

## **Genetic Parameters of Stayability of Different Categories of Dairy Animals**

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### **Summary**

The present investigation deals with the study of some genetic aspects of longevity of dairy animals in the herd. This aspect has been studied through the estimation of heritability of stayability, a term related to longevity, at different orders of lactation as well as genetic correlation between stayabilities at two different orders of lactation. The application, of the procedures studied, are made on the data collected at various Military Dairy Farms for different crossbreds, local breed of dairy cattle (Red Sindh) and graded buffaloes. From the results, different conclusions are drawn for different categories of animals. On the basis of the results it is concluded that probably there are some common genes with similar actions during the initial period of stayability of dairy animals.

*Key words* : Stayability, probability of survival, heritability of stayability and genetic correlation between stayabilities.

### **Introduction**

The concept of longevity in broad sense in dairy animal is mainly related to causes and components of the culling process which involves aptitude of an animal to remain productive in the herd. This aptitude along with culling which includes both voluntary and involuntary disposal has been termed as stayability or survivability. The causes of voluntary disposal are mainly low production, milking characteristics and general health etc. whereas the problems relating to reproduction, diseases and mortality are associated with the involuntary disposal. The concept of stayability in terms of probability of survival has been defined in detail by Narain and Bhatia [5] and Bhatia [1] by using various non-parametric techniques. Bhatia *et al* [2] further examined the relationship of this

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probability of survival with number of explanatory variables affecting the culling process using a logistic model. From this relationship study and as well as from other studies, it has been seen that stayability is highly related with milk yield. The consequence of this relationship is a strong correlated response for stayability on account of artificial selection on milk yield. In addition to this indirect effect of selection, an automatic selection on longevity always exists because long lived cows leave more progeny for replacement than cows culled in first and second lactations. It is thus expected that stayability is subjected to both natural and artificial selection at different lactations and therefore demands a through study on genetic and phenotypic trends. Since the stayability at the phenotypic level is expressed as an all-or-none manner, the conventional techniques of partitioning the total phenotypic variance of quantitative trait into genetic and environmental components of variation can not be applied directly. Further, genetic studies of all-or-none traits are facilitated by assuming a threshold model. This multifactorial model assumes an underlying continuous variable being the sum of many genetic and environmental effects. This therefore advocates that stayability will also have both genetic and non-genetic effects. With this in mind the present investigation deals with the study of some genetic parameters of stayability for drawing the inference about the inheritance of this trait. The parameters studied are heritability of stayability at different orders of lactation as well as genetic correlation between stayabilities at two different orders of lactation. The application of the procedures studied are made on the data collected at various Military Dairy Farms for different categories of dairy animals.

## 2. *Material and Methods*

The data for the present study have been taken from the breeding records of animals maintained at 13 Military Dairy Farms spread throughout the country for the period of about 40 years. From these farms, data for graded buffaloes, Red Sindhi (local breed of cattle) and nine categories of crossbreds with level of exotic inheritance ranging from 6.25% (called as 1/6ths crossbreds) to 87.5% (called as 7/8th crossbreds) are compiled for carrying out analysis on the genetic aspects of survival. From this data, the information for not only production characteristic but also the information on various other reproduction and survival traits of the animals at different orders of lactation are taken into account. The number of animals for different categories of animals for which

survival data are available varies from 145 (1/16ths crossbreds) to 761 (graded buffaloes). The rate of decline in the number of surviving animals differs for various categories of animals. For the category, half-breds (50% level of exotic inheritance) some animals are found to be retained for a quite long period to the extent of 15 lactations whereas for the category 1/16ths, animals are retained only upto 10 lactations. However number of animals for various categories becomes very small after about fifth and sixth lactations. Although in the present set up, the data available are from daughters having the information on their sires and dams but since the number of daughters available for each of the sire-dam family are very small, so the data used for the estimation of the genetic components are according to sire families only and dam's information has not been taken into consideration. The methods applicable to the present set up of the data for the estimation of heritability of stayability or survival and genetic correlation between two consecutive survival traits are described below.

