

**VARIATION DUE TO DIRECT AND MATERNAL GENETIC  
EFFECTS IN CANADIAN DAIRY GOATS**

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by  
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## **ABSTRACT**

### **Variation due to direct genetic and maternal genetic effects in Canadian dairy goats**

Derivative free restricted maximum likelihood (DFREML) was used to calculate variance and covariance components for cumulative milk yield, cumulative fat yield and cumulative protein yield, of Alpine, Toggenburg, Saanen and Nubian dairy goat breeds.

First lactation records of 691 Alpine, 641 Toggenburg, 439 Saanen and 433 Nubian goats freshening between 1986 and 1995, and a combined data set of all breeds, were analysed. Two basic models, either including or excluding coefficients for phantom groups, besides the random and fixed effects, were fitted for each trait and breed. Included fixed effects were age at first kidding and flock-year for the single breed data sets and an additional breed effect for the multiple breed data set. Random effects in sub-models were fitted to estimate direct effects (model 1), direct and maternal effects (model 2) and direct effects, maternal effects and the covariance between direct and maternal genetic effects (model 3).

Solutions for fixed effects were obtained, and estimates of heritabilities ( $h^2$ ) for the different breeds were between 0.17 and 0.30 for cumulative milk yield, 0.09 and 0.44 for cumulative fat yield and 0.04 and 0.25 for cumulative protein yield. There were marked differences between breeds for  $h^2$ . Values of the maternal genetic variances ( $m^2$ ) were small and statistically non-significant for all traits for Alpine, Toggenburg and Saanen goats. For Nubian the results for  $m^2$  were very high and statistically significant ( $p < 0.05$ ) for milk and fat yield and ( $p < 0.025$ ) for protein yield. Maternal effects estimated for the all breed data set were not significant for milk yield, but were significant ( $p < 0.05$ ) for fat and protein yield. Covariances between direct and maternal effects for all breeds and traits were not statistically significant. Fitting phantom groups in the model resulted in generally higher estimates. Best models to describe the data sets were those only fitting direct genetic effects in addition to fixed effects. The F-test revealed that fitting phantom groups had no effect in the single breed analyses, but had an effect in the multiple breed analysis.

## RÉSUMÉ

### **Variations de la production laitière dues aux effets génétiques directs et maternels chez les caprins au Canada**

L'utilisation du maximum de vraisemblance restreint et d'un algorithme sans dérivation (MVRSD) a été utilisé pour calculer les composantes de la variance et de la covariance des rendements cumulatifs en lait, matières grasses et protéines chez les chèvres de races Alpine, Toggenburg, Saanen et Nubian. Les analyses ont été réalisées sur les données de 691 Alpines, 641 Toggenburgs, 439 Saanens et 433 Nubians entrées en première lactation entre 1986 et 1995, ainsi que sur un ensemble de données de toutes les races combinées. Deux modèles de base prenant en compte les effets aléatoires ainsi que fixés et, incluant ou n'incluant pas les coefficients pour les groupes "fantômes", ont été ajustés pour chaque caractère et pour chaque race étudiés. Les effets fixés pour les données par races étaient l'âge des individus et l'année du troupeau. De plus, pour les données combinées les effets fixés comprenaient l'effet race. Les effets aléatoires des sous-modèles ont été ajustés pour l'estimation des effets génétiques directs (modèle 1), directs et maternels (modèle 2) et, directs, maternels, avec la covariance entre les 2 (modèle 3).

Les solutions aux effets fixés ont été calculées et, les valeurs de l'estimation de l'héritabilité ( $h^2$ ) pour les différentes races étaient comprises entre 0.17 et 0.30 pour le rendement cumulé en lait, 0.09 et 0.44 pour le rendement cumulatif en matières grasses, 0.04 et 0.25 pour le rendement cumulatif en protéines. Il existe donc des différences marquées de  $h^2$  entre les races. Les valeurs des variances de l'effet génétique maternel ( $m^2$ ) pour tous les caractères étudiés étaient minimales et non statistiquement significatives pour les chèvres Alpines, Toggenburg et Saanens. Pour les Nubians les résultats des  $m^2$  étaient statistiquement significatifs pour le rendement en lait et en matières grasses ( $p \leq 0.5$ ) et pour le rendement en protéines ( $p \leq 0.25$ ), mais les estimés de  $m^2$  étaient très élevés. Les effets maternels estimés pour l'ensemble des données combinées n'étaient pas significatifs pour le rendement en lait, mais étaient significatifs ( $p \leq 0.05$ ) pour le rendement en matières grasses et en protéines. Les covariances entre les effets directs et maternels n'étaient pas significatives pour aucun des caractères ni aucune des races. L'ajout des groupes "fantômes" au modèle a globalement augmenté les estimés. Les

meilleurs modèles pour décrire l'ensemble des données étaient ceux incluant seulement les effets génétiques directs en plus des effets fixés. Le test-F a révélé que l'ajout des groupes "fantômes" n'avait pas d'effet sur les analyses portant sur une seule race, par contre il avait un effet sur les analyses portant sur plusieurs races.

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## **1. INTRODUCTION**

The market situation for dairy goats in Canada is not promotional. However, there is a great potential for expansion of production to satisfy the current market. To select genetically superior animals, genetic evaluation is available to participants in milk recording programs. Replacement does are selected mainly according to dams milk production (63 %), litter size (60 %), conformation (55 %), body size at weaning (42 %), dams maternal ability (35 %). Bucks are selected according to conformation (69 %), dam/daughter milk (45 %), litter size (38 %) and other reasons such as average daily gain, sire's performance for growth, extended pedigree and breed characteristics (Nadarajah, 1998).

Dual-purpose goat breeds are dominant in many countries. In Canada, imported European breeds such as Alpine, Saanen, Toggenburg, and Nubian have been developed as single purpose breeds for milk production. In dairy goats, as in dairy cattle, profitability is dependent on the efficiency of milk production. For the development of effective selection plans, knowledge of genotypic and environmental parameters is necessary. The phenotype of an animal is the product of genetic and environmental effects. The genetic variance (effect) itself is composed of additive, maternal, dominance and epistatic genetic variance. The dam influences the phenotypic value of her offspring in two ways; first by contributing a sample half of her genes, and second by providing a maternal environment through mothering and supply of nutrients. Sire, on the other hand, contributes to the phenotype of the offspring through a sample half of his genes. The biometrical aspects of maternal effects in terms of linear genetic models were developed around 1950. Maternal effects, nowadays, are known to be present in beef cattle and sheep. Studies (e.g. Meyer, 1992, Robinson, 1996) show that between 0 to 20 % of the genetic variance is contributed by the maternal effect and that there are differences between breeds.

The development of computer programs allows the use of restricted maximum likelihood (REML) with animal models to estimate variance components (e.g. Meyer, 1989). The objective of this study was to estimate variance and covariance components due to direct and maternal genetic effects and environmental effects for milk production traits

(cumulative milk, fat and protein yield) using REML procedures under single trait animal models with data from Alpine, Toggenburg, Saanen and Nubian goats.

## **2. LITERATURE REVIEW**

Very little research is published on goat breeding and genetics. As in dairy cattle, the main interest is to increase performance in production, reproduction and conformation traits. The literature shows that many factors, environmental and genetic, play a role in affecting lactation traits; milk yield, fat yield (milk fat content) and protein yield (milk protein content). Most environmental influences are difficult to quantify, but there are known environmental effects. They are so consistent in influencing traits, that researchers have developed mathematical adjustment factors or adjustment procedures to account for them (Bourdon, 1997).

**Table 1. Examples of Environmental Effects for which Mathematical Adjustment Procedures and (or) Adjustment Factors are available [from Bourdon, 1997]**

<b>Species</b>	<b>Trait</b>	<b>Environmental Effect</b>
<b>Cattle (dairy)</b>	<b>Milk yield</b>	<b>Length of lactation</b>
	<b>Milk yield</b>	<b>Milking per day</b>
	<b>Milk yield</b>	<b>Age at calving</b>
	<b>Fat yield</b>	<b>Length of lactation</b>
	<b>Fat yield</b>	<b>Milking per day</b>
	<b>Fat yield</b>	<b>Age at calving</b>
	<b>Fat corrected milk yield</b>	<b>Fat yield</b>

The purpose of such adjustments is 1) to reduce sampling variance, 2) to remove systematic biases from comparison of animals or animal groups and 3) to estimate what a specific record would have been if taken at a standard age, season, length of lactation etc. (Iloeje et al, 1980).

### **2.1 Environmental and Genetic Causes of Variation in Production Traits**

Several genetic and environmental factors affect production in dairy animals. These factors which may cause variation in productivity of dairy goats should be considered in the evaluation and calculation of genetic components. One of the most important is the herd-

year-season, which includes all factors like flock environment (such as nutrition), flock management, year of birth and season of production. Year of birth is important, because there are existing phenotypic time trends, which could be genetic and/or environmental. Another important factor is age of doe at first kidding (parity) and the breed used. Studies in the United States indicate that milk yield of dairy goats is highly variable (Iloeje et al, 1981; Shelton, 1978). Effects of age, parity, and season of kidding on milk and fat yield were examined (Gipson et al, 1989; Kennedy et al, 1981), with the purpose of developing correction factors for use in genetic evaluation of breeding animals. A review of factors affecting production in goats is given by Iloeje et al, 1978.

### **2.1.1 Nutrition**

Nutrition is the easiest to influence and the fastest responding cause of variation. All lactation traits are affected by changing food supply. Comparing dairy goats and dairy cattle on the basis of the metabolic bodyweight, the calculated requirements for energy and protein for maintenance and production are very similar to those for dairy cattle (Sutton, 1990). Studies show that a well fed doe has a higher milk production. Research conducted in 1974 with Don goats showed that milk production was phenotypically significantly correlated with body weight (Orlyanskii et al, 1974). The correlation between milk production in the first lactation and body weight was 0.33 and in the second lactation 0.43. In the literature the correlation between body weight and milk production ranged from 0.19 to 0.43. Gall (1973) showed that about 60 % of the variation in milk yield could be attributed to body size, rumen volume, skeletal size, muscle volume, and fat.

After kidding, high producing does need a high amount of energy for milk synthesis and secretion in early lactation. Does can lose up to 6 kg live weight, consisting of protein as well as fat in early lactation, slowly regaining this weight later. In early lactation stage it is very important to supply the animals with the needed requirements, otherwise the doe will not be able to produce as much milk as her genotype would allow.

If the genetic potential of a doe is to produce 4 kg of milk per day, but she only receives enough nutrients to produce 2 kg, she will only produce 2 kg. Even if just one necessary nutrient is missing she will only produce as much milk as the supply of the restricted



nutrient allows. This is referred to as 'the principle of the first limiting nutrient' (Agriculture Canada, 1989).

Morand-Fehr and Sauvant (1978) stated that energy intake is the most important dietary factor influencing milk production regardless of the stage of lactation. The amount of energy really consumed by the goat appeared to be the most positively correlated factor with milk production whatever the composition of the diet may be (Morand-Fehr et al., 1978).

**Table 2. Correlation between intake of metabolisable energy and dairy goat performance**

	Correlation between intake of metabolisable energy and		
	Milk yield	Fat (%)	Protein (%)
1 <sup>st</sup> -8 <sup>th</sup> week of lactation	0.752*	+ 0.010	- 0.190
9 <sup>th</sup> -18 <sup>th</sup> week of lactation	0.794*	- 0.121	+ 0.188
19 <sup>th</sup> -28 <sup>th</sup> week of lactation	0.873*	- 0.157	+ 0.123

[from Morand-Fehr et al. 1978]

Ruminants obtain energy primarily from fibre, carbohydrates and fat in their ration. Studies show that improved energy efficiency from dietary fat increases milk production (Teh et al, 1994). The correlations between intake of metabolisable energy and trait yields shown in Table 2, indicate that milk yield increases progressively with advance in lactation and more energy is needed. In mid and late lactation fat percentage generally decreases whereas protein percentage increases.

### **2.1.2 Stage and length of lactation**

The stage and length of lactation is important for genetic evaluation based on cumulative milk yield, because with increasing length, the yields increase too. The cumulative milk, fat and protein yield is the actual amount of milk that a doe gives in her lactation up to a certain point and the longer a goat is in lactation the higher is her milk yield per lactation, all other things being equal. Within species and within breed, it is the stage of lactation that has the greatest influence on milk composition (Haenlein, 1995). To get unbiased results it is important to make sure that only goats with a complete lactation participate in the evaluation. The lactation curve of goats looks similar to that of dairy cattle and dairy

sheep. The lactation starts with a high increase in milk yield and reaches a peak after 30 days for sheep and around 45 days for goats and then declines until next kidding. (LKV, 1993; Sutton, 1990).

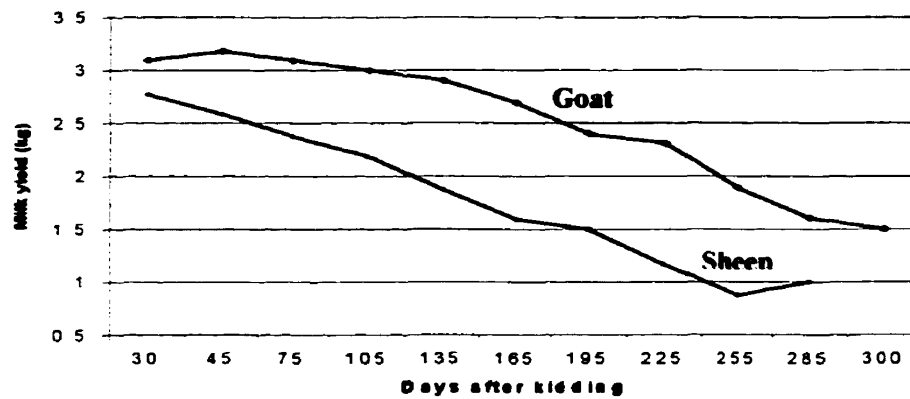


Figure 1. Average lactation curves of German sheep and German 'Alpine' goat populations [from LKV, 1993]

In literature reports, the averages of lactation length for dairy goats, depending on breed, are from 211 to 238 days (Ali et al., 1983). Ali et al (1983) and Kennedy et al (1982) reported a strong relationship between lactation length and lactation yield.

Sullivan (1988) concluded that if lactation length is determined mainly by environmental factors, there would be a large bias by failing to adjust for differences in lactation length and if lactation length is heritable, it would be inappropriate to simply adjust yield for lactation length.

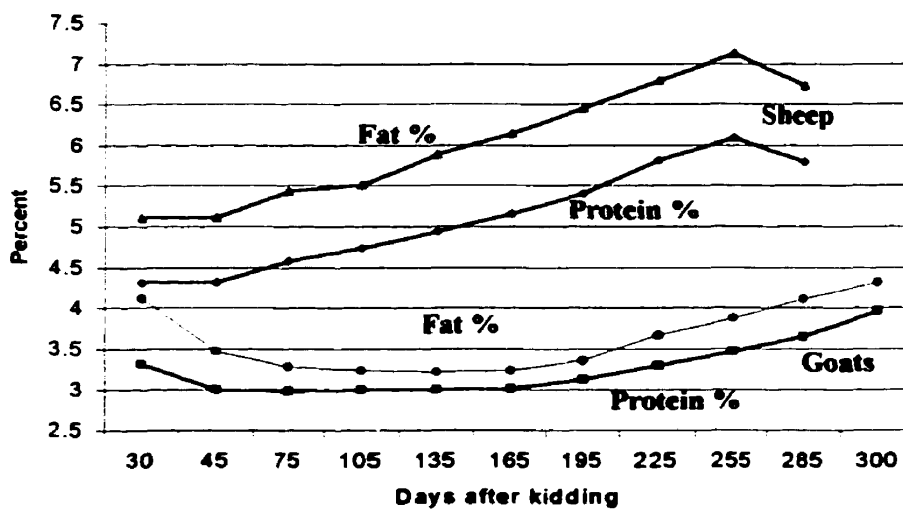


Figure 2. Protein and fat content of goats and sheep milk during lactation [from LKV, 1993]

Many components, especially fat and protein percentages, are high in ewe and goat colostrum, much lower thereafter in milk, and they rise again at the end of lactation (Anifantakis et al., 1980). Fat content in goat milk changed from 2.7 % in mid lactation to 4.6 % during the last week (42) of lactation, and protein content from 3.0 % to 4.2 % (Voutsinas et al, 1990). Similar trends were observed from the LKV Germany, (1993), which is illustrated in Figure 2.

