

## The Genetic Development of Sire, Dam and Progenies and Genotype × Environment Interaction in a Beef Breeding System

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**ABSTRACT** : The aim of this study was to investigate genetic development and genotype×environment interactions (GEI) in postweaning body weight of fattening bulls at the end of test period (WT-T) under various beef fattening environments. Data on a total of 24,247 fattening bulls obtained from the industrial farm, breeding farms and testing stations were used. Heritability estimates for WT-T in all environments were nearly similar. Significant genetic developments of sire, dam and progenies for WT-T were observed in all environments. However, many differences in annual genetic developments between the environments were significant. The genetic correlations for WT-T between industrial farm and breeding farms, industrial farm and testing stations and breeding farms and testing stations were respectively 0.004, 0.004 and 0.013. These low estimates of genetic correlations and significant differences in genetic developments among environments clearly show the existence of GEI for WT-T among various fattening environments. Results of this study indicate the need for environment-specific genetic evaluation and selection of beef bulls for commercial beef production. (*Asian-Aust. J. Anim. Sci.* 2004, Vol 17, No. 1 : 13-17)

**Key Words** : Beef Breeding, Genetic Development, Genotype-environment Interaction

### INTRODUCTION

The genetic development in beef breeding systems is a function of correlation between breeding values in performance test and breeding values in progenies, weighted by accuracy (Korver et al., 1987). Many studies (e.g. Averdunk et al., 1987; Oldenbroek et al., 1987) have shown that performance testing of young bulls is effective to improve fattening traits of progeny. Analysis of genetic developments simultaneously in males, females and their progenies could be more useful in this situation. However, selection on the basis of performance and/or progeny test results is effective for beef production as long as the fattening system is comparable. Unfortunately, genotype×environment interaction (GEI) is found to play an important role in beef breeding systems (e.g. Schoeman and Jordaan, 1998; Brown et al., 1993; Klautschek, 1989) because under this condition, response from selection in one environment is not likely to be fully transferred to other environments. Hence, in case of existence of significant GEI, the necessity of selecting stocks under the specific environment in which progeny of stocks will be reared has been expressed (Falconer, 1989). In beef breeding, selection of bulls for higher growth at the breeding farms or testing stations is a common practice where selection decision is usually made upon the performance of tested pure and crossbred animals. But at the industry level the fattening animals always have crossbred genetic make-up. Therefore, in recent years,

particularly in the poultry and swine industry, an increased concern over the use of both pure and crossbred information from both nucleus/central test stations and commercial/industrial units to make selection decision has been observed. Since selection decision is taken at one level while end animals being performed in another level, investigation of the magnitude of breeding developments in sire, dam and progenies along with the question of probable existence of GEI becomes important. The impact of GEI on breeding programs can be best estimated by quantifying the genetic correlation between the same or similar traits measured in different environments. Therefore, the objective of this study is to look at genetic developments while estimating genotype×environment interactions in post weaning body weight at test of fattening bulls under various beef fattening environments in the eastern part of Germany.

### MATERIAL AND METHODS

The study was based on the data from a beef breeding program carried out during early 1970s to 1990 in the Eastern part of Germany. The program had the objective to increase the quality and quantity of beef production. The design of breeding was a recurrent selection type and the Charolais and the German Beef Simmental were used as main beef breed resources. Details related to the breeding criteria, initiation of the breeding program, origin of experimental animal populations and production environments have been reported elsewhere (Löhrike and Klautschek, 1971; Wollert, 1985; Tilsch, 1986). In this breeding program, primarily selected young bulls were put under performance testing for next step selection followed by progeny testing to make final selection on the basis of

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**Table 1.** Summary of body weight of fattening at the end of test period data set

Variable	Industrial farm (IF)	Breeding farms (BF)	Testing stations (TS)
Mean (kg)	458.11	490.13	459.32
Standard deviation (kg)	45.84	51.62	40.15
Animals (heads)	4,118	5,432	1,4697
Sires (heads)	181	319	1,385
Dams (heads)	-	3,502	-
Number of farms	1	2	6
Year of births	1974-1981	1971-1989	1972-1988

**Table 2.** (Co)variance components and genetic parameters for body weight of fattening bulls at the end of test period at various fattening environments

Parameter	Industrial farm (IF)	Breeding farms (BF)	Testing stations (TS)
(Co) variance			
Residual	IF	1,047.83 (12.94*)	-
	BF	-	1,113.08 (16.11*)
	TS	-	616.08 (7.54*)
Animal	IF	1,036.29 (13.22*)	4.21 (7.30*)
	BF	-	1,119.79 (24.37*)
	TS	-	11.65 (6.66*)
Genetic parameter*	IF	0.500 (0.005*)	0.004 (0.007*)
	BF	-	0.500 (0.006*)
	TS	-	0.013 (0.008*)

