Prolactin Receptor (PRLR) Gen Polymorphism and Associations with Reproductive Traits in Pigs

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Abstract: The Prolactin Receptor (PRLR) gene was investigated as candidate gene for swine reproductive traits. 335 sows of 4 genetic groups: Yorkshire (Y), Landrace (L) Duroc (D) and YL were included. The traits studied were: Total Number of Born (TNB), Number Born Alive (NBA), Number of Weaned Piglets (NWP), Litter Weight at Birth (LWB) and Litter Weight at Weaning (LWW). The polymorphism was identified by PCR-RFLP. Allelic frequencies between each genetic group and Hardy-Weinberg equilibrium were tested by chi-square test. The association between PRLR genotypes with reproductive traits was evaluated by a linear model. Additive and dominance effects were estimated. The frequency of A allele was in general 0.46, with variation between genetic groups. D had the highest values for TNB. YL showed the best performance for NBA. AA genotype in D showed the best performance for NWP but no differences were found among genotypes L, YL and L. Differences in first parity were observed between genotypes for TNB, with highest value in BB (10.40 piglets). In general, additive effect per allele A resulted in a negative increase of 2.26 pigs (TNB) and positive of 0.42 kg (LWB) per litter. For TNB and LWB, dominance effect was -2.67 pigs and -0.56 kg, respectively. For LWW, additive in L resulted in -8.37 kg while dominance effect was 8.37 kg.

Key words: Prolactin receptor gene, litter size, reproduction, pigs

INTRODUCTION

Reproductive performance determines the economic efficiency in pig production systems because of its effects on productivity. Litter size is the most important economically and the most easily measured reproductive trait. Much effort has been made for its improvement (Johnson *et al*., 1999). However, as the heritability is low (10-15%, Johnson *et al*., 1999), the trait is limited to sex and expressed in late stages of development in the animal (Goliasova and Wolf, 2004), thus traditional genetic improvement for increased litter size has resulted only in slow genetic gain (Rothschild, 1996). The identification of individual genes controlling litter size or genetic markers associated with such trait and its use in direct selection programs could contribute to an increased rate of genetic gain in pig populations.

The candidate gene approach proposed by Rothschild and Soller (1997) is a procedure used to identify genes with significant influence on the expression of a quantitative character for possible use in genetic improvement programs. A gene is selected to be a potential candidate gene because of the physiological role it regulates in a given process or pathway (Korwin-Kossakowska *et al*., 2003).

Prolactin Receptor (PRLR) is the specific receptor for prolactin, which is an anterior pituitary peptide hormone involved in many different endocrine activities and is essential for reproductive success (Vincent *et al*., 1998). All actions of prolactin are mediated by its receptor (Van Rens *et al*., 2003). The prolactin receptor, encoded by PRLR gene, is a member of the growth hormone/ prolactin receptor gene family containing regions of identical sequences (Kelly *et al*., 1991). The prolactin and

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