

# PARTITIONING VARIANCE ON LITTER TRAITS OF *TRIBOLIUM CASTANEUM*<sup>1</sup>

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## SUMMARY

Litter traits were clarified as the measurements on the multiple individuals in the litters rather than litter dams. The genetic variance on litter traits was partitioned into ones of litter dam and service sire, and covariance between female and service sire. The estimations of the variance and covariance were demonstrated by the analysis on 773 observations on number of larva in *Tribolium castaneum* pedigree individuals.

**Key Words:** Litter, Covariance, Heritability, *Tribolium castaneum*

## INTRODUCTION

Searching suitable model for litter traits has been an effort to increase the accuracy of genetic evaluation for the improvement of reproduction in livestock. Litter traits are different from the traits that were measured on a single individual. For example, milk yield is measured on individual cow. Whereas, litter traits, e.g. litter size and litter weight, are measured on the multiple individuals in a litter. The performance of a litter is genetically determined by the litter dam and the sire of litter (the service sire of the female). Conventionally, litter traits were treated as the measurements on litter dams. The influence of service sire was ignored in most of situations. (Southwood 1990, Hoeschele 1991, Roehle 1993). However, significant contributions of service sire were founded recently. In pigs, service sire effect accounts for 1 to 2 % of total variation of pig born alive (See 1993).

This paper is to investigate the genetic covariance between service sire and litter dam, which could be another source of the variation of litter traits in some species. The estimations of the covariance and covariance were demonstrated by using the data on *Tribolium castaneum*.

## MATERIALS AND METHODS

**Data.** The data on litter trait were provided by the *Tribolium castaneum* experiment at the Institute of Animal Science, Chinese Academy of Agricultural Sciences. The *Tribolium*

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population of *Tribolium castaneum* was originally from Beijing Agricultural University (Zhang 1989). The culture medium consisted of 95 % whole-wheat flour and 5% dried brewer's yeast. The beetles were maintained at 32 °C and 70 % relative humidity.

Eight genetic lines were used in the experiment. Each genetic line was consisted with 20 random mating groups; each formed one male and one female. The male and female were put together for 24 hours for mating and producing eggs. The eggs laid by each mating group during this time were collected and developed afterward. The number of pupa at 21st day was recorded for each mating group. The experiment was carried out over 7 generations. Pedigrees were informative for all individuals except ones in base population. This information was cooperated in the relationship among individuals. The mean and standard error of the number of larva were 3.8 and .32 respectively. Table 1 showed the size and structure of the data.

**Table 1. Distribution of records of number of larva on genetic lines and generations**

Generations	Genetic lines								Total
	1	2	3	4	5	6	7	8	
1	7	8	5	4	8	9	9	10	60
2	5	12	8	9	10	23	11	12	89
3	5	13	10	14	12	13	12	10	89
4	17	16	15	15	19	17	14	15	128
5	18	17	19	16	17	18	18	15	138
6	17	16	19	17	18	18	17	16	138
7	14	17	20	15	19	16	13	17	131
Total	83	99	96	89	103	114	94	95	773

**Model.** Three models were used in the analysis. The full model involved fixed effect, random genetic effect of service sire and litter dam. The two reduced models (litter dam model and service sire model) excluded the effect of service sire and the effect of litter dam from the full model respectively. The full model was

$$Y = Xb + Z_1u_1 + Z_2u_2 + e$$

where,  $y$  was a vector of 773 observations on number of larva;  $b$  was a vector of 56 fixed effect of subclass of 8 genetic lines and 7 generations;  $u_1$  was a vector of random genetic effect of service sire with length of 773;  $u_2$  was a vector of random genetic effect of litter dam with length of 773;  $X$  and  $Z_1$  and  $Z_2$  were incidence matrices corresponding to  $b$ ,  $u_1$  and  $u_2$ ;  $e$  was a vector of random residual effects contributing to  $y$ . It was assumed that  $E(y)=Xb$ , and that the expectation of  $a$  was null. The (co)variance matrix of  $u_1$  and  $u_2$  was:

