## I. INTRODUCTION

Genetic parameters such as heritabilities and genetic or phenotypic correlation can be estimated by realized heritability or variance component using animal model. Many studies concerning this have been conducted for broiler population. For instance, Liu *et al.* (1994) revealed that realized heritability of 8-week body weight ranged from 0.22 to 0.28 for a high weight line and from 0.23 to 0.28 for a low weight line. Su *et al.* (1997) estimated heritability of body weight using animal model were of 0.25 (REML method) and 0.26 (Bayesian analysis), respectively. Heritability estimates of feed consumption and efficiency at constant age as summarized by Pym (1990), ranged from 0.2 to 0.8 and averaged at 0.45 for feed consumption; estimates for feed efficiency ranged from 0.18 to 0.56, and the average was 0.25. Khan (1976) reported a genetic correlation between 8- and 30-week body week of 0.86 ± 0.27 for normal and 0.15 ± 0.26 for dwarf broilers.

Although genetic aspect of both body weight and feed conversion has been studied intensively, additional research is still needed. For decision about an optimal selection program in broiler production, ample information is required on the heritability of body weight and of feed conversion. The aims of this study was to estimate and to compare realized heritability and estimated heritability of body weight and of feed conversion ratio.

## II. MATERIALS AND METHODS

Chickens originated from a line selected for growth and a line selected for feed conversion. In both lines, parents were selected on the basis of their own performance for body weight or feed conversion ratio. Two hatches were obtained with a maximum of 4 weeks between the youngest and oldest hatch. Random mating of the parent was used; the only restriction was the exclusion of matings between full and (or) half-sibs. At each generation, within line and hatch, 38 to 45 males and 106 to 130 females become candidates as sires and dams. Number of progeny per family used in this experiment ranged between 7 to 10 for BW line and 3 to 5 for FCR line.

For the BW line, at 41 days of age males and females were separated by a wire mesh fence and were fasted for 12 hours then weighed. The FCR line, at 21 days of age, 144 males and 144 females from each hatch (chosen at random, but approximately equal number per full sib family) were weighed and transfered to individual battery cages with individual feeders. Individual 21- and 42-day live weights were obtained after the birds were fasted about 12 hours. From 21 to 42 days of age weight gain and feed consumption were measured. Feed conversion was calculated by the ratio of feed consumed between 6 and 3 weeks and body weight gain from 3 to 6 weeks old.

To estimate heritability we used two methods in this experiment. First, estimated variance component using animal model with the aid of the package ASREML (Gilmour *et al*, 1998).and second, realized heritabilities were calculated over 9 generation of selection in the two selection lines by regression of generation mean of chicken on cumulative selection differential. Selection differential for body weight and feed conversion ratio were calculated by the difference in phenotypic mean value between the selected parents and the chickens of the parental generation before selection.

## III. RESULT AND DISCUSSION

### 3.1. Estimates of genetic parameters and Genetic trends

Estimates of heritabilities of, derived from animal model analysis (REML), phenotypic and genetic correlation between the two traits are shown in Table 3.1.

Table 3.1. Heritability of (diagonal), phenotypic (below diagonal) and genetic (above diagonal )correlation between body weight and feed conversion ratio in both lines.

| Traits | BW6(BW line) | BW6 (FCRline) | FCR (FCR line) |
|---|---|---|---|
| BW6(BW line) | 0.4153 (0.0302)* | | |
| BW6(FCR line) | | 0.5907 (0.0348) | 0.1839 (0.0627) |
| FCR (FCR line) | | -0.0267 (0.0379) | 0.4390 (0.0360) |

*) between brackets: the standard error

The estimates heritability of body weight in BW line and FCR line were 0.4153 and 0.5907, respectively. The heritability of feed conversion ratio was 0.4390. Genetic correlation between feed conversion ratio and body weight was positive while the opposite sign was found for phenotypic correlation.

Genetic trend of the two traits are presented in figure 3 1 and 3.2. This trend is derived from average breeding values from the REML analysis. The genetic level for body weight in BW line was notably increased by selection. The same trends was also found on chickens of FCR line, though only about 18.38% of BW line.

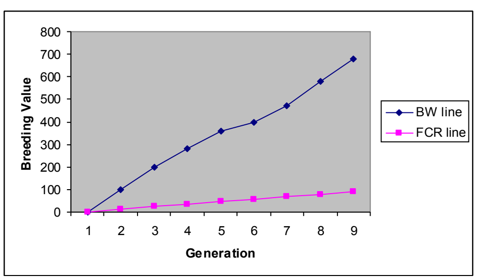


Figure 3.1. Genetic trend of body weight

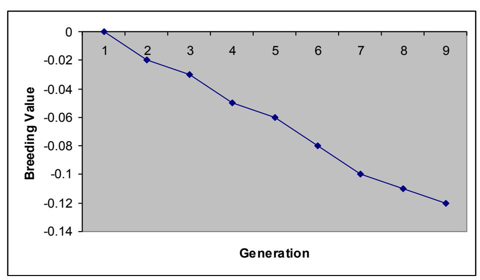


Figure 3.2. Genetic trends of FCR

The heritability of body weight of this study agreed well with most published (Leclercq *et al*, 1980; Chambers *et al*, 1984; Marks, 1985). However, the magnitude of heritability estimates for FCR line was higher than that for BW line. The differences in magnitude of both lines might be caused by the difference of housing system, individually for chickens of FCR line and as a group for chickens of BW line. As aconsequence chickens in BW line had more competion, social interaction and more space than those chickens in FCR line. To a small extent these differences might also be induced by the different number of birds used in each line. The number of chickens of BW line were much more than those of FCR line (9063 *vs* 4662 chickens). Becker *et al*. (1984) estimated heritabilities of some traits using sire model in broiler with small number of chickens (311 males and 341 females) and found the heritability estimates smaller than zero and larger than one. The other reason might be the base population of both lines have been previously selected for growth rate for many generation and this would tend to reduce the overall variability of the population.