\* Genetic correlations are above diagonal and heritabilities are on the diagonal. (\*)=standard error.

their pure-bred (with beef cows) and crossbred (with dairy cows-German Black and White) progeny performance. There were four different levels of the performance testing period viz. (a) 84-365 days, (b) 183-365 days, (c) 155-395 days and (d) 185-395 days. The performance as well as progeny testing of both pure and crossbred beef bulls was carried out under the conditions of industrial farm, breeding farms and testing stations. Body weight data of the fattening bulls at the end of test period (WT-T) under the conditions of industrial farm, breeding farms and testing stations were used for this study.

A summary of used WT-T data set is given in Table 1. The animals were sired by bulls of pure-bred Beef Simmental (FF), Charolais (CH), other beef breeds (sF), 1/2 FF-1/2 CH, 1/4 FF-3/4 CH,  $\geq 1/2$  FF-1/2 sF,  $\geq 1/2$  sF-1/2 FF, 1/2 sF-unknown sF,  $\geq 1/2$  FF-1/2 sF crossbred,  $\geq 1/2$  FF-1/2 CH,  $\geq 1/2$  FF-1/2 (sF cross+CH cross),  $\geq 1/2$  CH-1/2 FF crossbred,  $\geq 1/2$  sF-1/2 CH crossbred,  $\geq 1/2$  sF-1/2 (FF crossbred+CH crossbred),  $\geq 1/2$  FF-1/2 unknown cross of sF. Other beef breeds included continental European beef breeds such as Limousin, Chianina and Piemontese. However, progenies of the first four sire genotypes formed major part (96.5%) of the data set.

The original data were checked for animals' pedigree and performance. Pedigree of animals in the breeding farms was complete while that for industrial farm and testing stations had only their sires known. Any abnormal data were deleted from the data set.

For present study, the WT-T measures on animals in industrial farm, breeding farms and testing stations were

considered as three separate traits denoted respectively as WT-T1, WT-T2 and WT-T3. Preliminary fixed model analyses were undertaken with the GLM Procedure (SAS, 1996) to identify significant fixed effects to be included in the later mixed model analyses. The genetic groups were assigned only for animals with missing genetic relationships following Westell et al. (1988). Since animals had predominantly crossbred genetic make-up, analyses were carried out using data from all animals (pure and crossbred). (Co) variances and genetic parameters were estimated by restricted maximum likelihood method (REML), Patterson and Thompson (1971) and breeding values were estimated by best linear unbiased prediction, BLUP (Henderson, 1975) using a multi-trait animal model. For REML, VCE (Groeneveld, 1994) and for BLUP, PEST (Groeneveld et al., 1990) was used. The genetic group coefficients were incorporated in the mixed model equations by using group option in the animal model analyses. The animal model used to describe each of trait was:

$$y_{ijkl} = F_i + B_j + b(A_{ijk} + \bar{A}) + a_i + e_{ijkl}$$

where,  $y_{ijkl}$  is an observation of WT-T

$F_i$  is the fixed effect of farm

$B_j$  is the fixed effect of year of birth of animal

$b(A_{ijk} + \bar{A})$  is the fixed effect of age of animal in days (co variable)

$a_i$  is the random additive genetic effect of animal with variance  $\sigma_a^2$  and

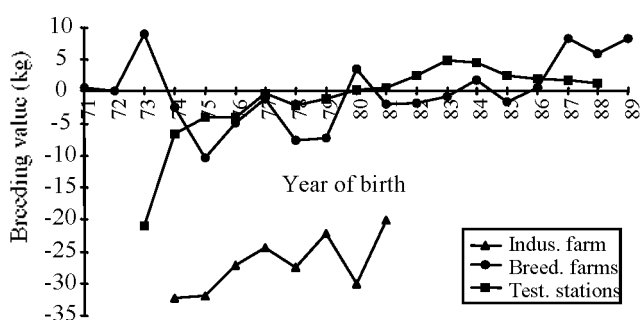
$e_{ijkl}$  is the residual with variance  $\sigma_e^2$ .

