RELATIONSHIPS BETWEEN MILKING MACHINES, SPEED OF MILKING AND SOMATIC CELL COUNT LEVELS IN DAIRY COWS

by

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Dedicated to: *The dairymen who gave of their time and who were so very cooperative and hospitable.*

ABSTRACT

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RELATIONSHIPS BETWEEN MILKING MACHINES,
SPEED OF MILKING AND SOMATIC CELL COUNT
LEVELS IN DAIRY COWS

Two distinct studies were carried out in relation to somatic cell count. In the first, two-minute milk yield and total milking time were measured on 2,619 sire identified Holstein-Friesian cows in test herds located in Quebec and Ontario. Milk samples were collected from each cow and analyzed for somatic cell count, while projected or completed 305-day or BCA milk and fat lactation production were available for the population. Two-minute yield and total milking time were adjusted for the effect of milk yield at sampling and the raw cell counts transformed to a natural log scale. Joint estimates of the fixed effects of herd, age of cow at calving, stage of lactation and season of calving and the components of variance of the random effects of sire and error were obtained by Maximum Likelihood (ML) methods. Heritability estimates of milking speed were greatest for adjusted two-minute yield (0.22 to 0.26), with the smallest values observed for adjusted total milking time (0.13 and 0.16). Phenotypic, genetic and rank correlations of sire breeding values indicated that all four measurements - adjusted and unadjusted two-minute yield and adjusted and unadjusted total milking time - were closely related and are useful measurements of milking speed. The phenotypic correlations were small between measurements of milking speed and somatic cell count (-0.05 to 0.09), while the corresponding genetic correlations with log somatic cell count were moderate to large and indicated an antagonistic

genetic relationship between faster milking speed and cell count. Small but significant phenotypic correlations were observed between unadjusted measurements of milking speed and lactation production (0.11 to 0.22), however, correlations were not significant when milking speed measurements were adjusted for the milk yield at sampling. The genetic correlations suggest an antagonistic relationship between two-minute yields and lactation production, while the genetic relationships between the lactation traits and milking time are small. Correlations between machine stripping and milking speed, somatic cell count and lactation production based on 953 records indicated that there was little benefit derived from this practice.

In the second study, parameters of milking machine design and performance and milking practices were measured for 46 herds on the Official Quebec Dairy Herd Analysis Program (DHAS) with monthly herd average somatic cell count data and 21 additional herds with a herd somatic cell count for the day of machine testing. Results were fairly consistent for one-way analyses of variance when herd average cell count and test day cell count were the dependent variables. Variables meeting the 0.1 level of significance in one-way analyses were included in stepwise regression analyses. The best regression equations for both herd average and test day somatic cell count included teat dipping with ratio fore teat or alternate pulsation, respectively. These models explained 40.8% and 33.8% of the variation in herd average and test day somatic cell count, respectively. However, the practice of teat dipping alone explained 33.2% and 27.5% of the variation for the corresponding somatic cell counts.

RESUME

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RELATIONS ENTRE LE SYSTEME DE TRAITE,
LA VITESSE DE TRAITE, ET LA NUMERATION
DES CELLULES SOMATIQUES CHEZ LA VACHE LAITIERE

Deux études distinctes ont été faites en rapport avec le comptage leucocytaire. Dans le premier cas, on a mesuré la production laitière des deux premières minutes de traite de même que le temps total de la traite pour 2619 vaches Holstein-Friesian dont le père est identifié et réparties dans des troupeaux contrôlés du Québec et de l'Ontario. On a effectué le comptage leucocytaire sur les échantillons de lait provenant de chaque vache, tandis que la production en 305 jours (projetée ou complétée) ou les MCR en lait et en gras étaient disponibles pour cette population. La production en deux minutes et le temps total de traite furent ajustés pour l'effet de la production laitière au moment de l'échantillonnage, et la numération cellulaire brute a été transformée à l'échelle logarithmique naturelle. L'estimation des effets fixes dus au troupeau, à l'âge de la vache au vêlage, au stade de lactation et à la saison de vêlage a été obtenue simultanément à celle des composantes de variance des effets randomisés du taureau et de l'erreur par la méthode du Maximum de Vraisemblance (ML)[1]. Les estimés de l'héritabilité pour la vitesse de traite furent plus élevées dans le cas de la production en deux minutes ajustée (0.22 à 0.26), les valeurs les plus faibles ayant été observées pour le temps total de traite ajusté (0.13 et 0.16). Les

[1] Maximum Likelihood Methods (ML).

corrélations phénotypiques, génétiques, de même que les corrélations de rang entre les valeurs génétiques des taureaux, ont indiqué que les quatre types de mesure - production en deux minutes ajustée et non ajustée, temps total de traite ajusté en non ajusté - sont étroitement reliés et constituent des mesures adéquates de la vitesse de traite. Les corrélations phénotypiques entre la vitesse de traite et le nombre de cellules somatiques étaient faibles (-0.05 à 0.09), alors que les corrélations génétiques correspondantes avec le log du nombre de leucocytes étaient de moyennes à élevées, indiquant une relation génétique antagoniste entre une plus grande vitesse de traite et le nombre des cellules somatiques. Des corrélations faibles mais significatives ont été observées entre les mesures non-ajustées de la vitesse de traite et la production totale pour la lactation (0.11 à 0.22); cependant, ces corrélations n'étaient plus significatives lorsque les mesures de vitesse de traite étaient ajustées pour la quantité de lait produite au moment de l'échantillonnage. Les corrélations génétiques suggèrent un effet opposé entre une production en deux minutes plus élevée et la production totale de la lactation, alors que les corrélations génétiques entre les mêmes caractéristiques de la lactation et le temps total de traite furent faibles. Les corrélations entre l'égouttement à la machine et la vitesse de traite, le nombre de leucocytes et la production pour la lactation, basées sur 953 données, ont indiqué qu'il y avait peu d'avantage à appliquer cette technique.

Dans la deuxième étude, on a mesuré des paramètres relatifs à la conception du système de traite et à son fonctionnement, et aux pratiques de la traite, dans 46 troupeaux du Programme d'Analyse des Troupeaux Laitiers du Québec, option officielle, pour lesquels des données moyennes mensuelles sur le comptage leucocytaire étaient disponibles; ces mêmes mesures ont été

effectuées dans 21 troupeaux additionnels pour lesquels le comptage leucocytaire a été fait sur un échantillon de lait prelevé le jour du test de la trayeuse. Les résultats des analyses de variance à une variable indépendante furent à peu près les mêmes dans des deux cas où la variable dépendante était soit la moyenne mensuelle du comptage leucocytaire soit la numération pour le jour du test. Les variables qui furent significatives au niveau de 0.1 en analyse à variable indépendante unique ont été soumises à l'analyse de régression par étape[1]. Dans le cas de la numération cellulaire mensuelle, la meilleure équation de régression a retenu le bain de trayons et le rapport de traite pour les quartiers avant, alors que dans le cas de la numération pour le jour du test, le bain de trayons et la pulsation alternée étaient retenus. Ces modèles ont expliqué 40.8% et 33.8% de la variation du comptage leucocytaire mensuel et du jour du test respectivement. Cependant, le bain de trayons à lui seul a expliqué 33.2% et 27.5% de ces mêmes variations.

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[1] Stepwise Regression.

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I. INTRODUCTION

Mastitis continues to cause large economic losses to the dairy industry. These were the words of the National Mastitis Council (NMC) in 1978, who also indicated that the largest loss of income was caused by subclinical mastitis. This type of mastitis shows no evidence of inflammation, but examination of the milk reveals udder infection and increased cell count and also alterations in chemical properties of the milk (International Dairy Federation (IDF), cited by Klastrup, 1975). Thus, the somatic cell count may be interpreted as a signal of udder inflammation. Moxley et al. (1978) reported that each increase of 100,000 cells/ml in herd average of somatic cell count was associated with a decline of 59 kg average production in the herd.

Due to the hereditary basis of milk flow rate, selection for this trait has been suggested as a means of reducing the labor input required to milk cows. The Milk-o-Meter digital totalizer, described by Sharaby et al. (1977), has been used to sample cows in Holstein herds in Ontario and Quebec for two-minute milk yield. These data have been used to obtain sire proofs for artificial insemination (AI) Holstein dairy sires for two-minute milk yield, a measurement of milking speed.

However, the relationships between two-minute yield and total milking time, as well as with measurements of udder health and lactation production have not been well established. We do not know the relative changes that would occur in these health and production related traits as a result of selection for two-minute yield.

Thus, the first study, which utilizes data from commercial dairy herds in Ontario and Quebec, was undertaken with the following objectives:

- to examine the environmental influences of herd, stage of lactation, age at last calving and season of calving on two-minute milk yield and total milking time
- to examine genetic and phenotypic relationships between two-minute milk yield and total milking time, as well as estimate the heritability of each trait
- to examine the genetic and phenotypic relationships between the measurements of milking speed, two-minute yield and total milking time, with somatic cell count
- to examine the genetic and phenotypic relationships between both measurements of milking speed and lactation 305-day milk and fat and BCA milk and BCA fat
- also, to examine the relationship between machine stripping and the measurements of milking speed, somatic cell count and lactation milk and fat production.

Secondly, Moxley et al. (1978) investigated the relationship between milking hygiene practices and somatic cell counts. Schalm et al. (1971) and Thiel (1975)indicated that much evidence exists with reference to mechanical milking and mastitis, yet few quantitative data are available to show the combined or separate importance of machine effects to the status of mastitis in herds. Thus, a study to investigate relationships between the design and operation of pipeline milking machines and herd somatic cell counts was also carried out.

II. REVIEW OF LITERATURE

Mastitis

Mastitis is an inflammation of the mammary gland, the inflammation being a reaction to injury (NMC, 1978; Jain, 1979). It is a disease complex resulting from numerous conditions or combinations of stress which injure the internal structure of the mammary gland. This injury to the internal tissues of the gland leads to an inflammatory response. The clinical signs characteristic of the disease are an expression of defense to eliminate or neutralize the irritant and allow for repair and a return to normal glandular function (Schalm et al., 1971; NMC, 1978).

Somatic Cells and Mastitis

The International Dairy Federation (IDF) defines mastitis as an inflammatory change of the mammary gland which, along with physical, chemical and microbiological changes, is characterized by an increase in numbers of somatic cells, particularly leucocytes in the milk and by pathological changes in the mammary tissue (cited by Weaver and Kroger, 1977). Somatic cells in milk are of two types: epithelial cells derived from local tissue as a result of physiological wear and leucocytes from the blood. They occur normally in milk as a result of udder wear and a small number of leucocytes occur physiologically as in other body fluids (Schalm et al., 1971), and there is a close relationship between the total somatic cell count and the number of polymorphonuclear (PMN) leucocytes (Waite and Blackburn, cited by Reichmuth, 1975; Paape et al., 1979).

Subclinical mastitis shows no evidence of inflammation, but examination of the milk reveals udder infection and an increased cell count and also alterations in chemical properties of the milk (IDF, cited by Klastrup, 1975). Thus, the somatic cell count may be interpreted as a signal of udder inflammation, allowing for the physiological factors which may influence the number and type of cells found in the milk (Sethar et al., 1979). A high bulk milk sample somatic cell count suggests the incidence of mastitis in a given herd (Reichmuth, 1975; NMC, 1978).

Fossomatic Somatic Cell Counting

Numerous methods have been developed for determining somatic cell numbers in milk. The National Mastitis Council Research Committee has developed reliable techniques for the direct microscopic somatic cell count (DMSCC) to serve as a standardized method for screening and regulatory procedures, as a research procedure, and as a standard method for evaluating all other cell count tests (NMC, 1978). Because this procedure is time consuming, automated cell counting procedures have been developed.

The Fossomatic is a fully automatic, fluoro-opto-electronic instrument which can count up to 180 preserved milk samples per hour (Downey et al., 1976; Mochrie and Monroe, 1978). Mochrie and Monroe (1978) reported the results of a collaborative study of the Fossomatic and DMSCC methods of somatic cell counting among six North American laboratories. As a result, the Association of Official Analytical Chemists (1978) recommended the Fossomatic Somatic Cell Counter as an acceptable method for counting somatic cells in milk.

Milking Speed

Due to the hereditary basis of rate of milk flow, selection for this trait has been suggested as a means to reduce needs for milking labor. The rate of milk flow is a useful proxy for milking machine time, as the time for evacuation of a cow's udder is a direct function of the quantity of milk contained and the rate of evacuation (Blake and McDaniel, 1978). Several methods have been used to define and measure the rate of milk flow.

Definitions of Milking Speed

Blake and McDaniel (1978) indicate that research has focused on three main families of similarly defined measures, peak flow rate, average flow rate, and milking machine time. Also, partial periods of milking have been used to approximate peak flow rate.

"Peak Flow" and "Maximum Rate of Flow" are defined as the maximum yield obtained in a single minute of milking time, these measurements being used by Touchberry and Markos (1970), Smith et al. (1974), Tomaszewski et al. (1975) and Miller et al. (1976). Measurements of "average flow rate" depend on the terminal point of milk flow used in its determination. Baxter et al. (1950) defined machine milking rate (yield/minute) as the yield prior to machine stripping averaged over that elapsed time. A few investigators defined average rate as the total milk output divided by the total time, including machine stripping (Blake and McDaniel, 1978).

Definitions of milking time also differ with respect to the end point. "Milking Machine Time" indicates termination of timing before the actual teat

cup removal. Tomaszewski et al. (1975) and Miller et al. (1976) included the milking time until the flow rate fell below 0.45 kg/30 sec, while Touchberry and Markos (1970) stopped timing when the rate fell below 0.14 kg/20 sec. "Total time" is the actual time the milking unit was on the cow (Miller et al., 1976).

The amount of milk in the first two minutes of milking was considered by Odegard (1967), Schmidt and Van Vleck (1969), Touchberry and Markos (1970), Tomaszewski et al. (1975) and Sharaby et al. (1979) as a measure of milking rate. Other intervals have been considered, with Tomaszewski et al. (1975) recommending that such measures be taken before the third minute of milking to avoid the problem of cows that complete milking earlier.

Measuring Milking Rate

Obtaining the measurements of milking rate was initially by one of two methods. The first involved suspending a milking machine bucket on a spring scale and recording the weight at timed intervals. The second method used a continuous feed Kymograph to obtain a graph of milk flow during machine operation. However, Tomaszewski et al. (1975) indicated the need for an easy field measure of milking rate, and Miller et al. (1976) stated that no measure of milking rate would be introduced into DHI testing until automatic recording equipment was available.

Sharaby et al. (1977) reported on the Milk-o-Meter (M-o-M) digital totalizer, which automatically registers two-minute yield and total milk yield. They reported a phenotypic correlation of 0.98 between a measurement of two-minute yield starting from the seating of the teat cups and reading

the M-o-M dial and the M-o-M digital totalizer two-minute yield. They concluded that the device shows promise as an inexpensive and accurate method of measuring milking speed of individual cows under field conditions.

Factors Influencing Milking Speed

Sharaby et al. (1979) found significant effects of stage of lactation ($P<0.05$) and the linear and quadratic effects of age of cow ($P<0.01$) on two-minute yield. Including total milking yield as a covariate resulted in these factors becoming not significant. Each 1 kg increase in total milking yield resulted in a 0.33 kg increase in the two-minute yield. Schmidt and Van Vleck (1969) and Touchberry and Markos (1970) observed a significant effect of days in lactation after adjusting for the variation in milk yield. They reported an increase in the rate of flow and a decrease in the milking time as the lactation progressed. Johansson and Malven (1960) noted that the decrease in the rate of flow with advancing lactation was rather slight in proportion to the decrease in milk yield. Smith et al. (1974) established 11 groups for the stage of lactation, and also found that when yield differences were removed, there was a significant increase in maximum rate to the end of lactation. They suggested this is due to wear and relaxation of the teat sphincter.

Tomaszewski et al. (1975) found a significant effect of lactation number on milk flow and concluded that cows be compared in the same lactation, or an adjustment for lactation number be applied. Schmidt and Van Vleck (1969), Markos and Touchberry (1970) and Miller et al. (1976) also reported a trend of increased milk flow rates with age. Rathore (1976) found a negative

relationship between age in years and average milk flow rate. Schmidt and Van Vleck (1965) found machine time to increase significantly with age.

Heritability and Relationships of Milking Speed Measures

Blake and McDaniel (1978), Sharaby (1977), and Miller et al. (1976) have reviewed the heritability estimates present in the literature for measurements of milking rate. Miller et al. (1976) reported that peak flow rate reflects genetic differences among animals to a greater extent than other measures of milk flow rate. However, Tomaszewski et al. (1975) reported heritabilities for several measures of milk flow, indicating that selection for these traits would be at least as rapid as for milk yield. Heritability estimates for two-minute yield and total milking time are presented in Table 1.

Table 1. Heritability estimates for two-minute yield and milking time

Study	Trait	h^2 Estimate	
Odegard, 1966	Milking time	0.17	0.18[a]
Colleau, 1971	Milking time	0.30	0.25[b]
Miller et al., 1976	Total time	0.17	
Tomaszewski et al., 1975	Two-minute yield	0.30	
Sharaby et al., 1979	Two-minute yield	0.25	0.24[c]

[a] Total time and machine time, respectively.
[b] First and second lactations of French Friesan cows, respectively.
[c] Unadjusted and adjusted for total milk yield, respectively.

Tomaszewski et al. (1975) reported within lactation repeatabilities of 0.51 to 0.78 for ten measurements of milking speed. Also, they reported large phenotypic and genetic correlations among eight measurements of milking rate. Odegard (1967) reported repeatabilities for lactation groups of 0.83 and 0.78 for milking time and two-minute yield, respectively. Correlations reported in the literature between two-minute yield, milking time, and other milking rate measurements appear in Table 2.

Table 2. Genetic and phenotypic correlations between two-minute yield, milking time and other milk flow measurements.

Study	Traits		Correlations	
			Phenotypic	Genetic
Tomaszewski et al., 1975	Two minute yield	Peak flow rate	0.93	0.98
	Two minute yield	Average flow rate	0.87	0.93
	Two minute yield	Machine time	-0.83	-0.87
Touchberry & Markos, 1970	Two minute yield	Initial flow rate	0.95	
	Two minute yield	Machine time	-0.57	
	Two minute yield	Maximum flow rate	0.97	
	Machine time	Initial flow rate	-0.65	
	Machine time	Maximum flow rate	0.60	
Miller et al., 1976	Total time	Peak rate		0.41
	Machine time	Peak rate		-0.24

Milking Speed and Mastitis

The National Mastitis Council (1978) stated that most researchers have found that ease of milking has a moderately high heritability, but the relation to mastitis remains unclear. Conflicting reports appear in the literature.

Dodd and Neave (1951) classified 94 first lactation cows into five groups according to their milking rates (peak flow) in early lactation. It was found that the frequency of cows with clinical mastitis increased from 5% in the group with the lowest peak flow (2.42 lb/min) to 44% in the highest peak flow group (6.79 lb/min).

They suggested that there is a strong correlation between milking rate and the incidence of clinical and subclinical mastitis. However, they did not agree with the proposal of McEwan and Cooper, cited by Dodd and Neave (1951), for the breeding of slow milking cows as a possible way of controlling mastitis.

Zeman and Neumann (1973) reported a significant increase in intramammary infections for easy to milk quarters of 63 third lactation cows, and a tendency to increased subclinical mastitis with increased milking rate in first calf heifers and third lactation cows. Schluep (1967) studying 215 Simmental cows in 59 herds reported the percentage of cows with healthy udders (milk with <80,000 ml somatic cells) declining almost linearly from approximately 67% to 33% as the maximum minute volume rose from <1.3 to >2.8 litres. This pattern was paralleled bacteriologically.

Schmidt and Van Vleck (1965) reported small and insignificant (<0.082) within herd correlations for machine on time with four measures of udder health. Andrus and McGilliard (1975) reported a phenotypic correlation of 0.11 between mastitis and milking time. Similarly, Politiek (1968) correlated peak flow and average number of infected quarters based on 583 cows in 38 herds. Correlations were small, the suggestion being that the incidence of mastitis hardly increased with peak flow. Afifi (1968a) found no significant differences between 5 subjective classifications of milking speed and cell count

in fourth lactation cows, and no pattern to first lactation progeny groups of 19 sires when leucocyte count was plotted against milking rate.

Bassalik-Chabielska and Ryniewicz (1978) observed 564 black and white cows owned by state farms. Cows were divided into 5 groups according to maximum yield per minute in litres. The lowest percent (10.6) of infected quarters were observed in the slowest milking group. However, this group had a high percent (2.3) of udder quarters with subclinical mastitis, and the highest percent (11.4) of unspecific inflammations. They concluded that cows milking quickly do not demonstrate an increased incidence of subclinical and clinical mastitis. If the mechanical milking is correct, the higher degree of udder latent infections in cows milking quickly does not lead to an exacerbation of the process and the beginning of inflammation.