The heritability estimate of FCR agreed well with most published (Pym, 1990; Wang *et al*.,1991; Chambers *et al*., 1994). Heritability estimation of efficiency of food conversion, either as gain : food ratio or its reciprocal (FCR) vary from approximately 0.1 to 0.6 and average about 0.4 (Pym, 1990).

Using REML analysis the genetic level for body weight in both line was notably increased by selection. The regression equation are y = 82.32x – 61.05 and y = 15.13x – 2.58, for BW line and FCR line, respectively. Slopes of the equation indicate that genetic gain of BW line was almost six time higher than those of FCR line. Although phenotypic trends in both line showed slightly progress in body weight, the genetical trend was considerable. Pym and Nicholls (1997) and Le Bihan-Duval *et al*. (1998) obtained the same genetic trend for body weight in broiler chickens. The trends of FCR and body weight shown in figure 3.1 and 3.2, both trends were in agreement with the estimated genetic correlation. the genetic trends of body weight increased from the first to ninth generation, while reverse was found for FCR indicated that there is a progress in genetic level after selection.

### 3.2. Realized heritabilities

Using regression of generation means on cummulative selection differential, the estimated realized heritabilities were 0.10, -0.14 and -0.03 for body weight BW line, body weight FCR line and feed conversion ratio, respectively. The realized heritabilities were considerably low for all traits and disagreed with most available publication (Pym and Nicholls, 1979). Negative signs of the realized heritabilities for the traits in FCR line is hard to explain. The possible reason is that there is no control line for this experiment such that correction for enviromental variation is not possible. Marks (1994) revealed that without correction for environmental variation resulted in large fluctuations in heritabilities across generations. Conectedness animals from one generation to another might be another reason for underestimate realized heritability. In this experiment, no chickens were kept for the next generation as a control group. However, using absolute value of heritabilities for all traits it can be concluded that high enviroment effect contributed in the realized heritabilities.

## IV. CONCLUSION

It can be concluded from the experiment that genetically, there was a high progress for all traits on both lines. However, the realized heritability resulted in unusually estimates. Using animal model, heritabilities for all traits agreed with published estimates. There is a discrepancy of estimates heritability and reaalized heritability.

## REFERENCES

Becker, W.A., Spencer, J.V.,Mirosh, L.W., Verstratem J.A., 1984. Genetic variation of abdominal fat, body weight and carcass weight in a female broiler line. Poultry Sci. 63: 607 – 611.

Chambers, J.R., Bernon, D.E., and Gavora J.S., 1984. Syntesis and parameters of new population of meat- type chickens. Theor. Appl. Genet. (1984) 69:23-30.

Chambers, J.R., Wang, L., and Mcmillan, I., 1994. Genetic variation of broiler feed concumption and efficiency corrected for differences in test body weights. Poultry Sci. 73: 1196-1203.

Gilmour, A.R., Cullis, B.R., Welham, S.J., Thompson,R., 1998. ASREML. Program user manual printed by NSW Agriculture, Orange Agricultural Institute, Forest Road, Orange, NSW, 2800, Australia. 150pp.

Khan A.G., 1976. Heritabilities and genetic correlations in related dwarf and normal broiler populations. Br. Poultry Sci. 17: 553-555.

Le Bihan-Duval, E., Mignon-Grasteu, S., Millet, N., and Beaumont, C., 1998. Genetic analysis of a selection experiment on increased body weight and breast muscle weight as well as on limited abdominal fat weight. Br. Poultry Sci. 39:346-353.

Leclercq, B., Blum. J.C., and Boyer, J.P., 1980. Selecting broiler for low or high abdominal fat: initial observations. Br. Poultry Sci.21:107-113.

Liu G., Dunnington E.A., and Siegel P.B., 1994. Response to long term divergent selection for eight-week body weight in chickens. Poultry Sci. 73: 1642-1650.

Marks, H.L., 1985. Direct and correlated respons to selection for growth. In PoultryGenetics and breeding. Br. Poultry Sci. Ltd. p. 47-57.

Marks, H.L., 1994. Selection for eight-week body weight in two randombred chicken populations under altered water to feed ratios. 1. Selection responses. Poultry Sci. 73: 1175-1182.

Pym, R.A.E, and Nicholls P.J., 1979. Selection for food conversion in broilers : Direct and correlated responses to selection for bodyweight gain, food consumption and food conversion ratio. Br. Poultry Sci. 20:73-86.

Pym, R.A.E., 1990. Nutritional genetics. Page 847-876 in: Poultry breeding genetics, R.D. Crawford, ed. Elsevier, New York. NY.

SAS Institute, 1996. SAS/STAT user quide: Statitics vol.2. SAS Institute Inc, Carry, NC

SAS, 1997. SAS/STAT software: Changes and enchancements throgh release 6.12. SAS Institute Inc, Carry, NC

Su, G., Sorensen, P., and Sorensen D., 1997. Inteference about variance components and selection response for body weight in chickens. Genet. Sel. Evol. 29: 413-425.

Wang, L., Chambers, R., and Mcmillan, I., 1991. Heritabilites of adjusted and unadjusted feed and abdominal fat traits in a broiler dam population. Poultry Sci. 70: 440-446.