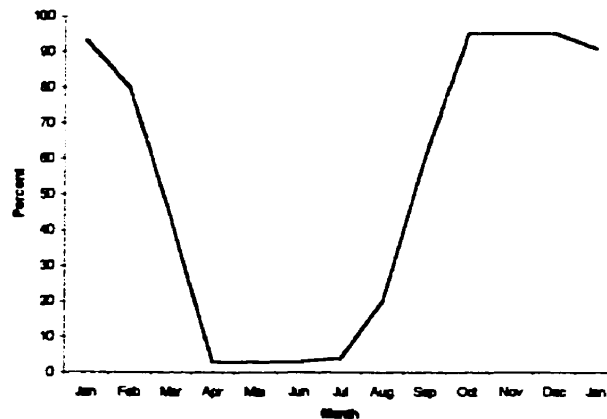
### **2.1.3 Season of kidding**

In Canada goats are like sheep in that they are highly seasonal in their breeding. Singh, Acharay and Biswas (1970) have found season of kidding to be a very important source of variation affecting milk production. Strong relationships between reproduction and production indicate that photo period may have an indirect effect on production traits (Ali et al., 1983; Kennedy et al., 1982). In the U.S. goats seem to be seasonal breeders (Shelton, 1978; Ali, et al., 1983; Mohammad, 1984; Amoah et al., 1996) and, as in other septentrional countries, related to length of photo period. Light introduces the fertile oestrous cycles, which generally begin 10 weeks after the longest day of the year (Agriculture Canada, 1989). This was also reported by BonDurant et al (1981) where the goats showed an endogenous annual rhythm of biological activity, which was responding to day length changes. Seasonal variation in photo period increased with increasing distance from the equator leading to the conclusion that breeding in dairy goats is more seasonal at northern than at southern latitudes because of differences in length of photo period (Ali et al, 1983; Mohammad, 1984).

On the other hand, some studies showed that the effect of latitude on reproductive performance is minor (Mohammad et al, 1984) and that even in the most northern regions of U.S., breeding in goats is not highly seasonal. The results suggest that factors other than length of photo period may be causing the seasonality of breeding of goats in the U.S., in particular, the interaction of feeding regimes, reproduction and management. The effects of season of kidding, lactation yield, temperature and humidity (climate) could cause variation in fat and protein content. It is reported that temperature (Johnson, H.D., 1965; McDonald et al, 1958) and humidity (Ingraham et al., 1979; Johnson J.C. et al.,

1962) influence the animal directly and cause adjustments in their behaviour which result eventually in a decline in milk energy output (Iloeje et al, 1980). However, artificial manipulation of photo period alters seasonality of reproduction and has been known for years as a way of controlling the breeding season (Henderson D., 1985).

Generally breeding season begins in early September and ends in February or March in the northern hemisphere. Amoah (1983) observed that there was negligible ovarian cycling



**Figure .3: Seasonality of ovulation in the female dairy goat in northern temperate regions. [from Ley, 1986]**

and reproductive activity in does between April and August. This observation corresponds with the breeding season, reported in the UK (Henderson D., 1985) and the US. Mohammad et al (1984) observed that the median month of conception was October and the five breeds (Alpine, Toggenburg, Saanen, Nubian and LaMancha) kidded most frequently in March. Similar findings are reported by Grossman and Wiggans (1980).

Results on seven dairy goat breeds (Amoha et al., 1996) show that most breeds start their seasonal breeding, approximately in June, reaching a peak in September to November. A small number of goats, about 5 % will cycle 1-2 months earlier or later than their flock mates (Agriculture Canada, 1989). Good nutrition will allow these animals to express this tendency, but this trait may also be genetic. Differences between breeds are also observed. Alpine and Toggenburg appear to be the most seasonal breeds and Nubians are less seasonal than Alpine, Saanen or Toggenburg (Mohammad et al., 1984). Another study also found that Nubian goats have an extended (8 to 11 month) breeding season (Amoah et al., 1996) which could be due to the lack of sensitivity to climate changes through the year, because of their origin in Africa. Further, it appears that interactions between age and season are significant for fat yield and approached significance for milk (Alderson,

1980) and that year of kidding, month of kidding and their interaction have a significant effect on milk production and lactation length (Mavrogenis et al., 1984). The season of freshening affects younger does more than their older flock mates (Iloeje et al., 1980). Studies showed that does which kidded earlier in the season (January through March) produced a higher milk yield than their flock mates that freshened later (Steine, 1975; Iloeje et al, 1980).

There are also clear seasonal differences in milk composition of the major and minor components (Renner, 1983), but these are confounded with climatic and dietary effects. Winter climate can affect milk yield and composition, and both are negatively correlated. Winter feeding usually provides different proportions and qualities of grazing, hay, silage and supplements, which influence milk composition considerably (Haenlein, 1995).

#### **2.1.4 Age at first kidding**

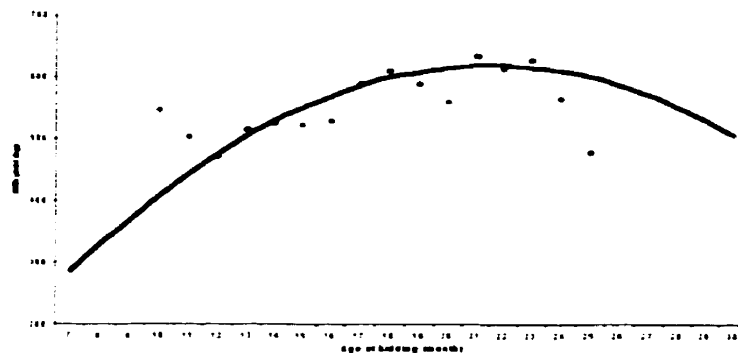
The fertile oestrus, or heat, of a doe starts as early as in her fourth month of age. Research on dairy cattle concluded (Iloeje, 1980) that age has no direct biological effect on production, but body weight does. In other words, age is an indicator of maturity and maturing has a biological effect on production since a growing animal needs a part of its energy intake for growth and development.

Many goat breeders recommend a body weight at first kidding of at least 32 kg. Does may reach this weight by 7-9 months (Sutton, 1990; Agriculture Canada, 1989). To some extent, breeding maturity (32 kg bodyweight) is dependent on genetic factors, but to a larger extent on management and feeding. Bred within 7-9 months, does would freshen, after a 5 month gestation period (~ 150 days), at 12 – 14 month of age. If does continue to grow during their first lactation, their milk production will be steady, but not as high as the milk production of fully grown does. For example, does bred at 18 months of age and freshening for the first time at 2 years of age milk less heavily compared to a second freshening two years old, but compared to a first freshening 1-year-old doe, the older doe will have a higher milk production (Agriculture Canada, 1989). Research in dairy goats, found that age is a very important source of variation affecting milk production.

Mavrogenis (1984) demonstrated that age of dam at kidding had a quadratic relationship with all traits studied except for lactation length. Iloeje (1978) and Rathore (1970) have shown that milk yield increases linearly with age until about the third to fifth lactation and tends to decrease in the following lactations. Expressed in age, does reach peak production at 24 to 50 months of age.

Results of a study made by Sullivan (1988) match with these from the literature (Finley et al. 1984; Kennedy et al, 1981), except that the quadratic effect of age was not significant. Solutions indicate that the effect of age on all traits in first lactation was initially large and positive, but quickly diminishes and eventually becomes negative after two years of age.

A plot of the age solutions for first lactation milk yield from the study made by Sullivan (1988) is given in Figure 4.



**Figure 4. Age solution curve (solid line) and unadjusted means (•) by age subclasses for first lactation milk yield. [from Sullivan, 1988]**

### **2.1.5 Parity**

Within a lifetime production a doe has a certain number of parities and her maximum production occurs between 24 and 50 months, which equals second to fourth parity, with a mean of about 40 months. Parity effects on production in dairy goats are large and significant (Ali et al., 1983; Finley et al., 1984; Kennedy et al., 1981). Kennedy et al (1981) calculated a set of factors for four groupings and showed that parity affected production. Differences between first and second parities of animals of the same age were as high as 217 kg of milk and 7.2 kg of fat. These amounts are about 20 % of the production for first parity. Differences among later parities were less.

Differences due to parity, lactation number or age of animal can be significant in gross milk composition, but this is also confounded with milk yield level. In sheep, the fat content of ewe milk changed linearly from the 1<sup>st</sup> to the 6<sup>th</sup> parity from 6.8 to 7.4 % and total protein content from 5.8 to 6.2 % (Casoli et al, 1989). Similar trends can be expected for goats. The cause of parity differences and the negative relationship between age and production within parity is unclear and could be genetic or environmental (Kennedy et al., 1982). Finley et al. (1984) recommends that the large effects such as the one between first and second parities should not be ignored.

### **2.1.6 Breed comparison for milk production**

In modern animal breeding, a “breed is conceived as a defined population, in which pure breeding is the rule and breeding animals are registered by a breeding organisation” (Gall, 1996). Within goat breeds, different types of goats have been developed or have evolved to serve specific functions or for adaptation to specific production or environmental conditions (Shelton, 1978). Some breeds developed for dairy purposes, others to produce milk and meat or just meat (Table 3).

**Table 3. Types and breeds of goats [from Shelton, 1978]**

<b>Type</b>	<b>Breed or genotype</b>	<b>Localisation</b>	<b>Source</b>
Dairy	Saanen	Temperate regions (world wide)	Guss (1975). Colby et al.
	Toggenburg	Europe and U.S.	Guss (1975). Colby et al.
	Anglo-Nubian	World-wide	Guss (1975). Colby et al.
	Alpine	Europe and U.S.	Guss (1975). Colby et al.
	LaMancha	U.S.	Guss (1975). Colby et al.
Meat and milk	Nubian	Sudan	Devendra. (1975)
	Damascus (Shami)	Syria and adjoining areas	Choveiri. (1973)
	Jamnapari	India and Pakistan	Singh and Singh. (1974)
	Barbari	India and Pakistan	Mittal and Pandey. (1971)
Meat	Boer	South Africa	Skinner. (1972)

Genetic differences of production yields within breeds have a wide range and numbers for milk, fat and protein yields are presented as mean values of the breeds as reported in the literature.

The most popular goat breeds used in Canada for milk production are Alpine, Toggenburg, Saanen and Nubian. All dairy breeds (Alpine, Saanen, and Toggenburg) have nearly the same milk yield per lactation, Nubians are lower in production. A possible explanation might be that this breed is a result of cross breeding where dual-purpose breeds were involved. Goat milk composition can differ greatly among breeds. For example, for milk fat from 2.3 % to 6.9 % with an average of 3.3 %; for milk protein from 2.2 % to 5.1 % with an average of 3.4. % (Juarez et al., 1986). A major portion of this variation is caused by negative correlation's between milk yield and composition, which means that low yields have higher contents and vice versa. (Haenlein, 1995).

The *Alpine* is a breed of goat that originated in the Swiss / French Alps. It is a medium to large goat and more variable in size than the Swiss breeds. Alpine females are reported as excellent milkers; milk yield is around 950 kg with 3,5 % fat (~33.5 kg) in a 259 days lactation period. (Sambras, 1994; Gall, 1996)

The *Toggenburg* is a Swiss dairy goat from the Toggenburg valley of Switzerland. They are thought to be oldest known dairy breed (since 1802). This breed is of medium size and slightly smaller than other Alpine breeds. They give their best performance in cooler conditions and they are noted for high milk production. Milk yield of 700–1000 kg with 3,3 % fat (~21.2 kg) in 267 days is common. (Sambras, 1994; Gall, 1996; Haenlein, 1996)

*Saanen* is probably the most developed dairy breed. Among goat breeds it occupies the place that the Holstein-Friesian has among cattle breeds. The Saanen dairy goat originated in Switzerland in the Saanen valley. It is of medium to large size with a milk yield of 750 to 1000 kg and 24.4 kg fat in 262 days. (Sambras, 1994; Gall, 1996; Haenlein, 1996)

The *Nubian* goat breed developed in England by crossing British and Swiss goats with Zaraibi, Jamnapari and Chitral goats from Pakistan. They are known as all-purpose goats, useful for milk, meat and hide production. It is a relatively large goat and described



as a not heavy milk producer (774 kg), but this breed has a very high fat yield with 4–5% (~35.4 kg). The average lactation length is 237 days, but, as mentioned earlier, their breeding season is much longer than that of the Swiss breeds and so it is possible to produce milk year round. (Sambraus, 1994; Gall, 1996; Haenlein, 1996)

Breeds differences are well reported under different conditions. Knowles and Watkins (1938) tabulated some breed comparisons under English conditions. Garcia, Castillo and Gado (1972) reported lactation yields under Venezuelan conditions. Gill and Dev (1972) reported lactation yields for Alpine and Nubian goats under Indian conditions and Dickinson and King summarised milk yield and fat content of U.S. dairy goats (Table 4.)

**Table 4. Lactation yields by breed and location. [from Shelton, (1978)]**

Breed	Current world record (kg)	England <sup>a</sup>		U.S. <sup>b</sup>		Vene- zuela <sup>c</sup>	India <sup>d</sup>
		Milk (kg)	Fat (%)	Milk (kg)	Fat (%)	milk (kg)	milk (kg)
Saanen	3430	1188	4.0	979	3.6	294.2	
Alpine	2194	1136	4.2	970	3.5	232.2	310.6
Toggenburg	2613	1087	4.5	921	3.3	283.4	
Nubian	2009	839	5.6	817	4.5	154.7	289.5

<sup>a</sup> Knowles and Watkins. 1938

<sup>b</sup> Dickinson and King. 1977

<sup>c</sup> Garcia et al., 1972

<sup>d</sup> Gill and Dev. 1972

In all four regions, Saanen had the highest milk production. Alpine and Toggenburg had similar high yields. Nubian does were lower in milk production, but had the highest fat percentages in the milk. Sutton (1990) and Iloeje (1980) made a detailed analysis of breed differences in milk yield, fat yield and fat %. Geerts (1975) summarised the performance of does of the five major dairy breeds.

The description of breeds of goats and their origin can be found in Haenlein (1981) and on the Oklahoma University Animal Science homepage. Later publications of the status of dairy goats in the U.S.A. can be viewed in Haenlein (1996).

### **2.1.7 Others**

A healthy dairy goat population will give a reasonable milk yield. Diseases caused by infection, parasites, nutritional and other reasons endanger the milk production of does. This variation appears because the animals are not able to make full use of the nutrients given in the ration (Agriculture Canada, 1989; Waite et al., 1963). Fortunately these factors, which influence the production, are reported in milk recording data, and it is possible to adjust genetic evaluations for environmental factors which are known. As it happens, there are further effects, but when not recorded, we can not account for them in a statistical analysis. Besides the already mentioned causes of variation, there is, for example, in sheep evidence that within the limits imposed by inherent ability and level of nutrition, milk production and the shape of lactation curve are affected by the suckling stimulus of the lamb or lambs. (Peart, 1968; Zygoiannis and Katsaunis, 1984; Zygoiannis, 1994). Also the number of kids born by a doe has been investigated. Results for a Research Institute flock indicate that mothers of twins gave proportionately 0.27 more milk than mothers of singles and mothers of triplets 0.47 more, and it was suggested that multiple fetuses led to a higher lactogenic activity, that results in higher milk yield post partum (Hayden, Thomas and Forsyth, 1979). More recent evidence from Spain also shows raised milk yields after multiple births (Subines, Lava, Ferrando and Boza, 1988). Williams, 1993 on the other hand could not find any evidence that the number of kids born affected either scale or persistency, which contradicts the work reviewed earlier. These results might be due to the husbandry of the goats surveyed, because housing and conserved forage and concentrate food were offered year around.

Some researchers mention that the number of milkings per day have a significant effect on milk production. Henderson et al (1983,1985) reported that thrice-daily milking increases milk yield immediately and in the long term. The immediate increase is believed to result from the more frequent removal of a chemical feedback inhibitor, which is present in the milk (Henderson and Peaker, 1984) and the long term increase seems to be caused by either growth or reduced regression of the thrice-daily milking gland (Henderson et al., 1985).

## **2.2 Components of an Individuals Performance**

For animal breeders, the most important economical characteristic of an animal is its production or performance. For each performance trait we can observe or measure a certain level, which is called the phenotype. An animal has as many phenotypes as there are traits to be observed or measured on this animal. In selection it is important to increase the phenotypic value which is possible through genetic and / or environmental improvement. The basic mathematical formula for expressing the phenotype is:

$$\mathbf{P = G + E}$$

where **P** stands for an animal's phenotype, **G** represents it's genotype and **E** the environmental effects (Bourdon, 1997). Through measuring the phenotype and adjusting for environmental effects, (these are all non-genetic effects) we can estimate the genotype. Accurate information on environmental factors helps obtain accurate estimation of the genotypic variance.

### **2.2.1 Variance Components**

Variation is the source of genetic change. If there is little variation in a trait, selection will be slow, because no animal is really genetically superior to another. To make genetic progress it is important for a population to have a wide range of variation. The amount of variation is measured and expressed as the variance. The total variance is the phenotypic variance ( $V_P$ ) which is the sum of the genotypic ( $V_G$ ) and the environmental ( $V_E$ ) variance. The genotypic variance itself can be divided into additive ( $V_A$ ), dominance ( $V_D$ ) and epistatic ( $V_I$ ) variance. The total variance is then:

$$\begin{aligned} V_P &= V_G + V_E \\ &= V_A + V_D + V_I + V_E \end{aligned}$$

**Additive variance** is the main cause of resemblance between relatives and therefore the chief determinant of the observable genetic properties of the population and of the response of the population to selection. It is also referred to as the direct genetic variance.

Estimates of additive variance are needed to estimate genetic parameters such as heritability, repeatability etc.

**Dominance variance** is caused by within locus interaction. For an accurate estimate, a complete pedigree with many different relationships is needed.

**Epistatic variance** ( $V_I$ ) occurs if the genotypes at different loci show epistatic interaction, but interactions involving large numbers of loci usually contribute so little variance that they can be ignored.