Miller et al. (1978) reported no significant regressions of infected/not infected on milking rate or time based on 770 lactations of 450 Holstein cows. They indicated these results do not support the belief that faster milking is associated with more mastitis.

Finally, Rathore (1976) working with 12 cows reported a significantly negative (-0.233) correlation between milk flow and cell count.

Milking Speed and Lactation Yield

Dodd and Foot (1953) studying one herd reported a 419 lb (190 kg) increase in lactation yield with each 1 lb (0.45 kg) increase in peak milking rate. They stated that it was reasonable to suppose that lactation yield is dependent on milking rate. Similar findings were reported by Sandvik (1957), Donald (1960) and Johansson and Malven (1960).

However, removing the effect of milk yield at the recorded milking resulted in no significant effects of milking speed measurements on lactation yield (Sandvik, 1957; Donald, 1960; Johansson and Malven, 1960). Correlations were reduced from 0.25 to 0.11 and 0.32 to 0.05, becoming not significant for lactation production with machine time and peak flow rate, respectively, after adjusting for milk yield (Sandvik, 1957). He stated that slow milking cows were not necessarily poor milk producers. Donald (1960) indicated an 11% reduction in the variation of lactation yield when peak flow rate was held constant. According to Blake and McDaniel (1978) the failure of peak rate to remove but 11% of the variation in milk yield refuted the presumed causal relationship of peak rate on milk yield, indicating the reverse: peak rate depends on yield. Andrus and McGilliard (1975) reported a phenotypic correlation between milk production and milking time (average per milking) of 0.06.

Markos and Touchberry (1970) estimated genetic correlations between milking rate and milk yield at the time the rate was measured, while Miller et al. (1976) estimated genetic correlations between measurements of milk rate and lactation production (Table 3). Miller et al. (1976) indicated that considerable apparent genetic improvement is made in milking rate due to selection for milk, while total milking time would increase slowly with selection for lactation milk production.

However, Sharaby et al. (1979) reported correlation coefficients among progeny test proof for sires of -0.10 and -0.21 for two-minute yield adjusted for total milk yield with BCA milk and BCA fat, respectively. These authors indicated a possible antagonistic relationship between high milk flow rates and high milk production.

Table 3. Genetic correlations of milking rate with milk production.

Study	Traits		Genetic correlation
Markos & Touchberry[a] 1970	Milk yield	Peak rate	0.40
	Milk yield	Initial rate	0.35
Miller et al., 1976	Lactation yield	Peak rate	0.69
	Lactation yield	Average rate	0.78
	Lactation yield	Time to .45 kg/min	0.37
	Lactation yield	Total time	0.50

[a] Average of single measurements in each of the first 6 months of lactation.

Machine Stripping

Machine stripping is the application of downward pressure on the clawpiece while massaging the udder (Smith et al., 1978). Its purpose is to force milk into the teat cistern, where it can be withdrawn by the milking machine.

Studies to examine the effects of machine stripping on production and udder health were carried out by Goff and Schmidt (1967), Little (1968), Rudovsky and Ebendorff (1977), and Smith et al. (1978). All reported no significant effect for the treatment (stripping vs non-stripping) on udder health. Smith et al. (1978) reported slight but non-significant increases in lactation milk, fat and solids not fat. Non-significant differences in production for the two treatment groups were also reported by Goff and Schmidt (1967) and Little (1968). Only Rudovsky and Ebendorff (1977) observed significantly higher milk production in cows that were machine stripped, with this being true only in the case of mature cows.

Miller et al. (1976) reported a phenotypic correlation of 0.09 between stripping time (minutes) and lactation milk production. Schmidt and Van Vleck (1965) reported a within herd correlation of 0.17 between stripping time and daily milk yield,while the correlations between stripping time and four measurements of udder health were small (0.048 to 0.073). They also reported a correlation of 0.28 between stripping time and machine on time. Little (1968) indicated that the total machine on time per milking averaged 36 seconds longer for stripped than not stripped cows.

Miller et al. (1976) reported a heritability estimate of 0.08 for stripping time.

Milking Machines and Mastitis

Thompson (1977) stated that the milking machine may affect the likelihood of mastitis by directly implanting pathogenic organisms into the streak canal, by engendering long-term deterioration of the teats, and by serving as a reservoir of pathogens. Schalm et al. (1971) and Thiel (1975) indicate that much evidence exists with reference to mechanical milking and mastitis. Yet, experiments are difficult to design and few quantitative data are available to show the combined or separate importance of machine effects to the status of mastitis in herds.

Vacuum Fluctuation

Vacuum fluctuation is a decline and recovery of vacuum level. There are two main types that occur: cyclic fluctuation is the change in the level

of vacuum at the teat end that occurs with each pulsation cycle, while irregular fluctation is a decline and recovery of vacuum that persists over several pulsation cycles. Irregular fluctuation is less frequent than cyclic, occurring randomly when air is allowed into the system (Kingwill et al., 1977).

Fell (1964) and McDonald (1969, 1975) describe the following milking machine characteristics which can lead to vacuum fluctation or affect its severity: inadequate vacuum reserve, too small a vacuum pump, malfunctioning vacuum regulator, improper slope to the milk pipeline, milk entering the bottom half of the milk line, elevation of milk, long vacuum or milk lines, inadequate vacuum line size and air leaks. McDonald (1975) indicated that nearly all aspects of design and operation of the system influence vacuum fluctuation.

Braund and Schultz (1963) studying 1,417 cows in 45 herds reported a highly significant correlation (0.39) between vacuum fluctuation on the line during milking and percent California Mastitis Test (CMT) positive quarters, even though the fluctuation did not exceed 8.5 kPa (2.5" Hg).

Beckley and Smith (1962) in a two year study of 12 herds with pipeline milkers reported a strong correlation between stable vacuum at the teat cup under full load and a low rate of reaction to CMT. Corrections made during the study resulted in improved CMT scores. Cousins, cited by McDonald (1975), observed more irregular fluctuations in systems of two herds with a high rate of infection than in two herds with a low infection rate.

Stanley et al. (1962) suggested that fluctuating vacuum affected udder health, and Nyhan and Cowhig, cited by McDonald (1975), associated irregular fluctuation with intramammary infection, under experimental conditions. Thiel et al. (1973) found that neither irregular or cyclic vacuum fluctuations

alone increased the infection rate, but that irregular fluctuation in combination with cyclic fluctuation did under the experimental conditions used. Wilson (1978) reported unstable vacuum resulted in a significant increase ($P<0.01$) in infections due to Streptococcus dysgalactiae and all other pathogens in a group of 6 cows exposed to S. dysgalactiae cultures, as compared to 6 cows exposed to the culture but milked with stable vacuum.

Westgarth (1978) reported on the use of shields in the teat cup inflation to prevent impacts on the teat end caused by vacuum fluctuation. Experimental results were encouraging, yet in a field trial the rate of infection was 11.1% in not shielded quarters versus 10.0% in shielded quarters. Thiel (1975) stated that the absence of a clearly demonstrated benefit from minimizing all vacuum fluctuations indicates that further knowledge is required before stronger recommendations are made.

Vacuum Reserve

Vacuum reserve is defined as air flow above the actual requirement of the system. Its purpose is to overcome air entering the system. Nyhan and Cowhig (1967) reported that low vacuum reserve was significantly associated with high prevalence of mastitis. They reported a correlation of -0.58 between vacuum reserve and cell count. Both Klastrup and Wilson, cited by McDonald (1975), reported similar findings.

Vacuum Level

Fell (1964) indicated that vacuum is the obvious force theoretically capable of causing trauma, since it acts on the teat end. Kingwill et al.

(1977) stated that greater vacuum levels will result in teat apex damage and higher vacuum levels in the teat sinus at the end of flow, thus it would be reasonable to expect an increase in new infection rate. Both experimental and field studies have investigated the effect of vacuum level on udder health.

Mochrie et al. (1953, 1955) reported no significant difference between 10, 13, and 17 inches Hg (34, 44, and 57.5 kPa) on the chloride content, pH and log cell count of milk. Porter et al., cited by Fell (1964), found no difference in effect of 10 and 13-1/2 inches of vacuum (34 and 46 kPa) on udder health. Neave et al., cited by Fell (1964), found no increased infection in cows milked at 20" (68 kPa) than 12-1/2" (42.5 kPa) even when teats were dipped in a culture of Staphylococcus aureus.

Braund and Schultz (1963) studying 1,417 cows in 45 herds reported a trend for increased vacuum to give increased percent positive quarters. Afifi (1968b) reported that in a field study of Friesian heifers increasing the vacuum above 40 cm Hg (53.5 kPa) resulted in a significant increase in leucocyte count. Fell (1964) reviewed reports by Little and Plastridge and Stevenson, where unsuspected high vacuum (>15", 51 kPa) resulted in clinical mastitis outbreaks. Decreasing the vacuum improved the situation. He suggested a possible interaction between management and level of vacuum.

Thompson (1977) concluded that vacuum >60 kPa imposes excessive stress on teats, while Kingwill et al. (1977) stated that vacuum in the limits of 40-55 kPa (12-16") does not appear to influence infection to any marked degree.

Pulsation

Kingwill et al. (1977) describes the main aspects of pulsation that may

influence the occurrence of udder disease as the rate, ratio, speed of movement and completeness of collapse of liner walls, and whether the four liners in a cluster pulsate alternately or simultaneously. They indicaed that no comprehensive study of the effects of pulsation on mastitis has been made, but field observations indicate that a complete breakdown in pulsation can result in a serious mastitis problem.

Bratlie, cited by Fell (1964), observed an increase in teat damage and cell count with rates of 75/minute as opposed to 40/minute. Watts, cited by Fell (1964), indicated that a milking machine with a rate >100/minute was more conducive to mastitis. However, Akam et al. (1977) concluded that provided effective pulsation occurs, wide differences in pulsator rate and ratio can be tolerated.

Afifi (1968b) reported from field observations a large increase in leucocyte count with a pulsator rate >50/minute, and a slight increase when the rate was <44/minute, leading to no clear relationship. Schmidt Madsen, cited by McDonald (1969), indicated that herd cell counts >300,000/ml were 2.3 times greater in herds with a pulsator ratio of 3:1 vs 1:1. Braund and Schultz (1963) found a significant correlation between pulsator deviation and percent positive quarters, but indicated that this trait was very confusing. Britt (1977) reported a major problem with wider than normal milk to rest ratio and a minor problem with pulsator speed in relation to herd infection. However, Nyhan and Cowhig (1967) reported no significant effect for pulsator rate or ratio on mastitis.

McDonald (1971) suggested that pulsator ratios above 2:1, especially when coupled with vacuum levels >33 cm Hg (44 kPa) at the teat end may increase teat canal erosion, eversion and irritation.

Other Factors

Bowman (1978) and Afifi (1968b) reported no significant effect for brand of milking machine on herd somatic cell count. Nyhan and Cowhig (1967) found no effect of age of milking machine on mastitis levels in herds. Schmidt et al. (1964) experimentally elevated milk 6 ft (1.83 meters) and reported no effect on CMT or leucocyte count when compared to no elevation of the milk. Noorlander (1977) indicated teat cup liner design can influence teat damage and contamination of the teat orifice.

III. SOURCE AND CLASSIFICATION OF DATA

Field data were collected on both the milking speed of Holstein-Friesan cows and the design and performance of the milking machine (pipelines), resulting in two independent data sets.

A. Milking Speed

Source

Milking speed data were obtained for 2,910 Holstein Friesan cows in 73 test herds located in Quebec and Ontario. The herds involved all made use of artificial insemination (AI), were on a milk recording program (ROP, Quebec DHAS or Ontario DHIA) and were visited between June, 1978 and February, 1979.

Milking speed was measured as two-minute milk yield recorded at a single milking using the Milk-o-Meter digital totalizer[1] and total milking time, the time from the seating of the teat cups until their complete removal, was recorded with a stopwatch. Accuracy and operation of the Milk-o-Meter digital totalizer under field conditions has been described by Sharaby et al. (1977).

The total milk yield for the test milking was also obtained from the Milk-o-Meter digital totalizer. Individual milk samples were collected from each cow, representative of the test milking, and sent to the Quebec Dairy Herd Analysis Service (QDHAS) laboratory. There they were analyzed for somatic cell count content by a Fossomatic Somatic Cell Counter[2].

[1] Technical Industries Inc., Fort Lauderdale, Florida.
[2] A/S N. Foss Electric, Hillerød, Denmark.

Lactation production data were obtained for each cow from the milk recording program on which the herd was enrolled. Completed or projected records for 305-day milk and fat and/or BCA milk and BCA fat were available.

The data, along with herd and cow identification, were punched on diskettes then transferred to magnetic tape. Fortran programs were used on an IBM 370 Model 125 computer belonging to QDHAS to read and edit the data tapes.

Data Classification

Only records with cows identified as to sire and containing complete birth dates, calving dates, test-day dates and herd identification were used in subsequent analyses. Because the objective was to look at relationships between traits sub-populations were identified with complete records on combinations of traits. This maximized the use of the collected data, as there were a number of missing values.

It was not always possible to obtain measurements of milking time on all cows, due to the restrictions of labor available to collect these data as well as to operate the milk-o-meters and collect milk samples. Also, not all of the milk recording programs predicted both 305-day milk and fat and BCA milk and fat lactation production. Five subsets of data were utilized, and are shown in Table 4.

Table 4. Subsets of milking speed data with complete cow identification and data on the listed traits.

Number of records	Record populations				
	2619	2604	2488	2235	2138
Traits	BCA milk	Somatic cell count	305-day milk	Somatic cell count	Total milking time
	BCA fat	Two-minute yield	305-day fat	Total milking time	BCA milk
	Two-minute yield	Total milk yield	Two-minute yield	Two-minute yield	BCA fat
	Total milk yield		Total milk yield	Total milk yield	305-day milk 305-day fat Total milk yield

The number of sires and herds in each population are in Table 5. Two herds had groups of cows tested on different days, and for the purpose of analysis these groups were considered as different herds. One of these herds was visited twice, while the other was visited a total of seven times with groups of approximately 15 cows being sampled each day to check the equipment and allow the technicians to become familiar with its usage.

Table 5. Summary of record populations by sires and herds.

	Record populations				
	2619	2604	2488	2235	2138
Herds	79	80	80	79	78
Sires	514	510	503	471	467

All data for each population were classified according to stage of lactation, age of cow at calving, and season of calving as follows:

a) Stage of lactation

Class	Stage of lactation days	Population distribution 2619	2604	2488	2235	2138
1	4-10	44	45	43	34	33
2	11-20	65	66	62	57	53
3	21-30	75	79	67	64	57
4	31-60	214	222	203	193	178
5	61-90	243	252	214	217	186
6	91-120	243	242	219	218	202
7	121-150	223	222	206	191	180
8	151-180	249	248	238	207	198
9	181-210	224	219	215	174	174
10	211-240	254	244	242	208	202
11	241-270	242	237	232	213	204
12	271-305	216	212	213	181	182
13	306-335	130	120	131	109	120
14	≥336	197	196	203	169	169

b) Season of calving

Class	Season of calving	Population distribution 2619	2604	2488	2235	2138
1	March - June	833	824	798	700	676
2	July - October	922	907	840	793	739
3	November - February	864	873	850	742	723

c) Age of cow at calving

Class	Age of cow at calving years	Population distribution 2619	2604	2488	2235	2138
1	≤2	619	625	568	539	497
2	3	547	540	507	469	437
3	4	400	393	386	331	325
4	5	310	316	300	276	262
5	6-7	411	401	401	334	334
6	≥8	332	329	326	286	283

Machine Stripping

Machine stripping data were also obtained for 953 cows in 31 of the herds described previously. Machine stripping was the time from the application of pressure to the milking machine cluster or the beginning of udder massage until the detachment of the machine from the udder. The data were classified by stage of lactation, age of cow at calving and season of calving; classifications being the same as for the milking speed data.

B. Milking Machines and Somatic Cell Counts

A milking machine fact sheet (Appendix Table 1) was prepared, based on suggested methods of machine analysis by Thomas et al. (1972), McDonald (1975), Britt (1977) and Husmann (1977).

Data were collected from 46 farms on the Official Quebec Dairy Herd Analysis Service (O-QDHAS) program. All herds were milking with a pipeline milking machine and were tested for somatic cell count at least eight times during the period from 12 months before to 2 months after testing the herd milking equipment and completing the milking machine fact sheet. Individual cow somatic cell counts were weighted by the cow's production and averaged to produce the herd somatic cell count.

All farms were visited by the same technician (Robert K. Moore) who made the observations and measurements of the milking machine. Measurements of vacuum level and air flow were obtained using an air flow meter, while pulsator performance was recorded using a Pulsograph[1]. Information on whether the

[1] De Laval Separator Company, Poughkeepsie, New York.

dairyman received a somatic cell count report, used a separate towel to wash udders, dried udders, and teat-dipped cows was available for these herds.

Also, similar data had been collected for 21 of the herds described in Section III.A.However, these herds had only the somatic cell count obtained at the time of testing available.

Fifty-two parameters were identified from the machine fact sheet, and the use of the four previously mentioned mastitis control practices was known. Seven variables, combinations of traits that were measured, were generated (Appendix Table 2). All data were keypunched onto cards for subsequent computer analysis. Measured characteristics were stored as the observed value, while the other data were classified with like responses being assigned the same class number within variables.

IV. METHODS OF ANALYSIS

Data relating to milking speed were analysed independently from the data on milking machine design and performance.

A. Milking Speed

Fortran programs used for the statistical analysis were written by B.W. Kennedy and A.K.W. Tong.

Preliminary Least Squares Analysis

The objective was to examine the linear and quadratic effects of total milk yield at the test period on the two-minute milk yield and total milking time. These effects were included as covariates in the following model with the fixed effects of herd, stage of lactation, age at calving and season of calving:

$$Y_{ijklm} = \mu + H_i + A_j + L_k + P_l + b_1 X_{ijklm} + b_2 X^2_{ijklm} + e_{ijklm}$$

where: Y_{ijklm} is the two-minute yield or total milking time of the $ijklm^{th}$ cow

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age of cow at calving

L_k is the fixed effect of the k^{th} stage of lactation

P_l is the fixed effect of the l^{th} season of calving

X_{ijklm} is the total milk yield

b_1 is the partial regression coefficient of Y_{ijklm} on X_{ijklm}

b_2 is the partial regression coefficient of Y_{ijklm} on X^2_{ijklm}

e_{ijklm} is the random error NID (o, σ^2_e).

Both the linear and quadratic effects of total milk yield were significant for the two-minute yield, while only the linear effect was significant for total milking time (Appendix Table 3). As a result, two variables were generated. The first adjusted the two-minute yield for the linear and quadratic effects of total milk yield, and the second adjusted the total milking time for the linear effect, the previous model having been run without the quadratic term. The formulae applied to adjust the data appear as follows:

Adjusted Two-Minute Yield[1]

$$Y_i = M_i - [(0.5209(X_i - 9.6787)) + (-0.0102(X_i^2 - 108.2016))]$$

where Y_i is the adjusted two-minute yield of the i^{th} record

M_i is the recorded two-minute yield of the i^{th} record

X_i is the recorded total milk yield of the i^{th} record

0.5209 and -0.0102 are the partial regression coefficients and 9.6787 and 108.2016 are the population means of X and X^2

Adjusted Milking Time[2]

$$Z_j = T_j - (13.3949(X_j - 9.6187))$$

where Z_j is the adjusted total milking time of the j^{th} record

T_j is the observed milking time of the j^{th} record

X_j is the recorded total milk yield of the j^{th} record

13.3949 is the partial regression coefficient and 9.6187 is the population mean of X.

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[1] 2604 record data set used

[2] 2235 record data set used

Variance Components by Maximum Likelihood

Maximum Likelihood (ML) procedures can be used to obtain joint estimates of unknown constants and variances under the general mixed model. The following, as given by Henderson (1973) and Schaeffer (1976), presents the methodology of deriving maximum likelihood estimates of variance components under a mixed linear model.

General Mixed Linear Model

Consider the following Model:

$Y = Xb + Zu + e$

where Y is a vector of observations of order n x 1

X,Z are the fixed and known matrices of n rows and p and q columns respectively

b is a vector of unknown fixed effects of order p x 1

u is a vector of random variables of order qx1 ~ (0,G)

e is a vector of random errors ~ (0,R)

Additionally, u and e are uncorrelated.

