

# EVALUATION OF CERTAIN MASTITIS DETECTION TESTS

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## ABSTRACT

A curvilinear regression resulted when the Feulgen-DNA test scores were plotted against the average concentration of leucocytes. Application of a logarithmic transformation to the average test data resulted in a linear correlation which slightly raised the correlation between the Feulgen-DNA Test and the leucocyte count. But, the application of a sample per cow transformation to the average test data from each of 30 representative cows, resulted in an approximate linear relationship and in significant correlations between the Feulgen, California, and Whiteside tests and the leucocyte count. Correlations in descending order were Feulgen > California > Modified Whiteside Test with respect to the leucocyte count.

The purpose of this report is to examine certain methods of evaluating mastitis detection tests based on the correlativity of a test with respect to the microscopic leucocyte count (3).

In a previous report concerned with the evaluation of certain mastitis screening tests, correlation coefficients were calculated without concern for type of linearity involved in plotting a particular variable against the leucocyte count (2, 3). This type of calculation, using raw data, assumes a linear relationship that may not obtain when qualitative are plotted against quantitative test results. Such a relationship was demonstrated by Paape, et al. (5), in plotting the Feulgen-DNA and the Milk Quality Test (MQT) scores against the Somatic Cell Count.

## MATERIALS AND METHODS

This part of the report is for the purpose of verifying the work of Paape, et al. (5) and duplication of their treatment applied to NDSU data was attempted with the following exceptions:

(a) Milk samples were selected at random from the University dairy herd and five commercial dairy herds so that there were 34 portions for each five Feulgen scores and 10 portions for the sixth score level.

(b) The Feulgen-DNA test was plotted versus the leucocyte count, modified (4).

Correlation coefficients were calculated by IBM 1620 computer<sup>1</sup> and Daniels Batch Processing Stepwise Multiple Linear Regression Program.<sup>2</sup>

The range of the true mean was applied to the test variables by means of "student" distribution<sup>3</sup> and appropriate statistical calculations.

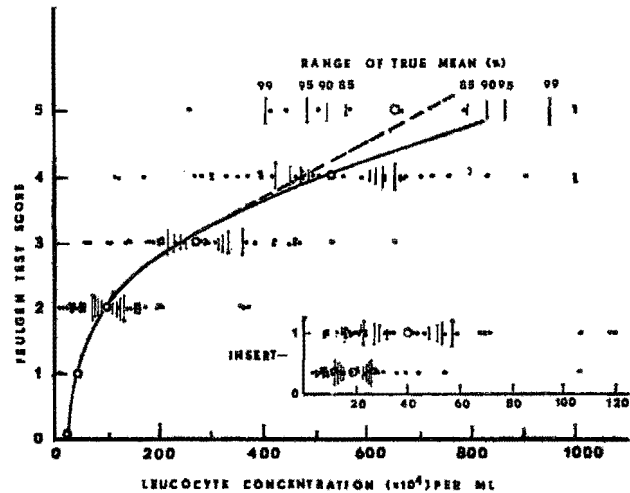


Figure 1. Feulgen mastitis test scores correlated with the concentrations of leucocytes resulting in a curvilinear relationship. Individual cell concentrations are indicated by ● and the average cell counts at each Feulgen score level by ○. Bars at the 80, 90, 95, and 99% levels indicate the range of the true mean. Insert demonstrates the distribution on an enlarged scale.

## RESULTS AND DISCUSSION

The vertical bars, Fig. 1, show the range of the true mean at the 80, 90, 95, and 99% levels. The use of the student distribution<sup>3</sup> signifies that the true mean cell count will fall within the bars for each quality score reading 80, 90, 95, and 99% of the time, but it does not mean that the values will fall within these ranges at all times, since they represent only mean values.