**Environmental variance** is defined as all variation caused by non-genetic factors. It can have many sources and its nature depends very much on the character and on the animal studied. In other words, environmental variance is a source of errors that reduces precision in genetic studies. Most common external causes are nutritional, managerial and climatic factors (Falconer and Mackay, 1996).

Partitioning the variance into its components allows us to estimate the relative importance of various determinants of the phenotype. In other words, we can determine the role of the components in heredity and environment. Estimates of phenotypic and additive genetic variances are needed for designing effective breeding programs. Iloeje et al (1981) reported variances for flock, year-season, sire, doe, and residual for five US dairy breeds (Alpine, Saanen, Toggenburg, LaMancha, and Nubian). Flock effects accounted for 22 to 31 % of the phenotypic variation for milk yield, 24 to 25 % for fat yield and 15 to 25 % for fat percentage. These results indicated large differences in production from feeding and overall flock management. Year-season accounted for 8 to 13 %, 8 to 14 % and 10 to 14 % of the total variation for milk yield, fat yield and fat percentage respectively. Sire components contribute 8 to 11 % of variation in these three traits. Because of the usually small sizes of goat flocks and only a few does per sire, it is hard to distinguish between effects of sire and year-seasons; therefore, some variation attributed to sire may be from confounding of sire effect with other effects. Doe component was 16 to 25 % of the total variation in milk yield, fat yield and fat percentage, which suggests that sire component was overestimated. Residual variances were about 34 % in milk and fat yield and 40 % for fat percentage. Sullivan (1988) working with Canadian dairy goats used two methods,

Schaeffer's and Van Raden's, to estimate variance components. The results are given in Table 5.

**TABLE 5. Estimates of Flock-year-season, sire, and residual components of variance [from Sullivan, 1988]**

<b>SCHAEFFER'S METHOD</b>						
Component (N)*	Milk yield	Fat yield	Fat %	Protein yield	Protein %	Lactation Length
Flock-year-season (730)	9837 (2098)	13.7 (3.1)	.031 (.009)	9.7 (1.9)	.0062 (.0026)	997 (150)
Sire (933)	5980 (1709)	6.1 (2.3)	.032 (.008)	4.7 (1.4)	.0050 (.0017)	443 (168)
Residual (1979)	46810 (2249)	62.8 (2.7)	.206 (.010)	44.1 (1.6)	.0630 (.0016)	3816 (149)

<b>VAN RADEN'S METHOD</b>						
Component (N)*	Milk yield	Fat yield	Fat %	Protein yield	Protein %	Lactation Length
Flock-year-season (730)	9626 (1817)	14.3 (3.0)	.034 (.008)	9.8 (1.8)	.0063 (.0023)	1119 (139)
Sire (933)	3919 (1687)	3.8 (2.7)	.037 (.007)	2.9 (1.3)	.0060 (.0017)	383 (169)
Residual (1979)	48140 (2123)	64.0 (2.7)	.202 (.010)	45.2 (1.7)	.0621 (.0014)	3805 (141)

\* N= number of levels of flock-year-seasons or sires or number of residual degrees of freedom

The flock-year-season component of variance ranged from 8 to 20 % of the total variance, which was similar to the results of Iloeje (1981). In Sullivan's study, percentage traits were less variable across flock-year season than were yield traits, but this varied depending on breed. In general, fat percent was more variable than milk and fat yields across year-season.

### **2.2.2 Heritability**

Each somatic cell in a goat's body contains 30 pairs of chromosomes; One half of each pair is inherited from its sire and the other half from its dam. Each chromosome carries a certain number of genes and the nature and position are controlling genetic characteristics. During formation of the ovum or sperm cells this genetic material is resorted. This gives each germ cell 30 chromosomes, each with its required number of genes, but in a combination, random from the original pair. These random combinations make genetic prediction incredibly complicated and we cannot predict the goat's characteristic with total confidence.

A superior doe can produce good quantities of milk persistently through her total lactation, and for many lactations. Such doe can pass these qualities to her offspring. Some traits are more easily improved through breeding than others, and are spoken of as having high heritabilities (Agriculture Canada, 1989). Heritability can be defined as "the fraction of total phenotypic variation attributable to genetic differences, and measure the accuracy of phenotype as an expression of genotype" (Cue, 1998). In algebraic terms, if  $p = \mu + g + e$ , where  $p$  is a phenotypic record on an animal,  $\mu$  is the population mean,  $g$  is the effect of genotype and  $e$  is the effect of environment such that  $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$ , then heritability ( $h^2$ ) is defined as:

$$h^2 = \sigma_g^2 / \sigma_p^2 \quad \text{assuming no covariance between } g \text{ and } e.$$

Heritability can be estimated in a broad and in a narrow sense. In the narrow sense,  $\sigma_g^2$  contains only additive genetic variance. In addition to the additive genetic variance, heritability in the broad sense,  $\sigma_g^2$  contains dominance and epistatic genetic effects. Theoretical limits of heritability estimates are  $0 \leq h^2 \leq 1$ . Results on heritabilities of milk yield are in a similar range for dairy cattle and goats (Auran, 1976; Iloeje et al., 1978; Steine, 1975).

**Table 6. Heritability estimates for dairy goat breeds**

Traits	Breed	$h^2$	Method	Source
Milk yield	ASTNL*	.25	BLUP	Boldman et al, 1984
Average yield per operational year for milk yield	Norwegian	.55		Ronningen, 1965
Butterfat %		.22		
Milk yield (morning yield)		.40		
Butter fat % (daily yield)		.10		
1 <sup>st</sup> lactation	Indian Beetal goat	.32		Prakesh et al, 1971
2 <sup>nd</sup> lactation		.29		
3 <sup>rd</sup> lactation		.32		
4 <sup>th</sup> lactation		.28		
5 <sup>th</sup> lactation		.16		
Milk production	ASTN *	.17 ± .20		Garcia, 1971
Fat production		.22 ± .20		
milk yield in first lactation	Indian Beetal goat	.25 ± .08		Singh et al, 1970
Unadjusted records	ASTN *	AST* N*	MINQUE	Kennedy et al, 1982
Milk yield		.69 .30		
Fat yield		.62 .48		
Fat %		.52 1.10		
Adjusted records	ASTN *	AST* N*	MINQUE	Kennedy et al, 1982
Milk yield		.68 .35		
Fat yield		.61 .54		
Fat %		.54 1.09		
Milk yield (per lactation)	Alpine	.60		Bouillon et al. 1976
Protein yield (milk)		.47		
Protein %		.58		
Fat yield		.47		
Fat %		.48		
Milk yield per lactation	Dairy breeds	.36		Ronningen, 1967
Fat yield		.30		
Fat %		.32		
Single-trait analysis	Murciano-Granadina		DFREML	Analla et al, 1996
Milk yield		.18		
Fat content		.16		
Protein content		.25		
Multiple-trait analysis	Murciano-Granadina		DFREML	Analla et al, 1996
Milk yield		.17		
Fat content		.14		
Protein content		.22		

\* A=Alpine, S=Saanen, T=Toggenburgs, N=Nubian, L=Lamancha

Heritabilities of dairy goats are summarised by Shelton (1978) and in Table 6. Estimates of heritabilities of traits can vary significantly from study to study. This depends on breed, population sampled, environmental and management conditions and error, both random and systematic, in the estimation procedures. The wide range of heritabilities reported would suggest that milk production has a medium heritability and fat and protein percentage have a high one.

### 2.2.3 Direct and Maternal Effects

Production traits such as milk yield, birth weight and early growth rate are determined not only by the animals' own genetic potential, but also by maternal effects. The maternal effect of a dam on her offspring is mostly environmental (with respect to the offspring) and represents mainly the dam's milk production and mothering ability, though effects of the uterine environment and extra chromosomal inheritance may contribute (Meyer, 1992). However, these abilities such as milk production and mothering are expressed according to genotype. The phenotypic differences among dams for the maternal effects are expressed in the phenotypic values of their young; i.e. offspring from good mothers have a better development and produce better later on.

A maternal effect defined by Willham (1972) is "a phenotypic value of a dam measurable only as a component part of her offspring's phenotypic value". These influences of a dam measurable on her offspring are recognised as a special case of the joint action of genotype and environment (Robison, 1981).

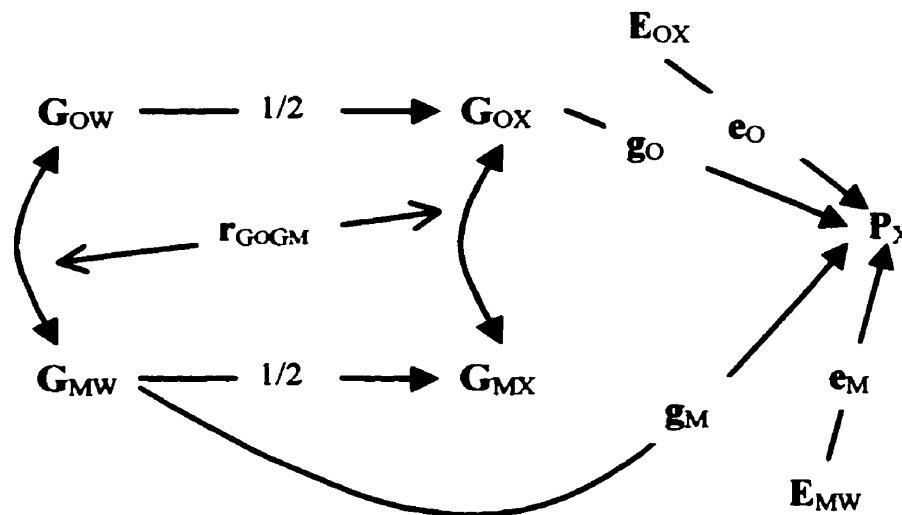


Figure 5. A path coefficient diagram showing the biometrical relationship when a direct and maternal effect are involved in the phenotypic expression of a trait [from Willham, 1972].

$G_{OX}$ : genotypic value of X for direct effects;  $E_{OX}$ : environmental value of X for direct effects;  $G_{MW}$ : genotypic values of W for the maternal effects;  $E_{MW}$ : environmental values of W for the maternal effects;  $G_{OW}$ : genotypic value of W for direct effects;  $G_{MX}$ : genotypic value of X for maternal effects.

Dickerson (1947), Koch and Clark (1955) and Kempthorne (1955) developed the biometrical aspects of maternal effects. Later, Willham (1963) put the biometrical aspects



in terms of linear genetic models. Falconer (1965) developed a genetic model in which the maternal effect was linearly related to the phenotype of the dam. Van Vleck (1971) devised selection index procedures for direct and maternal genetic components of traits (Willham, 1972).

The genetic principles behind the maternal effects are easiest to describe with a path coefficient diagram developed by Willham, 1972 (Figure 5):

$P_X$  represents the phenotypic value of individual  $X$ . For this model we have to assume only additive genetic effects and that covariances between genetic and environmental effects and between environmental effects ( $E_{MW}$ ,  $E_{OX}$ ) are zero. Under this assumption  $P_X$  is just influenced by the genotypic value of  $X$  and by the genotypic value of its dam ( $W$ ). Effects denoted by  $O$  are the direct effects and denoted by  $M$  are maternal effects. Then

$$P_X = P_{OX} + P_{MW}$$

For single traits, the phenotypic value is composed of the sum of genotypic variance and environmental variance accordingly

$$P_{OX} = G_{OX} + E_{OX}$$

$$P_{MW} = G_{MW} + E_{MW}$$

Here  $G_{OX}$  and  $E_{OX}$  are the genotypic and environmental values for the direct effects and  $G_{MW}$  and  $E_{MW}$  are the genotypic and environmental values for the maternal effects.

The total variance of  $P_X$  is then composed of:

$$V(P_X) = \sigma^2_{G_o} + \sigma_{G_o G_m} + \sigma^2_{G_m} + \sigma^2_{E_o} + \sigma^2_{E_m}$$

Unlike sires, which contribute just through transmitting genes to the offspring, dams make a 'direct' genetic contribution to the offspring through contributing genes and an 'indirect' genetic contribution through the environment she provides for the young (milk quality and quantity, nest structure, care of young etc.). This indirect contribution is genetic to the extent that these maternal qualities are heritable in the mother, even though experienced by her offspring as an environmental effect (Riska et al, 1985).

Research on maternal effects has been conducted mostly on beef cattle, meat sheep, swine or mice, where researchers and producers are convinced that maternal effects play a role. The little work done on dairy cattle gave contradictory results.

Meyer (1992) estimated variance components for birth, weaning, yearling and final weight in Australian Hereford, Angus and Zebu cross cattle by Restricted Maximum Likelihood. Using six models, significant maternal effects were found in all analyses except for final weight in Angus. Fitting a permanent environmental effect increased model fit markedly and identified a significant maternal effect contributing 8.3 (Angus) to 10.1 % (Hereford) of the total variation in birth weight. Estimates of the direct, maternal and total heritabilities were well within the range of estimates reported in the literature summarised by Meyer, 1992. Maternal genetic effects accounted for approximately 4 % (final weight) to 14 % (weaning weight). Genetic covariances between direct and maternal effect were essentially zero to very small (0.128 to 0.758 kg<sup>2</sup>) for birth weight, -203.1 to 14.7 kg<sup>2</sup> for weaning weight depending on breed, with Angus having a positive value. Covariance for yearling weight was -66.4 to 45.6 kg<sup>2</sup>, where again Angus had the positive value. For final weight, covariance's between direct and maternal effects were slightly lower and ranged from -6.7, 3.0 to 41.2 kg<sup>2</sup> for Hereford, Angus and Zebu Crosses. Variance components estimated by Robinson (1996) were slightly smaller. Maternal genetic effects were 7, 9 and 6 % for birth, weaning and yearling weights, respectively. Maternal effect for final weight was not significant. Van Vleck et al (1996) estimated direct and maternal effects for weaning weight of calves of dams at 2, 3 years of age and older with a derivative-free REML algorithm. For the three analyses for pure breeds, average proportions of phenotypic variance were 34, 31, and 27 % for direct genetic; 16, 15, and 12 % for maternal genetic; and 18, 20, and 17 % for maternal environmental effects. For composite breeds, average proportions of phenotypic variance were 44, 46, and 36 % for direct genetic; 6, 6 and 5 % for maternal genetic; and 16, 14, and 14 % for maternal environmental effects. A study by Eler et al. (1995) on growth traits of Nelore Cattle in Brazil, showed that maternal variance accounted for 12, 13 and 10 % of the total phenotypic variance and direct additive genetic variance accounted for 22, 14, 16 % of the total variance for univariate analysis of birth, weaning and yearling weight. Covariances between genetic and maternal effects were -0.49 for birth weight, 46.38 for weaning weight and 75.45 for yearlings' weight.

Research, using least square procedures, was undertaken to investigate maternal abilities on cross breeding sheep. A study made by Vesely et al. (1977) was designed to estimate heterosis, general specific combining abilities, maternal and sex-linked effects based on a diallel mating system among four breeds of sheep.

Maternal effects were measured only among progeny of crossbreeding type of mating and were found to be an important factor ( $p < 0.01$ ) influencing body weight, weaning weight, weight-per-day-of-age and final weight.

Research on crossbreeding animals (two-breed cross, back cross and 3 breed cross progeny) by Holtmann et al. (1969) showed an interaction between mating system and maternal effects attained significance with weights at 28 and 120 days and daily gain. Lambs raised by 3-year, 4-year and 5-year old ewes had highest body weight at 28 and 120 days of age, indicating that these age groups appeared to be at optimum in terms of the mothering ability of a ewe.

A similar study (Rastogi et al., 1982) also showed that maternal ability is a significant source of variation for birth weight, preweaning weight, preweaning average daily gain and weaning weight.

Direct and maternal effects for growth traits of Romanov sheep were estimated by Maria et al., (1993) using restricted maximum likelihood with an animal model, which included fixed effects for year x season, sex, rearing type and litter size, and random effects for the direct genetic effect ( $h^2$ ), the maternal genetic effect ( $m^2$ ), the permanent environmental effect ( $c^2$ ) and random residual errors. The estimates for  $h^2$ ,  $m^2$  and  $c^2$  were 0.04, 0.22 and 0.10 for birth weight; 0.34, 0.25 and 0.0 for weaning weight; 0.09, 0.01, and 0.07 for 90 day weight; 0.26, 0.17, and 0.02 for preweaning daily gain (birth to weaning); and 0.15, 0.01, and 0.03 for postweaning daily gain (weaning to 90 days) respectively. These estimates with sheep are similar to those with beef cattle and indicate that important maternal effects exist for birth and weaning weights and preweaning daily gain. Maternal effects in dairy cattle have been studied by Van Vleck and Bradford (1966), Van Vleck and Hart (1966), Gipson and Russel (1978), and Robison et al. (1981). Van Vleck and Bradford stated that the apparent pattern for heritability estimates for deviations is that the paternal half-sib correlation is about the same for all lactations but that daughter-dam

estimates are higher for first lactation records, with a gradual drop in second and third lactation to the level of estimates derived from paternal half-sib analyses. This result suggested a sizeable genetic maternal effect in first lactation, which drops in second lactation and disappears by third lactation. On the other hand Van Vleck and Hart (1966) regressed the actual covariance on the coefficient of additive direct genetic variance which gave a correlation of 0.92. These results suggested that in this research only additive genetic effects were important for first lactation. Gipson and Russel (1978) showed deviations of Ayrshire and Jersey from Holstein of 1574 and 1080 kg of milk. Of this, 61 and 72 % respectively were due to maternal effects. Robison et al (1981) analysed crossbreeding data, in which the model fitted included breed additive direct, heterotic and breed maternal effects. The deviation of Swiss and Ayrshire from Holstein were 1333 and 1366 kg, respectively. Approximately 36 and 44 % of these deviations were due to breed maternal effects. These results suggest that maternal effects play a large role in breed differences. No research on maternal effects with dairy goats has been reported. An understanding of the genetic variation in maternal effects and the relationship between direct genetic effects and maternal effects is essential for formulating optimum breeding programs (Robison, 1981).