The mixed model equations are:

$$\begin{pmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z+G^{-1} \end{pmatrix} \begin{pmatrix} \hat{b} \\ \hat{u} \end{pmatrix} = \begin{pmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{pmatrix}$$

If, K'b is estimable, then $K'\hat{b}$ is the best linear unbiased estimator (BLUE) of K'b. In the preceding, G and R are assumed known. If ML estimates of G and R are available, then these can be used and the resulting $K'\hat{b}$ and $\hat{u}$ are also ML estimates of K'b and the conditional mean of u given y. Further, it is possible to derive joint ML solutions for b, u, G and R in a single mixed model analysis.

Procedure

Partition u' and Z' into s subvectors and matrices corresponding to individual random effects in the model.

i.e. $u' = (u_1', u_2', \ldots u_s')$

$Z' = (Z_1', Z_2', \ldots Z_s')$

and, assuming $R = I_n \sigma_e^2$ and

$$G = \begin{pmatrix} I_{q_1}\sigma_1^2 & & & 0 \\ & I_{q_2}\sigma_2^2 & & \\ & & \ddots & \\ 0 & & & I_{q_s}\sigma_s^2 \end{pmatrix}$$

, where q_i is the order of u_i

then $\text{var}(y) = \left(\sum_{i=1}^{s} Z_i Z_i' \frac{\sigma_i^2}{\sigma_e^2} + I \right) \sigma_e^2$

If, u and e are uncorrelated and normally distributed, we can estimate b, σ_e^2, and $\sigma_1^2, \sigma_2^2, \ldots \sigma_s^2$ by ML.

A solution for b is obtained from the mixed model equations

$$\begin{pmatrix} X'X & X'Z \\ Z'X & Z'Z+D \end{pmatrix} \begin{pmatrix} \hat{b} \\ \hat{u} \end{pmatrix} = \begin{pmatrix} X'y \\ Z'y \end{pmatrix}$$

where

$$D = \begin{pmatrix} I_{q_1}\sigma_e^2/\sigma_1^2 & & & 0 \\ & \ddots & & \\ 0 & & & I_{q_s}\sigma_e^2/\sigma_s^2 \end{pmatrix} = G^{-1}\sigma_e^2$$

In partitioned form Z'Z+D

$$\begin{bmatrix} Z_1'Z_1 + I_{q_1}\,\sigma_e^2/\sigma_1^2 & Z_1'Z_2 \cdots\cdots & Z_1'Z_s \\ Z_2'Z_1 & Z_2'Z_2 + I_{q_2}\,\sigma_e^2/\sigma_2^2 & Z_2'Z_s \\ \vdots & \vdots & \vdots \\ Z_s'Z_1 & Z_s'Z_2 & Z_s'Z_s + I_{q_s}\,\sigma_e^2/\sigma_s^2 \end{bmatrix}$$

Let the inverse of Z'Z+D=T

$$\text{and } T = \begin{bmatrix} T_{11} & T_{12} \cdots\cdots & T_{1s} \\ T_{12}' & T_{22} & T_{2s} \\ \vdots & \vdots & \vdots \\ T_{1s}' & T_{2s}' & T_{ss} \end{bmatrix}$$

then, the ML estimates of σ_e^2, σ_1^2, σ_2^2,.... σ_s^2 are

$$\hat{\sigma}_e^2 = (y'y - \hat{b}' X'y - \hat{u}'Z'y) / n$$

$$\hat{\sigma}_i^2 = (\hat{u}_i'\hat{u}_i + \hat{\sigma}_e^2 \text{tr } T_{ii}) / q_i$$

Note for $\hat{\sigma}_e^2$, n is the total number of observations, thus the ML estimate of $\hat{\sigma}_e^2$ is not unbiased.

An unbiased $\hat{\sigma}_e^2$ is,

$$\hat{\sigma}_e^2 = (y'y - \hat{b}'X'y - \hat{u}'Z'y) / (n - r\,(X'X))$$

and this is used in the following analyses to compute the test statistic for $H_o = K'\hat{b} = 0$, with K chosen to estimate the difference from the last level within a fixed factor.

Prior Estimates and Iteration

These solutions require a starting point or prior estimates of σ_e^2/σ_i^2. Prior estimates were available for two-minute yield (Sharaby, 1977), while for the other traits starting values were guessed at. The first estimates of σ_e^2/σ_i^2 produced the first set of solutions and estimates of variance components. These results were then substituted and the new equations formed and solved. Repeated rounds of iteration were run until the difference between error to sire variance ratios in two successive rounds were$<|.01|$.

To hasten convergence, the following technique was utilized to estimate the variance rates at the point of convergence:

Analyses using high (R_h) and low (R_l) starting variance ratios were performed. For each analyses, new variance ratios (R_h^* and R_l^*) were computed based on the ML solutions of σ_e^2 and σ_i^2. The absolute difference between the input variance ratio and the output variance ratio ($d_h = |R_h - R_h^*|$ and $d_l = |R_l - R_l^*|$) was computed for each analyses and summed ($d_t = d_h + d_l$). The next input ratio was then computed as

$$R_n = R_h - (d_h/d_t) \times (R_h - R_l)$$

or $$R_n = R_l + (d_l/d_t) \times (R_h - R_l)$$

A numerical example follows:

Example:	Input	Output Ratio	|Difference|
Low ratio input	100	100.1322	0.1322
High ratio input	145	144.9584	0.0416
Difference between input ratios	45	Summation of |Difference|	0.1738

$$\therefore \text{ Next Input ratio} = 145 - \left(\frac{.0416}{.1738} \times 45\right) = 132.2$$

$$\text{or alternately next ratio} = 100 + \left(\frac{.1322}{.1738} \times 45\right) = 132.2$$

Mixed Model Analysis

Sire was included as a random effect under a mixed model including stage of lactation, age of cow at calving, season of calving and herd as fixed effects. The model was as follows:

$$Y_{ijklmn} = \mu + H_i + A_j + L_k + P_l + S_m + e_{ijklmn}$$

where Y_{ijklmn} is a record of the n^{th} cow for the trait being studied

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age of cow at calving

L_k is the fixed effect of the k^{th} stage of lactation

P_l is the fixed effect of the l^{th} season of calving

S_m is a random effect associated with the m^{th} sire $\sim(0, I\sigma_e^2)$

This model was analyzed according to ML techniques for all traits listed in the record populations (Table 4), except total test day milk yield, as well as the two adjusted measurements of milking speed and the log (natural) somatic cell count which was transformed from the raw observations. Classifications were as defined in Section III A.

This provided estimates of the variance components, best linear unbiased estimates (BLUE) of fixed effects and best linear unbiased predictors (BLUP) of random effects for the traits considered.

Also, this mixed model was used to provide ML estimates of the variances of two traits considered together, $\hat{\sigma}^2_{x+y}$, which were used to obtain estimates of the covariances between traits.

Heritability Estimation

Heritability may be defined as the fraction of total phenotypic variation attributable to genetic differences. In this study, the heritability was estimated by the Paternal Half Sib (PHS) method for all traits, assuming that sires are unrelated.

$$h^2 = \frac{4\,\hat{\sigma}_s^2}{\hat{\sigma}_p^2} = \frac{4\,\hat{\sigma}_s^2}{\hat{\sigma}_s^2+\hat{\sigma}_e^2}$$

where $\hat{\sigma}_s^2$ is the estimate of the sire variance

$\hat{\sigma}_e^2$ is the estimate of the error variance

$\hat{\sigma}_p^2$ is therefore the estimate of the phenotypic variance

Genetic and Phenotypic Correlations

The correlation between two variables indicates the degree to which the variables vary together. Product Moment Correlation (PMC) is a simple linear correlation defined by Pearson, and calculated in the following way:

$$\hat{r}_{xy} = \frac{\hat{\sigma}_{xy}}{\sqrt{\hat{\sigma}_x^2\,\hat{\sigma}_y^2}}$$

where r_{xy} is the estimated correlation coefficient between traits x and y

$\hat{\sigma}_{xy}$ is the estimated covariance between traits x and y

$\hat{\sigma}_x^2$ is the estimated variance of trait x

$\hat{\sigma}_y^2$ is the estimated variance of trait y.

Covariances between traits were estimated from variances obtained by ML as follows:

$$\hat{\sigma}_{x+y}^2 = \hat{\sigma}_x^2 + \hat{\sigma}_y^2 + 2\,\hat{\sigma}_{xy}$$

thus $$\hat{\sigma}_{xy} = \tfrac{1}{2}\,(\hat{\sigma}_{x+y}^2 - \hat{\sigma}_x^2 - \hat{\sigma}_y^2)$$

where $\hat{\sigma}^2_{x+y}$ is the variance component for the sum of trait x and trait y and the others are as previously defined.

Genetic correlations were calculated as:

$$\hat{r}_g = \frac{\hat{\sigma}_{sxsy}}{\sqrt{\hat{\sigma}^2_{sx}\ \hat{\sigma}^2_{sy}}}$$

where $\hat{\sigma}_{sxsy}$ is the sire covariance between trait x and trait y

$\hat{\sigma}^2_{sx}$ is the sire variance for trait x

$\hat{o}^2_{sy}$ is the sire variance for trait y

Phenotypic correlations were calculated as:

$$r_p = \frac{\hat{\sigma}_{pxpy}}{\sqrt{\hat{o}^2_{px}\quad \hat{\sigma}^2_{py}}}$$

where $\hat{\sigma}_{pxpy}$ is the phenotypic (sire plus error) covariance between trait x and trait y.

$\hat{\sigma}^2_{px}$ is the phenotypic variance for trait x

$\hat{\sigma}^2_{py}$ is the phenotypic variance for trait y.

Spearman rank correlation is a measure of association based on rank. It requires that the population has a bivariate normal distribution and that both variables are measured in an ordinal scale so that individuals may be ranked in two ordered series.

The formula for calculation, described by Siegal (1956) is shown below:

$$r_s = 1 - 6\ \frac{\sum_{i=1}^{N} d_i^2}{N^3 - N}$$

where d is the differences between ranks for each pair of observations

N is the number of pairs of observations

Spearman rank correlations were computed between the BLUP evaluations obtained for 56 sires for two-minute yield, adjusted two-minute yield, total milking time and adjusted total milking time in the 2235 record population. There were no tied observations in any of the variables, the preceding formula being the appropriate one.

Least Squares Analysis with Milking Speed Variables Treated as Fixed Effects

Two-minute yield and adjusted two-minute yield were classified into 10 classes and total milking time and adjusted total milking time into 7 classes, as illustrated below, for inclusion in a least squares analysis with the two measures of somatic cell count as dependent variables.

a) Classes of Two-Minute Yield:

Class	Two-minute or adjusted two-minute yield (kg)	Number of observations	
		Two minute yield	Adjusted Two-minute yield
1	<3.0	377	329
2	3.0<3.5	215	168
3	3.5<4.0	235	273
4	4.0<4.5	305	296
5	4.5<5.0	316	360
6	5.0<5.5	257	315
7	5.5<6.0	219	291
8	6.0<6.5	207	221
9	6.5<7.0	143	143
10	>7.0	330	208
		2604	2604

b) Classes of Total Milking Time:

Class	Total or adjusted total Milking Time (seconds)	Number of Observations	
		Total Milking Time	Adjusted Total Milking Time
1	<240	339	258
2	240<300	367	418
3	300<360	444	505
4	360<420	393	404
5	420<480	255	253
6	480<540	165	163
7	>540	272	234
		2235	2235

The model was as follows:

$$Y_{ijklmn} = \mu + H_i + A_j + L_k + P_l + T_m + e_{ijklmn}$$

where Y_{ijklmn} is a record of the n^{th} cow for the trait being studied

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age at calving

L_k is the fixed effect of the k^{th} stage of lactation

P_l is the fixed effect of the l^{th} season of calving

T_m is the fixed effect of the m^{th} level of the milking speed variable (two-minute yield, adjusted two-minute yield, total milking time or adjusted total milking time).

e_{ijklmn} is the random error associated with the $ijklmn^{th}$ record $\sim(o, \sigma_e^2)$.

All the other fixed effects were classified as in section III A. Herd effects were absorbed in the analyses.

Machine Stripping

A preliminary least squares analysis was run according to the following model to determine the effects of stage of lactation, age at calving, season of calving and herd on stripping time.

$$Y_{ijklm} = \mu + H_i + A_j + L_k + P_l + e_{ijklm}$$

where Y_{ijklm} is the stripping time for the $ijklm^{th}$ cow

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age of cow at calving

L_k is the fixed effect of the k^{th} stage of lactation

P_l is the fixed effect of the l^{th} season of calving

e_{ijklm} is the random error NID (o,σ_e^2)

Classifications were as defined in section III A. The effects of herd and age of cow were significant ($P<0.01$) as seen in Appendix Table 4.

As a result, the following model was run under ML analysis, to estimate variance components for sire and error terms:

$$Y_{ijkl} = \mu + H_i + A_j + S_k + e_{ijkl}$$

where Y_{ijkl} is the stripping time for the $ijkl^{th}$ cow

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age of cow at calving

S_k is a random effect associated with the k^{th} sire $\sim(o, I\sigma_s^2)$

e_{ijkl} is the random error associated with $ijkl^{th}$ record $\sim(o,I\sigma_e^2)$

Convergence was not achieved for σ_e^2/σ_i^2 for this model.

Phenotypic Product Moment Correlations were computed between machine stripping time and the variables that appear in Table 4, as well as the log (natural) somatic cell count. Also, the partial regression coefficients of stripping time for these 11 traits were computed by least squares analysis according to the following model:

$$Y_{ijklm} = \mu + H_i + A_j + L_k + P_l + b_1 X_{1ijklm} + e_{ijklm}$$

where Y_{ijklm} is record of the $ijklm^{th}$ cow for the trait being considered

μ is the population mean

H_i is the fixed effect of the i^{th} herd

A_j is the fixed effect of the j^{th} age of cow at calving

L_k is the fixed effect of the k^{th} stage of lactation

P_l is the fixed effect of the l^{th} season of calving

b_1 is the partial regression coefficient of stripping time for the trait being considered

X_{1ijklm} is the stripping time observation of the $ijklm^{th}$ cow

e_{ijklm} is the random error associated with the $ijklm^{th}$ record $\sim (o, \sigma_e^2)$

A similar model was used for 305-day milk and fat and BCA milk and BCA fat, including the effects of half-day milk yield as a second covariate in the model.

B. Milking Machines and Somatic Cell Counts

Data analysis was carried out using the SAS 76 (Barr et al., 1976) statistical package on the McGill University computing system.

All Variables

All identified milking machine and management characteristics (Section III B) were analyzed separately in a one-way analysis of variance with herd somatic cell count as the dependent variable. For the 46 herd population, the herd average somatic cell count was the dependent variable, and for the 67 herd population the dependent variable was the herd somatic cell count on the day the machine was tested.

Continuous variables were analyzed by least squares, according to the following model using GLM option of SAS 76:

$$Y_i = \mu + bX_i + e_i$$

where Y_i is the somatic cell count of the i^{th} herd

μ is a constant

b is the simple regression coefficient associated with the variable being tested

X_i is the value for the i^{th} herd for the variable being tested

e_i is the random error associated with the i^{th} herd $\sim(o, \sigma_e^2)$.

Classification data variables were analyzed by least squares according to the following model, also using the GLM option of SAS 76.

$$Y_{ij} = \mu + C_i + e_{ij}$$

where Y_{ij} is the somatic cell count of the ij^{th} observation

μ is the population mean

C_i is the effect of the i^{th} level of the classification variable being considered

e_{ij} is the random error of the ij^{th} observation $\sim(o, \sigma_e^2)$.

Variables from these first analyses that had a significance level of less than 0.1 were carried to the subsequent analyses, with the rest of the characteristics receiving no further consideration.

Selected Variables

Classification variables with two levels and continuous variables that met the 0.1 level of significance were included in a multiple regression type analysis using the STEPWISE option of SAS 76. Means of the continuous variables as well as product moment correlations between pairs of continuous variables were computed using the CORR procedure. Means and simple descriptive statistics for classification variables, as well as for all variables within a specific classification level, were obtained using the MEANS procedure of SAS 76. Finally, to include classification variables with more than two levels in multiple variable models, the GLM procedure was used. The multiple classification variables were considered in models with the variables that had been included in the best multiple regression equation, as selected by stepwise regression.

V. RESULTS AND DISCUSSION

A. Milking Speed

Means and standard deviations of the milking speed, somatic cell count and lactation production traits in the five record populations appear in Tables 6 and 7. the mean two-minute yield (4.85 kg) was almost equal to that observed by Sharaby (1977), while the mean somatic cell count (379,000/ml) was similar to that reported by Moxley et al. (1978), for Holstein-Friesan cows on official test in eastern Canada. The lactation production of these cows was above the breed average.

Table 6. Means and standard deviations of measurements of milking speed and somatic cell count.

No. of records	Population 2604		2235	
Trait	Mean	SD	Mean	SD
Two-minute yield (kg)	4.86	1.83	4.84	1.83
Adjusted two-minute yield (kg)	4.86	1.53	4.86	1.53
Somatic cell count ('000/ml)	381	805	377	782
Log somatic cell count	5.07	1.25	5.08	1.24
Total milking time (seconds)	--	--	375.7	142.7
Adjusted total milking time (seconds)	--	--	375.7	129.0

Table 7. Means and standard deviations of measurements of milking speed and lactation milk and fat production.

No. of Records	Population 2619		2448		2138	
Trait	Mean	SD	Mean	SD	Mean	SD
Two-minute yield (kg)	4.83	1.86	4.85	1.88	--	--
Adjusted two-minute yield (kg)	4.87	1.52	4.90	1.52	--	--
BCA milk	137.2	23.6	--	--	137.5	23.4
BCA fat	140.1	27.0	--	--	141.0	26.6
305-day milk (kg)	--	--	6697.2	1326.8	6680.1	1328.1
305-day fat (kg)	--	--	253.3	54.1	252.8	54.3
Total milking time (seconds)	--	--	--	--	371.8	142.2
Adjusted total milking time (seconds)	--	--	--	--	373.3	128.5

Fixed Effects

The significance of the fixed effects that were considered - herd, stage of lactation, age at calving and season of calving - for the traits analyzed in each record population appear in Appendix Tables 5 to 9.

Fixed effects were included in the model to account for known sources of variation. They all had a significant effect on all lactation production measurements. The significance of stage of lactation, age at calving and season of calving on lactation production, and in particular BCA milk and fat which are adjusted for age and season of calving, may be due in part to the use of projected records, cows in lactation for more than one year, and

older cows that have withstood the pressure of selection. Only season of calving was not highly significant ($P<0.01$) in its effect on somatic cell count and log somatic cell count, differing in this respect from the report of Kennedy et al. (1978).

The effects of herd and stage of lactation (with one exception) were highly significant ($P<0.01$) on two-minute yield, adjusted two-minute yield, total milking time and adjusted total milking time for all the record populations in which these traits appeared. Age at calving did not have a significant effect on two-minute yield, but its effect was significant after adjusting for the total milk yield. Age appeared as a highly significant factor on both measurements of milking time. Season of calving had no significant effect on any of the four milking speed measurements.

Best Linear Unbiased Estimates (BLUE) of significant effects of stage of lactation on two-minute yield and adjusted two-minute yield (2604 records), and total milking time and adjusted total milking time (2235 records) appear in Figures 1 to 4. These estimates are adjusted for the other previously mentioned fixed effects.

The two-minute yield peaked early in lactation, and then declined steadily as the lactation progressed. This decline with advancing lactation was also observed by Sharaby (1977). However, the pattern was completely reversed after adjusting for the linear and quadratic effects of milk yield, although the magnitude of the response was reduced. This increase in milking speed with advancing stage of lactation after adjusting for total milk yield has also been reported by Schmidt and Van Vleck (1969), Touchberry and Markos (1970) and Smith et al. (1974). The effect of stage of lactation did not become non-significant after adjusting for total milk yield as was the case for Sharaby et al. (1979).