## 2.1 Heritability of stayability or survival ( $h_p^2$ )

### 2.1.1 First Method

Although this method utilises the concept of regression of genotype on phenotype but in the present situation strictly speaking the method depends upon the intra-class correlation coefficient.

Let there be  $s$  sires in a given herd with  $i$ -th sire having  $n_i$  daughters in the first lactation such that  $n_i \geq 5$  for all  $i = 1, 2, \dots, s$ . Suppose the number of daughters of the  $i$ -th sire surviving to second lactation is  $a_i$  for  $i = 1, 2, \dots, s$ . This means that for  $i$ -th sire ( $n_i - a_i$ ) daughters were culled after the first lactation. An estimate of the phenotypic value of the overall survival to second lactation ( $\bar{p}$ ) in the herd will then be given by

$$\bar{p} = \frac{\sum_{i=1}^s a_i}{\sum_{i=1}^s n_i}$$

Following the technique used by Robertson and Lerner [6] in the case of poultry, we can consider, for the  $j$ -th daughter of the  $i$ -th sire ( $i = 1, 2, \dots, s$ ;  $j = 1, 2, \dots, n_i$ ) a random variable  $y_{ij}$  which takes the value one if  $j$ -th daughter survives to second lactation and takes

the value zero if she does not survive to the second lactation. We can perform an analysis of variance of  $y_{ij}$  with two sources of variation as between sires (B) with  $(s-1)$  d.f. and within sires (W) with  $(\sum n_i - s)$  d.f. with an ultimate goal to obtain an estimate of the component of variance due to the differences between sires similar to the situation of continuously distributed variables. The analysis of  $y_{ij}$  and expectation of mean squares for different components in the present situation can be found by including  $s_i$ , the effect of the  $i$ -th sire affecting the survival of his daughters which is treated as a random effect with mean zero and variance as  $\sigma_s^2$  and  $e_{ij}$ , the random effect for the survival of  $j$ -th daughter belonging to  $i$ -th sire. Like  $y_{ij}$ , here  $e_{ij}$  is a Bernoullian variable with parameter  $p$ . That is  $e_{ij}$  takes value one with probability  $p$  and takes the value zero with probability  $(1-p)$ . We then have  $E(e_{ij}) = p$  and  $V(e_{ij}) = p(1-p)$ . Under this situation, the expectation of sum of squares is  $E(W) = (N-s) p(1-p)$  and  $E(B) = (s-1) [p(1-p) + k\sigma_s^2]$  where

$N$  is the total number of daughters =  $\sum_{i=1}^s n_i$  and

$$k = \frac{1}{s-1} \left[ \sum_{i=1}^s n_i - \sum_{i=1}^s \frac{n_i^2}{N} \right]$$

Thus we get the expected value of the mean sum of squares between sires as

$$E \left[ \frac{B}{s-1} \right] = p(1-p) + k\sigma_s^2$$

Taking an estimate of  $p$  by the overall phenotypic survival

$$\bar{p} = \frac{\sum a_i}{\sum n_i} \text{ we get an estimate of } \sigma_s^2 \text{ as}$$

$$\hat{\sigma}_s^2 = \frac{B - \bar{p}(1-\bar{p})(s-1)}{k(s-1)}$$

Now we know that variance of the means of the sire groups i.e.  $\sigma_s^2$  is nothing but covariance between half sibs and as such equal to one quarter of the genetic variance. Thus for  $\sigma_g^2$ , the genetic variance we have  $\sigma_s^2 = \frac{1}{4} \sigma_g^2$  or  $\sigma_g^2 = 4 \sigma_s^2$

Now for developing a relationship between heritability of survival ( $h_p^2$ ), genetic variance of survival ( $\sigma_g^2$ ), and overall phenotypic survival value ( $\bar{p}$ ) in the present situation, we assume genotypic values for survival of  $N$  individuals (all the daughters of different sires with phenotypic values as  $y_{ij}$ ) be  $g_1, g_2, \dots, g_N$  with overall mean genetic value as  $\bar{g} = \frac{1}{N} \sum_{m=1}^N g_m$  and variance  $\sigma_g^2 = \sum_{m=1}^N \frac{g_m^2}{N} - \bar{g}^2$ .