**Table 3.** Genetic developments in body weight (kg) of fattened bulls at the end of test period by animal, sire and dam at various fattening environments

By	Regression <sup>1</sup> of breeding values on year of birth		
	Industrial farm (IF)	Breeding farms (BF)	Testing stations (TS)
Animal	1.38 <sup>a</sup> (0.16)	0.64 <sup>b</sup> (0.08)	0.59 <sup>b</sup> (0.03)
Sire	0.44 <sup>a</sup> (0.07)	0.95 <sup>b</sup> (0.12)	0.93 <sup>b</sup> (0.12)
Dam	0.67 <sup>a</sup> (0.04)	0.54 <sup>a</sup> (0.07)	0.14 <sup>b</sup> (0.04)

<sup>1</sup> all estimates statistically significant ( $p < 0.001$ ), regression coefficients with uncommon superscripts along the row differ significantly ( $p < 0.05$ ).

<sup>2</sup> The figure in the parentheses is standard error of the regression.



**Figure 1.** Genetic trends for body weight of fattening bulls at the end of test period under industrial farm, breeding farm and testing station.

Because of having only one level and non-significant ( $p > 0.05$ ) effect of farm on the WT-T data respectively under the conditions of industrial farm and breeding farms, the term  $F_1$  was not fitted in the animal model for WT-T1 and WT-T2. To find the degree of genetic developments for WT-T under different environmental conditions, the BLUP derived breeding values for WT-T under industrial farm, breeding farms and testing stations were regressed on the year of birth of animals, sires and dams. The differences in regression coefficients among environments were tested by t-test. The genetic correlations for WT-T among various fattening environments were regarded as estimates of GEI in the present study.

## RESULTS AND DISCUSSION

Estimates of (co)variances, heritabilities and genetic correlations are shown in Table 2. Heritabilities for WT-T were nearly identical in three fattening environments. For both industrial farm and breeding farms,  $h^2$  was 0.50 and for testing stations  $h^2$  was 0.53. (Co) variances and genetic correlations are above diagonal, variances and heritabilities are on the diagonal. (\*)=standard error.

### GENETIC DEVELOPMENT

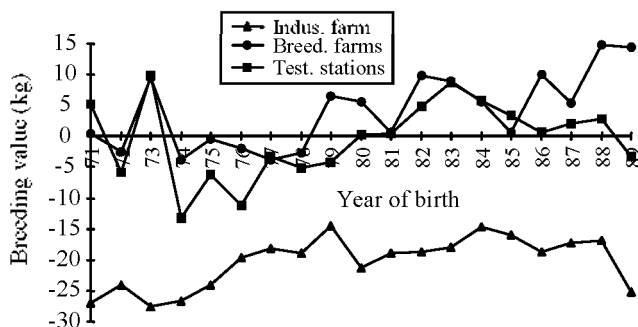
The genetic developments (i.e. genetic gain or genetic progress) measured as coefficient of regression of breeding values on the year of birth of animals, sires and dams under industrial farm, breeding farms and testing stations are

presented in Table 3. All regression coefficients were statistically significant ( $p < 0.001$ ). Moreover, many of the differences in regression coefficients among environments as shown in Table 3 were statistically significant ( $p < 0.05$ ).

The annual rate of genetic developments for WT-T estimated by animal under industrial farm (1.38 kg per) was double and more than double compared with those under breeding farms (0.64 kg) and testing stations (0.59 kg). It shows that progenies in the industrial farm developed very well for WT-T and this was probably because of their hybrid ( $F_1$  of beef×dairy) genetic make-up. Figure 1 shows these genetic trends at various fattening environments. In Figure 1, difference between industrial and breeding farm bulls and that between industrial and testing station bulls could be due to their 50% genetic make-up of dairy origin. Similar differences in fattening ability of beef×dairy and beef×dual purpose cattle has been reported by Frelch et al. (1998) under the conditions of Czech Republic. These results are also in agreement with Korver et al. (1987). In the same fattening environment (industrial farm), the annual rates of genetic development by animal and sire were 1.38 and 0.44 kg respectively. The rate of gain by animal is believed to be contributed by both additive and non-additive gene effect (1.38 kg) while that by the sire was composed only of additive gene effect. The rates of genetic development in breeding farms and testing stations by animal were 0.64 and 0.59 kg respectively and the same by sire were 0.95 and 0.93 kg respectively. In both cases, the differences in genetic developments between breeding farms and testing stations were statistically non-significant ( $p > 0.05$ ). It could probably be due to that males and females with the same amount of selection pressure were used to produce fattening bulls in these two environments.

The rates of genetic development by sire in industrial farm, breeding farms and testing stations were 0.44, 0.95 and 0.93 kg respectively and these trends are shown in Figure 2. The rate in industrial farm is half of that in breeding farms and testing stations. It could be due to that industrial farm sires are sharing only half of the genetic progress being attained among sires of breeding farms and testing stations.