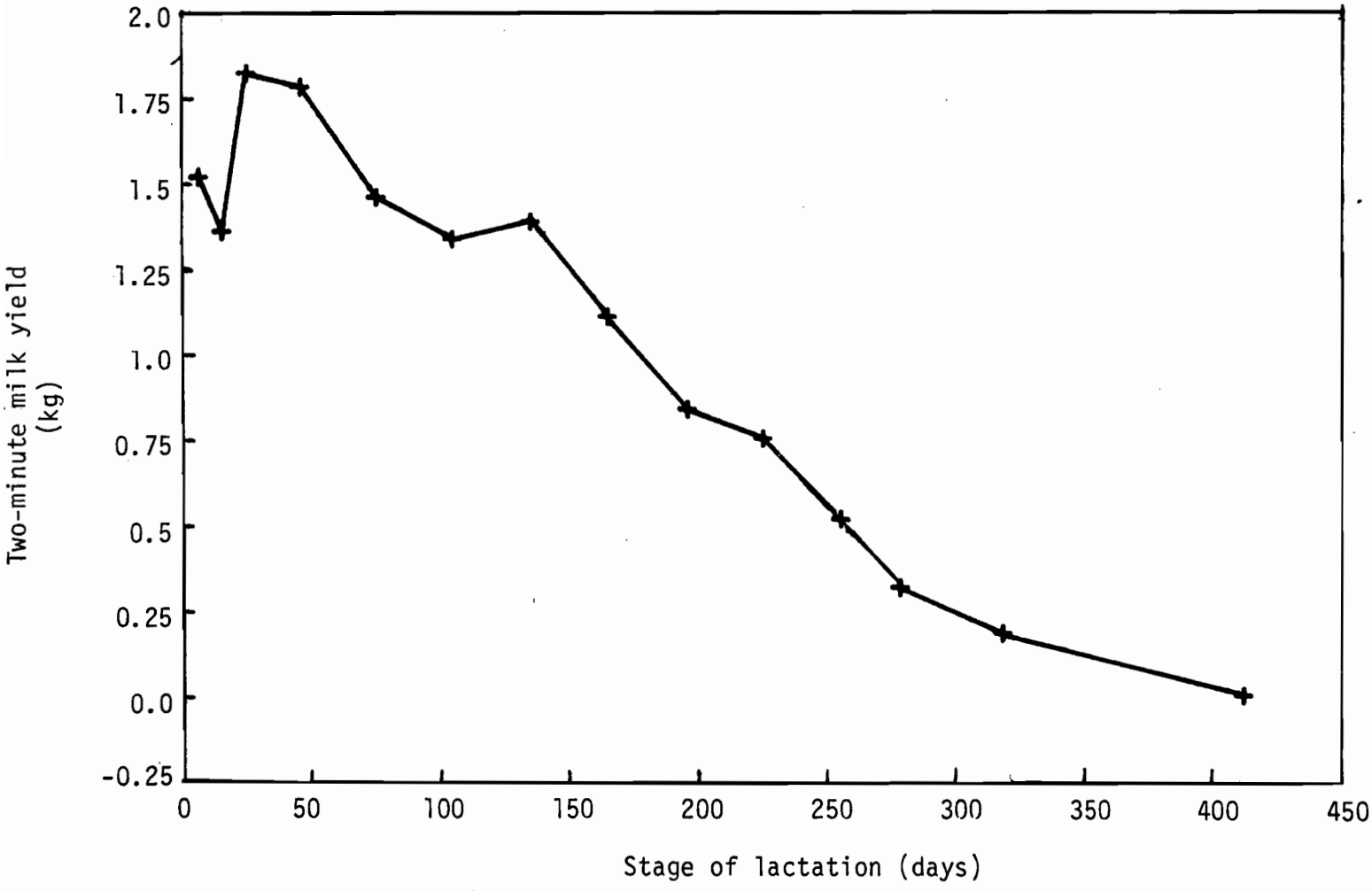

Figure 1. Best Linear Unbiased Estimates (BLUE) of the effect of stage of lactation on two-minute milk yield.

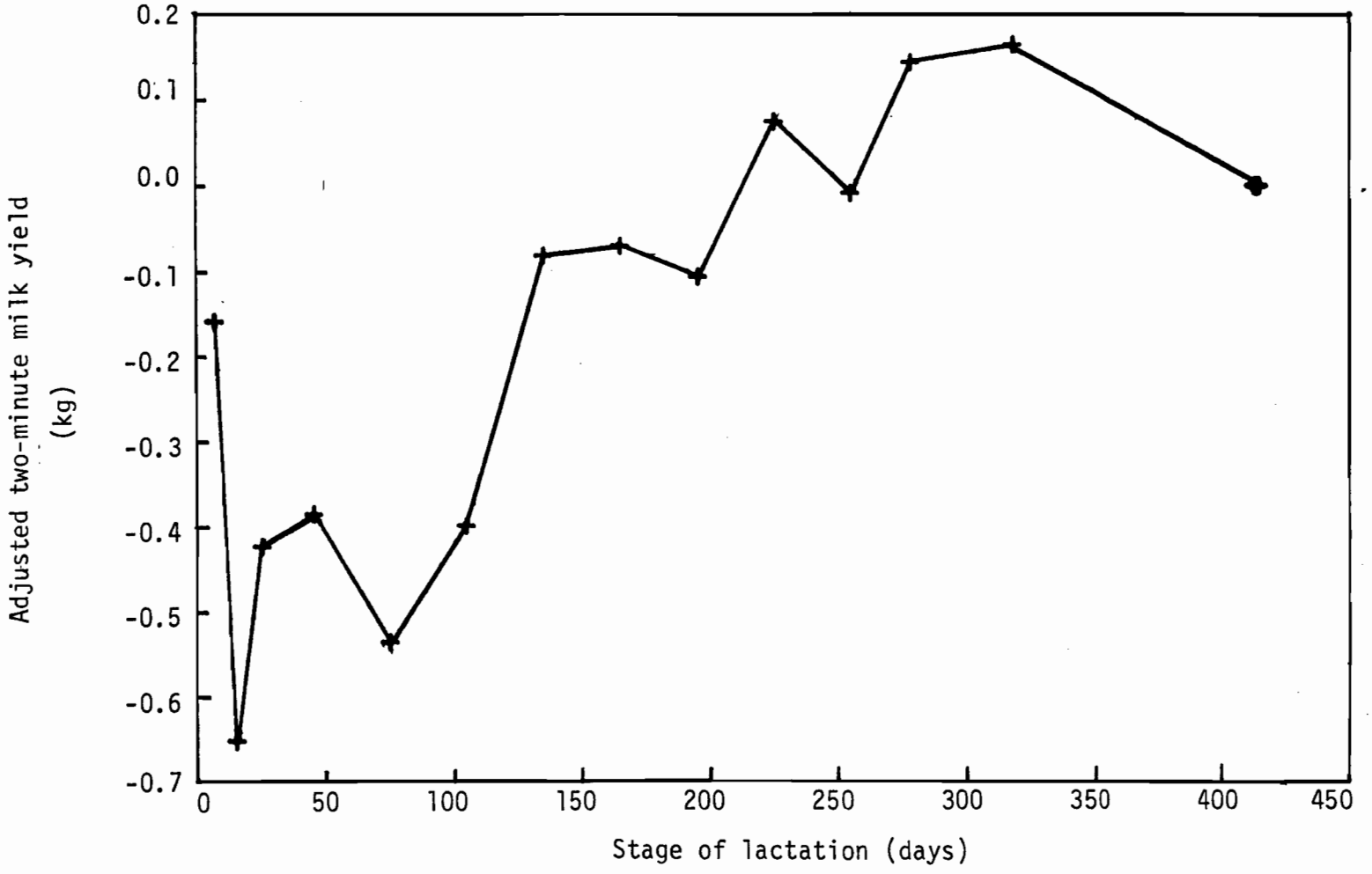

Figure 2. Best Linear Unbiased Estimates (BLUE) of the effect of stage of lactation on adjusted two-minute milk yield.

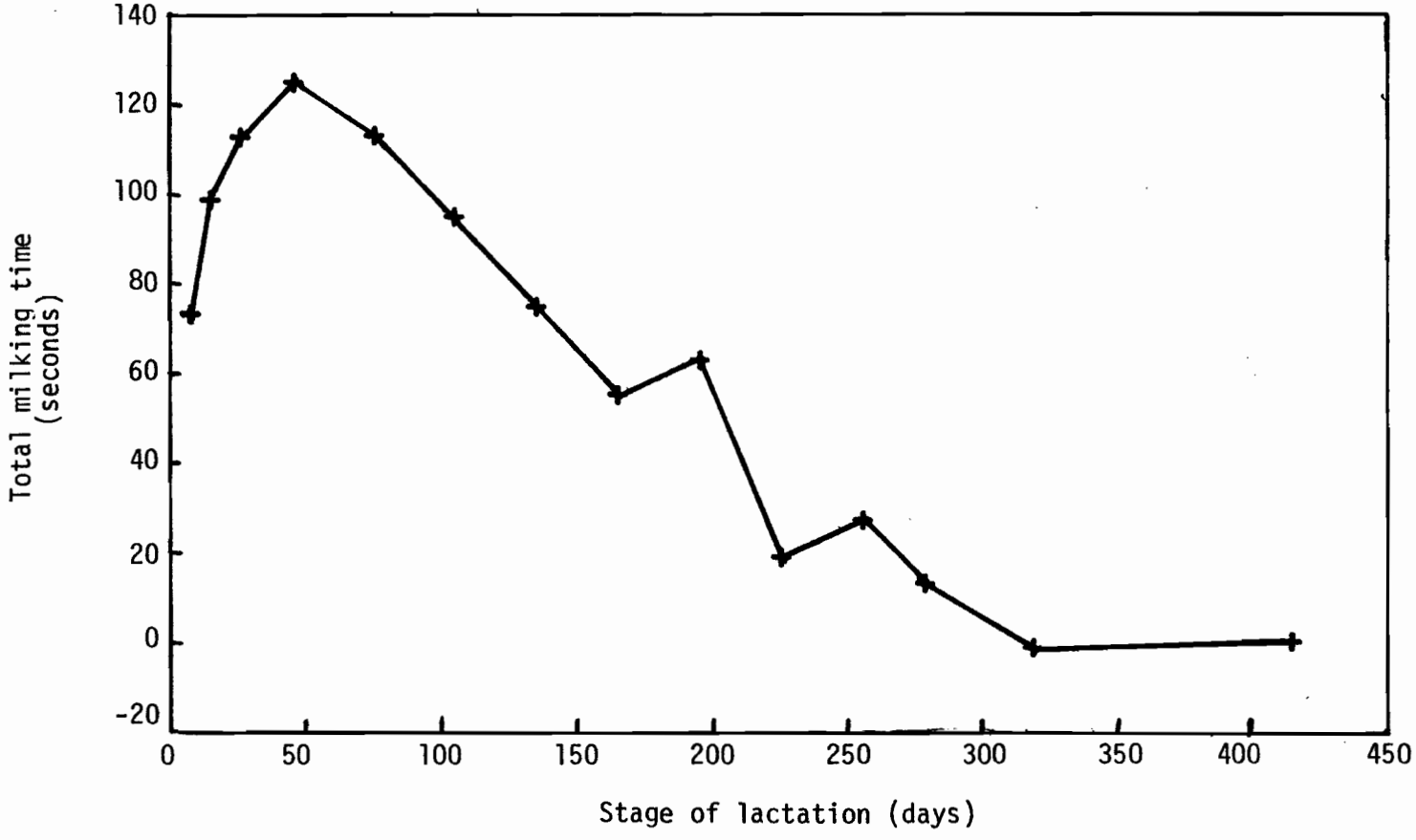

Figure 3. Best Linear Unbiased Estimates (BLUE) of the effect of stage of lactation on total milking time.

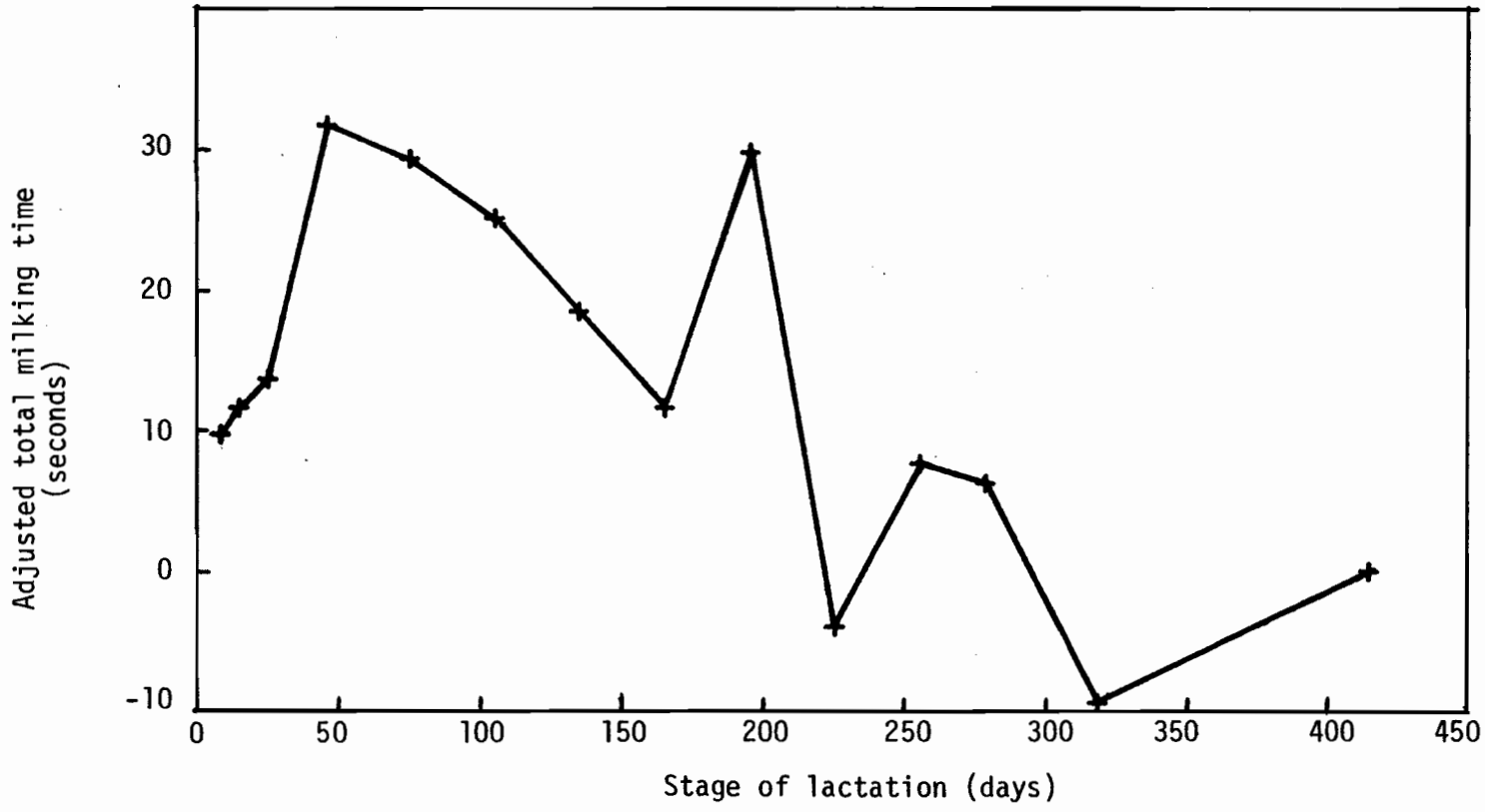

Figure 4. Best Linear Unbiased Estimates (BLUE) of the effect of stage of lactation on adjusted total milking time.

Total milking time followed a pattern similar to two-minute yield as the lactation progressed. Thus, even though the cows were milking more in the first two minutes early in lactation, it took a longer total time to remove all of the milk. When the adjustment was made for the total milk yield, cows early in lactation still took a longer time to milk. This is consistent with the lower adjusted two-minute yields early in lactation and was also reported by Schmidt and Van Vleck (1969) and Touchberry and Markos (1970).

Significant age of cow effects appear in Figures 5 to 7, with age of cow having no significant effect on two-minute yield. The only significant age difference for adjusted two-minute yield was between <3 and >8-year olds, with the younger cows milking faster and the older cows more slowly than the others. The non-significant effect of age on two-minute yield and significant effect when adjusted for total milk is in contrast to what was observed by Sharaby et al. (1979). An inverse relationship between age and milking rate was also reported by Rathore (1976).

With increasing age, the total milking time increased. Correcting for the total yield produced the same effect, although the difference in time was not as extreme for the younger classifications of cows. Schmidt and Van Vleck (1965) also found that machine time increased significantly with age.

Heritability Estimates

Variance components obtained by Maximum Likelihood analysis for milking speed, somatic cell count and lactation production traits were used to estimate the heritabilities of traits for each record population (Tables 8 and 9).

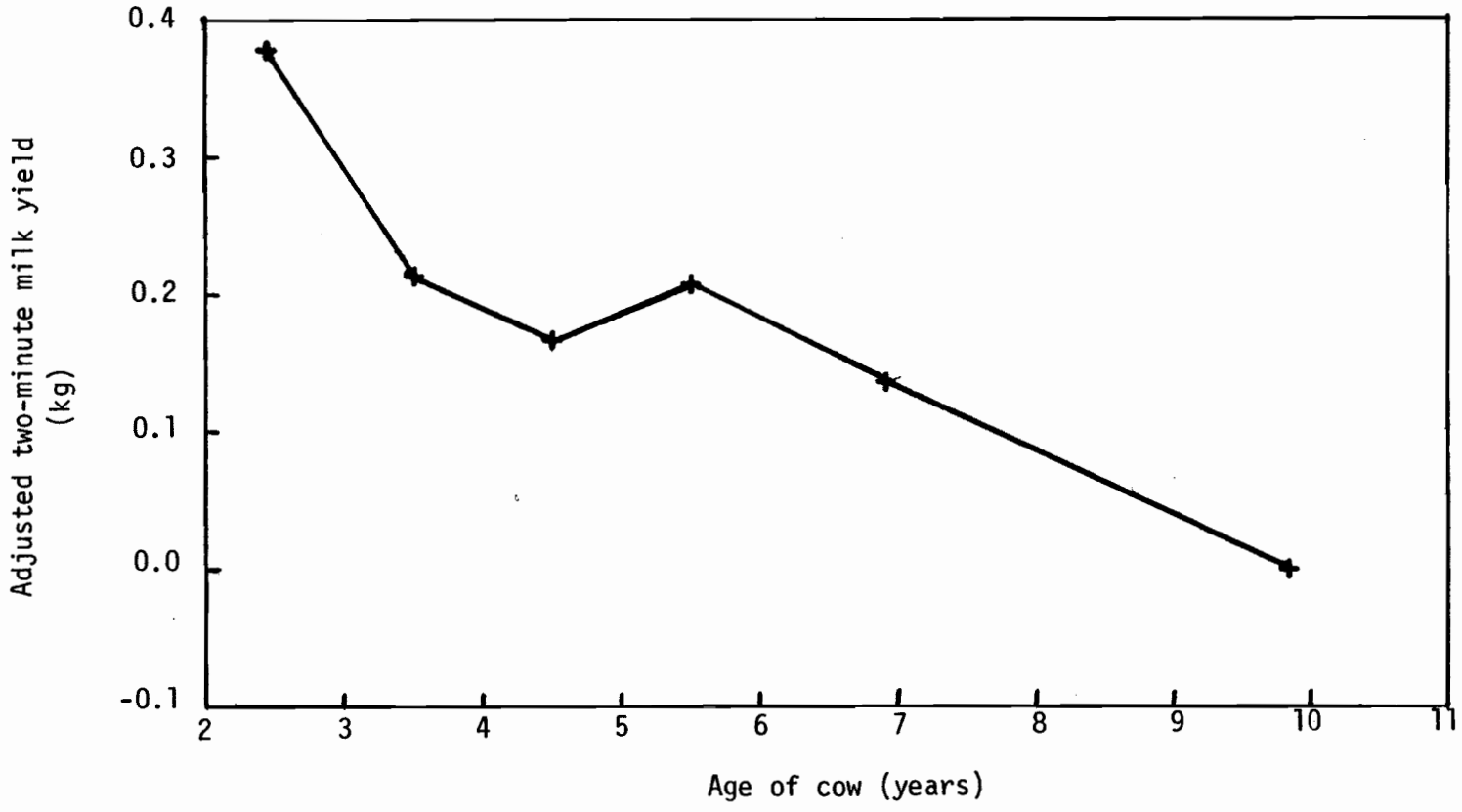

Figure 5. Best Linear Unbiased Estimates (BLUE) of the effect of age of cow on adjusted two-minute milk yield.

