

GENOMIC MARKERS IMPORTANT FOR HEALTH AND REPRODUCTIVE TRAITS IN PIGS

Vrtková I.¹, Matoušek V.², Stehlík L.¹, Šrubařová P.¹, Offenbartel F.³, Kernelová N.²

¹ Mendel University of Agriculture and Forestry Brno

² University of South Bohemia in České Budějovice

Introduction

The oedema disease and post-weaning diarrhoea in 4-12 weeks old pigs is associated with the colonization of the small intestine by toxigenic *Escherichia coli* strain with fimbriae F18. The FUT1 (α -1, 2 fucosyltransferase) gene has been determined as a marker gene for *Escherichia coli* F18 receptor locus. The M307 polymorphism of the FUT1 gene influences susceptibility to adhesion of *E. coli* F18 to intestinal mucosa and an outbreak of illness.

Enterotoxigenic *Escherichia coli* expressing fimbriae F4 frequently colonizes the intestine of neonatal and weaned pigs. Susceptibility to enterotoxigenic *Escherichia coli* with fimbriae F4 is determined with the marker gene MUC4 (sialomucin complex). Mucin 4 (MUC4) is a large membrane-bound O-glycoprotein that is abundant on the surface of gastrointestinal epithelial cells; it plays an important role in the lubrication and protection of mucosa (Peng, 2007).

Mx1 gene affects the capability of inhibition the proliferation of RNA virus. An 11-bp deletion in Mx1 gene results in the loss of the ability to suppress viral propagation.

Follistatin gene, found in pig chromosome 16, is a new genomic marker for reproductive traits in pigs. FS gene is indicative for the heritable traits of litter size, number born alive, number of fully formed fetuses, number of still-borns, number weaned, weaning weight, average daily gain, and feed efficiency in pigs. Polymorphism in the FS gene is related to reproductive and performance traits in pigs.

The main objective of this study was to evaluate presence of resistant alleles of FUT1, MUC4 and Mx1 genes in population of pigs in the Czech Republic and characterize new important gene because of its connection with reproductive and performance traits. Information about this new gene was found in Patent US2007/0186298.

Material and Methods

Samples of blood and/or tissue and/or hair roots of 213 pigs were analysed by PCR – RFLP methods in FUT1 and MUC4 genes. The same amount of animals (213) were used and PCR based detection of the 11-bp deletion in Mx1 gene was performed. There were analysed files of 81 breeding boars (different breeds – Large White (LW), Landrace (LA), Duroc (D)), 77 breeding sows of LW breed and 59 the Přeštice Black-Pied pigs (PBP).

The selected region of FUT1 gene was amplified by the polymerase chain reaction technique, using primers described by Meijerink et al. (1997).

For detecting MUC4 gene we used protocol from United States Patent 2006/0275763.

Methodology for detecting Mx1 gene was gathered from United States Patent 2006/0166188.

Results and Discussion

The resistant allele of FUT1, MUC4 and Mx1 gene is A, A and O, respectively.

In Tab.1 we can observe significant difference in genotype GG of FUT1 gene between pig commercial breeds and PBP. In the population of pig genetic resources (55 individuals) any sensitive individual was detected. Genotypes frequencies of MUC4 are comparable. Differences between genotypes frequencies indicating resistance to viral infection (Mx1) are almost same compare to genotypes frequencies indicating resistance to bacteria *Escherichia coli* (FUT1, MUC4).

Boars are the most selected individuals in pig's population. In comparison Large White and Landrace results (Tab.2), we can see the worst resistance to bacterial infection in Landrace breed. Difference between Large White boars and Large White sows is not so significant. The highest frequency of allele P of Mx1 gene is found in Landrace breed, as we can find in literature.

Differences between Duroc and Pietrain sire breeds are considerable in the case of bacterial infection (FUT1) (Tab.3). Genotype frequencies of Mx1 are almost the same.

Tab. 1.: Pig commercial breeds (LW, LA, D, PN) and pig genetic resources (Přeštice Black-Pied pig (PBP)) of the Czech Republic

| | Nr of pigs | FUT1 | | | MUC4 | | | Mx1 | | |
|---------------------------|------------|------|------|------|------|------|-----|------|------|-----|
| | | AA | AG | GG | AA | AB | BB | OO | OP | PP |
| Pig commercial breed | 431 | 9.5 | 41.3 | 49.2 | 62.4 | 28.1 | 9.5 | 62.2 | 29.4 | 8.4 |
| Pig genetic resources-PBP | 55 | 83.6 | 16.4 | 0 | 60.0 | 40.0 | 0 | 76.4 | 18.2 | 5.4 |

