18 *E. coli* is a predominant trait, while resistance to this infections is a recessive one (3).

Sequencing of the *FUT1* gene of pigs of BB and bb genotypes in ECF18R *locus* showed that these genotypes differ in the exchange of adenine (A) for guanine (G) in 307 nucleotide (27, 34, 53). The hypothetical genotype of resistance to diarrhea (*bb* in ECF18R *locus*) is equal to the AA genotype in *FUT1 locus* and BB and Bb (in ECF18R *locus*) genotypes are equal to GG and GA (in *FUT1 locus*), respectively. It was found that the level of the FUT1 enzyme (α(1,2) fucosyltransferase) was 28- to 45-fold higher in piglets resistant to diarrhoea as compared to the susceptible ones (34). Taking this into account, Swiss researchers developed a molecular test enabling the identification of a pig's genotype (33, 34).

The highest percentages of animals resistant to F18 *E. coli* were observed in the Large White breed (11%), whereas the highest percentage of susceptible animals (99%) was found in Landrace, Duroc and Hampshire breeds. The results of the studies conducted in Poland (22) show that the highest number of animals resistant to the *E. coli* F18-induced diarrhoea was found in the Zlotnicka Spotted breed (37.5%), while no resistant animals were observed in three other breeds: Polish Large White, Polish Landrace, and Zlotnicka White. The results suggest that old, native breeds may be an important source of genes responsible for the resistance of these animals to various diseases.

The genetic background of susceptibility/resistance to different diseases caused by infections has been reported by many authors. Heritability coefficients (h^2) in pigs have been determined. The h^2 coefficient of immunity to leptospirosis was 0.20 (42), 0.26 – to infectious atrophic nose inflammation (21), 0.12 – to enzootic pneumonia, and 0.13 – to pleuropneumonia (31). Also higher levels of postvaccine antibodies against Aujeszky's disease in Yorkshire and Chester White breeds as compared to Duroc and Landrace were observed (48). Experimental infection of pigs with *Sarcocystis sui hominis* revealed that animals of the Pietrain breed exhibited a significantly higher number of parasites in skeletal muscles and more severe clinical symptoms than pigs of the Meishan breed (46).

Susceptibility to stress

The data in literature show that also the anxiety of pigs resulting from disorders in the nervous system (2, 19, 30, 36) is worth attention. The susceptibility of pigs to stress (observed mainly in pigs on farms with an intensive breeding system) is often of genetic background.

Porcine stress syndrome (PSS), known also as malignant hyperthermia syndrome (MHS), is one of the earliest metabolic defects identified in pigs. Its physiological, biochemical, genetic and breeding background have already been well recognized. At the end of the 1950s, it was observed in a population of the Dutch Landrace that some animals responded to stress similarly, e.g. by a dangerous rise in body temperature to 42°C (27).

Individuals that have inherited one mutated allele ($RYR1^T$) from each parent, had $RYR1^T/RYR1^T$ genotype and were very sensitive to stress (PSS). In addition, the meat of these individuals exhibited characteristic changes, known as PSE (*pale*, *soft*, *exudative*) syndrome (7, 50). The PSE syndrome induced by physical and mental stressors is manifested with abnormal energy conversion in muscles, which is also of genetic background (24). As a result, glycogen and released adrenaline start a glycogenolytic process leading to the accumulation of lactic acid in muscles, lower pH, and as a consequence, low quality pork.

As has been found, the mortality of the pigs of Pietrain and Landrace breeds during transport was 0.7% (1), while that of less sensitive breeds, with higher body weight was markedly lower (0.1%-0.4%) (14). The losses caused by deaths of pigs and a reduced technological value of pork suggest that swine breeders should not neglect to test pigs on the presence of the mutated allele ($RYR1^T$) in order to eliminate the hosts of that allele from the herd (1, 14).

Genetic studies on the susceptibility of pigs to stress were conducted in Poland at the turn of the 1980s and 1990s (27). The susceptibility of pigs was defined by the halothane test, but after the 1991 the genotypes were detected in *RYR1 locus* (9). It was demonstrated that the $RYR1^CRYR1^C$, $RYR1^CRYR1^T$ and $RYR1^TRYR1^T$ genotypes are similar to the halothane *locus* genotypes which are identified by the haplotyping method (28). The aim of the studies was to find the incidence of the RYR^T allele in many breeds and lines, and to determine its influence on meat and carcass quality and on reproduction indices (29). Currently, in Poland, a programme of purging the mutated *RYR1* allele from pig herds is underway.

The results of the studies carried out by many authors show that the Hampshire (15), Zlotnicka Spotted (55) and Danish Landrace (26) breeds are resistant to stress, while pigs of the Duroc breed were relatively less resistant (15) to stress or resistant (8). Also pigs of the Yorkshire (15) and Polish Large White (55) breeds rarely exhibited susceptibility to stress.

Much more susceptibility to stress than Polish Landrace (8, 25) were Pietrain (9) and Belgian Landrace pigs (8).

The *RYR1* and *FUT1* genes are located very close to each other, on chromosome 6, and together with other genes they form a halothane linkage group (52). A very strong linkage between the *RYR1* and *FUT1* genes causes pigs resistant to stress to be more frequently affected by diarrhoea than pigs susceptible to stress (8). Hence, if only one of these traits (susceptibility/resistance to stress, susceptibility/resistance to infections with the F18 *E. coli* strain) is taken into consideration in selection, it seems quite likely that the number of animals characterized by the other trait will be increased. For this reason, the identification of the two genotypes and implementation of a programme aimed at freeing the herds of the two syndromes is necessary (8).

Conclusions

High performance of pigs has been obtained at the expense of their biotic potential. The genetic potential of contemporary swine breeds can be disturbed if animal welfare and management systems do not meet standard requirements. For this reason, environmental conditions, housing and feeding systems as well as veterinary inspection, including immunoprophylaxis and metaphylaxis are of primary importance, let alone, molecular genetics for testing the presence of expression genes in pigs, responsible for the performance and health condition of these animals.

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