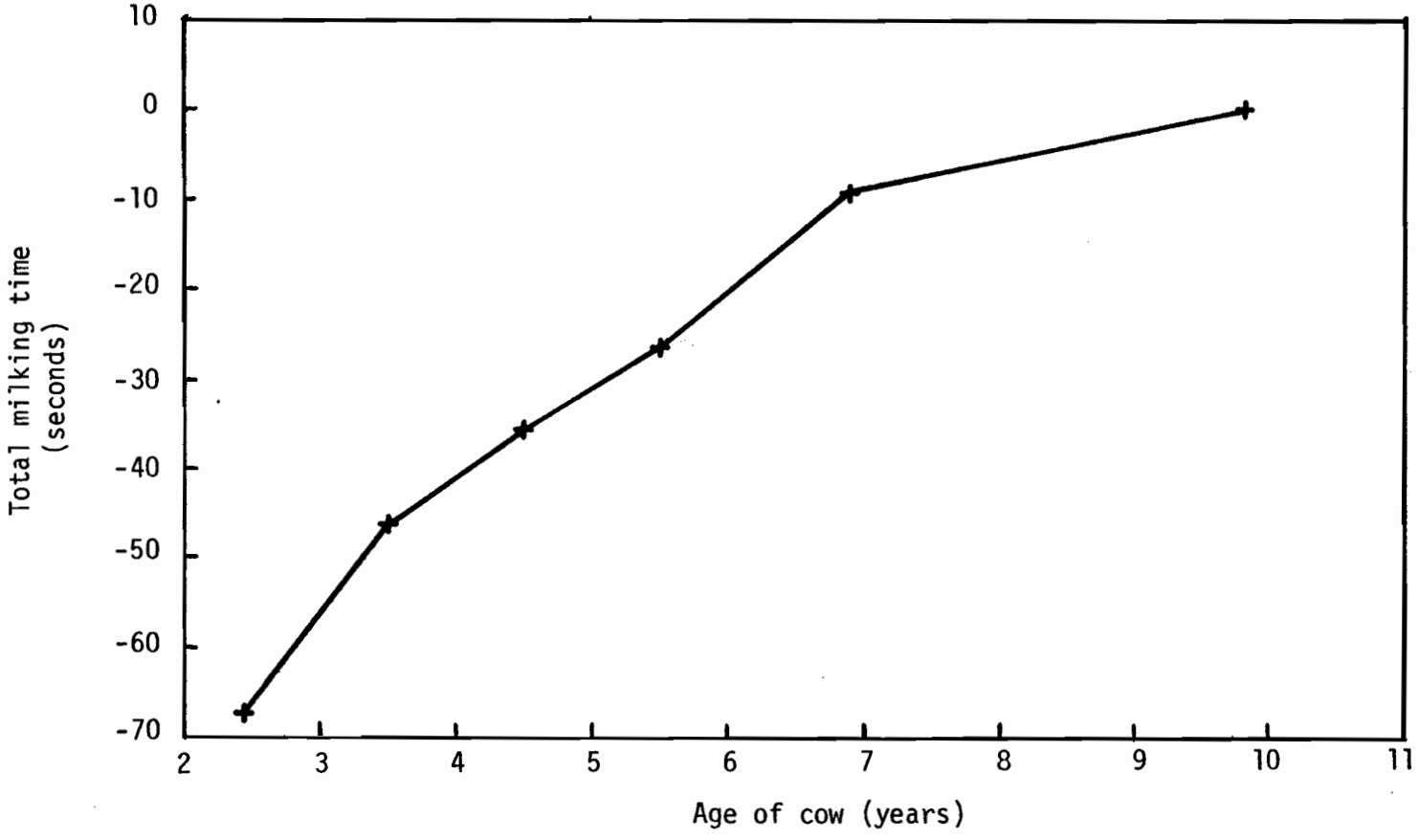

Figure 6. Best Linear Unbiased Estimates (BLUE) of the effect of age of cow on total milking time.

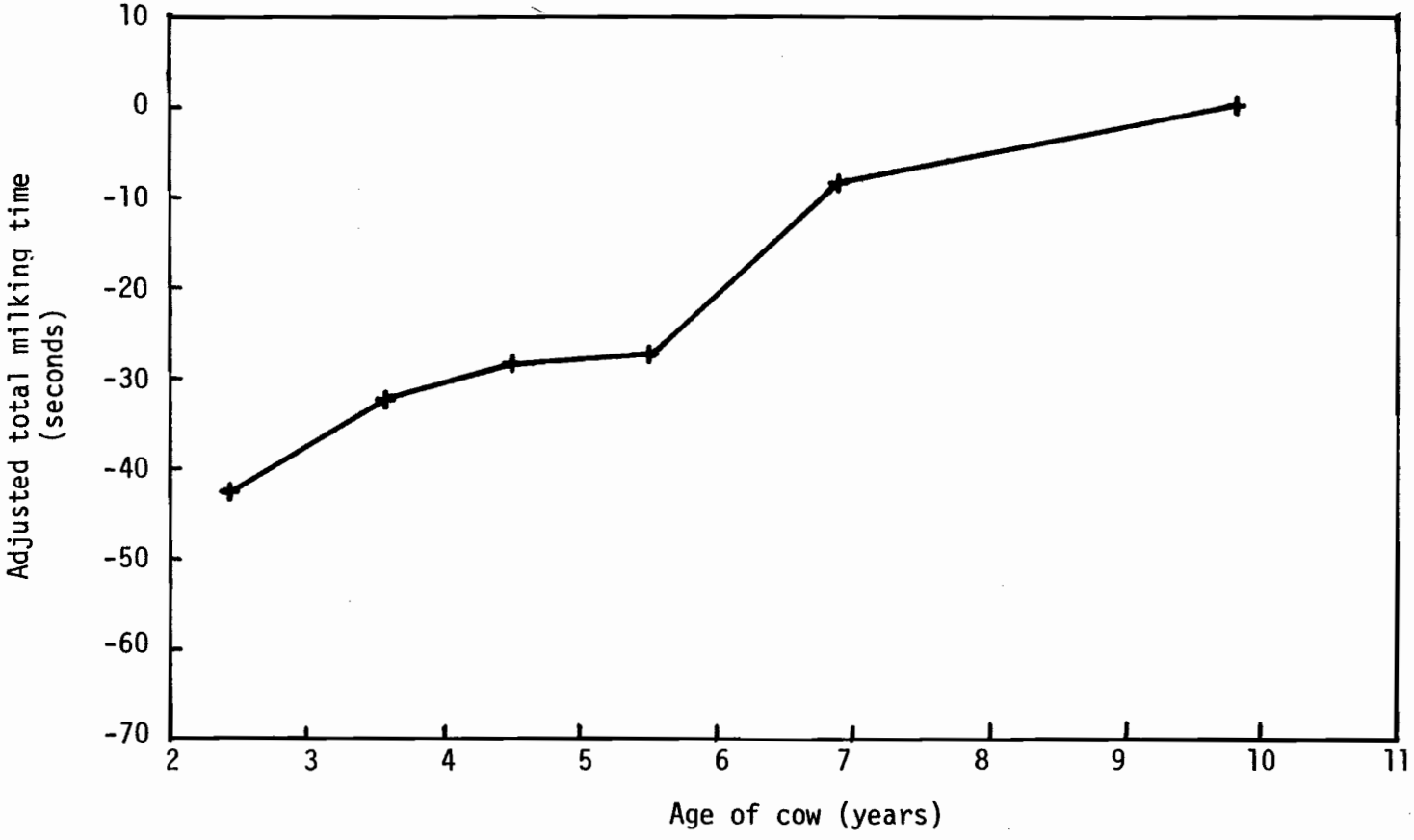

Figure 7. Best Linear Unbiased Estimates (BLUE) of the effect of age of cow on adjusted total milking time.

Table 8. Heritability estimates of measurements of milking speed and somatic cell count.

No. of Records	Population 2604	Population 2235
Trait		
Two-minute yield	0.18±0.06	0.23±0.07
Adjusted two-minute yield	0.23±0.06	0.26±0.07
Somatic cell count	0.06±0.04	0.02±0.03
Log somatic cell count	0.03±0.03	0.02±0.03
Total milking time	--	0.18±0.06
Adjusted total milking time	--	0.13±0.05

Table 9. Heritability estimates of measurements of milking speed and lactation milk and fat production.

No. of records	Population 2619	Population 2448	Population 2138
Trait			
Two-minute yield	0.20±0.06	0.17±0.06	--
Adjusted two-minute yield	0.23±0.06	0.22±0.06	--
BCA milk	0.21±0.06	--	0.20±0.06
BCA fat	0.32±0.07	--	0.32±0.08
305-day milk	--	0.15±0.05	0.15±0.06
305-day fat	--	0.30±0.07	0.28±0.07
Total milking time	--	--	0.20±0.06
Adjusted total milking time	--	--	0.16±0.06

The heritabilities of two-minute yield (0.17 to 0.23) were similar although slightly lower than that reported by Sharaby et al. (1979). The values for the adjusted two-minute yield (0.22 to 0.26) were slightly lower than that reported by Tomaszewski et al. (1975), but almost equal to the value reported by Sharaby et al. (1979). Adjusting the two-minute yield for the total milk yield resulted in higher heritability estimates, which is contrary to what was observed by Sharaby et al. (1979). The higher heritabilities after adjusting, suggest that the differing amounts of milk present at sampling may mask some of the genetic variance for milk flow rate.

The heritability estimates (0.18 and 0.20) for total milking time were lower than those reported by Colleau (1971), but almost equal to the values reported by Odegard (1966) and Miller et al. (1976). They are, however, larger than the values for the adjusted total milking time (0.16 and 0.13). Adjusting for the total milk yield reduced the genetic variance for the trait. The lower heritability estimates for measurements of total milking time than two-minute yield indicate a greater environmental influence on milking time. Measuring total milking time is much more dependent on the operator and the milking routine than is a measurement of two-minute yield.

The estimated heritabilities of both somatic cell count and log somatic cell count were very low (0.02 to 0.06). These estimates are based on a half-day milk sample. However, Sethar et al. (1979), using repeated observations on a large sample of cows, have shown the heritability of somatic cell count to be rather small (h^2=0.08).

The heritability estimates of the production traits are similar to those in the literature, keeping in mind that some projected records and different lactation numbers were used in their estimation.

Phenotypic and Genetic Correlations

Phenotypic and genetic correlations were calculated between milking speed, somatic cell count and lactation production traits from maximum likelihood estimates of variance and covariance. Correlations between measurements of milking speed and somatic cell count appear in Tables 10 and 11.

Table 10. Phenotypic and genetic correlations between measurements of milking speed and somatic cell counts (2604 records)

	Two-minute yield		Adjusted two-minute yield	
	Phenotypic	Genetic	Phenotypic	Genetic
Adjusted two-minute yield	0.88	0.96	--	--
Cell count	-0.01	0.05	0.08	0.13
ln cell count	0.00	0.94	0.09	0.79

Table 11. Phenotypic and genetic correlations between measurements of milking speed and somatic cell counts (2235 records)

	Milking time		Adjusted milking time	
	Phenotypic	Genetic	Phenotypic	Genetic
Two-minute yield	-0.27	-0.65	-0.43	-0.86
Adjusted two-minute yield	-0.48	-0.85	-0.50	-1.00
Cell count	0.00	0.03	0.02	0.08
ln cell count	-0.05	-0.40	0.00	-0.59
Adjusted milking time	0.95	0.97	--	--

Both the phenotypic and genetic correlations between the unadjusted and adjusted measurements of the same measure, two-minute yield or total milking time, were very high (0.88 to 0.97). Thus, it appears that even though both the linear and quadratic effects of total milk yield are significant on two-minute yield and the linear effect of total milk is significant on total milking time, correcting for these effects does not greatly alter the measurements recorded for the majority of the cows. The very high genetic correlations between the two measurements, unadjusted and adjusted, of both traits suggests that the half-day milk yield has little effect on the genetic expression of the these two traits.

The phenotypic correlations between two-minute yield and adjusted two-minute yield with total milking time and adjusted total milking time were moderately high, and negative. They ranged from -0.27 for the two traits unadjusted to -0.50 for the adjusted values of the two traits. The fact that the correlations were negative indicates that as the two-minute yields increased, the total milking times decreased. This was the case even when the two measures were not adjusted for yield at milking effects. Similar results were reported by Tomaszewski et al. (1975) and Touchberry and Markos (1970) for machine time with two-minute yield and other milk flow rate measurements.

The genetic correlations for the measurements of two-minute yield with the two measurements of total milking time were more highly negative than their corresponding phenotypic correlations. The smallest correlation (-0.65) was between two-minute yield and total milking time, and the largest (-1.00) was between the adjusted two-minute yield and adjusted total milking time. The genetic correlations with one milking speed measurement adjusted

and the other not were intermediate (-0.85 and -0.86). These high correlations suggest that essentially the same set of genes is controlling both the two-minute yield and the total milking time. Both traits measure how fast the cow is milking, with the highest correlations between them observed when we eliminate the influence of the total milk yield at sampling.

These results are in good agreement with Tomaszewski et al. (1975) who reported a genetic correlation of -0.87 between two-minute yield and machine time. However, they disagree with Miller et al. (1976) who reported genetic correlations of 0.41 and -0.24 for peak flow rate with total time and machine time, respectively.

The phenotypic correlations between cell count and log cell count with the four measurements of milking speed ranged from -0.05 to 0.09. Least squares analysis with somatic cell count (Appendix Table 10) and log somatic cell count (Appendix Table 11) as the dependent variables and the milking speed measurements treated in separate analyses as a fixed effect, resulted in only the adjusted two-minute yield having a significant effect on log somatic cell count.

The least squares estimates of the ten classes of adjusted two-minute yield on log somatic cell count appear in Figure 8. Only the cows in the two groups milking less than 3.5 kg in two minutes had log cell counts significantly lower than cows milking more than 7 kg in two minutes. From the graph of the least squares estimates, it appears that there is a point somewhere between 4 and 4.5 kg where further increases in adjusted two-minute yield do not adversely affect the log somatic cell count. Baxter et al. (1950) showed that teat canal diameter largely controlled milk flow rate, while the NMC (1978) indicates that susceptibility to infection increases with increasing teat canal diameter. From the results observed in this study, it may be that once the streak canal reaches a certain diameter, a larger diameter will have

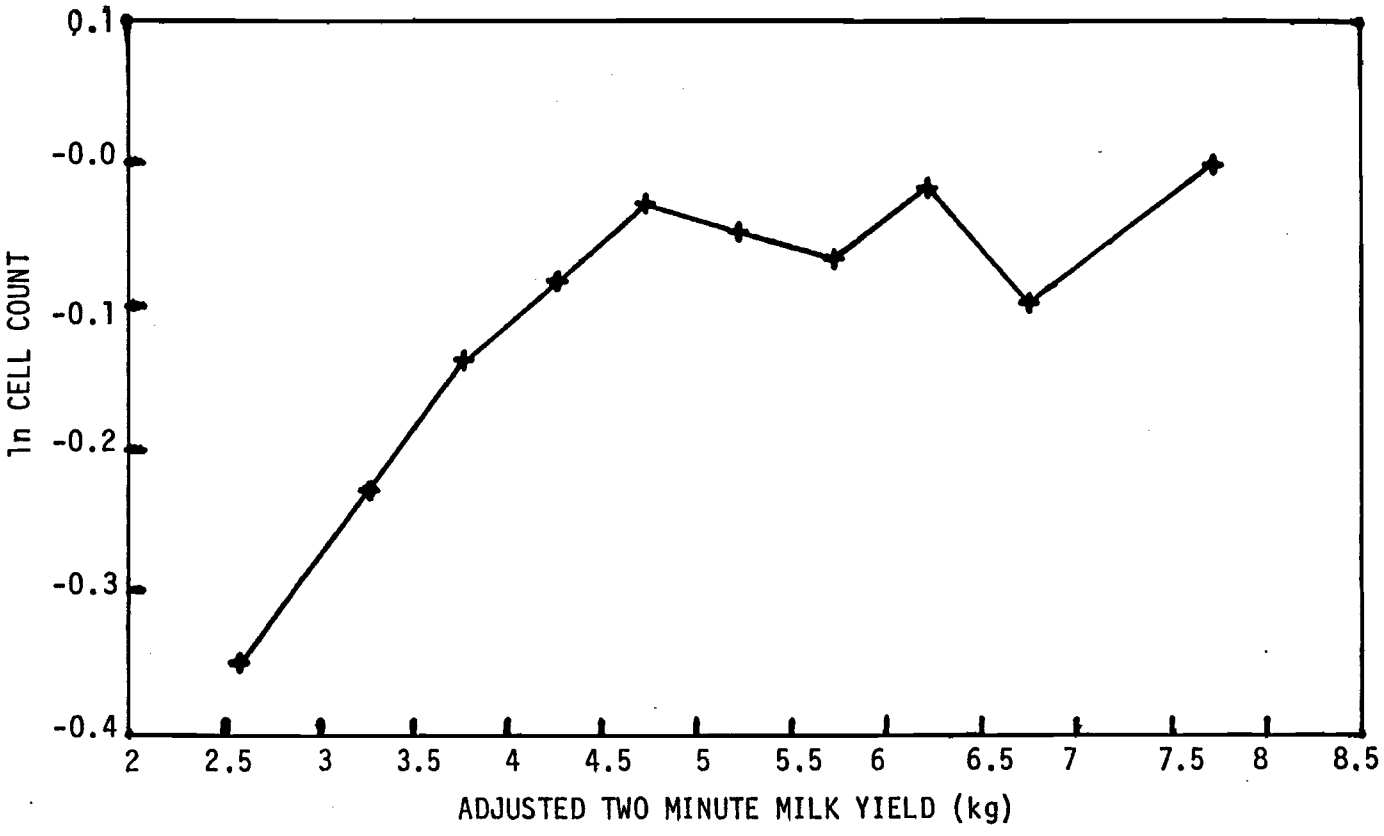

Figure 8. Least squares estimates of adjusted two-minute yield on ln somatic cell count.

little influence on the somatic cell count, although still influencing the milking speed.

The small and mostly non-significant phenotypic correlations between the measurements of raw and log somatic cell counts with the measurements of milking speed agree well with the results obtained by Schmidt and Van Vleck (1965), Politiek (1968), Afifi (1968a), Miller et al. (1978) and Bassalik-Chabielska and Ryniewicz (1978). They all reported small correlations between measurements of milking speed and udder health. These results are, however, in contrast to reports by Dodd and Neave (1951), Schluep (1967) and Zeman and Neumann (1973).

It is of interest to note that Dodd and Neave (1951), Schluep (1967) and Zeman and Neumann (1973) grouped cows according to speed of milking or somatic cell count level. In the present study, when cows were grouped according to the adjusted two-minute yield the two slowest groups for milking speed had significantly lower log somatic cell counts (Figure 8). However, the phenotypic correlation, which is a linear correlation over the range of values, between adjusted two-minute yield and log somatic cell count was small (0.09). This result is similar to reports by Schmidt and Van Vleck (1965), Politiek (1968), and Miller et al. (1978). The apparent difference between the two types of results may be explained by the curvilinear relationship between milking speed and log somatic cell count that is suggested in Figure 8. Real effects may be masked by analyzing the data by correlation if the underlying relationship is non-linear.

The genetic correlations between raw and log somatic cell count and the measurements of milking speed are also found in Tables 10 and 11. There were large differences between the genetic correlations of somatic cell count with milking speed variables and log somatic cell count with these same variables. One must keep in mind that cell counts do not follow a normal

distribution, and this was the reason for transforming them to a log (natural) scale. Also, genetic correlations appear to be much more subject to sampling error than phenotypic correlations. The estimates of the sire component of variance for both the raw and log somatic cell count were very small for these populations, and the heritabilities for these traits very low.

Nonetheless, the same pattern for the correlations of the four measurements of milking speed with log somatic cell count were observed. The genetic correlations were 0.94, 0.79, -0.40 and -0.59 between log cell count and two-minute yield, adjusted two-minute yield, total milking time and adjusted total milking time, respectively. They all indicate that a greater genetic potential for more rapid milking is associated genetically with a higher log somatic cell count. This relationship is greater for the measurements of two-minute yield than the total milking time measurements.

However, despite the antagonistic relationship between log somatic cell count and these four measurements of milking, direct selection for milking speed should not result in large genetic increases in log cell count because of its low heritability. Further, there exists the possibility that the genetic relationship may be non-linear, that is the situation may be similar to that suggested by the graph in Figure 8. Phenotypically, once a certain level of adjusted two-minute yield was reached, further increases in milking speed had little or no influence on the log somatic cell count.

No other estimates of genetic correlations between these traits were found for comparison. Afifi (1968a) reported no pattern in a graph of progeny groups of 19 sires in first lactation when leucocyte count was plotted against milking rate. However, no statistical analysis was carried out on the data nor were the cell counts transformed to the log scale.

The phenotypic and genetic correlations between the four measurements of milking speed with the four lactation measurements, 305-day milk and fat and BCA milk and BCA fat, appear in Tables 12 and 13.