The mean and standard deviations for leucocyte count  $\times 10^4$  at each Feulgen score level are tabulated as follows:

Feulgen-DNA score	0	1	2	3	4	5
Mean deviation	20	25	50	118	203	225
Standard deviation	16	37	58	145	246	269

Figure 1 demonstrates a curvilinear relationship between the Feulgen-DNA test scores and the concentration of leucocytes. Results are in substantial agreement with those reported by Paape, et al. (5), with respect to the relationship of the somatic cell concentration to the Milk Quality Test and Feulgen-DNA Test scores. Paape, et al. (5), performed a logarithmic transformation on the curvilinear data

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<sup>4</sup>G. W. Snedecor, Statistical Methods, Fifth Edition. Iowa State College Press (Ames).

<sup>5</sup>Calculations available.

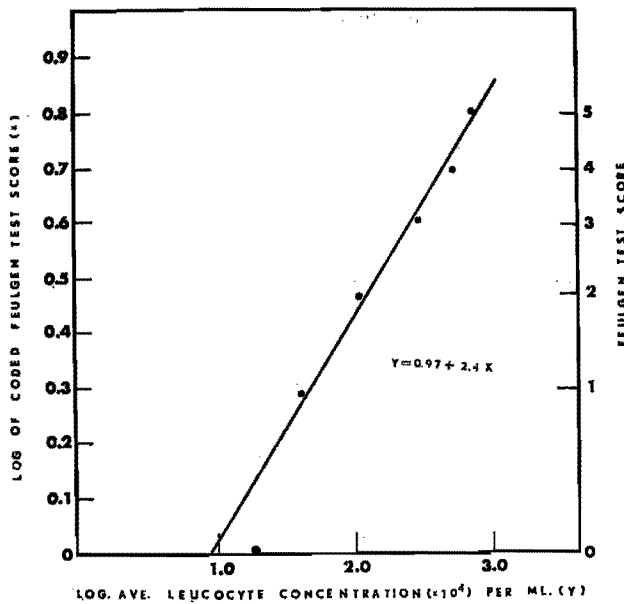


Figure 2. Application of a logarithmic transformation to the average mastitis test data.

which resulted in a linear relationship between the coded Feulgen-DNA score and the logarithms of the cell numbers, thus elevating the correlativity slightly over that of the score of the non-transformed data.

A similar transformation was applied to the NDSU average curvilinear data. The coded Feulgen score (score + 1), was correlated with respect to the logarithms of the numbers of leucocytes. A linear relationship resulted (Fig. 2) which is in general agreement with results reported by Paape, et al. (5).

The main criticism of this type of data transformation lies in reliance on the average microscopic cell count per Feulgen Test score, thus providing only one point per score and five points on a graph for both curvilinear and transformed data. It would seem that compilation of 4,945 samples in this manner might fail to represent true statistical validity.

One would expect that the mastitis test pattern of one cow to be distinctly different from that of other cows. This characteristic was observed in plotting the tests of samples from 30 individual cows against seasonal dates over a two year period.<sup>5</sup> This observation suggests that the application of a sample per cow transformation of mastitis test data might result in a closer relationship between the qualitative and the quantitative tests than with pooled data from two or more cows.

Thus a sample per cow transformation was performed as follows: 30 cows were selected from the University herd, each with about 78 test readings over a period of 2 years. The pooled average readings from each of 30 cows were plotted, a linear

<sup>5</sup>From author's unpublished data.

relation was noted and the correlation coefficients of the quality test scores versus the leucocyte concentration were computed by the IBM 1620 computer<sup>1</sup> and Daniels Stepwise multiple linear regression program.<sup>2</sup>

For comparative purposes the average and composite correlations of University herd and the aver-

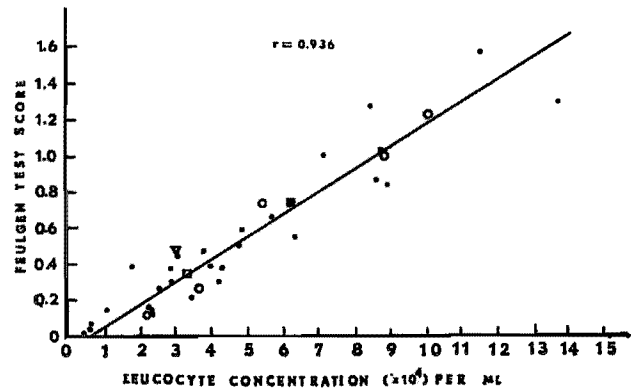


Figure 3. Sample per cow transformation; Feulgen - DNA versus Leucocyte Count ● average per cow samples 30 NDSU cows; ■ overall average 4,945 NDSU herd; ▲ overall average NDSU composites; ○ average per herd 5 commercial herds; □ overall average commercial herd samples.