The phenotypic value for the survival of the  $m$ -th individual is  $g_m + e_m$  where  $e_m$  is the environmental component. Since the expected values of  $\sum_{m=1}^N e_m$  is equal to zero so the mean genotypic value of the population is equal to mean phenotypic value  $\bar{g} = \bar{p}$ . Incidentally in our case the mean phenotypic value lies between 0 and 1. The mean genotype of survivors which is designated as  $\bar{g}_1$  to distinguish it from the mean genotype of all the individuals ( $\bar{g}$ ) is then given by

$$\bar{g}_1 = \frac{\sum_{m=1}^N g_m (g_m + e_m)}{\sum_{m=1}^N (g_m + e_m)}$$

$$\text{or } \bar{g}_1 = \frac{\sum_{m=1}^N g_m^2 + \sum_{m=1}^N g_m e_m}{\sum_{m=1}^N g_m + \sum_{m=1}^N e_m}$$

Under the assumptions  $\sum_{m=1}^N g_m e_m$  and  $\sum_{m=1}^N e_m$  both equal to zero

i.e. there is no correlation between genotype and environment and mean of environment deviations is zero we get

$$= \frac{\sum_{m=1}^N g_m^2}{\sum_{m=1}^N g_m} = \frac{N(\bar{g}^2 + \sigma_g^2)}{N\bar{g}} = \frac{(\bar{g}^2 + \sigma_g^2)}{\bar{g}}$$

Taking  $\bar{g} = \bar{p}$ , we get

$$= \frac{(\bar{p}^2 + \sigma_g^2)}{\bar{p}}$$

The expected difference in the survival over the two periods of time is thus given by

$$(\bar{g}_1 - \bar{g}) = \frac{(\bar{p}^2 + \sigma_g^2)}{\bar{p}} - \bar{p} = \frac{\sigma_g^2}{\bar{p}} \quad (1)$$

Now utilising the concept of regression of genotype on phenotype for estimation of heritability, we work out in the present situation regression of later lactation genotypic survival on the earlier phenotypic survival. This of course will not give us the true measure of heritability but an upper limit of heritability i.e. repeatability. As such denoting this repeatability by  $h_p^2$  as our guess estimate of heritability of survival by the following regression equation.

$$\left( \begin{array}{l} \text{Mean geno} \\ \text{typic value} \\ \text{of survivors} \end{array} - \begin{array}{l} \text{Overall} \\ \text{genotypic} \\ \text{mean} \end{array} \right) = \text{Regression} \left( \begin{array}{l} \text{of genotypic} \\ \text{on phenotypic} \\ \text{survival} \end{array} \right) \left( \begin{array}{l} \text{Mean pheno} \\ \text{typic value} \\ \text{of survivors} \end{array} - \begin{array}{l} \text{Overall} \\ \text{phenotypic} \\ \text{mean} \end{array} \right)$$

$$(\bar{g}_1 - \bar{g}) = h_p^2 (1 - \bar{p})$$

From (1) above

$$\frac{\sigma_g^2}{\bar{p}} = h_p^2 (1 - \bar{p})$$

or 
$$\hat{h}_p^2 = \frac{\hat{\sigma}_g^2}{\bar{p}(1 - \bar{p})}$$

Putting back in terms of  $\hat{\sigma}_s^2$  we get

$$\hat{h}_p^2 = 4 \frac{\hat{\sigma}_s^2}{\bar{p}(1 - \bar{p})}$$

$$= \frac{4 \left[ \frac{B - \bar{p}(1 - \bar{p})(s - 1)}{\bar{p}(1 - \bar{p})} \right]}{k(s - 1)}$$