Table 12. Phenotypic and genetic correlations between measurements of two-minute yield and lactation milk and fat production

	Two-minute yield		Adjusted two-minute yield	
	Phenotypic	Genetic	Phenotypic	Genetic
BCA milk	0.21	-0.18	-0.04	-0.36
BCA fat	0.17	-0.06	-0.02	-0.23
305-day milk	0.22	-0.36	-0.05	-0.48
305-day fat	0.17	-0.08	-0.03	-0.25

Table 13. Phenotypic and genetic correlations between measurements of total milking time and lactation milk and fat production (2138 records)

	Milking time		Adjusted milking time	
	Phenotypic	Genetic	Phenotypic	Genetic
BCA milk	0.16	0.10	0.01	-0.04
BCA fat	0.11	-0.05	-0.01	-0.18
305-day milk	0.17	0.14	0.02	0.01
305-day fat	0.13	-0.04	0.01	-0.14

Phenotypic correlations between the lactation traits and the unadjusted milking time were small but significantly positive, ranging between 0.11 and 0.22. All correlations between the lactation traits and both of the adjusted measurements of milking speed did not differ significantly from zero (-0.05 to 0.02). The elimination of significant relationship with lactation yield by adjusting for the total milk yield when sampled is consistent with the results obtained by Sandvik (1957), Donald (1960) and Johansson and Malven (1960). Cows that have higher test day yields will produce more milk during a lactation. These results suggest that higher test day yields increase two-minute yield, yet also lengthen the total time it takes to milk the cow. They support the view of Blake and McDaniel (1978) that the milking rate we observe is dependent upon the milk yield.

The genetic correlations between the four lactation production measurements and the adjusted two-minute yield were moderately negative (-0.23 to -0.48). A similar trend was observed between these same four variables and the raw two-minute yield, although the magnitude of the correlations was smaller (-0.06 to -0.36). The two measurements of milk yield were more negatively correlated with both of the measurements of two-minute yield than were the lactation measurements of fat yield.

These results indicate that the cows with a higher genetic potential for milk and fat production had a lower potential for two-minute yield, which is used as a measurement of milking speed. This possible antagonistic genetic relationship between high milk flow rates and high milk production has also been suggested by Sharaby et al. (1979), who examined correlations among sire proofs in a similar Canadian Holstein population. The results disagree with the report of Miller et al. (1976) who reported genetic correlations

between milking rate and lactation yield ranging from 0.69 to 0.78, which indicated that considerable apparent genetic improvement can be made in milking rate by selection for milk yield.

Also, Markos and Touchberry (1970) said that it is "...likely that most sires that have daughters with an unusually low average maximum rate of milk flow will also have a low breeding value for milk production." Milk proofs as of November, 1979, for the five slowest ranked sires for adjusted two-minute yield (Table 14) indicate that this is not necessarily the case. One of the five, Roybrook Starlite (308691) was in fact the fourth highest rated Holstein sire for milk in Canada, with a +17 rating. Further, the other four sires were all rated above the breed average for milk production.

It must be noted that the presence of bulls such as Roybrook Starlite with such an extreme negative relationship between milking speed and milk production may influence our estimate of the true genetic relationship that exists between these traits, in light of the limited sample population under study.

The genetic correlations between the lactation traits and both unadjusted and adjusted milking time were small, ranging between -0.18 and 0.14. Milking time showed a small positive relationship with lactation milk production, while the genetic relationship between these two traits after adjusting the total time for the milk yield at sampling was not significantly different from zero. The lactation 305-day fat and BCA fat were not significantly correlated genetically with total milking time, but there was a small negative relationship between these same traits and the adjusted total milking time. The small positive correlation between lactation milk yield and total milking time is in contrast to the larger genetic correlation (0.50) reported by Miller et al. (1976) between these traits.

Table 14. The upper and lower 10 of 56 sires ranked for adjusted two-minute yield, with their rank for two-minute yield (2604 records)

Sire Reg. No.	No. of daughters	No. of herds	Adjusted two-minute yield Rank	Adjusted two-minute yield kg	Two-minute yield Rank
329444	14	4	1	0.52	4
305966	14	8	2	0.44	5
288801	16	10	3	0.41	2
299855	29	12	4	0.39	1
310300	15	5	5	0.38	10
315487	22	5	6	0.37	7
317868	38	13	7	0.30	3
311498	39	19	8	0.28	8
293895	49	20	9	0.27	6
308942	10	5	10	0.26	14
⋮	⋮	⋮	⋮	⋮	⋮
311885	12	6	47	-0.25	40
271347	10	4	48	-0.25	36
289318	16	9	49	-0.27	44
283735	65	25	50	-0.30	48
322059	22	7	51	-0.30	35
308691	25	12	52	-0.38	49
314415	23	12	53	-0.40	55
320510	26	10	54	-0.50	52
283207	26	9	55	-0.57	54
275932	97	33	56	-0.60	56

The genetic correlations indicated a high degree of relationship between the measurements of two-minute yield and total milking time, both measuring how fast a cow will milk. Two-minute yield is more of a biological measurement, being less subject to the operator's discretion in defining the end point. However, the genetic relationships between both measurements of two-minute yield and log somatic cell count and lactation milk and fat production were more antagonistic than for total milking time.

Looking at the BLUP sire proofs (Table 14), the top and bottom 10 of 56 sires ranked for adjusted two-minute yield had very similar rankings for two-minute yield. A similar trend was observed in Table 15 for sire rankings based on adjusted total milking time and corresponding rankings based on total milking time. The adjusted rankings should provide a more absolute measure of the milking speed, being free of the influence of the milk yield at sampling. However, the rankings in these extreme groups were not greatly different for the majority of the sires between the adjusted and unadjusted trait.

Table 15 also contains the corresponding rankings for adjusted two-minute yield and two-minute yield for the top and bottom groups of 10 sires ranked on the basis of adjusted total milking time, with rank 1 representing the fastest milking proof in all cases. Rankings for adjusted total milking time were more similar to adjusted two-minute yield than unadjusted. Nonetheless, the sires that had a more negative proof for adjusted milking time also tended to be the ones with the more positive proofs for both measurements of two-minute yield.

Table 15. The upper and lower 10 of 56 sires ranked for adjusted two-minute yield, with ranks for the other milking speed traits (2235 records)

Sire Reg. No.	No. of daughters	No. of herds	Adjusted total milking time		Corresponding rank		
			rank	seconds	total milking time	Adj. 2-min yield	2-min yield
329444	13	4	1	-23.6	1	1	2
315487	21	5	2	-23.0	3	4	5
316123	15	10	3	-20.1	2	14	23
305966	13	8	4	-15.9	5	3	3
308942	10	5	5	-14.9	4	10	13
263781	42	21	6	-13.1	10	15	12
305887	13	5	7	-12.3	17	8	10
332846	8	5	8	-11.7	7	13	17
311498	29	17	9	-11.4	11	7	11
317868	34	12	10	-10.7	22	12	9
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
263475	11	10	47	6.8	46	26	21
303889	11	4	48	7.0	45	38	33
259668	13	9	49	9.3	47	27	19
320510	20	9	50	9.5	51	54	47
290516	90	33	51	10.8	48	35	31
275932	88	31	52	16.2	53	56	56
302981	41	15	53	19.8	52	44	50
289318	15	9	54	22.7	54	51	46
308691	10	5	55	24.8	55	53	53
283735	53	24	56	28.2	56	45	41

Spearman rank correlations between the estimated breeding values of the 56 sires for the four milking speed traits were intermediate between the corresponding phenotypic and genetic correlations (Table 16). The rank correlations emphasize the high degree of relationship between the unadjusted and adjusted measurement of the same trait, the correlation being 0.93 for both two-minute yield and total milking time. The largest rank correlation between the two traits was observed when both measurements were adjusted for the milk yield at sampling ($r_s = -0.71$). The rank correlations when one trait was adjusted and the other not were very similar (-0.63 and -0.61), while the smallest correlation was observed between the unadjusted two-minute yield and total milking time ($r_s = -0.44$).

Sires with a positive two-minute yield proof will in most cases be the ones with a negative total milking time proof, this agreement being better if the influence of the milk yield at sampling is removed. Both two-minute yield and total milking time will identify sires superior for milking speed.

Table 16. Spearman Rank Correlations between BLUP sire solutions of milking speed traits (2235 records)

Trait	Adjusted two-minute yield	Total milking time	Adjusted total milking time
Two-minute yield	0.93	-0.44	-0.63
Adjusted two-minute yield		-0.61	-0.71
Total milking time			0.93

Thus, in terms of identifying sires superior for milking speed, all four of the milking speed measurements discussed here could be used. More daughters would be needed to accurately rank sires for adjusted total milking time than for adjusted two-minute yield because of the lower heritability that was observed for the former trait.

Machine Stripping

The mean stripping time was 39.6 seconds for the 953 cows on which this trait had been measured (Table 17). Means of the other traits for cows with a measurement of stripping time also appear in Table 17. The means of these traits are similar to those in Tables 6 and 7 for the whole population.

Table 17. Means and standard deviations of traits for cows with a measurement of stripping time

Trait	Mean	SD
Stripping time (seconds)	39.6	44.6
Half-day milk yield (kg)	9.82	3.71
Two-minute milk yield (kg)	4.83	1.79
Adjusted two-minute milk yield (kg)	4.77	1.52
Total milking time (seconds)	375.9	132.4
Adjusted total milking time (seconds)	376.0	118.0
Somatic cell count ('000/ml)	419	683
Log somatic cell count	5.30	1.21
305-day milk yield (kg)	6754.6	1322.6
305-day fat yield (kg)	254.0	51.1
BCA milk	137.5	24.0
BCA fat	140.3	26.4

Simple phenotypic correlations between stripping time and measurements of milking speed, somatic cell count and lactation production appear in Table 18. This table also contains the partial regression coefficients of stripping time on these same traits. The relationships between stripping time and the other traits after adjusting for the effects of herd, age at last calving, stage of lactation and season of calving are consistent with the simple correlations.

Table 18. Phenotypic correlations and partial regression coefficients for stripping time with measurements of milking speed, somatic cell count and production

Trait	Phenotypic correlation with stripping time	Stripping time as a covariate (seconds)
Half-day milk yield (kg)	0.24**	0.0079±0.0021**
Two-minute milk yield (kg)	0.04	-0.0027±0.0014
Adjusted two-minute milk yield (kg)	-0.12**	-0.0046±0.0013**
Total milking time (seconds)	0.21**	0.5512±0.1041**
Adjusted total milking time (seconds)	0.16**	0.4578±0.0992
Somatic cell count ('000/ml)	0.04	0.9120±0.5631
Log somatic cell count	-0.02	0.0003±0.0009
305-day milk yield (kg)	0.20**	2.365 ±0.900 **
305-day fat yield (kg)	0.18**	0.094 ±0.036 **
BCA milk	0.15**	0.042 ±0.018 *
BCA fat	0.13**	0.044 ±0.020 *

* Significant at the 0.05 level.
** Significant at the 0.01 level.

Simple phenotypic correlations between stripping time and somatic cell count and log somatic cell count were 0.04 and -0.02, respectively, both being non-significant. The partial regression coefficients between stripping time and these same traits were also not significant. This lack of relationship between machine stripping and somatic cell count is in good agreement with other reports examining the relationship between machine stripping and udder health. Schmidt and Van Vleck (1965) reported small correlations between stripping time and four measurements of udder health. Goff and Schmidt (1967), Little (1968), Rudovsky and Ebendorff (1977) and Smith et al. (1978) all reported no significant effect of stripping vs not-stripping on udder health.

Of the four measurements of milking speed, only the unadjusted two-minute yield was not significantly correlated with stripping time. There is a small negative correlation (-0.12) between stripping time and adjusted two-minute yield, while the correlations were positive with total milking time (0.21) and adjusted total milking time (0.16). These correlations, especially with the adjusted two-minute yield, suggest that it is the cows that milk more slowly that are being machine stripped for a longer period of time. Each one-second increase in stripping time was associated with a 0.55-second increase in the total milking time. After adjusting for the half-day milk yield, a one-second increase in stripping time was still associated with a 0.46-second increase in milking time. The larger correlations between stripping time and both measurements of total milking time than with adjusted two-minute yield suggest that machine stripping may add to the total milking time in addition to being associated with the slower milking cows.

Schmidt and Van Vleck (1965) also found a positive correlation between stripping time and total milking time. Little (1968) reported that the total machine on-time per milking was longer for stripped than not-stripped cows.

The phenotypic correlations between the four measurements of lactation production and stripping time were small yet significantly positive, ranging from 0.13 to 0.20. The partial regression coefficients of stripping time were also highly significant for the 305-day production, and significant for BCA milk and BCA fat. This would suggest a higher lactation production for cows machine stripped longer.

However, the largest correlation observed was between stripping time and half-day milk yield (0.24). Each one-second increase in stripping time was associated with a 0.008 kg increase in milk yield. When half-day milk yield was included with stripping time as covariates in models with the lactation production traits as the dependent variables, the effect of the half-day milk yield was highly significant in all four cases while the stripping time had no significant effects (Table 19). Thus, the apparent higher lactation production in cows machine stripped longer is really only the effect of cows with higher test-day milk yields being subjected to more machine stripping.

A positive relationship between stripping time and daily milk yield was also reported by Schmidt and Van Vleck (1965). Miller et al. (1976) observed a small positive correlation between stripping time (minutes) and lactation milk production. However, in experiments comparing machine stripping to not-stripping, Goff and Schmidt (1967), Little (1968) and Smith et al. (1978) found no significant differences in production for the two treatment groups.

Table 19. Partial regression coefficients of stripping time and half-day production on lactation production

Trait	Covariate 1 Stripping time (seconds)	Covariate 2 half-day milk (kg)
305-day milk yield (kg)	0.24 ±0.76	241.51±12.75**
305-day fat yield (kg)	0.028±0.033	7.54± 0.56**
BCA milk	0.001±0.016	4.59± 0.26**
BCA fat	0.010±0.018	3.81± 0.30**

** Significant at the 0.01 level

Convergence was not achieved when estimating σ_e^2/σ_i^2 for stripping time, and the heritability estimate of this trait continually approached zero. Miller et al. (1976) reported a low heritability for stripping time (0.08).

Thus, the cows with higher test day yields, as well as those tending to milk more slowly are subjected to more machine stripping. When the effect of the milk yield for the observed milking is removed, there is no significant effect of machine stripping on lactation production. Also, there was no relationship between machine stripping and somatic cell count. There appears to be little benefit obtained from machine stripping, with the suggestion that this practice may add to the total milking time.

B. Milking Machines and Mastitis

As previously described, 63 variables relating to the design and performance of the milking machine and milking practices were analyzed by least squares procedures in a one-way analysis of variance to determine their effects on somatic cell count. This preliminary analysis was carried out to select variables for inclusion in a multiple regression analysis. All variables that were significant at the 0.1 level of probability for either the 46 or 67 herd sample appear in Table 20. This level of probability was used as it provided a good separation of the variables. Most variables were either significant at this probability level or had an F value greater than 0.2, with very few variables having a significance level between 0.1 and 0.2.

Eleven variables were significant at the 0.1 level for both herd average somatic cell count in 46 herds and the somatic cell count on the day the machine was tested in 67 herds. Only six variables were significant at this level in one of the test populations but not both. This was despite the fact that short interval random effects may influence the results of single tests of bulk milk (Reichmuth, 1975), and the larger sample included 21 herds whose somatic cell count was based on a half-day milk sample taken one year prior to the milk samples in the other herds. These 21 herds did not have the option of receiving a somatic cell count report, and the definition of the subjective measurement of variability of the slope of the milk line was changed in the year between the milking machine evaluation in these and the other 46 herds.

Means, standard deviations and ranges of the herd average somatic cell

Table 20. Milking machine and management variables with a probability less than 0.1 in a one-way analysis of variance for average monthly herd somatic cell count.

Source	Description	d.f.	Probability > F: Av of monthly Cell counts (46 herds)	Probability > F: Last test day cell count (67 herds)
Teat dip	Classif.	1	0.0001**	0.0001**
Separate towel	Classif.	1	0.0713	0.0414*
Vacuum line 2	Classif.	4	0.0933	0.0132*
Alternate pulsation	Classif.	1	0.0157*	0.0012**
Brand of inflation	Classif.	4	0.0846	0.0549
Rate of pulsation	Cont.	1	0.0892	0.0049**
Ratio rear teat	Cont.	1	0.0535	0.0987
Ratio fore teat	Cont.	1	0.0188*	0.0288*
Milking phase fore	Cont.	1	0.0307*	0.1090
Rate x ratio rear	Cont.	1	0.0357*	0.0214*
Rate x ratio fore	Cont.	1	0.0192*	0.0095**
Teat end vacuum (static)	Cont.	1	0.0670	Not avail.
Air phase fore	Cont.	1	0.0605	0.1355
Variability of slope	Classif.	1	0.0083**	0.5587
(Required-Rated) airflow	Cont.	1	0.0706	0.5951
(NM Required-Rated) airflow	Cont.	1	0.0992	0.5317
Receives report	Classif.	1	0.5894	0.0426*
Units per operator	Classif.	6	0.3763	0.0987
Length of milk hose	Cont.	1	0.6894	0.0976

** Significant at 0.01 level.

* Significant at 0.05 level.

count and the ten continuous variables significant at the 0.1 level appear in Table 21. This and subsequent analyses were done with the 46 herds that were tested in the same year and on which there were at least 8 herd somatic cell counts available.

Table 21. Means, standard deviations and ranges of herd average somatic cell count and continuous variables meeting the 0.1 level of probability (46 herds).

Variable	Mean	SD	Range
Herd average somatic cell count ('000/ml)	350.7	126.4	593.0
Rate of pulsation (#)	56.6	6.5	23.0
Ratio rear teat	1.70	0.60	1.88
Ratio fore teat	1.61	0.65	1.88
Milking phase fore (%)	59.5	8.5	26.0
Air phase fore (%)	35.7	9.0	28.0
Static teat end vacuum (kPa)	50.4	3.5	18.6
Rate x ratio rear	97.0	40.0	122.5
Rate x ratio fore	92.9	43.2	126.5
(Required-Rated) Airflow (l/min)	140.7	255.3	1248.0
(NM Required-Rated) Airflow (l/min)	84.8	259.1	1248.0

Seven of these variables relate to the operation of the pulsator. A graph of pulsator performance and an explanation of these variables appear in Appendix Figure 1. Static teat end vacuum is the level of vacuum at the teat end when the milking machine was operating, but not milking any cows. The airflow is the litres of air per minute being displaced by the vacuum

pump. The airflow requirements were calculated according to Agriculture Quebec (1977), both with (Required) and without the requirements for milk meters (NM Required), while the airflow ratings of the vacuum pumps were obtained from the same source. A positive value for (Required-Rated) Airflow indicates that the vacuum pump is below its required capacity.

The frequency of each class of the 6 classification variables as well as the means of the continuous variables within each class of a classificiation variable appear in Tables 22 to 27. Also, these tables contain the means of teat dip, separate towel, alternate pulsation, and variability of slope within each class. The first three were coded as 1-yes 2-no, while for variability of slope it was 1-high and 2-moderate to good. The variable vacuum line 2 refers to the diameter of the vacuum line connecting the vacuum distribution tank to the moisture trap.

Table 22. Means of significant milking machine traits (0.10) by use of teat dip

Trait	Frequency	Teat dip	
		Yes	No
		34	12
Herd average somatic cell count ('000/ml)		308.0 ±15.2	471.9 ±40.8**
Rate of pulsation (#)		55.5 ± 1.2	59.6 ± 1.1
Ratio rear teat		1.68± 0.1	1.74± 0.2
Ratio fore teat		1.56± 0.1	1.74± 0.2
Milking phase fore (%)		58.9 ± 1.5	61.2 ± 2.6
Air phase fore (%)		36.3 ± 1.5	34.2 ± 2.9
Static teat end vacuum (kPa)		49.9 ± 0.6	51.7 ± 0.7
Rate x ratio rear		94.6 ± 6.9	103.9 ±11.8
Rate x ratio fore		89.0 ± 7.5	103.9 ±11.8
(Required-Rated) airflow (l/min)		97.4 ±45.6	263.4 ±52.0
(NM Required-Rated) airflow (l/min)		43.3 ±46.3	202.1 ±54.6

** Significant at the 0.01 level

Table 23. Means of significant milking machine traits (0.10) by use of separate towel

Trait	Frequency	Separate towel Yes 24	Separate towel No 22
Herd average somatic cell count ('000/ml)		318.6 ±20.1	385.8 ±31.0
Rate of pulsation (#)		56.8 ± 1.4	56.4 ± 1.3
Ratio rear teat		1.66± 0.1	1.73± 0.14
Ratio fore teat		1.57± 0.1	1.65± 0.15
Milking phase fore (%)		59.1 ± 1.6	59.8 ± 2.0
Air phase fore (%)		39.5 ± 1.8	36.0 ± 2.0
Static teat end vacuum (kPa)		50.3 ± 0.8	50.4 ± 0.6
Rate x ratio rear		95.8 ± 8.2	98.3 ± 8.7
Rate x ratio fore		91.3 ± 8.8	94.7 ± 9.4
(Required-Rated) airflow (l/min)		110.6 ±48.9	173.7 ±58.2
(NM Required-Rated) airflow (l/min)		36.3 ±51.2	137.6 ±58.2
Teat dip		1.13± 0.07	1.41± 0.11*

* Significant at the 0.05 level.