The regression coefficients of genetic development by dam were respectively 0.67, 0.54 and 0.14 kg respectively under industrial farm, breeding farms and testing stations.



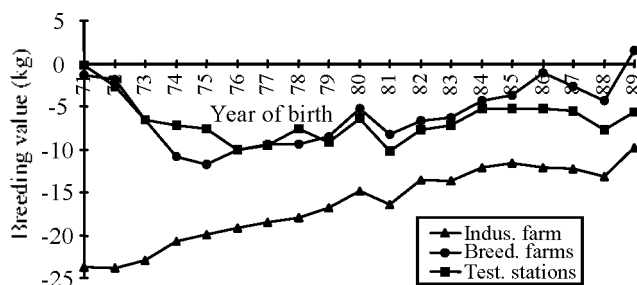
**Figure 2.** Trends in genetic development by sires for body weight of fattening bulls at the end of test period.

The corresponding trends are shown in Figure 3. The WT-T development was highest in industrial farm dams and lowest in testing station dams. In Figures 1 to 3, positive genetic trends were evident. However, the scale of trends and value of intercepts for the regression lines indicate that with further generations of selection there could be overlapping of trend lines from three fattening environments.

#### GENOTYPE×ENVIRONMENT INTERACTIONS

The genetic correlations for WT-T between industrial farm and breeding farms, between industrial farm and testing stations and between breeding farms and testing stations were respectively 0.004, 0.004 and 0.013 (Table 2). These very low estimates of genetic correlations were largely based on genetic relationships developed through beef sires which were tested in three fattening environments. A total of 1,575 sires used as common mainly contributed to develop genetic links among progenies (animals) in the three fattening environments. These correlations indicate that WT-T was an independent trait in the environmental conditions of industrial farm, breeding farms and testing stations and as a result, selection of candidates across fattening environments will change their ranking. Under this situation, genetic evaluations of beef sires on the basis of either performance and/or progeny testing in one environment may not be adequate predictors of progeny performance in another environment.

The observed differences in genetic developments coupled with low estimates of genetic correlations among WT-Ts under three fattening environments might have occurred through differences in feeding and management system, housing system, age of the fattening hybrids at admission and at the start of the test period, exposure to diseases with poor health controls. However, using earlier data material from the same population, Klautschek (1989) defined differences in environmental conditions to be small, medium and large between the farms and found the existence of genotype x environment interactions for daily



**Figure 3.** Trends in genetic development by dams for body weight of fattening bulls at the end of test period.

weight gain on test and yearling weight. Similar genotype x environment interactions for 365 d weight of Angus, Brahman and reciprocal-cross animals (Brown et al., 1993), for 205 d and end-of-test weight of Hereford bulls (Pahnish et al., 1985) under USA conditions, for postweaning liveweight gains of young bulls (Schoeman and Jordann, 1998) under Australian conditions were reported.

In the present study, body weight of fattening bulls at the end of test period (WT-T) measured at three different environments was regarded not as one character but as three. Analyses revealed very low estimates of genetic correlations which on the contrary expresses very high scale of genotype x environment interactions for WT-Ts among fattening environments (Table 2). The differences in the rate of genetic developments for WT-T in three beef fattening environments (Table 3 and Figure 1 to 3) indicate that it can not be used as one trait to rank and select beef bulls for breeding purposes.

Both pure-bred and crossbred information were utilised to estimate (co)variance components, genetic parameters, genetic developments and genotype-environment interactions. Ideally, pure-bred and crossbred performance should be treated as genetically different traits because of evidence of empirical differences between pure and crossbred genetic parameters (Wie et al., 1991). Therefore, combined analysis carried out in the present study might have given to a certain degree of biasness in the genetic parameters as well as GEI estimates. Another limitation for this study could be not including herd-year-season effect in the used animal model as suggested by Engellandt et al. (1998) for the progeny field test of German Simmental. However, due to only one farm in the industrial fattening situation and small sub-class sample sizes in other situations it could not be considered in the used animal model.

Nevertheless, since the scale of genetic correlations were very low and many of the differences in genetic developments among fattening environments were statistically significant, then WT-T in three fattening environments represent completely different traits meaning that these traits are not controlled by the same set of genes.

Finally, since the final aim of all beef crossbreeding systems is to produce high quality crossbred fattening animal, results of present study therefore indicate that the breeding goal should be defined at the crossbred or industry level and for that matter environment-specific genetic evaluation and bull selection program has to be adopted.

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