$$= \frac{4 \left[ \frac{B}{\bar{p}(1-\bar{p})} - (s-1) \right]}{k(s-1)}$$

The data on survival according to sire group can also be looked upon as (2×s) contingency table giving the number of survivors and non-survivors of each of the s sire groups. The heterogeneity chi-square for this table is

$$\chi^2 = \frac{B}{\bar{p}(1-\bar{p})} \text{ with } (s-1) \text{ d.f.}$$

In terms of this  $\chi^2$ , the heritability can then be expressed as

$$h_p^2 = \frac{\chi^2 - (s-1)}{k(s-1)}$$

Since  $E(\chi^2)$  is (s-1), this shows that  $h_p^2$  depends upon the excess of the observed  $\chi^2$  above its expected value. Cochran (3) has shown that for small numbers the expected value of  $\chi^2$  is slightly greater than (s-1). The exact expression of this expected value with a constant number n in each of s groups is given by

$$E(\chi^2) = (s-1) + \frac{1}{n} \left[ 1 - \frac{1}{s} \left( 1 - \frac{1}{n} \right) \right]$$

In the present case, however, n is required to be replaced by k in order to take into account the different number of observations in the various sire-groups. It is also possible to give some estimate of the standard error of the estimate of heritability, since the method used above is similar to the determination of the intra-class correlation in the case of continuous variation. Fisher (4) has shown that in the case similar to that discussed above and using the same symbols,

$$\sigma_t = [1 + (n-1)t] (1-t) \left( \frac{2}{n(n-1)(s-2)} \right)^{1/2}$$

where t denotes the intra-class correlation and n is to be replaced by k in the present case. Since heritability is equal to 4t the standard error of the estimate of heritability is given by  $4\sigma_t$ , which is only a rough estimate.

### 2.1.2 *Second Method*

The above method involves conducting the analysis of variance for a binomial variable and is therefore not strictly valid, since in this case the variance is not independent of mean. Further, it is also noted that the heritability obtained by using the analysis of variance on the raw binomial data is the heritability on the binomial or p-scale. Heritabilities determined on the p-scale however cannot be compared between populations unless they have the same average incidence of the trait under consideration. This is because a fundamental requirement of analysis of variance that the error variances be equal in all subgroups and be independent of the mean, is not met for binomial data with only two classes. As such it is desirable to use an angular transformation which makes the variance independent of mean and therefore justifies the use of analysis of variance technique. This method is therefore, based on this logic and following Snedecor and Cochran (7) the ones and zeros in the various sire groups are converted to proportions and then the proportions are transformed to angles by applying arc sine transformation and thereafter the usual analysis of variance technique meant for half sibs is applied on angles to estimate the heritability. Further, we have assumed that in our situation observations i.e. probability of survival are influenced by genetic component (sire component) only in addition to random error component. But in practice this is not true and in fact the survival of an animal besides sire component also depends upon by certain non-genetic causes such as herd environment and feeding conditions which include broadly the farm effect, period effect and season of calving effect. It is therefore desirable that before going for the estimation of heritability of survival from the angles by half-sib analysis, the angles must be adjusted for the various non-genetic causes.

### 2.2 *Genetic Correlation between stayability at two different orders of lactation*

In order to study the relationship between the culling policies at different lactations the genetic correlation between stayabilities i.e. probabilities of survival at two different lactations are to be worked out. These can be estimated by following the usual half-sib analysis technique.