Table 24. Means of significant milking machine traits (0.10) by variability of slope of the milk line

Trait	Frequency	Variability of slope: High 14	Variability of slope: Moderate to good 32	
Herd average somatic cell count ('000/ml)		423.4 ±40.6	318.9 ±17.7	**
Rate of pulsation (#)		60.2 ± 0.9	55.0 ± 1.2	*
Ratio rear teat		2.15± 0.17	1.49 ± 0.08	**
Ratio fore teat		2.15± 0.17	1.37 ± 0.08	**
Milking phase fore (%)		66.5 ± 1.9	56.4 ± 1.3	**
Air phase fore (%)		27.6 ± 1.6	39.3 ± 1.3	**
Static teat end vacuum (kPa)		51.2 ± 0.7	50.0 ± 0.7	
Rate x ratio rear		128.5 ± 9.7	83.2 ± 5.9	**
Rate x ratio fore		128.5 ± 9.7	77.3 ± 6.5	**
(Required-Rated) airflow (l/min)		181.6 ±87.1	122.8 ±39.1	
(NM Required-Rated) airflow (l/min)		121.0 ±85.0	68.9 ±41.1	
Teat dip		1.43± 0.14	1.19 ± 0.07	
Separate towel		1.57± 0.14	1.44 ± 0.09	

* Significant at the 0.05 level

** Significant at the 0.01 level

Table 25. Means of significant milking machine traits (0.10) by use of alternate pulsation

Trait	Frequency	Alternate pulsation Yes 11	Alternate pulsation No 35	
Herd average somatic cell count ('000/ml)		271.7 ±18.1	375.6 ±22.3	*
Rate of pulsation (#)		48.4 ± 1.7	59.2 ± 0.7	**
Ratio rear teat		1.48 ± 0.06	1.76 ± 0.11	
Ratio fore teat		1.12 ± 0.04	1.76 ± 0.11	**
Milking phase fore (%)		52.1 ± 0.9	61.8 ± 1.4	**
Air phase fore (%)		42.2 ± 1.0	33.7 ± 1.6	**
Static teat end vacuum (kPa)		46.7 ± 0.7	51.5 ± 0.5	**
Rate x ratio rear		71.4 ± 3.4	105.1 ± 7.2	*
Rate x ratio fore		54.3 ± 3.0	105.1 ± 7.2	**
(Required-Rated) airflow (l/min)		43.4 ±88.9	171.3 ±40.2	
(NM Required-Rated) airflow (l/min)		-18.4 ±96.7	117.2 ±39.3	
Teat dip		1.00 ± 0.0	1.34 ± 0.08	*
Separate towel		1.36 ± 0.15	1.51 ± 0.09	
Variability of slope		2.00 ± 0.0	1.60 ± 0.08	*

* Significant at the 0.05 level

** Significant at the 0.01 level

Table 26. Means of significant milking machine traits (0.10) by brand of inflation

Trait	Frequency	Brand of inflation 2	3	4	5	6
		7	6	5	12	16
Herd average somatic cell count ('000/ml)		361.9 ± 55.2	286.7 ±32.9	253.8 ± 5.8	418.4 ± 43.7	349.4 ±27.2
Rate of pulsation (#)		62.9 ± 1.2	45.8 ± 0.02	51.4 ± 3.5	60.7 ± 0.9	56.4 ± 0.8**
Ratio rear teat		1.51± 0.05	1.57± 0.02	1.38± 0.12	2.64± 0.04	1.21± 0.04**
Ratio fore teat		1.51± 0.05	1.03± 0.02	1.23± 0.06	2.64± 0.04	1.21± 0.04**
Milking phase fore (%)		59.9 ± 0.9	50.7 ± 0.2	53.8 ± 1.7	72.2 ± 0.7	54.8 ± 0.9**
Air phase fore (%)		33.6 ± 0.8	44.5 ± 0.8	39.4 ± 1.1	22.8 ± 0.3	41.9 ± 1.2**
Static teat end vacuum (kPa)		50.8 ± 1.4	47.4 ± 0.6	45.9 ± 1.2	51.9 ± 0.5	51.5 ± 0.9**
Rate x ratio rear		94.7 ± 2.7	71.9 ± 0.8	70.8 ± 7.8	160.1 ± 2.7	68.3 ± 2.5**
Rate x ratio fore		94.7 ± 2.7	47.3 ± 0.8	62.6 ± 4.2	160.1 ± 2.7	68.3 ± 2.5**
(Required-Rated) airflow (l/min)		80.9 ±126.7	53.3 ±99.2	31.4 ±169.3	294.4 ± 52.1	118.6 ±50.4
(NM Required-Rated) airflow (l/min)		24.3 ±114.8	-12.7 ±86.9	-25.2 ±200.1	226.1 ± 50.0	76.1 ±55.1
Teat dip		1.57± 0.20	1.00± 0.0	1.00± 0.0	1.33± 0.14	1.25± 0.11
Separate towel		1.57± 0.20	1.50± 0.22	1.20± 0.20	1.50± 0.15	1.50± 0.13
Variability of slope		1.43± 0.20	2.00± 0.0	2.00± 0.0	1.33± 0.14	1.88± 0.09**
Alternate pulsation		2.00± 0.0	1.00± 0.0	1.00± 0.0	2.00± 0.0	2.00± 0.0**

** Significant at the 0.01 level

Table 27. Means of significant milking machine traits (0.10) by vacuum line 2 diameter

Trait	Frequency	Vacuum line 2				
		2.54 cm	3.18 cm	3.81 cm	5.08 cm	5.72 cm
		1	22	7	14	1
Herd average somatic cell count ('000/ml)		302	351.9 ±25.2	451.7 ±67.8	291.4 ±23.1	395
Rate of pulsation (#)		63	59.5 ± 1.0	56.9 ± 1.1	52.0 ± 2.0	45**
Ratio rear teat		1.49	1.74± 0.15	1.94± 0.30	1.52± 0.08	1.54
Ratio fore teat		1.49	1.74± 0.15	1.94± 0.30	1.27± 0.10	1.05
Milking phase fore (%)		60	61.5 ± 1.9	63.7 ± 3.7	54.5 ± 1.3	51
Air phase fore (%)		33	34.3 ± 2.1	32.9 ± 3.7	39.4 ± 1.7	46
Static teat end vacuum (kPa)		50.8	52.0 ± 0.7	50.7 ± 0.8	48.1 ± 0.9	47.4**
Rate x ratio rear		93.9	104.5 ± 9.6	111.6 ±19.0	79.2 ± 5.9	69.3
Rate x ratio fore		93.9	104.5 ± 9.6	111.6 ±19.0	67.3 ± 7.2	47.3
(Required-Rated) airflow (l/min)		308.5	177.9 ±39.5	184.8 ±90.4	68.5 ±95.7	-89.2
(NM Required-Rated) airflow (l/min)		223.6	122.6 ±41.3	116.0 ±85.7	11.9 ±98.5	-89.2
Teat dip		2.0	1.32± 0.10	1.29± 0.18	1.07± 0.07	1.0
Separate towel		1.0	1.41± 0.11	1.71± 0.18	1.43± 0.14	2.0
Variability of slope		2.0	1.64± 0.10	1.57± 0.20	1.86± 0.10	2.0
Alternate pulsation		2.0	2.00± 0.0	2.00± 0.0	1.14± 0.13	1.0**

** Significant at the 0.01 level

Simple regression coefficients between the 10 continuous variables and herd average somatic cell count appear in Table 28. Four variables relating to the pulsator performance, ratio fore teat, milking phase fore, rate x ratio rear and rate x ratio fore were significant (0.05) in their effect on herd average somatic cell count. Each one unit increase in the milking-to-rest-phase ratio of the fore teats was accompanied by a 67,000 increase in cell count. Similarly, an increase in the milking phase increased the somatic cell count as did a higher value for the product of the rate x ratio of the pulsator in both the front and rear quarters.

Table 28. Simple regression coefficients of variables with a probability less than 0.1 for average monthly herd somatic cell count (46 herds)

Variable	Estimate	PR>|T|
Rate of pulsation (#)	4.95± 2.85	0.0892
Ratio rear teat	59.91±30.20	0.0535
Ratio fore teat	67.04±27.48	0.0188*
Milking phase fore (%)	4.74± 2.12	0.0307*
Air phase fore (%)	-3.94± 2.04	0.0605
Static teat end vacuum (kPa)	9.98± 5.31	0.0670
Rate x ratio rear	0.98± 0.45	0.0357*
Rate x ratio fore	1.01± 0.41	0.0192*
(Required-Rated) airflow (l/min)	0.13± 0.07	0.0702
(NM Required-Rated) airflow (l/min)	0.12± 0.07	0.0992

* Significant at 0.05 level.

Schmidt Madsen, cited by McDonald (1969) and Britt (1977) both indicated a problem of wider pulsator ratios in relation to herd somatic cell counts and infection. Britt (1977) had also reported a problem with faster pulsator speed in relation to herd infection while Bratlie, cited by Fell (1964), had observed increases in cell counts with pulsator rates of 75 per minute as opposed to 40 per minute. However, these results and the results observed in this study do not agree with Nyhan and Cowhig (1967) who reported no significant effect of pulsator rate or ratio on the incidence of mastitis.

There was a trend for higher levels of vacuum to be associated with higher cell counts. A similar trend was reported by Braund and Schultz (1963) when looking at the percent positive quarters. Afifi (1968b) reported that increasing the vacuum above 40 cm Hg (53.5 kPa) resulted in a significant increase in cell count. But, both Mochrie et al. (1953, 1955) and Neave et al., cited by Fell (1964), found no significant differences on measurements of udder health in cows milked at different levels of vacuum.

Both measurements of airflow suggest that the vacuum pumps that had a rating closest to the requirements (these requirements included a 50% reserve) had lower herd somatic cell counts. The greater the deficiency of the pump, the higher the cell count tended to be. Nyhan and Cowhig (1967) found that low vacuum reserve was significantly associated with a high prevalance of mastitis.

Single variable analysis least squares estimates of the effects of the six classification variables appear in Table 29. Two of the four mastitis control practices, teat dipping and the use of separate towels to wash the udder, met the 0.1 level of significance for herd average somatic cell count. Herds using a teat dip had somatic cell counts 163,950 cells/ml lower than those not teat dipping, the relationship being highly significant.

Table 29. Least squares estimates of average monthly herd somatic cell count for variables with a probability less than 0.1 (46 herds)

Variable	Level	Estimate	PR>/T/
Teat dip	Yes	-163.95± 35.07	0.0001**
	No	0.0	
Separate towel	Yes	- 67.15± 36.33	0.0713
	No	0.0	
Vacuum line 2	2.54 cm	-149.71±129.03	0.2528
	2.18 cm	- 99.81± 52.38	0.0639**
	5.08 cm	-160.36± 55.87	0.0065**
	5.72 cm	- 56.71±129.03	0.6626
	3.81 cm	0.0	
Alternate pulsation	No	103.84± 41.30	0.0157*
	Yes	0.0	
Brand of inflation	2	12.42± 54.41	0.8206
	3	- 62.77± 57.48	0.2812
	4	- 95.64± 61.51	0.1277
	5	68.98± 45.85	0.1401
	6	0.0	
Variability of slope	High	104.49± 37.80	0.0083**
	Moderate	0.0	

** Significant at 0.01 level.

* Significant at 0.05 level.

There was a tendency for herds using a separate towel to have lower cell counts, although this effect was not significant. Moxley et al. (1978) reported significantly lower ($P<0.01$) somatic cell counts in herds teat dipping and lower somatic cell counts when separate towels were used to wash udders in 581 official test herds on the Quebec Dairy Herd Analysis Service.

Highly variable sloping of the milk line was associated with herd somatic cell counts 104,490 cells/ml higher than in herds with moderate to good sloping lines. Both Fell (1964) and McDonald (1969, 1975) indicated that an improper slope to the milk pipeline can lead to vacuum fluctuations or affect their severity. Vacuum fluctuation has been associated by a number of authors, Beckley and Smith (1962), Stanley et al. (1962), Braund and Schultz (1963) and Wilson (1978), with udder health. The methods of data collection in this study did not permit the direct observation of vacuum fluctuation.

Herds with single pulsation had higher cell counts than those using alternate pulsation, the effect being highly significant. Also, vacuum line 2 with a 5.08 cm diameter was associated with significantly lower herd somatic cell counts than a 3.81 cm diameter line. Brands of inflation were not significantly different for herd cell count when compared to brand 6.

Thus, we have looked at the effects of these milking machine and management practices individually on herd somatic cell count. But, each of these variables was part of the milking machine system, with no control over the rest of the systems characteristics as we studied one particular design or performance criteria. The simple correlations between the continuous variables may be found in Table 30.

Table 30. Simple correlations between continuous variables

	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
1) Ratio rear	0.96**	0.91**	-0.89**	0.97**	0.92**	0.28	0.11	0.31*	0.27
2) Ratio fore		0.97**	-0.95**	0.98**	0.98**	0.46**	0.23	0.35**	0.31*
3) Milking phase fore			-0.95**	0.96**	0.97**	0.54**	0.24	0.28	0.25
4) Air phase fore				-0.94**	-0.95**	-0.55**	-0.17	-0.32*	-0.29
5) Rate x ratio rear					0.98**	0.39**	0.21	0.29*	0.25
6) Rate x ratio fore						0.51**	0.28	0.32*	0.30
7) Rate of pulsation							0.39**	0.09	0.06
8) Static teat end vacuum								-0.09	-0.07
9) (Required-Rated) airflow									0.97*
10) (NM Required-Rated) airflow									

** Significant at 0.01 level.
* Significant at 0.05 level.

All seven pulsator traits were highly significantly correlated, the lone exception being ratio rear with rate of pulsation. If we exclude rate of pulsation, the magnitude of the correlations between the other six pulsator variables was 0.89 and greater. Thus it appears that these six traits, ratio fore, ratio rear, milking phase fore, air phase fore, rate x ratio rear and rate x ratio fore all are really describing the same thing, pulsator performance.

The simple phenotypic correlations for five of the above pulsator variables were significant with the required-rated airflow, with the correlation between milking phase fore and required-rated airflow being positive but not significant. The direction of the correlations were similar between these six variables and teat end vacuum and NM required-rated airflow, but most were not significant. The rate of pulsation was positively correlated with the teat end vacuum (0.39), with neither of these two traits being significantly correlated with airflow.

The significance between the classifications of the six variables of this type and the continuous variables in Tables 22 to 27 indicate relationships between these two types of variables. The milking management traits, teat dipping and use of separate towels, were not associated with significant differences between the yes and no groups for any of the ten continuous traits. Significantly more of the herds that were teat dipping were also using separate towels in this study.

All continuous pulsator variables except ratio rear teat differed significantly between the group of herds with alternate pulsation and those without. There were also differences in the static teat end vacuum, variability of slope and use of teat dip amongst the herds with or without

alternate pulsation. Group differences between high and moderate to good slope variability of the milk line were also significant with all pulsation traits. Group differences for brand of inflation were highly significant with all variables other than airflow, teat dip and separate towel. Finally, the rates of pulsation, static teat end vacuum and use of alternate pulsation were significantly different between the groups of herds with different sized vacuum lines between the vacuum distribution tank and the moisture trap.

Fourteen of the 16 variables significant at the 0.1 level in a one-way analysis of variance with herd somatic cell count were suitable for inclusion in a multiple regression analysis. The exceptions were brand of inflation and vacuum line 2, because of their multiple classes.

Stepwise regression (SAS 76) enters the independent variable having the largest partial correlation with the dependent variable in the model. It continues adding variables to the model by selecting the variable with the largest partial correlation, from the remaining variables. This procedure only retains variables in the model that have significant partial F values with the dependent variable.

The best regression equation for predicting herd average somatic cell count as selected by stepwise regression appears in Table 31, the model being highly significant. Only the variables teat dip and ratio fore teat were significant in explaining variation in the herd somatic cell count. The regression equation explained 40.81% of the variation in cell count. Teat dipping, coded as 1-yes, 2-no, was associated with lower cell counts when practiced, as was a lower milk-to-rest ratio of pulsation in the front teats. The mean of the ratio fore teat was lower than the mean of the ratio rear teat. One brand of milking machine uses a lower ratio and rate of pulsation for the front quarters as a method to avoid overmilking these lower producing quarters.

Table 31. Best regression equation by stepwise regression for average monthly herd somatic cell count (46 herds)

Analysis of variance Source	d.f.	SS	F value	PR>F
Teat dip	1	207614.669	20.99	0.0001**
Ratio fore teat	1	54817.310	5.54	0.0232*
Error	43	718500.870		

* $P<0.05$; ** $P<0.01$

EQUATION: $\hat{Y}_i = 69.417 + 154.173$ Teat Dip + 54.060 Ratio Fore Teat

R^2 (% explained variation) = 40.81%

It is of interest to note, however, that teat dipping alone explained 33.18% of the variation in herd somatic cell counts in the 46 herd population. The inclusion of all 14 variables in the multiple regression analysis explained only 47.18% of the variation in somatic cell count and this model was not significant.

Finally, including vacuum line 2 in the analysis with teat dip resulted in both variables being significant in their effect on herd somatic cell count (Table 32). However, it was the seven herds with an intermediate vacuum line (3.81 cm) that had significantly higher somatic cell counts than when this line was 3.18 cm or 5.08 cm. This suggests that this effect is not associated with the amount of space available for airflow from the vacuum distribution tank to the moisture trap. The diameter of the vacuum line at three other places was not significant at 0.1 in the preliminary analyses.

Table 32. General linear models procedure considering the effects of teat dip and vacuum line 2 on herd somatic cell count (45 herds)

Source	d.f.	SS	F value	PR>F
Teat dip	1	218745.63	23.44	0.0001**
Vacuum line 2	4	115762.87	3.10	0.0262*
Error	39	707601.11		

* $P<0.05$; ** $P<0.01$

R^2 (% explained variation) = 48.56%

Vacuum line 2 was associated with significant differences between classes for rate of pulsation and static teat end vacuum, but the seven herd class was intermediate for these traits. All of these seven herds had single pulsation, but so did the 22 herds with a line diameter of 3.18 cm. Thus, there may be a detrimental effect associated with this 3.81 cm diameter vacuum line. However, it seems that with this small sample, when we included vacuum line 2 with teat dip in the analysis the multiple classes of this trait merely identified this seven herd group as having high herd somatic cell counts. The variable vacuum line 2 had a probability greater than F of only 0.0933 in the one-way analysis.

The similarity that was observed for significant variables in the one-way analyses of variance for the 46 and 67 herd samples was also evident when a multiple regression analysis was carried out for the test day somatic

cell counts. Teat dipping alone accounted for 27.48% of the variation in the cell count. The best regression model included the variables teat dip and alternate pulsation, accounting for 33.83% of the variation in herd test date somatic cell count. In the 46 herd group, the use of alternate pulsation was closely related to the ratio of the fore teat.

Moxley et al. (1978) found that the use of a teat dip was the most important factor in having lower herd somatic cell counts of all the management practices examined in that study. The analyses in the present study indicate that teat dipping is also more important than any of the milking machine design and performance characteristics studied in relation to lower herd somatic cell counts.

Of the milking machine traits, only ratio fore teat and alternate pulsation were significant in multiple regression analyses for herd average somatic cell count and herd test day cell count, respectively. However, these two closely related traits did not greatly increase the percentage of explained variation for somatic cell count. Further study of the effects of pulsation on udder health is indicated, as Kingwill et al. (1978) indicated that no comprehensive study of the effects of pulsation on mastitis has been made.

In the absence of major malfunctions of the milking system, it is suggested that milking management and specifically teat dipping are more important than the machine towards lower herd average somatic cell counts.

VI. SUMMARY AND CONCLUSIONS

A. Milking Speed

The linear and quadratic effects of the milk yield at sampling had a significant effect on two-minute yield, while only the linear effect was significant for total milking time. Both measurements of each trait, unadjusted and adjusted, were utilized in the subsequent analyses.

Maximum Likelihood (ML) procedures were used to obtain estimates of unknown constants and variances under mixed models. Both herds and stage of lactation had a highly significant effect on two-minute yield, adjusted two-minute yield, total milking time and adjusted total milking time. Best Linear Unbiased Estimates (BLUE) indicated that the two-minute yield peaked early in lactation, then declined steadily. However, adjusting for the milk yield at sampling indicated the opposite, that the cows were actually milking faster late in lactation. The total milking time followed a pattern similar to that for two-minute yield. The adjusted milking time was also longer early in lactation and declined with advancing lactation. This is consistent with the results obtained for the adjusted two-minute yield, in that adjusting for the total milk yield indicates that cows milk at a faster rate as the lactation progresses.