### **3. MATERIAL AND METHOD**

The final cumulative milk, fat and protein yields of the first lactation of Alpine, Saanen, Toggenburg, and Nubian does were used to estimate:

1. Basic statistical parameters
2. Variance components such as additive genetic effects, maternal genetic effects, and covariance between additive genetic and maternal genetic effects
3. Resulting genetic parameters

Basic statistical parameters were calculated using SAS for OS/2, release 6.12 and variance components were estimated using the DFREML package version 2.1 for the derivative-free REML algorithm (Meyer, 1993).

#### **3.1 Data Source**

A total of 88965 test day records from all registered breeds in Canada, recorded from 1985 to 1995, were available through the Quebec Dairy Herd Analysis Service (QDHAS). As with dairy cattle, monthly measurements of milk yield are taken, and analysed for fat and protein content. These monthly measurements are used to estimate cumulative milk, fat and protein yields. The information included in the test day records is: flock, QDHAS goat number, testing program (official or self testing), breed, goat identification number, nip letter of goat, sire identification number, dam identification number, nip letter of dam, date of birth, lactation number, date of kidding, date of testing, lactation code, test day milk, test day fat, test day protein, 305 days milk yield, 305 days fat yield, 305 days protein yield, cumulative milk yield, cumulative fat yield, cumulative protein yield, handling code.

Genetic evaluation for dairy goats in Canada is undertaken by the Canadian Centre for Swine Improvement from which the pedigree file, containing registered goats from all breeds, was received. The file contained 108545 records. Information included in the pedigree was goat, sire and dam identification number, sex of the animal, name, foreign identification number and date of birth. The pedigree was used to extract ancestors and build up the relationship matrix.

## **3.2 Data Editing**

### **3.2.1 Test day records**

Each animal, tested by the QDHAS, had an average number of 8 to 10 monthly measurements (or test day records) per lactation. For a separate analysis of Alpine, Saanen, Toggenburg and Nubian data, the test day records were divided into records by breed. Alpine had 24265 records on all lactations, Toggenburg had 23364 records, Saanen had 17797 records and the number for Nubian test day records for all lactations was 15611. The rest, counting 7928 records, belonged to breeds like LaMancha, Boer etc., which were excluded from the analysis. Data from each breed was edited separately. The number of records and reasons for editing are summarised for all four breeds in Table 7.

**Table 7. Edits per breed**

	Alpine	Toggenburg	Saanen	Nubian
<b>TEST DAY RECORDS</b>	<b>24265</b>	<b>23364</b>	<b>17797</b>	<b>15611</b>
<b>Editing</b>	<b># of records edited</b>	<b># of records edited</b>	<b># of records edited</b>	<b># of records edited</b>
Reg. # ≠ 0, Sire = 0, Dam = 0	562	138	624	594
Not first lactation records	14049	14465	10514	9351
Differ. from kidding to first-test-day >365	270	641	189	149
Animals with just one record	36	24	13	35
Animals which have not finished lactation	1626	649	1059	835
Other reasons	628	589	600	184
<b>Clean test day records</b>	<b>7094</b>	<b>6858</b>	<b>4798</b>	<b>4463</b>
<b>NUMBER OF ANIMALS</b>	<b>786</b>	<b>711</b>	<b>501</b>	<b>534</b>
Cumulative milk yield less than 50 kg	8	4	6	13
Single granddaughters	69	37	44	74
Single animal flocks	18	29	12	14
<b>Final Number</b>	<b>691</b>	<b>641</b>	<b>439</b>	<b>433</b>

Test day records missing sire or dam registration number were discarded. The evaluation in this study was based on first lactation records only. After eliminating second and higher lactation records, the following edits were based on first lactation test day records: Records which had a difference larger than 365 days between date of kidding and first day of testing were considered to be wrong records and also excluded from the evaluation. Animals with just one record on their first lactation were dropped to avoid any wrong data

and resulting bias. All animals, which had not finished their lactation, because of selling, or nursing reasons etc. were excluded.

Other reasons to edit records included animals, which were declared to be in first lactation but had a lactation continuing far beyond 305 days. By manually checking the records, they showed extreme variation considering the lactation curve, such as increasing yield over a few months and after the peak the yield decreased until again an increase occurred. Furthermore, animals which were younger than 10 months or older than 30 months for age at first kidding were excluded, because does younger than 10 months would have been bred at 5 months of age and that is quite unlikely, and after 30 months a doe is probably in her in second lactation. Animals with cumulative milk yield less than 50 kg, single granddaughter animals and animals which were the only animal in a flock were excluded from this study. For animals without siblings or cousins, or single animal flocks, the flock fixed effects can not be separated from the sire effect, which means these effects are confounded and those animals have to be deleted.

### 3.2.1.1 Time period of test day records

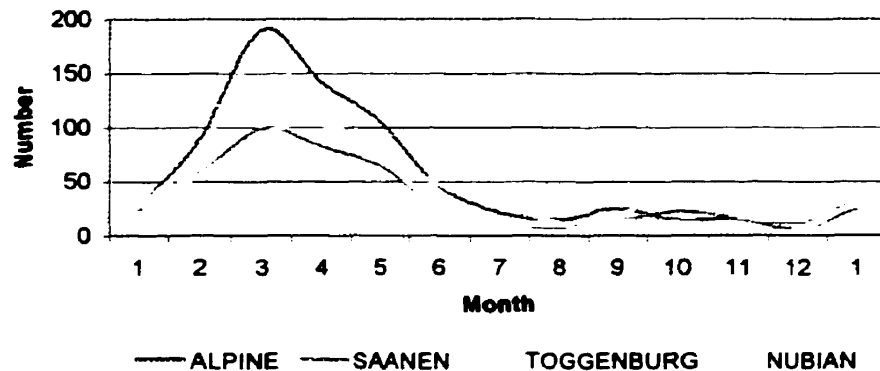
The numbers of records for breed and year of animals' date of birth, which passed editing, are given in Table 8. Also given are the numbers of animals for breed and year the production was recorded. Animals included in the analysis were born between 1984 and 1995, and the time period in which the production traits for the animals are recorded is from 1986 to 1996.

**Table 8. Number of records per year and breeds for animals' date of birth and year of recording**

BREED	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996
<b>Year of birth</b>													
Alpine	13	52	86	69	55	61	86	109	57	42	52	9	-
Saanen	5	34	56	50	56	43	63	41	43	26	20	2	-
Toggenburg	2	33	62	37	59	87	111	94	79	71	6	0	-
Nubian	1	31	56	48	38	31	69	63	49	21	25	1	-
<b>Year of recording</b>													
Alpine	-	-	35	94	73	54	60	69	108	73	49	61	15
Saanen	-	-	18	58	57	41	64	49	49	43	25	32	3
Toggenburg	-	-	14	62	44	40	75	113	72	111	68	40	2
Nubian	-	-	10	54	53	39	37	43	65	71	27	25	9

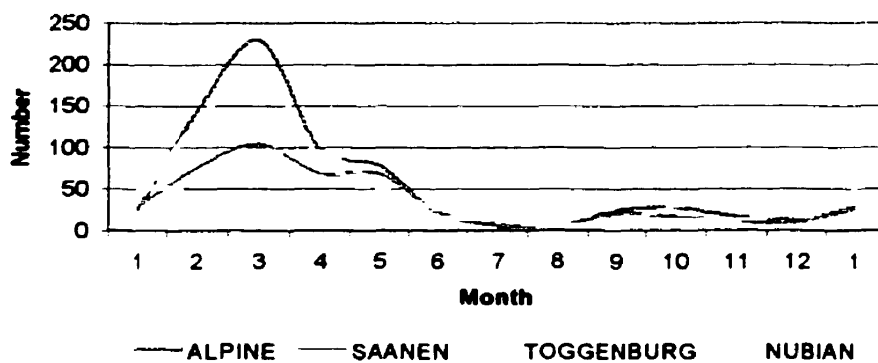
### **3.2.1.2 Season of kidding**

The months of kidding in the data set used are similar to the seasons described in the literature. Most of the animals included in the analysis were born between January and June (Figure 6). After reaching sexual maturity, these animals were bred, around September, October or November and gave birth five month later in January to April.



**Figure 6. Date of birth distribution of does for first lactation across 12 month**

It is interesting that the shape of Figure 6, which is the graph of the number of does born in the different month, is similar to that of Figure 7 which represents the number of does kidding in the different months of the year.



**Figure 7. Kidding distribution of does for first lactation across 12 month**



Raw means by breed and months of kidding for cumulative milk, fat and protein yield of first parity does are given in Table 9 to 12.

**Table 9. Number of observations and raw means by month of kidding for lactation traits (ALPINE)**

month	N	cum. Milk (kg)	cum. Fat (kg)	cum. Protein (kg)
January	25	541.80	18.32	16.14
February	89	746.60	26.75	22.97
March	190	750.39	25.44	22.58
April	141	796.33	27.71	24.05
May	105	656.54	22.44	19.73
June	46	862.20	30.50	25.94
July	21	743.81	26.47	22.61
August	14	642.57	25.91	21.15
September	25	753.68	27.26	24.47
October	14	602.00	23.81	19.78
November	15	696.27	23.00	20.67
December	6	928.17	28.81	28.49
<b>Total</b>	<b>691</b>	<b>740.01</b>	<b>25.74</b>	<b>22.48</b>

For all breeds, most of the animals were born in March to May. Almost 63 % of the Alpine does, 55 % of the Toggenburg does, 56 % of the Saanen does and 63 % of the Nubian does gave birth in these three months.

**Table 10. Number of observations and raw means by month of kidding for lactation traits (TOGGENBURG)**

month	N	cum. Milk (kg)	cum. Fat (kg)	cum. Protein (kg)
January	27	827.48	27.33	24.98
February	77	836.35	26.17	23.55
March	172	880.64	27.81	24.70
April	103	676.28	21.38	19.07
May	79	770.56	24.70	22.39
June	47	656.15	21.12	18.68
July	29	801.69	26.57	23.55
August	12	913.50	28.39	25.40
September	18	519.17	16.69	14.52
October	44	797.66	27.93	22.91
November	18	824.94	26.40	23.26
December	15	1155.87	34.55	32.79
<b>Total</b>	<b>641</b>	<b>796.29</b>	<b>25.46</b>	<b>22.64</b>

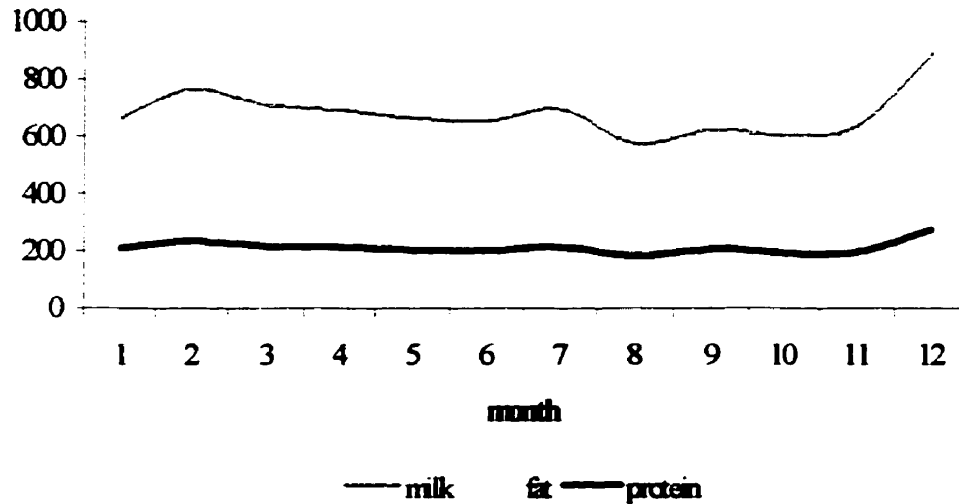
**Table 11. Number of observations and raw means by month of kidding for lactation traits (SAANEN)**

month	N	cum. Milk (kg)	cum. Fat (kg)	cum. Protein (kg)
January	31	860.06	30.22	26.07
February	58	953.31	30.58	27.64
March	99	829.94	26.54	24.63
April	82	758.12	23.82	22.73
May	64	755.16	23.95	22.71
June	27	817.96	26.36	24.53
July	9	808.78	24.98	24.83
August	6	767.33	27.51	22.43
September	13	769.31	27.32	23.55
October	22	961.73	30.28	28.59
November	16	856.69	27.52	25.40
December	12	752.25	29.32	24.43
<b>Total</b>	<b>439</b>	<b>825.68</b>	<b>26.74</b>	<b>24.65</b>

Observing raw means, Toggenburg does which gave birth in September had a significant drop in milk, fat and protein yield. It was not obvious that Nubians were more or less seasonal than the other breeds. The highest milk, fat and protein yields were for animals, which gave birth in September, and the lowest for animals, which were kidding in July.

**Table 12. Number of observations and raw means by month of kidding for lactation traits (NUBIAN)**

month	N	cum. Milk (kg)	cum. Fat (kg)	cum. Protein (kg)
January	31	548.61	26.39	20.29
February	56	484.43	22.96	17.13
March	93	529.74	25.07	19.58
April	104	487.41	22.49	17.48
May	74	498.66	23.55	18.95
June	26	395.08	20.54	15.22
July	9	334.56	15.12	11.74
August	4	496.50	25.82	18.37
September	13	741.00	37.65	29.33
October	12	502.08	23.08	19.07
November	6	430.17	20.14	16.04
December	5	452.60	20.63	17.73
<b>Total</b>	<b>433</b>	<b>500.61</b>	<b>23.74</b>	<b>18.48</b>



**Figure 8. Least square means for month of kidding for cumulative milk, fat and protein yield**

Using the combined data set of all four breed, the SAS procedure 'proc glm' was used to fit a fixed effects model with age, breed, month of kidding and flock-year, to estimate least-squares-means for cumulative milk, fat and protein yields (Figure 8).

The graph shows just a small difference between months for cumulative milk yield and almost no change in cumulative fat and protein yield. This led to the decision that season has almost no effect on cumulative milk, fat and protein yield and just flock-year instead of flock-year-season was fitted later in the final model and analysis for all four breeds.

### **3.2.1.3 Age at first kidding**

Unadjusted means by kidding age for lactation traits for first parity does for Alpine, Toggenburg, Saanen, and Nubian are given in Tables 13 to 16. Some animals are listed to be 9 months old, despite the fact, that it is an editing criterion. These animals were manually checked and reintegrated in the process, because they were found to be below 10 months (9 months and 20 days old). For Alpine, relatively few does were kidding between the ages of 16 to 20 months. This is explainable since most does born between February and May would have to conceive outside of the natural breeding season in order to kid within these ages (Sullivan, 1988).

**Table 13. Number of observations and unadjusted means by age at kidding for lactation traits. (Alpine)**

Age	N	Cumulative	Cumulative	Cumulative
9	7	444.71	13.43	12.34
10	17	533.24	18.50	16.10
11	45	630.38	21.27	18.75
12	116	685.42	24.11	20.86
13	123	768.83	26.35	23.33
14	55	670.47	23.67	20.35
15	49	751.53	26.87	23.54
16	34	843.38	28.62	25.82
17	37	828.00	29.51	26.23
18	25	731.12	27.62	23.10
19	17	731.76	24.55	21.53
20	16	722.06	23.47	21.32
21	19	700.74	23.74	20.45
22	35	850.29	30.47	25.67
23	48	768.31	27.02	22.98
24	25	780.68	26.26	23.76
25	13	870.46	29.08	25.56
26	4	1296.50	45.61	39.48
27	3	997.00	33.29	28.93
28	2	868.50	28.70	25.00
29	1	743.00	29.78	25.72

Most of the animals for each breed gave birth at 12 or 13 months of age. The general pattern for all breeds was an increase in cumulative milk yield, cumulative fat yield, and cumulative protein yield with age. However, for Alpine a drop in milk yield, fat yield and protein yield was observed at 14 / 15 months of age.

**Table 14. Numbers of observations and unadjusted means by age at kidding for lactation traits (TOGGENBURG).**

Age (months)	N	cum. milk yield (kg)	cum. fat yield (kg)	cum. protein yield (kg)
9	2	807.00	25.48	21.60
10	7	639.57	19.72	19.30
11	30	632.10	20.66	18.62
12	48	633.85	19.57	17.64
13	65	598.28	18.95	16.91
14	56	675.95	22.00	19.48
15	44	912.70	29.24	25.96
16	45	812.07	25.14	22.57
17	39	857.95	27.63	24.21
18	33	832.33	27.45	23.66
19	36	890.33	30.21	25.76
20	27	788.48	25.83	22.44
21	32	932.47	29.53	26.58
22	36	1024.25	31.15	29.32
23	46	844.33	26.59	23.75
24	51	857.71	27.47	24.58
25	19	1031.95	34.00	29.12
26	11	688.09	21.99	19.75
27	8	767.13	24.51	21.57
28	4	773.00	23.88	21.88
29	1	892.00	27.96	22.58
30	1	640.00	20.84	19.28

The trend that in some months the number of kiddings is reduced was not so clear with Toggenburg, but the drop of milk, fat and protein yields could also be observed for this breed. It occurred at the age of 13 and 18 months.