### 3. Results and Discussion

Using the methodology discussed above, the heritability of stayability or survival has been calculated first of all by two methods: (a) by regression of genotype on phenotype or heterogeneity chi-square and (b) by using angular transformation. Along with the heritability of stayability to different orders of lactation by the two methods, their standard errors have also been worked out. From the results which are presented in Table 1, firstly it is concluded that for a particular order of lactation, the values of heritabilities obtained by the two methods do not differ markedly. It is further observed that for almost all the eleven categories of animals, the trend of the estimates of heritability to different lactation is approximately an increasing one in the initial few orders of lactation and thereafter no definite trend is observed. The increasing trend for different categories of animals is visualised up to 4th and 5th lactation. This increase in the heritabilities to first few lactations may be due to the rapid reduction of animals surviving to successive lactations and increase in genetic correlation of survivors. The reasons for not getting a definite trend in the later lactations, that the various causes of culling and milk yield might have different genetic elements at different orders of lactation. If we assume that either the causes other than yield have no genetic element or are controlled by same set of genes as that of lactation milk yield in different culling processes, then to some extent we can predict the expected trend of the heritability of stayability to different lactations. In practice none of the two assumptions are satisfied, and hence no trend can be predicted. The other reasons for not getting any trend are possibly fewer number of observations on which estimates are based along with their high standard errors in the later lactations.

Further, since survival is related to fitness so the heritability of stayability is expected to be very low but in our case the estimates are very high and sometimes yield an inadmissible estimates. The reasons for not getting a precise and appropriate estimates of heritabilities are (a) inflation of between sire- component of variance to a large extent by various non-genetic factors such as farms, periods, seasons etc. as the progenies of sires are distributed over a long period of time and also over different Military Dairy Farms having different agro-climatic conditions, and (b) the number of daughters available for different sires are very small. In order to take care of (a) mentioned above, the estimates of the heritabilities of stayability to different orders of lactation for each category of animals are thus worked out by using adjusted angles and are

presented in Table 2. Using the transformed adjusted variables (angles) for probabilities of survival to various lactations, the genotypic and phenotypic correlation between stayability traits of two different lactation have also been worked out and the results are presented in Table of heritabilities of stayability mentioned above. It is observed from Table 2 that the revised estimates (estimates free from non-genetic effects) of heritabilities of stayability are having considerable small values in comparison to the values obtained earlier, but having almost similar trend as that observed for heritabilities of stayability estimated from raw data. Further on examining these estimates of heritability of stayability to different lactations, it is concluded that probably selection for longevity of animals would not be that effective because of the low values of the heritabilities of stayability.

On further seeing the Table 2, it is found that while the phenotypic correlation between probabilities of survival to two consecutive lactations is low, this phenotypic correlation between probability of survival to given lactation and probability of survival to any other lactation decreases as the difference between the two lactations increases. On the other hand this type of behaviour is not noticed for the genotypic correlations between the probabilities of survival to different lactations. From the estimates of genetic correlations for different categories of animals it is concluded that there are some common causes or genes which influence the culling processes in the initial lactations as the genetic correlations in the first five culling processes are seen to be high among themselves. It is also interesting to observe that at many occasions the survival at two points are phenotypically poorly related but because of some common genes or factors they are highly positively genetically correlated. The most probable common cause may be the first lactation milk yield.

## REFERENCES

- [1] Bhatia, V.K., 1984. Some aspects of yield survival relationship in dairy cattle, unpublished Ph.D. Thesis, IARI, New Delhi.
- [2] Bhatia, V.K., Narain, P. and Malhotra, P.K., 1987. Use of logistic models in studying the relationship between all-or-none response variate and other explanatory variables in dairy cattle breeding, IASRI Souvenir on 40th Anniversary of India's Independence., 182-192.
- [3] Cochran, W.G., 1936. The  $\chi^2$  distribution for a Binomial and Poisson series with small expectations, *Annals of Eugenics*, **7**, 207-217.
- [4] Fisher, R.A., 1941. Statistical methods for research workers. Oliver and Boyd, Edinburgh.
- [5] Narain, P. and Bhatia, V.K., 1984. Some aspects of culling patterns in Indian herds of dairy cattle. IASRI Silver Jubilee Souvenir, 161-173.
- [6] Robertson, A. and Lerner, I.M., 1949. The heritability of all-or- none traits: viability of poultry, *Genetics*, **34**, 395-411.
- [7] \*Snedecor, G.W. and Cochran, W.G., 1967. Statistical Methods, Iowa State University Press, Ames, Iowa.

