

Chatchai Chansomboon 2011: Genetic Analyses for Weaning to First Service Interval in a Thai Commercial Swine Population. Doctor of Philosophy (Animal Science), Major Field: Animal Science, Department of Animal Science. Thesis Advisor: Assistant Professor Skorn Koonawootrittriron, Ph.D. 119 pages.

Genetic analysis for weaning to first service interval (WSI) and litter traits (i.e., number of piglets born alive, NBA; litter weight at birth of live piglets, LBW; number of piglets at weaning, NPW and litter weight at weaning, LWW) were evaluated base on the pedigree and phenotypic data from a commercial swine herd in Northern Thailand. The original data contained 1,341 Landrace (L) and 795 Large White (W) and reciprocal crossbred sows (163 LW and 169 WL) were collected during 1989 to 2008. Primiparous sows had a longer WSI than multiparous sows ($P < 0.0001$). Crossbred sows had longer WSI than purebreds sows ($P < 0.0001$), whereas WSI between L and W sows were no difference. Variance-covariance components were estimated with an animal model for WSI and a sire-dam model for litter traits. Heritabilities for direct genetic effects were low for WSI (0.04 ± 0.02) and litter traits (ranged from 0.05 ± 0.02 to 0.06 ± 0.02). Maternal heritabilities for litter traits were 20% to 50% lower than their direct genetic heritabilities. Repeatabilities for WSI was similar to its heritability, whereas repeatabilities for litter traits ranged from 0.15 ± 0.02 to 0.18 ± 0.02 . Direct genetic correlations between WSI and litter traits were close to zero, contrarily with positive and high correlation among litter traits (except between litter traits at birth and LWW). Thus, a single trait analysis could be used for WSI, whereas litter traits must be multiple traits analysis. Boar genetic trends were small and significant only for NBA ($P = 0.0042$). Sow genetic trends were small, negative and significant for WSI ($P = 0.0113$), NBA ($P = 0.0071$), LBW ($P = 0.0109$), NPW ($P = 0.0234$) and LWW ($P = 0.0034$). In addition, one polymorphism and 2 alleles of the adiponectin (ADIPOQ; G and A) and follicle stimulating hormone receptor (FSHR; C and T) genes were studied for allele substitution and genotypic effects. Neither allelic nor genotypic effects were significant for either the ADIPOQ or the FSHR gene. Thus, the ADIPOQ and FSHR genes will be of little help for selecting pigs in this population.

Student's signature

Thesis Advisor's signature