**Table 15. Numbers of observations and unadjusted means by age at kidding for lactation traits (SAANEN)**

Age (months)	N	cum. milk yield (kg)	cum. fat yield (kg)	cum. protein yield (kg)
9	4	637.75	19.62	18.56
10	16	727.69	22.81	21.12
11	36	668.39	21.29	20.10
12	71	692.17	21.00	20.47
13	51	792.47	25.77	24.01
14	54	755.81	23.79	22.38
15	31	839.32	28.62	25.57
16	18	926.83	32.63	27.54
17	26	1030.92	33.73	30.73
18	15	896.80	29.18	26.95
19	8	681.50	22.29	21.17
20	19	942.95	29.18	27.47
21	18	875.44	28.10	25.53
22	24	1034.42	34.38	30.96
23	24	963.42	33.15	29.00
24	12	1050.33	36.00	31.56
25	9	984.22	31.22	29.09
26	2	553.00	21.01	17.59
30	1	1245.00	35.45	43.18

Saanen also had a reduced number of does kidding between 16 and 21 months. A drop in the milk, fat and protein yield could be observed for 12 and 20 months of age.

**Table 16. Numbers of observations and unadjusted means by age at kidding for lactation traits (NUBIAN).**

Age (months)	N	cum. milk yield (kg)	cum. fat yield (kg)	cum. protein yield (kg)
10	4	595.25	28.66	21.71
11	20	485.55	22.12	17.11
12	58	508.14	24.11	18.60
13	64	454.05	22.07	17.07
14	52	476.58	23.40	17.80
15	28	471.89	22.99	17.83
16	20	537.20	25.09	19.70
17	17	464.24	23.45	18.27
18	13	503.31	24.37	19.28
19	15	575.13	27.05	20.83
20	20	674.50	30.38	24.26
21	25	435.08	18.61	15.57
22	28	471.86	22.85	17.31
23	27	573.96	27.30	21.48
24	17	455.88	21.24	16.27
25	9	573.89	28.46	20.16
26	8	496.63	24.18	18.96
27	5	570.60	21.75	20.84
29	3	507.67	20.11	18.25

The milk, fat and protein yields for 19 month old Nubians, were 32 % less than those of animals which were 18 month old when they gave birth and even 42 % less compared to animals which were 20 month of age. The reduced number of kiddings between 16 and 20 months of age was not so clear as with Alpine or Saanen.

To check whether age has a significant effect on milk yield or not, SAS was used to fit a fixed effects model including age and flock-year, to estimate least-square-means of cumulative milk yield for age at first kidding.

SAS results (Figure 9) showed a clear trend upward, despite some fluctuations, leading to the conclusion that age had to be fitted in the final model of analysis.

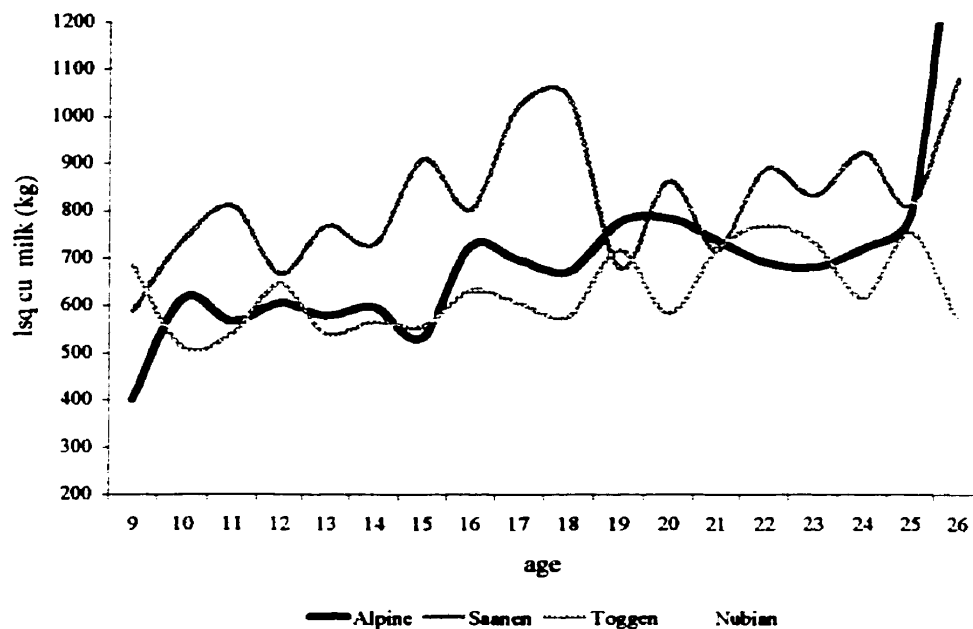


Figure 9. Least square means for age of first kidding for cumulative milk yield

### **3.2.1.4 Animal, sire and dam distribution per flock, per breed**

#### **Animals**

Table 17 contains the number and size of flocks per breed. Of 58 Alpine flocks, 18 were smaller than five animals per flock with a minimum size of 2 animals. This equals 31 % of Alpine flocks. Three of the flocks had 51, 68, and 80 animals, which equals 29 % of all Alpine does. Toggenburg animals were distributed in 39 flocks and 45 % of the flocks were smaller than 5 animals. One flock had 217 animals, which is almost 34 % of the whole number of animals (641). 50 % of the total number of Saanen flocks (50) were smaller than 5 animals and the biggest flock contained 53 animals. Nubian flocks were relatively small. Most of them (78 %) had 2 to 10 animals and just a few had higher numbers of animals with a maximum size of 35 animals. The average flock size was 11.91 animals for Alpine, 16.44 animals for Toggenburg, 8.78 animals for Saanen and 8.02 animals for Nubian.

**Table 17. Number of flocks and different sizes per breed**

<b>Flocks with</b>	<b>Alpine</b>	<b>Toggenburg</b>	<b>Saanen</b>	<b>Nubian</b>
< 5 animals	18	17	25	22
5-10 animals	19	6	14	20
11-15 animals	3	5	3	5
16-20 animals	2	4	1	3
21-30 animals	2	3	5	2
31-50 animals	3	3	1	2
51-100 animals	3	-	1	-
101-200 animals	-	-	-	-
>200 animals	-	1	-	-
<b>Total number of flocks</b>	<b>58</b>	<b>39</b>	<b>50</b>	<b>54</b>
<b>Average # of animals per flock</b>	<b>11.91</b>	<b>16.44</b>	<b>8.78</b>	<b>8.02</b>

#### **Sire**

The frequencies of sires and dams per flock are shown in Table 18 and 19 respectively. The average number for Alpine was 3.10, for Toggenburg 3.92, for Saanen 3.15 and for Nubian 2.78 sires per flock. Two Alpine flocks had 18 and 28 different sires respectively.

Toggenburg had one flock with 32 sires and for Saanen the maximum number of sires per flock was 15. The maximum number of sires for a Nubian flock was 13 animals.

**Table 18. Frequency distribution of sires per flock**

Number of sires	Alpine	Toggenburg	Saanen	Nubian
1	9	4	9	7
2	11	12	12	14
3	14	5	8	11
4	6	3	8	5
5	7	3	2	8
6	1	3	2	2
7	2	1	2	0
8	3	2	3	0
9	0	2	0	1
10	2	1	1	2
11-20	1	1	2	3
21-30	1	1	0	0
<b>Total # of flocks</b>	<b>58</b>	<b>39</b>	<b>50</b>	<b>54</b>
<b>Average # of sire per flock</b>	<b>3.10</b>	<b>3.92</b>	<b>3.15</b>	<b>2.78</b>

### Dam

Most of the flocks had two to three dams. The average number for Alpine was 8.91, for Toggenburg 11.67, 6.56 for Saanen and 5.39 for Nubian (Table 19).

**Table 19. Frequency distribution of dams per flock**

Number of dams	Alpine	Toggenburg	Saanen	Nubian
2	18	8	13	16
3	7	7	11	7
4	3	5	4	4
5	6	2	5	6
6	7	3	5	8
7	3	1	0	2
8	0	0	1	0
9	1	2	1	3
10	0	0	1	1
11-20	5	6	5	3
21-50	6	3	3	3
>50	1	1	0	0
<b>Total # of flocks</b>	<b>58</b>	<b>39</b>	<b>50</b>	<b>54</b>
<b>Average # of dams per flock</b>	<b>8.91</b>	<b>11.67</b>	<b>6.56</b>	<b>5.93</b>



### **3.2.1.5 Offspring per sire**

Table 20 shows the frequency distribution of numbers of daughters per sire. 46 Alpine bucks had just one daughter, which equals almost 26 % of all sires. 10 of the alpine sires had from 11 up to 39 daughters. 21 % of Toggenburg sires had one daughter, and 12 of the total number of 153 sires had 11 to 31 daughters. For Saanen, 30 sires, which equals 24 % had one daughter. Six sires had more than 10 daughters. 44 Nubian sires had just one daughter, which equals 29 %, and just three had more than 10 daughters (11, 14, and 16). The average number of daughters per sire was 3.84 for Alpine, 4.19 for Toggenburg, 3.57 for Saanen and 2.89 for Nubian.

**Table 20. Frequency distribution of numbers of daughters per sire.**

Number of daughters	Alpine	Toggenburg	Saanen	Nubian
1	46	32	30	44
2	45	39	34	47
3	30	22	17	18
4	16	19	10	16
5	10	7	13	11
6	7	8	7	5
7	5	7	3	2
8	5	2	2	0
9	2	3	1	3
10	4	2	0	1
11	2	2	0	1
> 11	8	10	6	2
Total # of sire	180	153	123	150
Average # of daughters per sire	3.84	4.19	3.57	2.89

### **3.2.1.6 Offspring per dam**

The frequency distribution of numbers of daughters per dam is summarised in Table 21. Out of 517 Alpine dams, 389 had just one daughter. The maximum number of daughters was 6. Of 455 Toggenburg dams 323 had one daughter, (71 %) and 1 dam had 6 daughters. Saanen had a total number of 328 dams, 76 % of these dams had one daughter. Like the previous breeds, just one dam had more than 5 daughters (6). The maximum number of daughters per Nubian dam was 5. In total 320 dams were known and 75 % of these dams had one daughter. The average number of daughters per dam is 1.37 for Alpine, 1.41 for Toggenburg, 1.34 for Saanen and 1.35 for Nubian.

**Table 21. Frequency distribution of numbers of daughters per dam.**

Number of daughters	Alpine	Toggenburg	Saanen	Nubian
1	389	323	248	240
2	95	94	59	52
3	23	27	14	24
4	8	7	5	3
5	1	3	1	1
>5	1	1	1	0
<b>Total # of dams</b>	<b>517</b>	<b>455</b>	<b>328</b>	<b>320</b>
<b>Average # of daughters per dam</b>	<b>1.37</b>	<b>1.41</b>	<b>1.34</b>	<b>1.35</b>

### **3.2.2 Pedigree**

The pedigree file received from the Canadian Centre for Swine Improvement was used to build up an unique pedigree for each breed. No editing concerning incorrect records had to be done. Steps for building up the pedigrees for each breed is summarised in Table 22.

**Table 22. Steps for building up the pedigree**

<b>ALPINE - PEDIGREE</b>		
	<b>Records</b>	<b>Zero Birth date</b>
Animals with records	691	0
Extracted ancestors	2408	1101
Phantom parents	772	772
<b>Total records</b>	<b>3871</b>	<b>1873</b>
<b>TOGGENBURG - PEDIGREE</b>		
	<b>Records</b>	<b>Zero Birth date</b>
Animals with records	641	0
Extracted ancestors	1530	657
Phantom parents	471	471
<b>Total records</b>	<b>2642</b>	<b>1128</b>
<b>SAANEN - PEDIGREE</b>		
	<b>Records</b>	<b>Zero Birth date</b>
Animals with records	439	0
Extracted ancestors	1501	702
Phantom parents	532	532
<b>Total records</b>	<b>2472</b>	<b>1234</b>
<b>NUBIAN - PEDIGREE</b>		
	<b>Records</b>	<b>Zero Birth date</b>
Animals with records	433	0
Extracted ancestors	1805	839
Phantom parents	663	703
<b>Total records</b>	<b>2901</b>	<b>1542</b>
<b>COMBINED ALL BREED - PEDIGREE</b>		
	<b>Records</b>	<b>Zero Birth date</b>
Animals with records	2204	0
Extracted ancestors	6774	2936
Phantom parents	2034	2034
<b>Total records</b>	<b>11012</b>	<b>4970</b>

Difficulties in identifying animals occurred because in the test day records the animal's identification is based on an eight-digit number, but in the pedigree file, country-breed codes are used in addition to the eight-digit number. Matching with just the number was impossible, because some numbers were used more than once in the pedigree. What made the animals unique in the pedigree file was the combination of country-breed code and that eight-digit number. The solution was matching test day record and pedigree animals with all their criteria (goat, sire and dam identification and date of birth) and assigning all test day record animals the country-breed code found in the pedigree file. Over 95 % of the animals were successfully renumbered without possible mix-up.

For the pedigree file all animals, even those with missing parents or date of birth were kept. Using FORTRAN programs, ancestors of all breeds were extracted from the pedigree file and for missing dams, sires or birth dates phantom parents and calculated birthdates were assigned. Data handling for the pedigree is summarised in Table 22. For the use in DFREML, the pedigree input file was sorted in logical order (oldest animals in the beginning followed by their offspring etc.) and renumbered from 1 to N.

### **3.2.2.1 Genetic grouping**

Under the assumption that knowing relationships (pedigree) account for the effect of selection on the related ancestors, there is no need to assign groups when both parents are known. In case of having many animals with one or both parents unknown genetic groups must be assigned to account for genetic selection and trends. For example, migration of animals into a population results in a need for grouping to account for genetic merit of the migrant, or selection on parents for which records are not available (Westell et al, 1988). Pollak and Quaas (1983) demonstrated that the need for grouping decreases with increasing completeness of the genetic relationship information. To group animals, phantom parents for all animals with missing sire or dam information were assigned to replace each of the unknown animals. Phantom parents are assumed to be average representatives of the genetic group of animals selected to be parents at the same time. The concept of grouping by their year of birth for genetic evaluation was introduced by

C.R. Henderson (Henderson, 1973). An alternative approach, developed by Westell (1984), is to group only those animals missing one or both parents. Animals can be grouped by different criteria. Gianola and Fernando (1986) and Howson and Urbach (1989) formed genetic groups using non-data-based (diffuse) prior information. Genetic grouping based on birth period or selection criteria are proposed by Quaas and Pollak (1981), Robinson (1986), Quaas (1988), Westell et al. (1988) and Van Vleck (1990). Principles of assigning phantom parents are developed by Westell, 1984.

**3.2.2.2 Example of assigning phantom parents [from Westell et al, 1988]:**

Consider a case of having a pedigree where not all relatives' information is available (Figure 10).

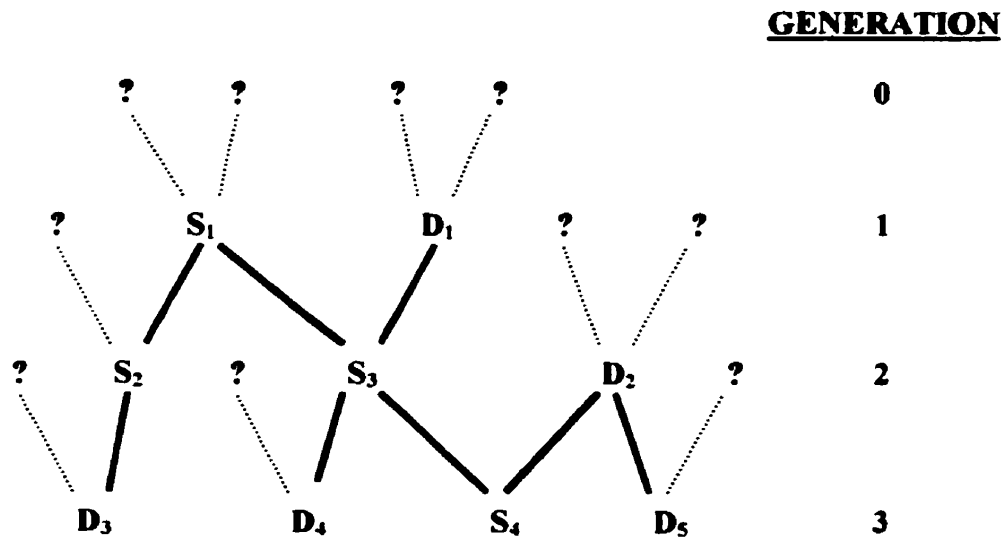


Figure 10. Sample Pedigree [from Westell et al, 1988]

Both parents are unknown for S<sub>1</sub>, D<sub>1</sub>, D<sub>2</sub>; one parent is unknown for D<sub>3</sub>, D<sub>4</sub>, D<sub>5</sub>, and S<sub>2</sub> and both parents of S<sub>3</sub> and S<sub>4</sub> are known. Figure 11 shows the phantom parents assigned in the example of Figure 10 and one half of the effect of the phantom parent genetic group is attributed to its progeny.