Table 1. Heritabilities of stayability based on raw data to a given lactation for different categories of animals.

Breed	Order of lactation	Heterogeneity Chi-square				Angular Transformation			
		2	3	4	5	2	3	4	5
Graded Buffaloes		0.55	0.67	0.67	0.77	0.56	0.70	0.70	0.84
		(0.13)	(0.14)	(0.14)	(0.15)	(0.13)	(0.14)	(0.14)	(0.15)
Cattle Red Sindhi (Local)		0.28	0.45	0.56	0.64	0.20	0.38	0.47	0.61
		(0.16)	(0.20)	(0.22)	(0.24)	(0.14)	(0.18)	(0.20)	(0.22)
Cattle Crossbreds		0.78	0.34	0.16	0.65	0.86	0.37	0.13	0.70
		(0.35)	(0.28)	(0.24)	(0.33)	(0.35)	(0.28)	(0.23)	(0.33)
1/16		0.14	0.05	0.08	0.12	0.05	0.01	0.03	0.07
		(0.15)	(0.13)	(0.14)	(0.15)	(0.13)	(0.11)	(0.13)	(0.14)
3/16		0.11	0.63	0.84	0.81	0.09	0.67	0.89	0.88
		(0.17)	(0.26)	(0.28)	(0.28)	(0.16)	(0.26)	(0.28)	(0.28)
1/4		0.13	0.47	0.38	0.71	0.13	0.53	0.42	0.77
		(0.14)	(0.18)	(0.17)	(0.21)	(0.14)	(0.19)	(0.18)	(0.21)
3/8		0.40	0.72	0.95	**	0.39	0.79	**	**
		(0.16)	(0.18)	(0.20)		(0.15)	(0.19)		
1/2		0.25	0.69	**	0.96	0.20	0.69	**	**
		(0.12)	(0.17)		(0.15)	(0.12)	(0.17)		
5/8		0.33	0.65	0.99	**	0.33	0.65	0.99	**
		(0.12)	(0.16)	(0.20)		(0.12)	(0.16)	(0.19)	
3/4		0.63	0.99	**	**	0.61	0.99	**	**
		(0.15)	(0.19)			(0.15)	(0.18)		
7/8		0.49	0.51	0.77	**	0.54	0.57	0.91	**
		(0.27)	(0.27)	(0.31)		(0.27)	(0.28)	(0.32)	

\*\* Indicate inadmissible estimates

Figures in parentheses denote standard errors

**Table 2.** Heritability, Phenotypic and Genotypic Correlation of probabilities of survival at different orders of lactations (Based on adjusted angles) for different categories of animals.

Graded Buffaloes				
Order of lactation	2	3	4	5
2	0.14 (0.09)	0.99 (0.01)	0.48 (0.27)	0.24 (0.28)
3	0.58 (0.03)	0.25 (0.10)	0.88 (0.06)	0.70 (0.12)
4	0.39 (0.03)	0.71 (0.02)	0.27 (0.10)	0.96 (0.02)
5	0.28 (0.03)	0.53 (0.03)	0.76 (0.02)	0.42 (0.12)

Red Sindhi (Cattle Local)				
Order of lactation	2	3	4	5
2	0.002 (0.07)	0.41 (0.37)	0.65 (0.53)	**
3	0.57 (0.04)	0.005 (0.09)	**	**
4	0.39 (0.05)	0.70 (0.04)	0.06 (0.11)	0.80 (0.40)
5	0.24 (0.05)	0.43 (0.05)	0.64 (0.04)	0.70 (0.11)

Cattle Crossbreds 1/16				
Order of lactation	2	3	4	5
2	0.67 (0.34)	0.52 (0.21)	0.34 (0.60)	0.68 (0.22)
3	0.49 (0.07)	**	0.34 (0.49)	0.57 (0.23)
4	0.35 (0.08)	0.53 (0.07)	0.10 (0.18)	0.65 (0.46)
5	0.26 (0.08)	0.39 (0.08)	0.68 (0.06)	0.41 (0.29)

Table 2 (Contd.)