$$\text{Var} \begin{pmatrix} u_1 \\ u_2 \end{pmatrix} = \begin{bmatrix} G_{11} & G_{12} \\ G_{21} & G_{22} \end{bmatrix} \\ = \begin{bmatrix} A_{11} \sigma_1^2 & A_{12} \sigma_{12} \\ A_{21} \sigma_{12} & A_{22} \sigma_2^2 \end{bmatrix}$$

where,  $\sigma_1^2$  was the genetic variance of service sire;  $\sigma_2^2$  was the genetic variance of litter dam;  $\sigma_{12}$  was the genetic covariance between service sire and litter dam;  $\sigma_e^2$  was residual variance;  $A_{11}$  was relationship matrix among service sires;  $A_{22}$  was relationship matrix litter dams;  $A_{12}$  was relationship matrix between service sires and litter dams;  $A_{21}=A_{12}$ . The covariance between  $u_1$  and  $e$  and covariance between  $u_2$  and  $e$  were assumed be null. The variance of residual effect was assumed be  $\text{Var}(e)=I \sigma_e^2$ . The mixed normal equation is:

$$\begin{bmatrix} X'X & X'Z_1 & X'Z_2 \\ Z_1'X & (Z_1'Z_1 & Z_1'Z_2) \\ Z_2'X & (Z_2'Z_1 & Z_2'Z_2) \end{bmatrix} + \begin{bmatrix} A_{11}\sigma_1^2 & A_{12}\sigma_{12} \\ A_{21}\sigma_{12} & A_{22}\sigma_2^2 \end{bmatrix}^{-1} \sigma_e^2 \begin{bmatrix} b \\ u_1 \\ u_2 \end{bmatrix} = \begin{bmatrix} X'y \\ Z_1'y \\ Z_2'y \end{bmatrix}$$

The variance and covariance components  $\sigma_1^2$ ,  $\sigma_2^2$  and  $\sigma_{12}$  were estimated by using DMU package (Madsen, Jensen and Thompson, 1994). The convergence criterion was  $10^{-8}$ .

**Heritability.** The total variance of litter trait under alternative models were as following:

$$\begin{aligned} \sigma_p^2 &= \sigma_1^2 + \sigma_2^2 + 2\sigma_{12} + \sigma_e^2 && \text{(Litter model)} \\ &= \sigma_2^2 + \sigma_e^2 && \text{(Litter dam model)} \\ &= \sigma_1^2 + \sigma_e^2 && \text{(Service sire model)} \end{aligned}$$

Heritability on litter, litter dam and service sire were defined as the proportion of corresponding genetic variance over the totals.

$$\begin{aligned} h^2 &= \sigma_1^2 + \sigma_2^2 + 2\sigma_{12} / \sigma_p^2 && \text{(Litter heritability)} \\ &= \sigma_2^2 / \sigma_p^2 && \text{(Litter dam heritability)} \\ &= \sigma_1^2 / \sigma_p^2 && \text{(Service sire heritability)} \end{aligned}$$

## RESULTS AND DISCUSSION

Estimates of variance and covariance for the number of larva were shown in Table 2. The contribution of litter dam was greater than that of service sire. Whereas service sire effect accounted 2% and 13% of total variance for number of pupa under service sire model and full model respectively. Estimates of the heritabilities under alternative models were shown in Table 3. The conventional heritabilities on litter traits resulted from literature are actually litter dam heritabilities. This finding indicated that the model for genetic evaluation on litter traits should

be different from the traits that are measured on individuals. By capitalizing on genetic differences of litter traits, the improvement of reproductive efficiency through selection can be speeded.

**Table 2. Estimates of variance components for litter trait**

Model	$\sigma_1^2$	$\sigma_2^2$	$\sigma_{12}$	$\sigma_e^2$
Full	4.6	19.7	-9.5	35.9
Litter dam	NA	16.8	NA	44.8
Service sire	4.8	NA	NA	45.4

**Table 3. Heritability on litter, litter dam and service under alternative models**

Model	Heritability		
	Litter	Litter dam	Service sire
Full	.13	.48	.11
Litter dam	NA	.27	NA
Service sire	NA	NA	.10

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