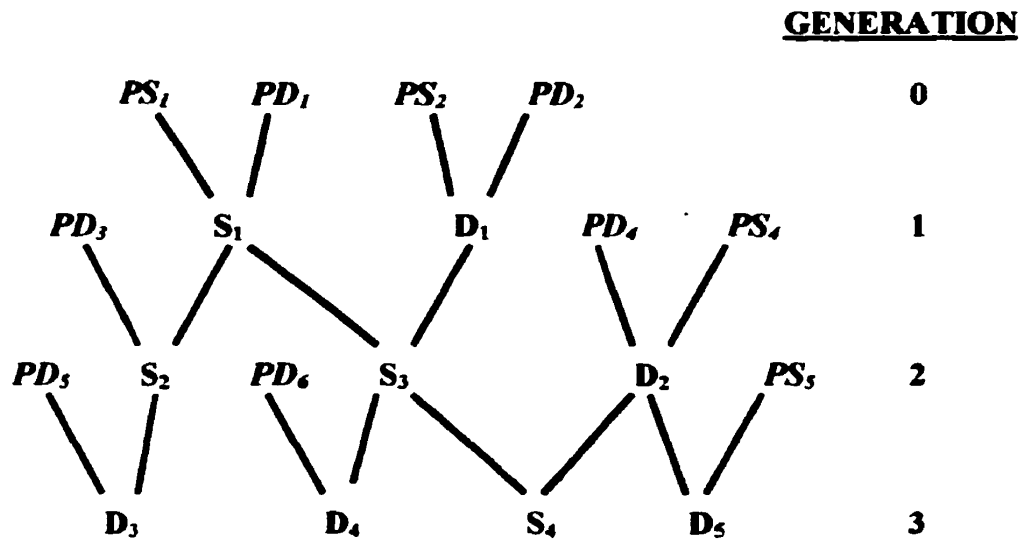


Figure 11. Assignment of phantom parents [from Westell et al, 1998]

Table 23 shows the assigned phantom groups and the resulting coefficient matrix, which will be included in the model to account for missing relatives and resulting bias.

Table 23. Pedigree and resulting coefficient matrix for example of Figure 13.

Pedigree information				Coefficient Matrix						
Animal	Sire	Dam	Generation	PS1	PD1	PS2	PD2	PS3	PD3	Sum
D1	0	0	1	0.5	0.5	0	0	0	0	1
S1	0	0	1	0.5	0.5	0	0	0	0	1
D2	0	0	2	0	0	0.5	0.5	0	0	1
S3	S1	D1	2	0.5	0.5	0	0	0	0	1
S4	S3	D2	3	0.25	0.25	0.25	0.25	0	0	1
D5	0	D2	3	0	0	0.25	0.25	0.5	0	1
D4	S3	0	3	0.25	0.25	0	0	0	0.5	1
S2	S1	0	2	0.25	0.25	0	0.5	0	0	1
D3	S2	0	3	0.125	0.125	0	0.25	0	0.5	1

Principles of assigning phantom groups, equivalent mixed model equations and rules for calculating coefficients due to groups can be reviewed in Westell et al, 1988 and Westell, 1984.

### **3.2.2.3 Phantom groups**

Selection differential may be different between phantom male and phantom females, so it is useful to set at least two parallel groups representing phantom sire and phantom dams.

The decision was made to assign four groups (born before 1966, 1966-1970, 1971-1975 and born after 1975) for phantom sire and four groups for phantom dams by estimated date of birth, ending up with eight different genetic groups. The numbers of animals per group are given in Table A1 (Appendix). To assign missing birth dates to animals, the average generation interval for the four selection pathways (phantom sire of buck, phantom sire of doe, phantom dam of buck and phantom dam of doe) were estimated (Table 24) of each breed and sex and subtracted from the birth date of the oldest offspring.

**Table 24. Generation interval in years**

Breed	Path of selection			
	Dams to produce does	Dams to produce bucks	Sire to Produce does	Sire to produce bucks
Alpine	3.28	4.64	2.65	3.05
Toggenburg	3.15	4.46	2.81	3.22
Saanen	3.48	4.93	2.89	3.32
Nubian	2.90	4.10	2.94	3.37
All breeds	3.20	4.53	2.82	3.24

### **3.4 Statistical Analysis**

SAS for OS/2, release 6.12 was used for to test the data sets for normality. The data sets were found to be slightly skewed.

The lactation length was quite similar for Alpine, Saanen and Toggenburg and was in the range reported in the literature. The longest milking period had Toggenburg with 255 days followed by Alpine and Saanen. With a length of 172 days, the Nubians are significantly shorter in lactation than the other breeds (Table 25).

The number of flock-years was similar for all breeds. Nubians had the highest number with 157 flock years, followed by Alpine 155 and Saanen 146. Toggenburg had the lowest number of flock-years with 133. Maternal genetic effects can be estimated in different ways with different relationships of the animals in the data set. Probably the most important ones are the daughter-dam pairs. These pairs show how many animals have a dam with records in the data set. Alpine had the lowest number and percentage of

daughter-dam pairs and Toggenburg had the highest number. The mean of daughter-dam pairs for all breeds was around 18.4 % of all animals in the data set (Table 25).

**Table 25. Lactation length and number of flock-year-seasons per breed.**

Breed	Lactation length (days)	Year-seasons (N)	Daughter- Dam pairs (N)	Daughter- Dam pairs (%)
Alpine	247	155	106	15.3
Toggenburg	255	133	146	22.8
Saanen	246	146	78	17.8
Nubian	172	157	75	17.3
All breeds	230	485	405	18.4

### **3.4.1 Mixed Model analysis**

Computations of genetic and phenotypic parameters of cumulative first lactation traits were carried out using derivative-free REML for estimating variance and covariance components for univariate animal models by restricted maximum likelihood (Meyer, 1989). An animal mixed model including additive genetic effects and maternal genetic effects as additional random effects was fitted for data sets of the four breeds. The mixed model included effects of flock-year, age at first kidding and regressions on phantom groups as fixed effects, and additive, maternal and residual components as random effects. All known additive genetic relationships amongst animals in the pedigree were used to construct the relationship matrix.

### **3.4.2 The Models**

The following basic models (1) and (2) were used for single breed data sets:

$$y_{ijklmn} = \mu + hy_i + age_j + r.e. + e_{ij(klm)n} \quad (BM1)$$

$$y_{ijklmnop} = \mu + hy_i + age_j + \sum_{k=1, 4} b_k PS_k + \sum_{l=1, 4} b_l PD_l + r.e. + e_{ijkl(mno)p} \quad (BM2)$$

For the multiple breed data sets the following basic models (1) and (2) were used:

$$y_{hijklmn} = \mu + \text{breed}_h + hy_i + \text{age}_j + \text{r.e.} + e_{hij(klm)n} \quad (\text{BM1})$$

$$y_{hijklmnop} = \mu + \text{breed}_h + hy_i + \text{age}_j + \sum_{k=1,4} b_k PS_k + \sum_{l=1,4} b_l PD_l + \text{r.e.} + e_{hijkl(mno)p} \quad (\text{BM2})$$

With three sub-models depending on which random effects were included in the basic model, 6 different models were fitted for each data set.

where: **r.e. = Random effects:**

Model 1 :  $a_m$

Model 2 :  $a_m + m_n$

Model 3 :  $a_m + m_n [c_o]$

where,  $Y_{hijklmnop}$  = the  $hijklmnop^{\text{th}}$  first lactation cumulative milk yield, fat yield or protein yield

$\text{breed}_h$  = the fixed effect of the  $h^{\text{th}}$  breed (4 levels)

$hy_i$  = the fixed effect of the  $i^{\text{th}}$  flock-year of first kidding  
(Alpine: 155 levels, Toggenburg: 133 levels, Saanen 146 levels,  
Nubian: 157 levels, all breeds 485 levels)

$\text{age}_j$  = the fixed effect of age at first kidding  $j$ , in month  
(Alpine: 21 levels, Toggenburg: 22 levels, Saanen 19 levels,  
Nubian: 19 levels, all breeds 22 levels)

$\sum_{k=1,4} b_k PS_k$  = linear regression coefficients for  $y$  on the sum of phantom groups of sires ( $n = 4$ )

$\sum_{l=1,4} b_l PD_l$  = linear regression coefficients for  $y$  on the sum of phantom groups of dams ( $n = 4$ )

$a_m$  = the  $m^{\text{th}}$  random direct genetic effect, assumed to be normally distributed with mean 0 and variance  $\sigma_a^2$



- $m_n$  the  $n^{\text{th}}$  random maternal genetic effect, assumed to be normally distributed with mean 0 and variance  $\sigma_m^2$ ,
- $e_{ijklmnop}$  the random residual associated with the doe ijklmnop, assumed to be normally distributed with mean 0 and variance  $\sigma_e^2$ .

$c_0$  refers to the covariance between direct genetic and maternal genetic effects, which was included when fitting Model 3 only.

### 3.4.3 DFREML procedure

The DFREML 2.1 package by Karin Meyer (1993) was obtained via ftp from the University of New England. The DFREML package is a Fortran program using subroutines for estimating genetic parameters using derivative-free restricted maximum likelihood. Theoretical steps and main computational steps can be summarised as follows:

The general mixed model is

$$Y = Xb + Zu + e$$

- where
- $Y$  is the vector of  $N$  observations
  - $b$  is the vector of  $NF$  fixed effects (including regression coefficients)
  - $u$  is the vector of  $NR$  random effects
  - $e$  is the vector of residuals
  - $X$  is the  $N \times NF$  incidence matrix pertaining to  $b$
  - $Z$  is the  $N \times NR$  incidence matrix pertaining to  $u$

It is assumed that:

$$\begin{aligned} V(u) &= G, & E(u) &= 0 \\ V(e) &= I\sigma_e^2 = R, & E(e) &= 0 \\ \text{Cov}(u, e) &= 0, & E(y) &= Xb \end{aligned}$$

Then:  $V(y) = ZGZ' + R$

The mixed model equations are:

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

Under an animal model,  $\mathbf{u}$  always contains the vector of animal's direct additive genetic effects,  $\mathbf{a}$ . Maternal additive effects are taken into account by fitting vectors of maternal genetic effects ( $\mathbf{m}$ ), if traits analysed are subject to maternal effects (Meyer, 1996).

$$\mathbf{u} = \begin{pmatrix} \mathbf{a} \\ \mathbf{m} \end{pmatrix}$$

with corresponding partitioning  $\mathbf{Z} = (\mathbf{Z}_A | \mathbf{Z}_M)$ . Further let  $\mathbf{A}$  denote the numerator relationship matrix between animals in the univariate case,

$$\mathbf{G} = \mathbf{V} \begin{pmatrix} \mathbf{a} \\ \mathbf{m} \end{pmatrix} = \begin{pmatrix} \sigma^2_{\mathbf{A}}\mathbf{A} & \sigma_{\mathbf{AM}}\mathbf{A} \\ \sigma_{\mathbf{AM}}\mathbf{A} & \sigma^2_{\mathbf{M}}\mathbf{A} \end{pmatrix}$$

The likelihood is:

$$L = \frac{1}{(2\pi)^{\frac{n}{2}} |\mathbf{V}|^{\frac{1}{2}}} e^{-\frac{1}{2} (\mathbf{y} - \mathbf{X}\mathbf{b})' \mathbf{V}^{-1} (\mathbf{y} - \mathbf{X}\mathbf{b})}$$

$$\ln L = -\frac{n}{2} \ln 2\pi - \frac{1}{2} \ln |\mathbf{V}| - \frac{1}{2} (\mathbf{y} - \mathbf{X}\mathbf{b})' \mathbf{V}^{-1} (\mathbf{y} - \mathbf{X}\mathbf{b})$$

where  $-\frac{n}{2} \ln 2\pi$  is a constant and  $\mathbf{V}$  is the determinant of the variance, covariance matrix.

Restricted Maximum likelihood theory can be reviewed in Meyer (1983), Meyer (1985), Meyer (1986), Meyer (1989) and Meyer (1993).

For maximising the likelihood function, an initial estimate of the optimum must be used, and corresponding function values obtained. Iteration must be done until the point of maximum is reached, or, in other words, the aim of each iteration is to replace the worst point, e.g. for a maximising problem the point with the lowest function value. The next point, which is defining the next simplex, is chosen in a direction away from the discarded point. The procedure allows the simplex to rescale itself automatically in each iteration, changing shape and size according to the landscape of the surface being searched. This adaptability is achieved by a combination of so-called reflections, expansion and contraction steps. Iterations are repeated until the simplex finds the optimum (Perotto, 1992)

#### **3.4.4 Likelihood ratio test**

The likelihood ratio test evaluates the significance of a model containing one or more additional parameters, compared to another identical model, except for the omission of those parameters. The numerical values of the maximum of the likelihood function are required under both, the null ( $H_0$ ) and the alternative hypothesis ( $H_A$ ). Minus twice the difference in the two logL asymptotically has a  $\chi^2$  distribution with degrees of freedom equal to the number of parameters tested, i.e. it can be compared to tabulated  $\chi^2$  values in order to decide whether to accept or reject the  $H_0$ . (Meyer, 1992) Manual DFREML

#### **3.4.5 F-test**

The F-test was used to evaluate both basic models as to whether phantom groups have an effect and the null hypothesis can be accepted or must be rejected. Animals were seen to be nested within phantom groups and the following equation was used to calculate  $F_c$ -values.

$$F_c = \frac{SSR(R) - SSR(F) / N}{\sigma^2_E(F) + \sigma^2_A(F)}$$

where:

<b>SSR (R)</b>	= Sums of square for residual from the reduced model
<b>SSR (F)</b>	= Sums of square for residual from the full model
<b><math>\sigma^2_E</math> (F)</b>	= Error Variance of full model
<b><math>\sigma^2_A</math> (F)</b>	= Additive Variance of full model
<b>N</b>	= Number of phantom groups fitted

## **4. RESULTS AND DISCUSSION**

### **4.1 Basic statistics**

Means, standard deviations, minima, and maxima were calculated. The data given by breed for the lactation traits, of first parity does are given in Table 26.

**Table 26. Number of observations (N), unadjusted means, standard deviation, minimum and maximum for the different breeds**

Breed	Trait	N	Mean	S. D.	Minimum	Maximum
Alpine	Cumulative milk yield (kg)	691	740.01	371.06	50.00	2182.00
	Cumulative fat yield (kg)		25.74	13.81	1.52	85.92
	Cumulative protein yield (kg)		22.48	11.43	1.40	65.61
Toggenburg	Cumulative milk yield (kg)	641	796.29	427.67	53.00	1984.00
	Cumulative fat yield (kg)		25.46	14.00	2.36	69.08
	Cumulative protein yield (kg)		22.64	12.11	1.93	58.20
Saanen	Cumulative milk yield (kg)	439	825.68	442.95	54.00	2081.00
	Cumulative fat yield (kg)		26.74	15.31	1.94	103.30
	Cumulative protein yield (kg)		24.65	13.26	1.78	68.98
Nubian	Cumulative milk yield (kg)	433	500.61	279.67	53.00	1520.00
	Cumulative fat yield (kg)		23.74	14.32	2.43	79.79
	Cumulative protein yield (kg)		18.48	10.66	2.20	57.89
All breeds	Cumulative milk yield (kg)	2204	726.41	405.06	50.00	2182.00
	Cumulative fat yield (kg)		25.46	14.29	1.52	103.30
	Cumulative protein yield (kg)		22.17	12.03	1.40	68.98

There were large differences between breeds. Nubian does had a much lower milk yield than that of the other breeds, but they had higher fat and protein percentages (4.7 and 3.7 % respectively). Saanen does had the highest milk, fat and protein yields, Alpine and Toggenburg had slightly smaller yields than Saanen. Milk components of these three breeds were also similar with 3.5 % fat and 3.0 % protein for Alpine, 3.2 % fat and 3.0 % protein for Saanen and 3.2 % fat and 2.8 % protein for Toggenburg. The milk yield differences between Nubian and the other three breeds are explainable through the fact that Nubian does had a 31 % shorter lactation length (average of 172 days) than Alpine (247), Toggenburg (255) and Saanen (246 days). The short lactation length of Nubian

does agree with findings in the literature, but in this study the lactation length was much shorter than reported (237 days), (Sambraus, 1994).

The phenotypic means for cumulative milk, fat and protein yield calculated in this study are close to those reported in the literature (Sambraus, 1994; Gall, 1996; Haenlein, 1996). Alpine had slightly smaller milk yields (740 kg) than reported (~950 kg). Saanen often described as the most developed dairy breed had the highest milk yield at 826 kg. Nubians are described in the literature as not heavy milkers, but with a very high fat yield. This could also be observed in this study. Raw means have to be compared carefully, because not each flock contained all breeds and these breed differences might be due to different flock management/ environment.

The highest variation or standard deviation (S.D.) for all traits had the Saanen breed, followed by Toggenburg and Alpine. Nubians had the smallest standard deviation of all breeds for milk and protein yield, but had a very high standard deviation for cumulative fat yield compared to the other breeds.

