Archiv Tierzucht 53 (2010) 4, 497-499, ISSN 0003-9438

Porcine prolactin receptor genotypes and production and reproduction traits in Hungarian Large White and Landrace sows (Brief Report)

Porcines Prolaktionrezeptor (PRLR) Genotypen und Produktions- und Reproduktionseigenschaften bei Ungarischen Large White und Landrasse Sauen (Brief Report)

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Background

Prolactin is an anterior pituitary hormone involved in many endocrine activities and plays and essential role in reproduction. Its receptor (PRLR) was detected in various tissues including brain, ovary, placenta, an uterus in several mammalian species (BOLE-FEYSOT *et al.* 1998). Reproductive performance of sows is a crutial point in pig production with significant economic importance and may be estimated with the help of markers. Porcine prolactin receptor gene is said to be a candidate genetic marker for reproductive traits. It has been mapped to porcine chromosome 16 (VINCENT *et al.* 1997). There is a C/G SNP in PRLR gene (KMIEC *et al.* 2001) at the position of 203 (GAN: U96306) which eliminates an AluI cleavage site. The effect of this polymorphism on litter size in various breeds has been estimated (VINCENT *et al.* 1998, ROTHSCHILD *et al.* 1998, VAN RENS *et al.* 2002, KMIEC and TERMAN, 2004, DRÖGEMÜLLER *et al.* 2001, KORWIN-KOSSAKOWSKA *et al.* 2003). The influence of the bovine hormone variant was also estimated (RATNA-KUMARI *et al.* 2008). The aim of the study was to estimate PRLR *Alu*I polymorphism effects on litter size in Hungarian Large White (HLW) and Hungarian Landrace (HL) breeds.

Procedures

202 HLW and 71 HL sows and 412 HL piglets (offsprings of the 71 HL sows) were included in this experiment. Primer sequences were as follows:

PRLR-F: 5'- CCC AAA ACA GCA GGA GGA CG-3' and
PRLR-R: 5'- GGC AAG TGG TTG AAA ATG GA-3'.

Primers were designed to amplify a 457 bp fragment using DNA sequence of porcine PRLR gene (GenBank acc. no. U96306). PCR reactions were performed in a total volume of 10 µl, containing 200 µM of each dNTP, 0.2 µM primers, 10 x PCR buffer, 0.5 unit Dynazyme DNA polymerase and 100 ng genomic DNA. The PCR cycling profile consisted of denaturation at 94 °C for 2 min, 35 cycles of denaturation at 94 °C (for 30 s), annealing at 58 °C (for 1 min), and extension at 72 °C (for 1 min), followed by a final extension at 72 °C for 3 min (after KMIEC *et al.*

2001). Digested fragments (by AluI endonuclease) were resolved in 4 % agarose gel stained with ethidium bromide and visualised under UV light. Genotypes were determined based on the fragment lengths such as: 125, 91, 79, 77, 66 and 19 bp for C allele and 125, 110, 79, 77 and 66 bp for T allele. Genotypes and reproduction performance (total number of born piglets (TNB), number of piglets born alive (NBA) and number of weaned piglets (NWP)) of HLW and HL sows were recorded. Live weight data of piglets at the 1st and 21st days in HL breed were also collected. Allele frequency and population balance were examined in the population. Method of univariate and multivariate analysis of variance and estimated marginal means were used to estimate relationship between the locus and reproduction data of HLW sows. Whereas method of non-parametric measure of correlation was applied (due to deviation from normal distribution) in case of HL piglets.

Results

Allele frequency data (HLW: C: 0.38, G: 0.62; HL: C: 0.5 G: 0.5) were similar to the results of KMIEC and TERMAN (2004) in case of HLW breed and to the findings of KMIEC et al (2001) and DRÖGEMÜLLER *et al.* (2001) in HL pigs. The calculated x^2 values did not indicate Hardy-Weinberg equilibrium in the populations. All studied traits showed significant changes between genotypes. Total number of born piglets (TNB) and piglets born alive (NBA) presented the highest value in CC genotype group. Significant differencies ($P<0.05$) could be detected between CC, CG and GG genotypes in the results of TNB and NBA. (TERMAN 2005, KMIEC and TERMAN 2004). GG sows had the highest number of weaned piglets, but this advantage was not proved to be significant. However difference between CC and CG genotypes in NWP was significant ($P<0.05$) for the benefit of CG group.

There was significant difference from normal distribution in database of litter size (including TNB, NBA and NWP) of HL breed. Data could not be normalised due to its nature. Therefore non-parametric tests were used, such as rank transformation. Friedman test was applied as a non-parametric probe. There was significant difference ($P<0.05$) between genotype groups in TNB and NBA, however verifiable difference could not be found in case of NWP. Litter size results showed normal distribution. So the methods of univariate analysis of variance and estimated marginal means were allowed to use. The effect of PRLR locus was only significant ($P<0.05$) in case of 21st day live weight data, however live weight at birth was not influenced by this locus significantly. Although sex of piglet was a significant factor ($P<0.05$) in weight at birth. Impact of fathers was strongly significant ($P<0.05$) in both traits, indicating the importance of a number of loci inherited from the father and affecting live weight gain. As the result of Fisher LSD test, least square differences could only be found between genotypes in case of 21st day live weight. CG genotype group had the highest results and 21st day weight data of this genotype were significantly ($P<0.05$) higher comparing to the similar data of CC and GG genotype piglets. This outcome may reflect to the feed conversion and utilization capacity of piglets and their grow capacity and certainly to the maternal ability of sows.

In conclusion it can be said that porcine prolactin receptor locus may be linked indirectly to loci responsible for the control of reproductive performance of sows and live weight gain of piglets. Litter size traits of sows, as it was presented above, had a correlation to PRLR AluI

polymorphism in both HLW and HL breeds. CC genotype resulted always the most beneficial one for litter size results. If 21st live weight is considered, CG genotype was seemed to achieve the best data.

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