

China Supakorn 2007: Effect of Growth Hormone and Growth Hormone Receptor Genes for Prewaning Growth Traits in a Multibreed Beef Population. Doctor of Philosophy (Animal Science), Major Field: Animal Science, Department of Animal Science. Thesis Advisor: Associate Professor Sornthep Tumwasorn, Ph.D. 110 pages.

The research was designed to screen polymorphism of the growth hormone (*GH*) and growth hormone receptor (*GHR*) genes by using Single Strand Conformation Polymorphism (SSCP) method. The study was carried out at Buffalo and Beef Production Research and Development Center (BPRDC), Kasetsart University. One hundred and thirty animals from six breed groups of crossbreeding among Charolais, Brahman and Thai Native were used in this study.

The first trial was designed to identify and to characterize polymorphisms of *GH* and *GHR* genes. The *GH* gene was studied at six fragments taking into account almost the entire length of gene (*GH1* to *GH6*) and the *GHR* gene was studied at three fragments (*GHR1* to *GHR3*). Three point mutations and five SNPs were detected in *GH* and *GHR* genes of this cattle population. Two SNPs were detected at position -303 and 670 bp of *GH1* and *GH2* fragments. The other two SNPs were located at position 2,141 and 2,354 bp of *GH5* fragment. The last one SNP was detected at position 1,867 on *GHR3*. Fourteen genotypes and twenty three haplotypes of *GH* and *GHR* genes were found in this study.

The second trial was carried out to evaluate the effect of the genetic polymorphisms of *GH* and *GHR* on BW and WW. The analysis of SNPs effect of *GH* and *GHR* genes indicated that *GH1* influenced on BW ($P<0.01$) and WW ($P<0.05$) but *GH5* influenced only on BW ($P<0.05$). Haplotypic effect influenced on BW ($P<0.01$) and WW ($P<0.05$). Also, the SNPs of *GH1* should be considered for genetic marker in order to select the high WW animals.

The third trial was conducted to compare the best fit models among model with and without molecular information (SNPs, regression of allelic and haplotypic effects). Testing among models with and without molecular information indicated that model with haplotypic effect showed the lowest of mean square error but the highest coefficient of determination, -log likelihood. Moreover, this model gave the highest means accuracy of prediction (ACC) for both traits from univariate and bivariate analysis. However, the means ACC of EBV_a for BW and WW from bivariate analysis showed the highest in model with regression of allelic effect but they were non significant with model with haplotypic effect.

The last trial was estimation direct heritability from the bivariate analysis using model with haplotypic effect. The direct heritabilities were found to be 0.33 for BW, and 0.27 for WW. Estimated maternal heritabilities were found to be 0.06 for BW, and 0.19 for WW. The direct genetic, maternal genetic and phenotypic correlations between BW and WW were found to be 0.88, 0.81 and 0.47, respectively. An antagonistic direct-maternal correlation for within traits (-0.28 for BW and -0.69 for WW) and between traits (-0.21 and -0.07 for BW and WW and vice versa) was found in this population. The ranges of EBV_a and EBV_m for both traits were found to be wide. The rank correlation of EBV_a and EBV_m of the whole population and 50 percent of top dataset for BW and WW were found to be positive. Both EBV_a and EBV_m getting from the model considered haplotypic effect that ranking by its order and the order from the model without haplotypic effect were different ($P<0.05$). Therefore, the producers should consider molecular information linked to conventional breeding for increasing the economic efficiency in the population.

Student's signature

Thesis Advisor's signature