Tab. 2.: Pig dam breeds of the Czech Republic

| Breed | Nr of pigs | FUT1 | | | MUC4 | | | Mx1 | | |
|----------|------------|------|------|------|------|------|------|------|------|------|
| | | AA | AG | GG | AA | AB | BB | OO | OP | PP |
| LW boars | 48 | 2.1 | 35.4 | 62.5 | 18.8 | 62.4 | 18.8 | 81.2 | 18.8 | 0 |
| LW sows | 77 | 2.6 | 42.9 | 54.5 | 28.6 | 46.8 | 24.6 | 100 | 0 | 0 |
| LA boars | 19 | 0 | 21.1 | 78.9 | 26.3 | 31.6 | 42.1 | 57.9 | 26.3 | 15.8 |

Tab. 3.: Pig sire breeds of the Czech Republic

| Breed | Nr of pigs | FUT1 | | | MUC4 | | | Mx1 | | |
|-------|------------|------|------|------|------|------|-----|------|------|------|
| | | AA | AG | GG | AA | AB | BB | OO | OP | PP |
| PN | 171 | 8.8 | 41.5 | 49.7 | 76.6 | 22.2 | 1.2 | 43.9 | 42.1 | 14.0 |
| D | 102 | 20.6 | 48 | 31.4 | 92.2 | 7.8 | 0 | 54.0 | 39.2 | 6.8 |

For the FS gene we do not have any own results. But it is important to know that FS gene was observed to be useful genomic marker in growth and reproductive traits. We discuss results from experiment; US patent nr 2007/0186298. They worked with 730 sows and 1464 litters of three different breeds - Chester White, Yorkshire and Landrace. Animals were divided into four groups - populations. Polymorphic variant of FS gene were detected using PCR-RFLP and statistical analysis were done by PROC GLM. We decided to observe these traits – nr of born alive (NBA), nr of stillborn (NSB), born weight (BW), average weaning weight (AWW) and nr after transfer (NAT). Genotype was found to be a significant, contributing factor to the differences seen among individuals for mentioned traits.

Least square (LS) means were calculated for each trait and are presented in Tab.4. When looking at pair wise differences of LS means for each genotype the genotypes were found to differ for several traits.

When examining the LS means for raw litter data, BB individuals were found to be superior to other genotypes for traits such as NBA, BW, NSB, AWW, and NAT. These individuals averaged 0.55 more pigs born alive, 0.205 kg heavier per individual weaned and 0.55 more pigs after transfer than average of the alternative genotypic groups.

Tab. 4.: Least Square Means for litter trans (Source: US 2007/0186298)

| Genotype | NBA | BW [kg] | NSB | AWW [kg] | NAT | n |
|----------|----------------------|--------------------|---------------------|----------------------|----------------------|-----|
| AA | 9.80 ^a | 12.27 | 1.10 ^{c,c} | 5.31 ^{D,DD} | 9.60 ^e | 730 |
| AB | 9.50 ^A | 11.82 ^b | 0.80 ^c | 5.63 ^D | 9.50 ^E | |
| BB | 10.20 ^{A,a} | 12.72 ^b | 0.80 ^C | 5.68 ^{DD} | 10.10 ^{E,e} | |

$P^A = 0.004$; $P^a = 0.08$

$P^b = 0.09$

$P^C = 0.0014$; $P^c = 0.0677$

$P^D = 0.05$; $P^{DD} = 0.004$

$P^E = 0.015$; $P^e = 0.056$

Conclusion

Frequency of „resistant“ allele of marker FUT1 in particular files - breeding boars; breeding sows of LW breed and PBP pigs was: 0.20; 0.24 and 0.08. Frequency of „resistant“ allele of marker MUC4 in particular files - breeding boars; breeding sows of LW breed and PBP pigs was: 0.52; 0.52 and 0.80. Frequency of Mx1 allele associated with the capability of inhibition the proliferation of RNA virus was 0.85 in breeding boars; 1.00 in breeding sows of LW breed and 0.85 in PBP pigs.

New genomic marker FS was observed to be associated with reproductive traits according to US patent 2007/0186298. Genotype BB has a positive effect to some of reproductive traits such as nr of born alive (NBA), born weight (BW), nr of stillborns (NSB), average weaning weight (AWW), and nr after transfer (NAT). Genotype was found to be a significant source of variation for several traits. Based on this information it can be concluded that FS marker can be used to explain some of the variation among individuals when considering phenotypic litter data and breed values as well as growth traits EBVs (estimated breeding value).

References

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