#### **4.2 Breeding season**

In Canada goats are seasonal breeders (Figure 6 and 7). Most of the kiddings occurred between January and July. That means they were mated between September and December to kid 5 month later, which corresponds with the reported breeding season for goats in the northern hemisphere (Shelton, 1978; Ali, 1983; Mohammad, 1984 and Amoha, 1996). Singh, Acharay and Biswas (1970) found season to be a very important source of variation affecting milk production, but this was not further investigated in this study.

#### **4.3 Distribution of data**

The distribution of all traits in each of the data sets was found to be slightly skewed. In statistical analyses, an important assumption is that the data has to be normally distributed otherwise results are biased, but previous studies using REML methodology revealed that heritabilities and genetic and phenotypic correlation of log transformed traits were unchanged from the untransformed traits (Jairath, 1992). Various authors (Harville, 1977;

Banks et al., 1985) indicated that REML estimates may be an appropriate choice even if normality does not hold. Based on these findings, the data sets were not transformed.

#### **4.4 Fixed effects included in the Model**

The most limiting factor in this study was the small number of animals with data on cumulative milk, fat and protein yields per breed. Working with such small data sets (small number per flock-season and age at first kidding groups) gives almost no alternative than to accept that the results will be biased. A common fitted effect for dairy cows is the combined effect of flock-year-season (f-y-s), but the numbers of records for each level of f-y-s was so small that the decision had to be made either to accept the small numbers or to fit just flock-year instead of flock-year-season. The least-squares means showed that there was a small difference for milk yield between months and almost no difference for fat and protein yield. Since the final model used was supposed to be fitted for all traits, it seemed appropriate to include just flock-year as a fixed effect. The differences for age at first kidding were clear for all breeds and were fitted as a second fixed effect.

For the combined data set (all four breeds), just breed as an additional fixed effect was fitted. If there would have been more than one observation per animal, breed nested within flock, must have been fitted.

The relatively small flock size for dairy goats, the few sires used in the average flock and the small number of different flocks a sire was used in might result in the possibility that differences between sires are confounded with flock effect.

#### **4.5 Generalised Least Squares (GLS) - solutions for age at first kidding**

DFREML obtained solutions for all effects fitted for arbitrary values of the (co) variance by direct inversion of the coefficient matrix, after absorbing random effects.

When estimates of environmental effects (in this case fixed effects), such as flock, breed of animal and age of doe at first kidding are plotted over time, they reveal environmental trend-changes in the mean performance of a population.

Solutions for age at first kidding for cumulative milk yield per breed are shown in Figure 12a to 12d and for cumulative fat and protein yield per breed in Figure 13a to 13d.

All solutions are presented as deviations from the first level, which is 9 and 10 months respectively. The first age effect level is set to zero, for a better comparison. Age differences in production are given in kg for milk, fat and protein yield.

Generalised least squares solutions plotted for age at first kidding show for all traits and breeds a slight increase in production with increasing age. Sullivan (1988) had similar results, that increasing ages at first kidding caused an initial increase in yield and after a peak (26 months of age) the milk, fat and protein yield decreased with age.

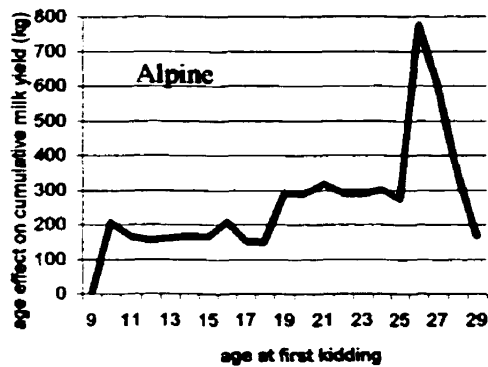


Figure 12a

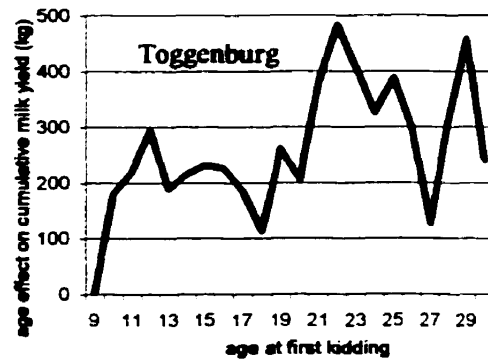


Figure 12b

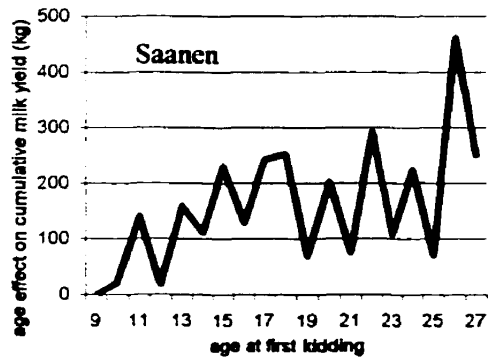


Figure 12c

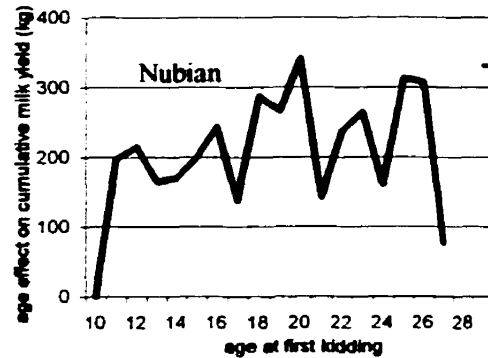
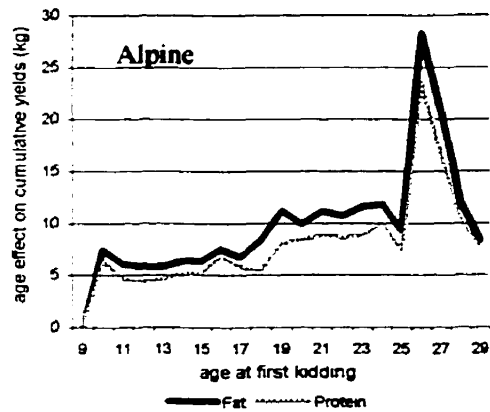


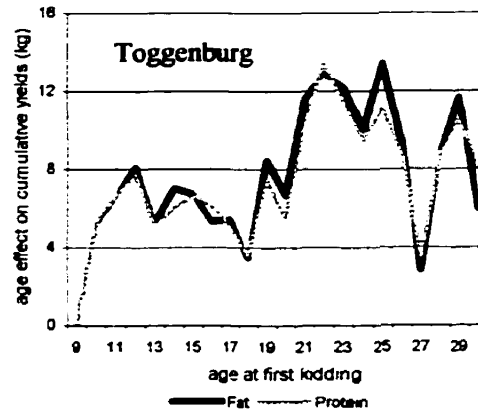
Figure 12d

Figure 12a-12d. GLS- solutions for age at first kidding effect on milk yield per breed

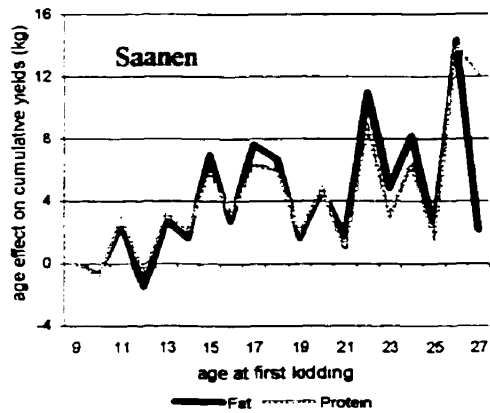




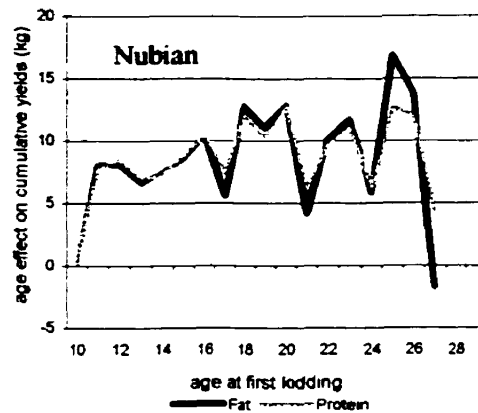
**Figure 13a**



**Figure 13b**



**Figure 13c**



**Figure 13d**

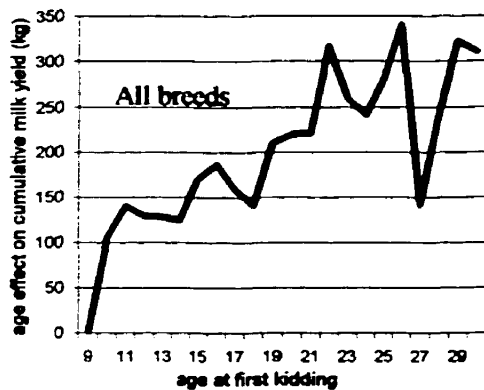
**Figure 13a-13d. GLS- Solutions for age at first kidding effect on cumulative fat and protein yield per breed**

Fixed effects solutions for age at first kidding must be interpreted carefully in this study, due to the small number of animals considered to be a population. Alpine, Toggenburg and Nubian solutions show a high initial increase in cumulative milk, fat and protein yield and all breeds show a final high peak in production, in the last month of age at first kidding

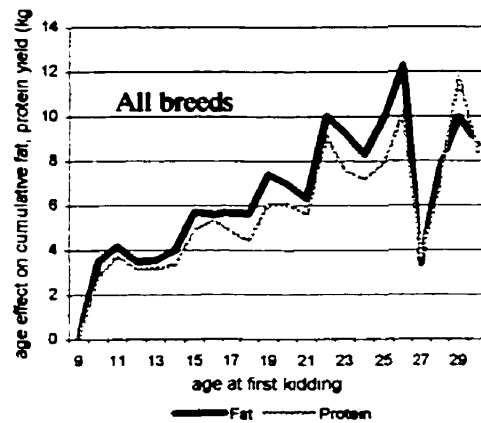
Solutions reveal environmental trend changes in the mean performance of a population, meaning you get the most representative results for fixed effects, when the number of animals is equally distributed through age groups. In this study, the early age group

(9months) and the final age group (26–30 months) solutions are estimated with maximum 10 animals, which might result in bias.

The final high peak around 26-28 months, might also be less comparable, caused by animals, which are actually in second lactation, but were listed to be in first. Following the literature (Sullivan, 1988) an age span between 9 and 30 months of age was chosen, but maybe a closer range (12 to 24 months of age at first kidding) would have been more appropriate.



**Figure 14a**



**Figure 14b**

**Figure 14a,14b. GLS solutions for age at first kidding effect on cumulative milk, fat and protein yield for the combined, all breed data set.**

The combined data set (all breeds) demonstrates more clearly the positive effect of age at first kidding. The plotted solutions show, that with increasing age the milk yield is up to ~300 kg higher when first kidding occurs at 24 months instead of at 9 months of age (Figure 14a). The trends are similar for fat and protein yield. The age effect increases fat and protein yield by approximately 10 and 9 kg respectively (Figure 14b).

All breeds combined in one data set increased not just the total animal number, but also the number of animals per age group, which might explain, why fluctuations in numbers plotted are less severe than in the single breed analyses.

#### 4.6 Generalised Least Squares (GLS) - solutions for breed

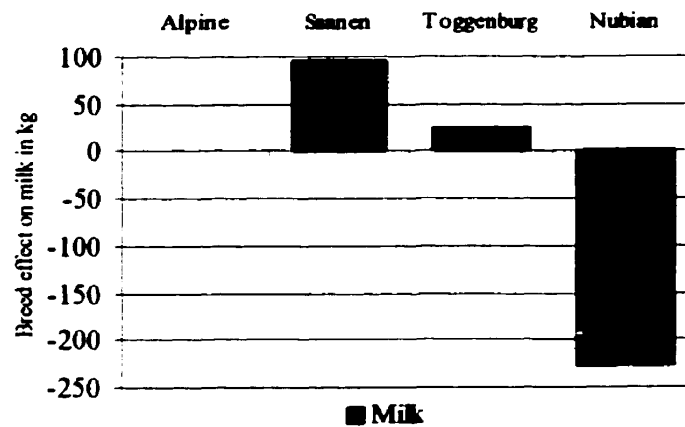


Figure 15. GLS solutions for breed effects on cumulative milk yield, Alpine set to 0

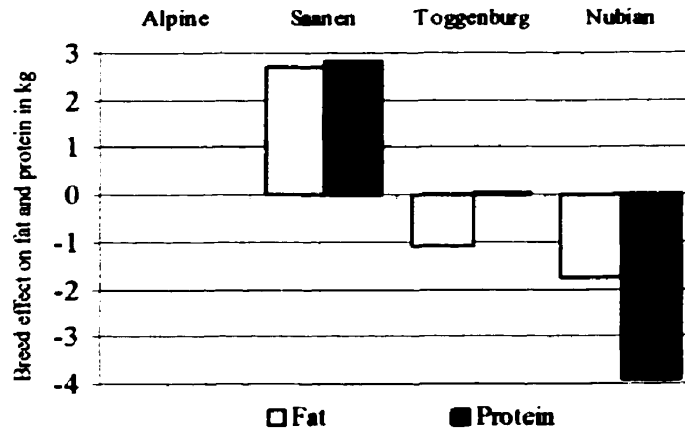


Figure 16. GLS solutions for breed effects on cumulative fat and protein yield, Alpine set to 0

Breed effects on milk, fat and protein yield for Toggenburg, Saanen and Nubian compared to Alpine which was set to be the operational zero are presented in Figure 15 and 16. Alpine and Toggenburg had similar milk yield, but about 100 kg less production than Saanen. Nubian had lowest yield with 250 kg to 300 kg less than the other breeds. The breed differences for fat yield were much smaller than observed for milk yield, but differences in breed effects on protein yield showed similar trends than those for milk yield.

Values for fixed effects solutions and corresponding standard errors are given in Table A3 to A14 (Appendix).

## 4.7. Results for variance components and resulting parameter estimates

### 4.7.1 Alpine

Table 27. Variance components and resulting parameter estimates for Alpine

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	26329.41	19135.87	34239.37	26934.65	15317.57	27265.23
$\sigma^2_M$	-	6831.1	15580.47	-	10002.56	17377.03
$\sigma_{AM}$	-	-	-12445.53	-	-	-10073.01
$\sigma^2_E$	60521.12	61128.84	51054.78	60124.84	60689.72	53543.13
$\sigma^2_P$	86850.53	87095.81	88429.08	87059.49	86009.85	88112.38
$h^2 = \sigma^2_A / \sigma^2_P$	0.3032	0.2197	0.3872	0.3094	0.1781	0.3094
s.e.	0.1253	0.1533	0.2486	0.1307	0.1616	0.2589
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0784	0.1762	-	0.1163	0.1972
s.e.	-	0.0862	0.1379	-	0.0903	0.1223
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.1407	-	-	-0.1143
s.e.	-	-	0.1577	-	-	0.1372
Log L	-4375.160328	-5466.766474	-5466.363733	-4167.172493	-5410.504087	-5410.229099
Fat yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	21.51	15.79	24.8	27.24	19.86	30.48
$\sigma^2_M$	-	5.58	11	-	7.40	13.87
$\sigma_{AM}$	-	-	-7.47	-	-	-9.04
$\sigma^2_E$	93.41	92.8	87.7	90.17	89.81	84.12
$\sigma^2_P$	114.92	114.16	116.03	117.41	117.08	119.43
$h^2 = \sigma^2_A / \sigma^2_P$	0.1872	0.1383	0.2137	0.2320	0.1697	0.2552
s.e.	0.1282	0.1482	0.2200	0.1349	0.1587	0.2385
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0488	0.0948	-	0.0632	0.1162
s.e.	-	0.0853	0.1292	-	0.0882	0.1372
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.0644	-	-	-0.0757
s.e.	-	-	0.1366	-	-	0.1488
Log L	-2672.44966	-3764.330634	-3764.221708	-2493.673349	-3737.612126	-3737.476646
Protein yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	16.98	10.1	23.01	19.34	8.89	19.84
$\sigma^2_M$	-	6.9	15.2	-	10.10	17.43
$\sigma_{AM}$	-	-	-11.04	-	-	-9.86
$\sigma^2_E$	63.15	62.64	54.65	61.64	61.92	54.80
$\sigma^2_P$	80.13	79.64	81.81	80.98	80.92	82.21
$h^2 = \sigma^2_A / \sigma^2_P$	0.2119	0.1268	0.2812	0.2389	0.1099	0.2413
s.e.	0.1258	0.1484	0.2267	0.1299	0.1539	0.2272
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0887	0.1858	-	0.1249	0.2120
s.e.	-	0.0832	0.1362	-	0.0893	0.1409
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.1350	-	-	-0.1199
s.e.	-	-	0.1453	-	-	0.1482
Log L	-2566.942844	-3669.432024	-3669.005314	-2398.888016	-3642.029984	-3641.700594

Estimates of (co) variance components, resulting parameters such as heritability ( $h^2$ ), maternal heritability ( $m^2$ ), genetic covariance, corresponding standard errors and maximum ( $\log$ ) likelihood values for each trait and basic model for Alpine are given in Table 27. Fitting basic model 2 gave, for each trait, slightly higher estimates for  $\sigma^2_A$ ,  $h^2$  and  $\log L$ , and smaller estimates for  $\sigma^2_E$ . Including maternal effects decreased values of  $\log L$  markedly over those for model 1 and reduced estimates for  $\sigma^2_A$  in both cases.

