A STATISTICAL AND GENETICAL STUDY OF BOVINE LEUKEMIA

Un estudio estadístico y genético de la leucemia bovina

Statistische und genetische Untersuchungen der Rinderleukose

L. K. ERNST *
P. G. KLABUKOV *
D. V. KARLIKOV *
R. O. GRINBERG *

An interest for genetic aspects of bovine leukemia has been shown by research workers almost as soon as the discovery of this disease was made (1). Research reports in this field were reviewed by ENGELBRETH-HOLM (2), WIESNER (3) and others. Up to now there have been several viewpoints on the nature of hereditary transmission of resistance to bovine leukemia. Hereditary predisposition to disease is transmitted according to a monogenic mode with three pairs of alleles the susceptibility to different forms is thought to be due to dominant ones (4, 5). According to other investigators the resistance is controlled by a dominant allele at single locus (6). A hypothesis of genetic control was also proposed according to which a provirus occuring in the host genome appears as a dominant factor of disease the action of the provirus becomes apparent in the absence of non-allelic dominant repressor R (7).

In view of the vagueness of etiology of bovine leukemia we consider the most acceptable approach to population studies will be to count the predisposition as polygenic character where the additive effects of equally acting genes will be seen on reaching a certain threshold. Other approaches may be considered on elucidating the etiology of disease.

In this report the results of statistical and genetical analysis of bovine leukemia in Brown Latvian breed of cattle are given.

MATERIAL AND METHODS

The population investigated consisted of above 50,000 cows within herds of collective and state farms in the Latvian S. S. R. where artificial insemination has

* Department of Genetics, All-Union Animal Research Institute, Moscow-Dubrovitsy 142012, USSR.

been employed. For this study the data of disease incidence in cows, their sires and dams were used. Only lactating adult cows 2.5 years old or older were included. Clinical and hematological diagnosis of condition was carried out by local state veterinary laboratories. Animals are considered as affected if they have the number of leucocytes per cubic mm and percentage of lymphocytes above standards accepted in the diagnostic practice (8), otherwise they are considered as normal (or apparently healthy).

Binomially distributed data of incidences were examined by analysis of variance (9). The heritability was estimated based on the correlation between paternal halfsibs.

RESULTS AND DISCUSSION

Within investigated population a retrospective analysis of incidence in daughters produced by sires and dams with known phenotype was carried out (Table I).

TABLE 1

INCIDENCE OF DISEASE IN DAUGHTER GROUPS

Group	Type of mating		Daughters			
			Affected		Normal	
	Sire	Dam	Number	Per cent ± S. E.	Number	Per cent ± S. E.
I	Affected	Affected	69	14.2 ± 1.59	416	85.8 ± 1.59
II	Affected	Normal	225	6.4 ± 0.41	3271	93.6 ± 0.41
III	Normal	Affected	640	12.4 ± 0.46	4520	87.6 ± 0.46
IV	Normal	Normal	2739	6.3 ± 0.011	41296	93.8 ± 0.011
	Total		3673	6.9 ± 0.01	49503	93.1 ± 0.01

The highest percentage of affected daughters was resulted in the matings between affected sires and affected dams (14.2 per cent). Differences between this group and other groups statistically were significant (1 versus II group and 1 versus IV group $P < 0.001$, and 1 versus III group $P < 0.05$). The following group is group III which significantly differs from group II and IV ($P < 0.001$). Finally the group produced by matings between normal sires and dams gave the lowest incidence and the difference was not significant statistically.

Similar data on the incidence were obtained in our previous investigation (10) where on 44,174 pairs daughter-dam and daughter-sire was established that affected dams produced 13.1 per cent affected daughters while normal ones produced only 6 per cent; affected and normal sires produced 9 and 6,4 per cent affected daughters respectively.

Analysis of variance of incidence in 34,029 cows sired by 467 bulls (there were 26 affected bulls among them) showed the presence of statistical highly significant differences between halfsib groups (Table 2).

188

The difference between groups of cows descending from affected and normal sires was not significant.

TABLE 2

ANALYSIS OF VARIANCE OF INCIDENCE

Source of variation	Degree of freedom	Sums of squares	Mean squares
Group of sires (affected and normal)	1	0.220	0.220
Sires within group	465	99.58	0.214 (*)
Error	33562	1,746.40	0.052

(*) $P < 0.001$.