Cattle Crossbreds 1/8				
Order of lactation	2	3	4	5
2	0.01 (0.12)	-0.75 (0.70)	**	**
3	0.64 (0.04)	**	-0.91 (0.05)	**
4	0.40 (0.06)	0.66 (0.05)	**	-0.80 (0.11)
5	0.31 (0.06)	0.52 (0.05)	0.78 (0.04)	**

Cattle Crossbreds 3/16				
2	0.04 (0.11)	-0.32 (0.66)	0.58 (0.35)	0.64 (0.40)
3	0.66 (0.05)	0.12 (0.17)	**	0.64 (0.52)
4	0.46 (0.06)	0.69 (0.05)	0.23 (0.20)	0.99 (0.01)
5	0.35 (0.06)	0.52 (0.06)	0.77 (0.04)	0.15 (0.18)

Cattle Crossbreds 1/4				
2	0.12 (0.14)	**	**	**
3	0.61 (0.04)	0.39 (0.17)	**	**
4	0.43 (0.05)	0.70 (0.04)	0.12 (0.14)	**
5	0.33 (0.05)	0.51 (0.04)	0.74 (0.03)	0.28 (0.16)

Table 2 (Contd.)

Cattle Crossbreds 3/8				
Order of lactation	2	3	4	5
2	0.09 (0.12)	0.91 (0.12)	**	0.99 (0.01)
3	0.58 (0.04)	0.17 (0.13)	0.94 (0.05)	0.98 (0.02)
4	0.40 (0.04)	0.70 (0.03)	0.25 (0.14)	**
5	0.28 (0.04)	0.51 (0.04)	0.74 (0.03)	0.29 (0.15)

Cattle Crossbreds 1/2				
2	0.01 (0.09)	**	**	**
3	0.63 (0.03)	0.23 (0.12)	**	**
4	0.41 (0.04)	0.66 (0.03)	0.34 (0.13)	**
5	0.26 (0.04)	0.46 (0.04)	0.69 (0.03)	0.06 (0.09)

Cattle Crossbreds 5/8				
2	0.13 (0.09)	0.99 (0.02)	**	0.76 (0.13)
3	0.62 (0.03)	0.22 (0.10)	**	**
4	0.40 (0.04)	0.66 (0.03)	0.28 (0.11)	0.99 (0.04)
5	0.27 (0.04)	0.46 (0.03)	0.70 (0.03)	0.40 (0.13)

Table 2 (Contd.)

Cattle Crossbreds 3/4				
Order of lactation	2	3	4	5
2	0.09 (0.09)	0.89 (0.10)	0.85 (0.12)	0.96 (0.05)
3	0.58 (0.03)	0.21 (0.10)	0.91 (0.06)	0.67 (0.26)
4	0.36 (0.04)	0.64 (0.03)	0.21 (0.10)	**
5	0.23 (0.04)	0.42 (0.04)	0.72 (0.03)	0.10 (0.09)

Cattle Crossbreds 7/8				
2	0.19 (0.21)	**	0.13 (0.69)	-0.37 (0.36)
3	0.58 (0.06)	**	0.96 (0.17)	-0.52 (1.26)
4	0.21 (0.07)	0.44 (0.07)	0.24 (0.22)	-0.60 (0.24)
5	0.05 (0.07)	0.28 (0.07)	0.52 (0.06)	**

Note : \*\* Indicate inadmissible estimates. Figures in parentheses denote standard errors. Diagonal terms are heritabilities of stayability or survival. Values below diagonal are phenotypic correlations. Values above diagonal are genotypic correlations.