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Brief Communication

GENETIC VARIATION IN THE SERUM LYSOZYME ACTIVITY IN CATTLE

Widely distributed in nature, lysozyme (LZM) occurs in various vertebrates, invertebrates, bacteria, phages and plants. In animals this enzyme can be determined in, or isolated from, various body fluids, tissues and secretions (*Jollès* 1976). LZM is a protein of comparatively low molecular weight. Among other properties, it possesses a markedly cationic charge and an unspecific bacteriolytic activity. This activity cleaves the link between n-acetyl-muramic acid and n-acetyl-glucosamine of a mucopolysaccharide in the bacterial cell wall (*Salton* 1957). Extensive studies during the last decade might now indicate that the original hypothesis of *Fleming* (1922) is correct. This hypothesis postulates that LZM plays a role in the body's defence against infection. *Vakil et al.* (1969) found that several Gram-positive and Gram-negative bacteria were susceptible to different degrees to purified LZM from bovine and human milk. As reviewed by *Jollès*, several investigations demonstrate the indirect immunopotentiating effect of LZM, arising during the course of its action on bacteria, as some of the decomposition products behave as adjuvants (*Adam et al.* 1972, 1973, *Hiu* 1972, *Migliore-Samour & Jollès* 1972). Also co-operation between LZM and antibody/complement in the lysis of Gram-negative bacteria has been demonstrated (*Glynn & Milne* 1967, *Hill & Porter* 1974). Recently, it has been asserted that serum LZM activity reflects the homeostatic expression of the reticuloendothelial system (RES), which is one of the most fundamental defence mechanisms against infection. Moreover, experimental findings have produced evidence for LZM being an index of macrophage functional status (*Di Luzio* 1979).

The object of this investigation was to study the genetic influence of the serum LZM activity in cattle.

At a performance testing station, serum samples were collected from 294 bulls which consisted of 19 half sib groups (sire families). Environmental conditions were standardized and the effect of age was considered negligible (mean age 229 days, standard deviation 8 days). The samples were drawn during a period of 2 years and stored frozen. Consequently, the influence

of seasonal variation and duration of storage on the LZM activity had to be separated from the effect of sires (the heritability). This was achieved by employing the method of least squares analysis.

The LZM assay procedure employed was that described by *Parry et al.* (1965), with some modifications: 2 ml of a Micrococcus lysodeikticus* suspension (approx. 0.20 mg per ml sodiumphosphate buffer, pH = 6.2) was pipetted into a glass cuvette (lightpath = 1 cm), placed in the thermoregulated cellholder (38°C) of a spectrophotometer. At zero time 200 μl enzyme (serum or LZM standard) was added, immediately followed by mixing and reading the absorbance at 520 nm (A_{520}). Thereafter, the decrease in absorbance per minute (ΔA_{520}/min) was recorded by reading A_{520} with 2 min intervals for about 10 min. Besides, in order to confirm linearity of the enzymatic action, a chart recorder was simultaneously used. Standard LZM solutions were prepared by dissolving crystalline egg-white LZM** in phosphate buffer (pH = 6.2). Accordingly, the LZM activity of the serum samples was expressed as μg egg-white LZM per ml.

In only 5 of the 294 serum samples LZM was not detectable. In the total material LZM activity varied from zero to 2.63 with a mean activity of 0.39 ± 0.32 (mean ± s) μg per ml. The difference between half sib groups was highly significant with regard to serum LZM activity ($P < 0.0005$). The main source of intergroup variation was caused by a single sire family, comprising 30 offspring with extremely high LZM activity. The mean LZM activity of this particular group was almost 3-fold the mean level of the total bull material. This discontinuous variation might perhaps be caused by the effect of a so-called "major gene", overshadowing the polygenes, which probably ordinarily regulate the LZM activity. The difference between half sib groups when the extreme one was excluded, was also significant ($P < 0.025$) and the corresponding heritability was 0.27 ± 0.18 ($h^2 \pm s.e._{h^2}$).

The results of this study might be interpreted as follows: The serum LZM activity in cattle is probably influenced at least at 2 different genetic levels: Firstly, in accordance with the esti-

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* Prod.No. M-0128. SIGMA Chemical Company, St. Louis, USA.
** Prod.No. L-6876. SIGMA Chemical Company, St. Louis, USA.

mated heritability, polygenes probably regulate the LZM activity. Secondly, a possible LZM controlling gene, occurring at a relatively low frequency in the population, is perhaps responsible for the existence of individuals having an extremely high LZM level.

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