The heritability of differences was estimated on the basis of halfsib correlation according to formula:

$$h^2 = \frac{4\,(\sigma^2_e - \sigma^2_e)}{\sigma^2_s + (n_o - 1)\,\sigma^2_e}$$

where σ^2_s is the variance due to sires; σ^2_e is within subgroup (error) variance and n_o is weighted mean number of daughters per sire equal to

$$n_o = \frac{1}{g-1}\left[N - \frac{\sum\limits_{i}^{g} n^2_i}{N} \right]$$

where g is the number of halfsib group; N is total number of daughters and n_i is the number of daughters i-th sire ($i = 1, 2, \ldots g$).

On the basis of these formulae the heritability of differences in predisposition to bovine leukemia is estimated to be 0.1622. Since this estimate obtained on the binomial scale the genetically more accurate heritability on the normal scale can be obtained by dividing factor $z^2/p\,(1 - p)$, where z is the ordinate on the normal distribution at the threshold point corresponding to a fraction p of the population having the character. As a result of correction for continuity of distribution the estimate of heritability was increased to 0.072.

These results should be taken into account in selection and selective matings for lower incidence of bovine leukemia.

SUMMARY

Analysis of the matings between tested to leukemia sires and dams has shown that affected parents produced the highest per cent of affected daughters. The effect of dams on the incidence was more pronounced than the effect of sires. Highly significant differences in the incidence between sire groups were revealed. The heritability of differences in incidence is estimated to be low and moderate.

SUMARIO

El análisis de los cruzamientos entre padres y madres probados con respecto a la leucemia bovina demuestra que los padres afectados producen el mayor porcentaje de hijas afectadas. El efecto de las madres en la frecuencia fue más pronunciado que el de los padres. Se revelaron diferencias altamente significativas en la frecuencia entre grupos paternos. La heredabilidad de las diferencias en la frecuencia se estima como baja y moderada.

ZUSAMMENFASSUNG

Die Unterzuchungen der Anpaarungen auf Leukose geprüfter Bullen und Kühen ergeben, daß der grösste Anteil von kranker Nachkommenschaft von kranken Eltern bekommen werden. Die Wirkung der Mütter auf die Erkrankunghäufigkeit ist höher als die der Väters. Es wurden significante Differenze in der Erkrankungshäufigkeit von Töchtern verschiedener Bullen festgesellt. Die Veranlagungserblichkeit der Rinder zur Leukose ist mäßig und mittels.

LITERATURE CITED

1. HARTENSTEIN, F. (1896): *Ber. Vet. Kgr. Sach.*, 41, 141.
2. ENGELBRETH-HOLM, J. (1942): *Spontaneous and experimental leukemia in animals.* Edinburgh, Oliver & Boyd.
3. WIESNER, E. (1967): *Die Leukosen des Rindes.* 2nd ed., Gustav Fischer, Jena.
4. GÖTZE, R., und ZIEGENHAGEN, G. (1953): *Dtsch. Tierärztl. Wschr.*, Suppl. Fortpfl. u. Besam., 3, 55.
5. BÖTTGER, T. (1954): *Zschr. Tierzücht. Zücht. Biol.*, 63, 223.
6. EMEL'JANOV, A. S.; SMOLINA, K. A., and SMETANINA, G. K. (1970): *Zivotnovodstvo*, Nr. 7, 53.
7. IVANOVA, O. A. (1973): *Genetics* (USSR), 9, No. 7, 49.
8. VASIL'EV, N. T.; RUM'JANTSEV, N. V., and CHERNYAK, V. V .(1966): *Leukoses in farm animals* (Russian), Moscow, Kolos.
9. ROBERTSON, A., and LERNER, I. M. (1949): *Genetics*, 34, 395.
10. ERNST, L. K.; KLABUKOV, P. G.; KARLIKOV, D. V.; ZIVOTOVSKY, L. A.; CALITIS, A. A.; GRINBERG, R. O.; PRIEDNIEK, O. K., and AUZINA, A. K. (1973): *Bull. Nauch. Rabot.* VIZ, vypusk, 34, 15.