

P-1. Change of genetic parameter of parity number with advancing birth year in Holstein(Abstracts of the International Symposium on Recent Advances in Animal Science(IS-RAAS),Joint meeting of 2nd IS-AS and 3rd IS-IFS)

著者	Sasaki O., Aihara M., Hagiya K., Ishii K., Nagamine Y.
journal or publication title	Tohoku journal of agricultural research
volume	56
number	1/2
page range	36-36
year	2005-11-25
URL	http://hdl.handle.net/10097/30082

Poster Sessions

P-1. Change of genetic parameter of parity number with advancing birth year in Holstein

O. Sasaki¹, M. Aihara², K. Hagiya³, K. Ishii¹ and Y. Nagamine¹

¹National Institute of Livestock and Grassland Science, ²Livestock Improvement Association of Japan, ³National Livestock Breeding centre

In the efficient dairy farming management, it is important to increase the average number of parity of a herd. The observable number of parity of cow is shortened with advancing birth year, because very limited number of parity can be observed from young cow. The objectives of this study were to estimate the genetic parameters of last parity numbers (LPN) and investigate the change of these parameters with advancing of birth year.

Data of parity number between 1975 and 2001 were obtained from Livestock Improvement Association of Japan. If the last parity of a cow was observed more than two years ago in the latest record book of her own herd, it was used as LPN of the cow. A total of 585,937 records from 918,135 Holstein cows were used for analysis. The animals were divided into the four groups by their birth year. Heritabilities and genetic correlations were estimated by the four traits animal model.

The observable period of cows, which were born after 1984, were restricted. The heritability of LPN was diminished with advancing birth year, because the genetic variance decreased more than the decrement of residual variance with limited observable period. The genetic correlations among birth year groups were as large as 0.73-0.94. The trends of annual average of breeding values of LPN were similar in all birth year groups. This result showed that the breeding value of LPN can be predicted by using the one genetic parameter.

P-2. Genetics of residual feed intake and its consequences in selection program of Japanese Black cattle

T. Oikawa^a, M.A. Hoque^a, and P.F. Arthur^b

^aGraduate School of Natural Science and Technology, Okayama University, Japan

^bElizabeth Macarthur Agricultural Institute, NSW 2570, Australia

Comparison between different measures of feed efficiency and their genetic relationships with component traits on 740 bulls (sire population) and with carcass traits on 1,774 progeny (1,281 steers and 493 heifers) for Japanese Black cattle were estimated with REML. Bull traits included daily gain (ADG), metabolic weight (MWT), feed intake (FI), feed conversion ratio (FCR) and residual FI computed from linear (RFI_{reg}), phenotypic (RFI_{phe}) and genetic (RFI_{gen}) regression of FI on MWT and ADG. Progeny traits were carcass weight (CWT), rib eye area, subcutaneous fat and marbling score. The genetic and phenotypic correlations between RFI_{phe} and RFI_{gen} were >0.95 implying that they may be regarded as the same trait. FCR genetically strongly correlated with RFI_{phe} and RFI_{gen} . The heritabilities for RFI_{phe} and RFI_{gen} were moderate while for RFI_{reg} and FCR were low. RFI_{phe} was phenotypically independent of its component traits (MWT and ADG), and RFI_{gen} was genetically independent of MWT. The genetic correlations of RFI of bulls with CWT and marbling of their progeny were favorably negative. The correlated responses in CWT of progeny were higher to selection against RFI_{phe} or RFI_{gen} than those to selection against RFI_{reg} or FCR of bulls. This study provides evidence that selection against RFI_{phe} or RFI_{gen} is preferred over selection against RFI_{reg} or FCR in sire population for genetic improvement of feed efficiency and getting higher correlated responses in progeny carcass traits.