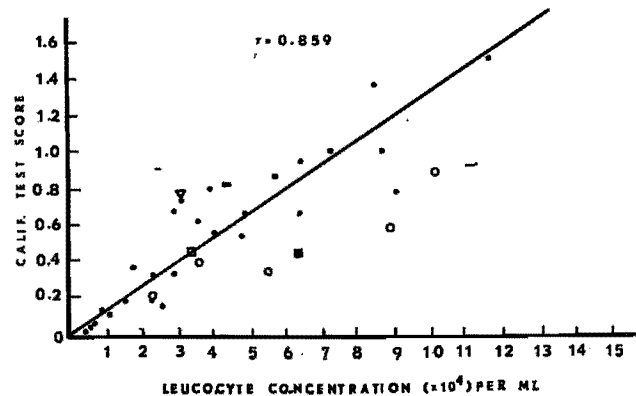


Figure 4. Sample per cow transformation; California Mastitis Test versus leucocyte count. Key is the same as in Fig. 3.

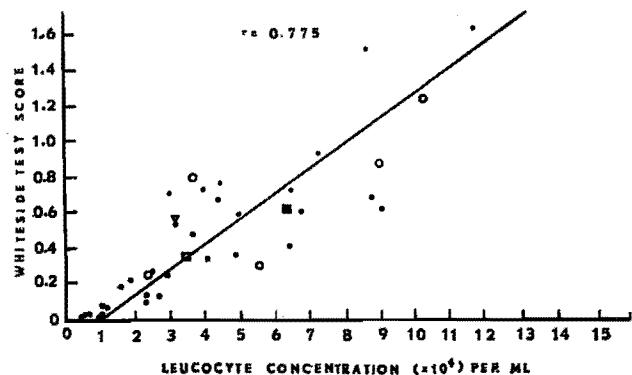


Figure 5. Sample per cow transformation; Modified Whiteside Test versus Count. Key is the same as in Fig. 3.

TABLE 1. EFFECT OF DATA TREATMENT ON CORRELATION COEFFICIENTS OF CERTAIN MASTITIS TESTS VERSUS LEUCOCYTE COUNT<sup>1</sup>

Data treatment	Test correlated vs leucocyte count		
	Feulgen r	California r	Modified Whiteside r
Sample per cow			
Transformed	0.936	0.859	0.775
Untransformed	0.691	0.602	0.554
Difference	0.245	0.257	0.221

<sup>1</sup>Simple correlation coefficients of average (4,945) NDSU samples.

age values of 720 samples from five commercial herds also were plotted.

The pooled average scores from the Feulgen-DNA (5), California (7), and the Modified Whiteside test (4), each were plotted against the average leucocyte concentration and results are demonstrated in Fig. 3, 4, and 5.

Results (Fig. 3, 4, and 5) demonstrate an approximate linear relationship of the qualitative mastitis tests to the leucocyte count, when a sample per cow transformation is applied to the curvilinear data. This transformation also takes into account variations among test readings from the University herd and from five commercial herds. In all instances, the check points fall close to the linear graph plotted

against the average test readings from the 30 University cows employed in the analysis.

Correlation coefficients of tests evaluated (Fig. 3, 4, and 5) compared with corresponding correlations of the average untransformed NDSU herd test data are presented in Table 1.

Results show that in each instance the sample per cow transformation of average test data caused a definite elevation in correlations over the untransformed data.

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