Age of cow at last calving had no significant effect on two-minute yield. However, the results obtained for the other three measurements of milking speed indicated that younger cows milk at a faster rate than do older cows. Season of calving did not significantly influence any of the measurements of milking speed.

The heritability estimates obtained using ML variance estimates were greater for adjusted two-minute yield (0.22 to 0.26) than for two-minute yield (0.17 to 0.23). The higher heritabilities after adjusting suggest that the amount of milk present at sampling may mask some of the genetic variance for two-minute yield. Lower heritability estimates were observed for total milking time (0.18 and 0.20) and adjusted total milking time (0.13 and 0.16). The lower heritabilities of milking time than two-minute yield are not unexpected in that total milking time is more dependent on the operator and the milking routine.

Both the phenotypic and genetic correlations between the unadjusted and adjusted measurements of the same trait were very high (0.88 to 0.97). Phenotypic correlations between the measurements of two-minute yield with the measurements of total milking time were moderately high, all being negative (-0.27 to -0.50). The corresponding genetic correlations were more highly negative (-0.65 to -1.00). The negative correlations indicate that higher two-minute yields are associated with less total milking time. The high genetic correlations suggest that the same set of genes are controlling both the two-minute yield and the total milking time. Both measurements indicate how fast a cow is milking, with the highest correlations observed when we eliminate the influence of the total milk yield at sampling.

The phenotypic correlations between the four measurements of milking speed with somatic cell count and log somatic cell count were small (-0.05 to 0.09). Least squares analysis indicated that only the two classes with the lowest adjusted two-minute had significantly lower log somatic cell counts. There appears to be a point between 4 and 4.5 kg after which further increases in the adjusted two-minute yield do not adversely affect the log somatic

cell count.

Genetic correlations were highly positive between log somatic cell count with both measurements of two-minute yield (0.94 and 0.79), while the genetic correlations with the measurements of total milking time were moderately negative (-0.40 and -0.59). However, direct selection for milking speed should not result in large genetic increases in somatic cell count because of the low heritabilities (0.02 and 0.03) and small sire components of variance observed for log somatic cell count.

Phenotypic correlations between the four lactation traits - 305-day milk and fat and BCA milk and BCA fat - and the two unadjusted milking speed measurements were small but significantly positive (0.11 to 0.22). However, the corresponding correlations with the adjusted measurements were not significantly different from zero (-0.05 to 0.02). The relationships with the unadjusted measurements resulted from the cows with higher lactation production having had a higher milk yield at sampling. The milking rate we observe is dependent upon the milk yield at sampling.

The genetic correlations between the lactation production traits and adjusted two-minute yield were moderately negative (-0.23 to -0.48), being larger than the corresponding correlations with two-minute yield (-0.06 to -0.36). Genetic correlations between the measurements of milking time and the four lactation traits were generally small, ranging between -0.18 and 0.14. There appears to be an antagonistic genetic relationship between higher two-minute yields and lactation milk production, while the genetic relationship between the lactation traits and milking time is small.

Spearman rank correlations between the estimated breeding values of 56 sires for the four milking speed traits were intermediate between the phenotypic and genetic correlations. They emphasize the high degree of relationship between these traits, especially the unadjusted and adjusted measurements of the same trait (r_s=0.93). Thus, two-minute yield, adjusted two-minute yield, total milking time and adjusted total milking time are all useful measurements for indicating milking speed.

The choice of which measurement of milking speed to use is dependent upon the ease of measuring the trait, its heritability, and its relationship with other economically important traits that are part of the selection program. The adjusted two-minute yield has the highest heritability but the most negative relationship with production. Conversely, the adjusted total milking time has the lowest heritability of the four traits, but is not adversely related to lactation production. Both measurements of two-minute yield had a more negative relationship with log somatic cell count than measurements of total milking time.

Thus, the final decision depends upon the economic importance of milking speed in relation to other traits of interest, and the relationships between milking speed measurements and these traits. It may be of value to investigate these relationships further, in view of the relatively small sample size available in this study. Somatic cell counts were based on a half-day milk sample, while the use of multiple tests to produce a lactation measurement for this trait may better reflect the genetic relationships that do exist between cell count and milking speed.

Machine stripping time was not significantly correlated with somatic

cell count, log somatic cell count and two-minute yield. There was a small negative correlation between stripping time and adjusted two-minute yield (0.12) while the correlations were positive with total milking time (0.21) and adjusted total milking time (0.16). It appears that slower milking cows are subjected to more machine stripping.

The largest correlation was observed between stripping time and half-day milk yield (0.24). Cows that were milking more were subjected to more machine stripping. Simple phenotypic correlations between stripping time and lactation production were positive (0.13 to 0.20). However, when half-day milk yield and stripping time were considered as covariates in models with production as the dependent variable, only the half-day milk yield had a significant effect on lactation production.

There appears to be little benefit obtained from machine stripping based on the results of this study. This practice may in fact add to the total milking time.

B. Milking Machines

Eleven variables were significant at the 0.1 level on both herd average somatic cell count in 46 herds and somatic cell count on the day the machine was tested in 67 herds. Only six variables were significant at this level for one or the other populations. These variables were the only variables significant at the 0.1 level out of 63 variables relating to the design and performance of the milking machine and milking practices that were analyzed in one-way analyses of variance with somatic cell count as the dependent variable.

There were ten continuous and six classification variables that were significant at the 0.1 level on herd average somatic cell count. Of these, eight of the variables were related to the performance of the pulsator. Simple correlations between six of these - ratio rear, ratio fore, milking phase fore, air phase fore, rate x ratio rear and rate x ratio fore were $|0.89|$ and larger. Pulsator rate was significantly correlated ($P<0.01$) with all but ratio rear, while there were significant differences between many of these traits in the groups with or without alternate pulsation. Thus, it appears that all of these different measurements describe the same thing, pulsator performance. A higher ratio fore teat, milking phase fore, rate x ratio fore, rate x ratio rear and the use of alternate pulsation were all significantly ($P<0.05$) associated with higher herd somatic cell counts.

Those farms that were using a teat dip had significantly ($P<0.01$) lower cell counts than those not, as did milking machines with a moderate to good slope of the milk line when compared to those with a highly variable slope. The other factors that were significant on herd somatic cell count at the 0.1 level of significance were the use of separate towels, the size of the vacuum line between the vacuum distribution tank and moisture trap, the brand of inflation, the static teat end vacuum and two measurements of the air flow of the system.

Multiple regression analysis was used to study the combined effects of the variables on herd somatic cell count. Two variables, the brand of inflation and the size of the vacuum line were not suitable for inclusion in this type of analysis because of their multiple classes.

The best regression equation for predicting herd average somatic cell count as selected by Stepwise regression (SAS 76) included only the variables teat dip, with 1-yes and 2-no, and ratio fore teat. The equation, which appears below, explained 40.81% of the variation in herd average somatic cell count.

$$\hat{Y}_i = 69.42 + 154.17 \text{ Teat Dip} + 54.06 \text{ Ratio Fore Teat}$$

However, teat dip alone explained 33.18% of the variation in herd somatic cell count. Also, including the multiple class variable vacuum line 2 in a model with teat dip explained 48.56% of the variation in cell count. There was, however, no pattern distinguishable for this variable with the highest herd somatic cell counts observed in seven herds with an intermediate vacuum line size. This intermediate vacuum line size may have a negative association with somatic cell count. However, it seems more likely that with this small sample size and the multiple classes of this variable, that it identified this seven herd group as having high herd somatic cell counts.

Multiple regression analysis that included the variables that were significant at the 0.1 level on herd average test day somatic cell counts yielded similar results. The best regression equation included the variables teat dip and alternate pulsation, explaining 33.83% of the variation in test day cell count. Teat dipping alone explained 27.48% of the variation in the cell count.

Thus, of the milking machine traits, only ratio fore teat and alternate pulsation were significant in multiple regression analyses for herd average somatic cell count and herd test day cell count, respectively.

However, these two closely related traits did not greatly increase the percentage of explained variation for somatic cell count. In the absence of major malfunctions of the milking system it appears that milking practices, and specifically teat dipping, are more important towards lower herd somatic cell counts than the milking machine.

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Appendix Table 1. Milking machine design and performance data

Herd No. _____ Date _____

1) Year of acquisition of present milking system _____.

2) Is the system
   i) As installed
   ii) Expanded or changed
   iii) Upgraded

3) Vacuum pump(s)
   a) Brand _____
   b) Model _____
   c) H.P. _____
   d) Air flow rating _____
   e) Number of pumps _____

4) Air flow measured at the vacuum pump _____

5) Number of vacuum controllers _____

6) Position of vacuum controllers
   i) After vacuum pump or distribution tank
   ii) Just before moisture trap
   iii) Other

7) Condition of vacuum controllers
   i) Clean
   ii) Dirty

8) Vacuum line sizes
   a) Vacuum pump to distribution tank _____
   b) Distribution tank to moisture trap _____
   c) Moisture trap to receiver jar _____
   d) Pulsator line _____

9) Length of vacuum line installation _____

10) Vacuum line
   a) Is it a
      i) Closed circuit
      ii) Dead end
      iii) Closed, but contains a dead-end portion
   b) Installed inside the barn with as few bends and elbows as possible
      1) If not, number of extra _____

Continued.....

Appendix Table 1 (Cont'd)
Page two

11)	Milk line	a) Diameter	_____
		b) Slope i) double	
		ii) single	
		c) Slope variability i) highly variable	
		ii) good to slight variability	
		d) Pitch per slope	_____
		e) Highest elevation from floor	_____
		f) Position of milk inlets i) top	
		ii) middle	
		iii) bottom	
12)	Static vacuum levels	a) Milk Line	_____
		b) Vacuum line	_____
		c) Teat cup	_____
		d) Pulsation chamber	_____
13)	Milking unit	a) Number	_____
		b) Type of inflation	
		i) brand	_____
		ii) number	_____
		c) Length of service of inflation	_____
		d) Are two sets of inflations alternated	_____
		e) Inflation bore	
		i) large	
		ii) narrow	
14)	Milk hose	a) Type i) rubber	
		ii) plastic	
		b) Length	_____
		c) Diameter	_____
15)	Pulsators	a) Type i) pneumatic	
		ii) electric	
		b) i) single acting	
		ii) alternate acting	
		c) Rate per minute	_____
		d) Opened to closed ratio	
		i) fore	_____
		ii) rear	_____
		e) Milk phase	
		i) fore	_____
		ii) rear	_____
		f) Air phase	
		i) fore	_____
		ii) rear	_____
		g) Recovery time after 5 sec. air admission	_____

Continued.....

Appendix Table 1 (Cont'd)
Page three

16) Number of units per operator _____

17) Is the vacuum closed before the teat cups are removed _____

18) Is the system checked regularly or only when a breakdown occurs _____

19) How long since the system was tested by a dealer and maintenance carried out _____

20) a) Is the vacuum line flushed out _____
b) If yes, how often _____

21) Calculation of required vacuum pump capacity[1]

Milking units _____	x 169.8 l/min (6 CFM)	_____
Stall cocks _____	x 2.83 l/min (1/10 CFM)	_____
Milk inlets _____	x 2.83 l/min (1/10 CFM)	_____
Vacuum controllers ____	x 84.9 l/min (3 CFM)	_____
Sanitary elbows _____	x 1.41 l/min (1/20 CFM)	_____
Milk meters _____	x 28.3 l/min (1 CFM)	_____

Minimum required America standard @ 50 kPa (includes a 50% reserve) Total _____

22) a) Formula to evaluate period of teat cup usage:[1]

$$1200 \div (\text{No. of cows} \times 2 \div \text{No. of milking units}) = \text{No. of days}$$

b) Use of teat cups in relation to formula
i) less
ii) ~ equal
iii) more .

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[1] Le système lactoduc, Agriculture Québec.

Appendix Table 2. Generated milking machine variables

1.	Required vacuum pump capacity (air flow) - rated vacuum pump capacity
2.	Required vacuum pump capacity - measured vacuum pump capacity
3.	Pulsation rate x pulsation ratio rear
4.	Pulsation rate x pulsation ratio fore
5.	Required vacuum pump capacity $\div$ vacuum line length
6.	Required pump capacity (not including requirements for milk meters) - rated vacuum pump capacity
7.	Required pump capacity (not including requirements for milk meters) - measured vacuum pump capacity

Appendix Table 3. Analysis of variance for two-minute yield and total milking time with two covariates included in the model

Source	Two-minute yield d.f.	Two-minute yield M.S.	Total milking time d.f.	Total milking time M.S.
Herd	79	11.32**	78	147612.66**
Stage of lactation	13	6.13**	13	15697.26
Age at calving	5	5.16*	5	67050.53**
Season of calving	2	1.11	2	386.25
Total milk - linear	1	453.36**	1	418796.68**
Total milk - quadratic	1	95.08**	1	24436.32
Error	2502	1.87	2134	10787.18

* Significant at the 0.05 level.

** Significant at the 0.01 level.

Appendix Table 4. Analysis of variance for machine stripping

Source	d.f.	Mean square
Herd	30	16900.97**
Stage of lactation	13	1380.16
Age at calving	5	8370.48**
Season of calving	2	1415.73
Error	896	1458.00

** Significant at the 0.01 level.

Appendix Table 5. Analysis of variance of fixed effects for the traits in the 2619 record population

	d.f.	Two-minute yield M.S.	Adjusted two-minute yield M.S.	BCA milk M.S.	BCA fat M.S.
Herd	78	17.73**	11.22**	4354.42**	6153.91**
Stage of lactation	13	66.19**	8.70**	2360.51**	1525.84**
Age at calving	5	4.05	6.21**	2228.10**	1202.97*
Season of calving	2	4.56	0.94	1471.10*	4120.98**
Error	2520	2.49	1.84	385.26	472.61

* Significant at the 0.05 level.

** Significant at the 0.01 level.

Appendix Table 6. Analysis of variance of fixed effects for the traits in the 2604 record population.

	d.f.	Two-minute yield M.S.	Adjusted Two-minute yield M.S.	Somatic cell count M.S.	Log somatic cell count
Herd	79	16.93**	11.15**	1342593**	8.14**
Stage of lactation	13	54.19**	9.82**	1794876**	15.20**
Age at calving	5	5.07	5.21*	15706654**	72.31**
Season of calving	2	6.78	1.16	351575	0.97
Error	2504	2.45	1.85	573870	1.09

* Significant at the 0.05 level.

** Significant at the 0.01 level.

Appendix Table 7. Analysis of variance of fixed effects for the traits in the 2488 record population

Source	d.f.	Two-minute yield M.S.	Adjusted two-minute yield M.S.	305-day milk M.S.	305-day fat M.S.
Herd	79	15.87**	10.01**	9950985**	18171.60**
Stage of lactation	13	68.76**	6.44**	6566115**	6310.33**
Age at calving	5	2.61	5.14*	148799170**	175949.67**
Season of calving	2	4.08	0.25	31665345**	66443.93**
Error	2388	2.56	1.86	961402	1617.31

* Significant at the 0.05 level.

** Significant at the 0.01 level.

Appendix Table 8. Analysis of variance of fixed effects for the traits in the 2235 record population

Source	d.f.	Two-minute yield M.S.	Adjusted two-minute yield	Total Milking time	Adjusted total milking time	Somatic cell count	Log somatic cell count
Herd	78	15.37**	10.29**	158262.09**	149211.77**	1308000**	7.96**
Stage of lactation	13	44.28**	9.96**	276665.52**	23474.19**	1319166**	11.20**
Age at calving	5	4.50	3.89*	176003.91**	70134.46**	12375731**	59.69**
Season of calving	2	5.41	1.10	11771.73	373.50	153947	0.84
Error	2136	2.40	1.82	11870.63	10870.63	545103	1.05

* Significant at the 0.05 level.

** Significant at the 0.01 level.

Appendix Table 9. Analysis of variance of fixed effects for the traits in the 2138 record population

Source	d.f.	Total milking time M.S.	Adjusted Total milking time M.S.	BCA Milk M.S.	BCA fat M.S.	305-day milk M.S.	305-day fat M.S.
Herd	77	159023.25**	147097.46**	3766.04**	5174.46**	9201375**	17359.03**
Stage of lactation	13	245735.14**	15581.96	2223.79**	1324.90**	6780728**	6716.53**
Age at calving	5	144949.88**	54048.11**	1559.79**	1539.58**	128193810**	158082.39**
Season of calving	2	7387.00	854.46	1052.26	2896.20**	26122360**	57895.83**
Error	2040	11670.22	10643.71	379.41	465.07	9452	1605.13

** Significant at the 0.01 level

Appendix Table 10. Analysis of variance of fixed effects for somatic cell count with milking speed variables treated as fixed

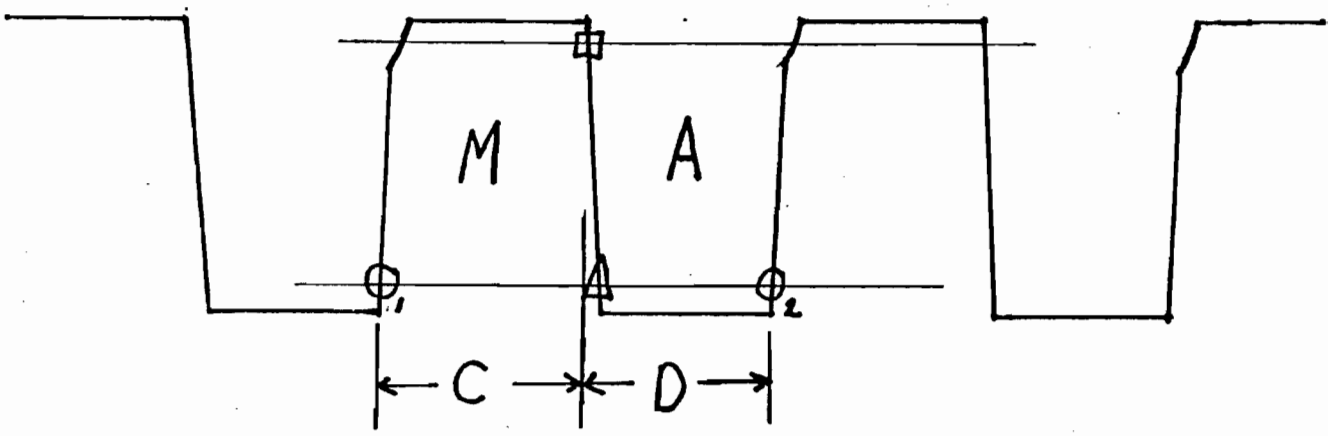
Source	Somatic cell count M.S.					
	Fixed milking speed variable					
	d.f.	Two-minute yield	Adjusted Two-minute yield	d.f.	Total milking time	Adjusted total milking time
Stage of lactation	13	1744324.50**	1579210.40**	13	1240275.90**	1298932.50**
Age at calving	5	17020308.00**	17477768.00**	5	12998454.00**	12699330.00**
Season of calving	2	233919.12	270886.89	2	179279.68	134003.04
Milking speed	9	957966.97	478196.72	6	790107.39	342107.53
Error	2495	581632.49	583290.98	2130	547424.90	548686.87

** Significant at the 0.01 level.

Appendix Table 11. Analysis of variance of fixed effects for log somatic cell count with milking speed variables treated as fixed

Source	Log somatic cell count M.S.					
	Fixed milking speed variable					
	d.f.	Two-minute yield	Adjusted two-minute yield	d.f.	Total milking time	Adjusted total milking time
Stage of lactation	13	14.42**	12.63**	13	8.40**	10.93**
Age at calving	5	74.08**	78.11**	5	62.82**	61.21**
Season of calving	2	0.87	0.86	2	0.87	0.70
Milking speed	9	1.96	3.38**	6	2.19	1.20
Error	2495	1.10	1.09	2130	1.05	1.05

** Significant at the 0.01 level.



Rate of pulsation: the number of complete pulsation cycles per minute. On graph, one cycle is shown between the two circles(O).

Pulsation ratio: the ratio of the milking-to-rest-phase of pulsation, the rest phase $\frac{C}{D}$ including the transition from opened-to-closed.

Milking phase: the percentage of time the pulsator is opening or completely open in the milking phase. On graph, the percent of the total cycle between O_1, and □.

Air phase: The percentage of time the pulsator is completely closed On graph, the percent of the total cycle between Δ and O_2.

Alternate pulsation: if not all four teats are being milked in the same opened-to-closed phase of pulsation.

Appendix Figure 1. Pulsator tracing