

Association analyses of candidate single nucleotide polymorphisms on reproductive traits in swine

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Abstract :

The ability to identify young females with superior reproduction would have a large economic impact on commercial swine production. Previous studies have discovered SNP associated with economically important traits such as litter size, growth rate, and feed intake. The objective of this study was to test for association of candidate SNP with sow prolificacy reproductive traits in gilts of a Landrace-Duroc-Yorkshire composite population. Association analyses regressed additive (A), dominant (D), and imprinting (I) SNP effects on each trait with an animal model. A carnitine palmitoyltransferase 1A SNP and a glycogen synthase 1 SNP were associated with age at puberty (AP; D = 10 d; $P = 0.0037$ and A = 3.8 d; $P = 0.0078$, respectively). Four *IGF2* SNP were associated with AP as well, having additive or dominant effects (3.2 to 5.8 d; $P \leq 0.0052$). Two mannosidase 2B2 SNP and 2 prolactin receptor (*PRLR*) SNP were also associated with AP. Solute carrier 22, subfamily member 5 SNP was weakly associated with AP (D = 3.9 d; $P < 0.10$). Polymorphisms within glycogen synthase 1 and protein kinase AMP-activated, gamma 3 noncatalytic subunit had associations with ovulation rate. Estrogen receptor (*ESR*) 1, *ESR2*, PPAR gamma coactivator 1, and *IGFBP3* SNP were significantly associated with weaning-to-estrus interval. Two *PRLR* SNP were associated with total number of piglets born (A = 0.57 piglets; $P = 0.0095$ and D = 0.61 piglets; $P = 0.0016$, respectively). A SNP within *PRLR* was also associated with number of piglets born alive (D = 0.61; $P = 0.0016$). The PPAR gamma coactivator 1 SNP was associated with total number of piglets born (D = 0.38 piglets; $P = 0.0391$) and number of piglets born alive (D = 0.53 piglets; $P = 0.0032$). The SNP within *ESR1* (A = 0.65 piglets; $P = 0.0950$), *ESR2* (A = -0.33 piglets; $P = 0.0176$), *IGF2* SNP (A = -0.26 piglets; $P = 0.0032$), and *IGFBP3* SNP (D = 0.35 piglets; $P = 0.0683$) were associated with number of piglets born dead. Leptin SNP was associated with mummified fetuses (D = 0.09 piglets; $P = 0.0978$). Many of the SNP analyzed in this study are from genes involved in regulation of metabolism, suggesting that there is an important link between physiological events associated with reproduction and energy utilization. Furthermore, these reproduction and growth trait SNP may serve to assist in selection of young females for superior reproductive performance.

Key Word :

pig, reproductive trait, single nucleotide polymorphism, sow longevity, swine

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