### **Cumulative milk yield**

With estimates of the maternal heritability of 7.8 and 11.6 % (BM1 and BM2 respectively), the direct heritability ( $h^2$ ) was reduced from 30.3 to 22.0 % and from 30.9 to 17.8 % for cumulative milk yield. The change in likelihood values was small compared to the models ignoring  $\sigma_{AM}$ . Estimates of the covariance between direct and maternal effects for milk yield were -14.1 % (BM1) and -1.4 % (BM2) of the phenotypic variance. The negative covariance caused higher estimates for  $\sigma^2_A$  and  $\sigma^2_M$  compared to the models ignoring genetic covariance.

### **Cumulative fat yield**

Heritability was reduced by 4.9 and 6.3 % from 18.7 to 13.8 % and from 23.2 to 16.9 % respectively, fitting models allowing maternal genetic effects. Estimates of  $m^2$  were 4.9 and 6.3 %. The additional random animal effect decreased the  $\log L$  value significantly, while reducing  $\sigma^2_A$  correspondingly. The genetic covariance between direct and maternal effects was moderate and negative and accounted for 6.4 and 7.6 % of the total phenotypic variance. Including  $\sigma_{AM}$  in the model reduced  $\log L$  values slightly compared to a model ignoring  $\sigma_{AM}$ , but increased  $\sigma^2_A$  and  $\sigma^2_E$ , respectively. The phenotypic variance slightly increased through the negative covariance.

### **Cumulative protein yield**

Cumulative protein yield showed similar results to cumulative fat yield. The direct heritability was reduced by 8.5 % from 21.2 to 12.7 % for BM1 and by 12.9 % from 23.9 to 11.0 % for BM2, in which maternal effect was fitted. Maternal effects were estimated

to account for 8.9 and 12.5 % of the total variance. Allowing for direct-maternal covariance yielded a negative estimate amounting to 13.5 and 12.0 %.  $\log L$  values went down by 51 % when fitting  $\sigma^2_M$  in the model, but changed very little compared to model 2 by fitting  $\sigma_{AM}$  in addition.

Genetic correlations ( $r_{AM}$ ) between direct and maternal genetic effects are presented in Table 28. Estimates of  $r_{AM}$  were high and negative for all traits. BM2 gave generally smaller estimates than BM1.

These results indicate that the higher the estimates of the direct genetic variance, the smaller the estimates of the maternal genetic variance and vice versa.

**Table 28. Genetic correlation between direct and maternal genetic effects - Alpine**

Trait	Basic Model 1	Basic Model 2
Cumulative milk yield	-0.5388	-0.4628
Cumulative fat yield	-0.4522	-0.4397
Cumulative protein yield	-0.5906	-0.5302

The Likelihood ratio was used to test the fit for each model for the data set and to test the significance of parameters included in the model. Minus twice the difference in the  $\log L$  values  $[-2(\log_1 - \log_2)]$ , has a  $\chi^2$  distribution with degrees of freedom equal to the number of parameters tested. As the smaller log likelihood values for all traits clearly demonstrate, the data was best described by fitting just direct effects (sub-model 1). Estimates for maternal effects and covariance between direct and maternal effect were not statistically significant for all traits (Appendix Table A16). The likelihood ratios, were 0.8994, 0.3496 and 1.1332 for BM1 and they were all smaller than the tabulated  $\chi^2$  values for a probability level of 10 %. Similar results were found for BM2.

### 4.7.2 Toggenburg

Table 29. Variance components and resulting parameter estimates for Toggenburg.

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	20323.99	18401.25	12145.09	22268.37	22126.35	15340.97
$\sigma^2_M$	-	1144.79	1293.72	-	9.13	796.39
$\sigma_{AM}$	-	-	3961.06	-	-	3439.35
$\sigma^2_E$	98765.89	99017.99	101095.05	96604.73	96704.34	98724.80
$\sigma^2_P$	119089.89	118564.03	118494.93	118873.10	118839.82	118355.51
$h^2 = \sigma^2_A / \sigma^2_P$	0.1707	0.1552	0.1025	0.1873	0.1862	0.1296
s.e.	0.1530	0.1884	0.1988	0.1572	0.2068	0.2247
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0097	0.0101	-	0.0001	0.0067
s.e.	-	0.0865	0.1002	-	0.0936	0.1099
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0334	-	-	0.0295
s.e.	-	-	0.1009	-	-	0.1118
Log L	-3939.714968	-4704.760849	-4704.555165	-3797.473109	-4652.934982	-4652.811248
Fat yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	25.53	7.59	5.05	24.49	10.79	7.45
$\sigma^2_M$	-	13.59	8.02	-	10.62	5.71
$\sigma_{AM}$	-	-	6.36	-	-	6.50
$\sigma^2_E$	101.48	104.96	106.11	101.67	103.74	105.47
$\sigma^2_P$	127.01	126.15	125.54	126.16	125.16	125.13
$h^2 = \sigma^2_A / \sigma^2_P$	0.2010	0.0602	0.0402	0.1941	0.0862	0.0595
s.e.	0.1386	0.1440	0.1231	0.1444	0.1622	0.1512
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.1078	0.0639	-	0.0849	0.0456
s.e.	-	0.0838	0.1033	-	0.0885	0.1031
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0507	-	-	0.0520
s.e.	-	-	0.0777	-	-	0.0819
Log L	-2271.514742	-3035.649869	-3035.459859	-2153.460898	-3008.412123	-3008.189177
Protein yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	15.78	10.66	7.98	17.96	17.92	12.42
$\sigma^2_M$	-	3.14	1.52	-	0.061	0.60
$\sigma_{AM}$	-	-	3.48	-	-	2.73
$\sigma^2_E$	79.16	80.07	81.37	77.20	76.97	79.06
$\sigma^2_P$	94.94	93.88	94.35	95.16	94.95	94.81
$h^2 = \sigma^2_A / \sigma^2_P$	0.1663	0.1135	0.0846	0.1887	0.1887	0.1310
s.e.	0.1478	0.1810	0.1852	0.1516	0.1968	0.2071
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0335	0.0161	-	0.0006	0.0063
s.e.	-	0.0746	0.1008	-	0.0917	0.0976
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0369	-	-	0.0288
s.e.	-	-	0.0879	-	-	0.0992
Log L	-2202.757769	-2967.734426	-2967.510865	-2086.115286	-2941.577182	-2941.471424

Estimates of (co) variance components, genetic parameters and corresponding maximum (log) likelihood values for each trait and each analysis are summarised for Toggenburg in Table 29. Results for direct variance, phenotypic variance and direct heritabilities were slightly higher for BM2 fitting phantom groups, except for fat yield. Maternal genetic variance was much lower with BM2 than with BM1.

### **Cumulative milk yield**

The maternal effect included in BM1 decreased the direct variance by 9.5 % from 20324 to 18401. The direct heritability ( $h^2$ ) went down by 1.5 % from 17 to 15.5 % and the estimate of the maternal heritability ( $m^2$ ) was 0.96 %, which leads to the conclusion that almost no maternal genetic effects are present for milk yield in Toggenburg goats.

Fitting  $\sigma_{AM}$  increased the maternal genetic variance by just 1.1 % but decreased the direct genetic variance by 34 %. The covariance between direct and maternal effects fitted was positive and accounted for 3.3 % of the total variance.

Same trends were observed for milk yield using BM2, but values were higher for direct variance and direct heritability and smaller for  $\sigma^2_M$  and  $\sigma_{AM}$ . Fitting just additive direct variance in model 1 gave estimates for  $h^2$  of 18.7 % of the total variance. Estimates for maternal heritabilities were 0 % and  $h^2$  was hardly reduced fitting maternal effects in addition. Allowing for a covariance between direct and maternal effects reduced  $h^2$  to 13 % and increased  $m^2$  to 0.06 %. Results for  $\sigma_{AM}$  were smaller when phantom groups were fitted (2.9 % of  $\sigma^2_P$ ). Log likelihood values decreased with the inclusion of maternal effects, but increased slightly when  $\sigma_{AM}$  was fitted in both basic models.

### **Cumulative fat yield**

Direct heritability for fat yield was 20.1 % (BM1) and 19.4 % (BM2). Maternal heritability ranged from 8.4 % (BM1) to 8.9 % (BM2). A high estimate of the maternal genetic variance resulted in a relatively small estimate for direct genetic variance for BM1. Different starting values for the parameters always lead to the same maximum. Basic model 2 gave more acceptable results. The estimates for  $m^2$  were 8.5 % and 8.6 % of the direct heritability. Adding the direct-maternal covariance as an additional random effect



(Model 3) increased  $\sigma^2_E$  and decreased  $\sigma^2_A$ ,  $\sigma^2_M$  and  $\sigma^2_P$ . The covariance between direct and maternal effect counted for ~ 5 % of the phenotypic variation in both basic models.

### Cumulative protein yield

Heritability for protein yield was 16.6 % in BM1 and 18.9 % in BM2. Fitting model 2 increased  $\log L$  values for both basic models and gave estimates of 3.3 % (BM1) and 0 % (BM2) for maternal genetic effects. The covariance between direct and maternal genetic effects was positive but fairly small (3.7 and 2.9 % of  $\sigma^2_P$ ) and changed the likelihood values slightly compared to models ignoring  $\sigma_{AM}$ .

Genetic correlations between direct and maternal genetic effects are given in Table 30.

**Table 30. Genetic correlation between direct and maternal effects - Toggenburg**

	Basic Model 1	Basic Model 2
Cumulative milk yield	0.9860	0.9994
Cumulative fat yield	1.00	0.9974
Cumulative protein yield	0.9960	0.9981

Genetic correlations between maternal and direct effects are positive and very high for Toggenburg. The results indicate that increase in direct variance results in a corresponding increase in maternal variance.

As with Alpine goats, the log likelihood value of models 1 demonstrate clearly that maternal genetic effects and the covariance between direct and maternal effects do not improve the goodness of fit, and that the models only including direct effects provide the best fit for the data. Maternal effects for all traits were not statistically significant (Appendix - Table A17).

### 4.7.3 Saanen

Table 31. Variance components and resulting parameter estimates for Saanen

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	f	0.93	4756.31	f	1.80	21293.36
$\sigma^2_M$	-	2307.97	10265.22	-	5861.61	33594.25
$\sigma_{AM}$	-	-	-6983.55	-	-	-26742.64
$\sigma^2_E$	f	129676.75	124597.79	f	129571.76	110796.46
$\sigma^2_P$	f	131985.65	132635.76	f	135435.16	138941.44
$h^2 = \sigma^2_A / \sigma^2_P$	f	0.0000	0.0359	f	0.0000	0.1533
s.e.	f	0.1542	0.2960	f	0.2588	0.2294
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0175	0.0774	-	0.0433	0.2418
s.e.	-	0.1113	0.1386	-	0.1498	0.1496
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.0527	-	-	-0.1925
s.e.	-	-	0.0375	-	-	0.0003
Log L	f	-3194.788771	-3194.501076	f	-3139.706979	-3139.909288
Fat yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	14.89	0.0065	10.61	18.28	0.040	45.84
$\sigma^2_M$	-	13.96	37.92	-	16.21	56.78
$\sigma_{AM}$	-	-	-20.05	-	-	-43.99
$\sigma^2_E$	143.6	143.91	131.21	143.75	145.05	109.65
$\sigma^2_P$	158.49	157.87	159.69	162.03	161.30	168.28
$h^2 = \sigma^2_A / \sigma^2_P$	0.0939	0.0000	0.0664	0.1128	0.0002	0.2724
s.e.	0.1625	0.1631	0.4608	0.1795	0.2495	0.3851
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0884	0.2375	-	0.1005	0.3374
s.e.	-	0.1115	0.2862	-	0.1453	0.2893
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.1256	-	-	-0.2614
s.e.	-	-	0.2771	-	-	0.2701
Log L	-1589.723288	-2267.572374	-2267.388625	-1561.013863	-2238.874601	-2238.400188
Protein yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	4.85	0.0021	11.89	12.01	0.0063	18.58
$\sigma^2_M$	-	8.02	16.26	-	10.08	35.57
$\sigma_{AM}$	-	-	-9.37	-	-	-24.93
$\sigma^2_E$	115.28	112.47	103.54	112.43	113.57	97.61
$\sigma^2_P$	120.13	120.5	122.33	124.43	123.65	126.84
$h^2 = \sigma^2_A / \sigma^2_P$	0.0404	0.0000	0.0972	0.0965	0.0001	0.1465
s.e.	0.1842	0.2643	0.3308	0.1986	0.2737	0.2758
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0666	0.1329	-	0.0815	0.2805
s.e.	-	0.1457	0.2187	-	0.1516	0.2511
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.0766	-	-	-0.1966
s.e.	-	-	0.1962	-	-	0.1771
Log L	-1553.210892	-2231.103234	-2230.834603	-1526.308188	-2204.259897	-2203.475363

Estimates of (co) variance components and resulting heritabilities (maternal and direct), together with the maximum (log) likelihood values for each trait and model are given for Saanen in Table 31. Basic model 2 (fitting coefficients for phantom groups) gave generally higher results for  $\sigma^2_A$  and  $\sigma^2_P$ .

### **Cumulative milk yield**

No results for model 1 of BM1 and BM2 could be obtained, even after trying different starting values, very small step sizes and small convergence criteria. The estimates became very small and eventually negative, which caused the DFREML program to fail.

Basic model 1 gave very small estimates for  $h^2$  and  $m^2$  for all sub-models. Including the covariance as an effect increased the estimate of  $h^2$  from 0 to 3.6 % and  $m^2$  from 1.7 to 7.7 %. The covariance between direct and maternal effect ( $\sigma_{AM}$ ) was negative and accounted for 5.3 % of the total variance. Estimates using sub-models of BM 2 were slightly higher than with BM1. Better results for direct and maternal heritabilities were obtained by fitting the covariance between direct and maternal effects in BM2. The direct and maternal genetic effect contributed 15.3 and 24.2 % to the phenotypic variance. The covariance between both effects was negative and had a value of 5 and 19.2 % of the total variance respectively. Log likelihood values changed with fitting different random effects or phantom group coefficients. The highest value was reached with model 2 of BM2.

### **Cumulative fat yield**

Heritabilities, for models fitting just additive direct effects were 9.4 % (BM1) and 11.3 % (BM2). Fitting additive maternal effects in addition decreased  $h^2$  almost to zero for BM1 and from 11.2 to 0.02 % for BM2. The reductions were attributed to maternal effects of 8.8 and 10.1 %. Likelihood values decreased significantly by including maternal effects. In addition the covariance increased likelihood values only slightly, but gave higher estimates of  $h^2$  and  $m^2$ . Neither value of  $h^2$  (6.6 and 27.2 %) seems very. Maternal heritability estimated with sub model 3 accounted for 23.7 and 33.7 % of the total variance. The covariance between direct and maternal effects was negative and relatively high (12.6 and

26.1 % of  $\sigma^2_P$ . Changes of  $\log L$  were high when fitting maternal effects in addition, but changed then very little with the covariance included.

### **Cumulative protein yield**

Estimates of genetic parameters for cumulative protein yield showed a trend similar to fat yield. For both basic models likelihood values decreased with included maternal genetic effects and increased the covariance between direct and maternal effects. The two estimates of  $h^2$  for protein yield were 4 and 9.6 %. Fitting maternal effects gave higher results for  $m^2$  (6.7 %) than for  $h^2$  (0%) (BM1), but on the other hand, the direct heritability (9.6 %) estimated with model 2 (BM2) declined when maternal effects were included. Allowing for the covariance between direct and maternal effects gave higher results of  $h^2$  (9.7 and 14.7 %) and increased  $m^2$  estimates to 13.3 and 28 %. Covariance estimates were negative and accounted for 7.7 and 19.7 % of the total variation. The highest log likelihood value was obtained with model 1 of BM2.

Genetic correlations between direct and maternal genetic effects are given in Table 32.

**Table 32. Genetic correlation between direct and maternal effects**

	Basic Model 1	Basic Model 2
Cumulative milk yield	-0.9994	-0.9999
Cumulative fat yield	-0.9999	-0.8622
Cumulative protein yield	-0.6736	-0.9696

Genetic correlations between direct and maternal effects for Saanen were found to be high and negative.

Minus twice the difference between the maximum log likelihood values  $[-2(\log_1 - \log_2)]$  of the two models gives answers in how good the model fits the data set. It is demonstrated clearly that maternal genetic effects and the covariance between direct and maternal effects included in the model decrease the likelihood values, hence the 'best' models are just fitting direct genetic effects. Estimates for maternal genetic effects were not statistically

significant. All calculated  $\chi^2$  - values were smaller than the tabulated ones for a 10 % probability level (Appendix Table A18).

All results obtained for Saanen appear somewhat questionable. Maternal heritabilities were all small and close to zero, but so were the estimates for direct heritability. Reason for doubting these results are also the very high standard errors and the structure of the data set used. Saanen had the smallest pedigree, and the smallest number of sires and grand sires with progeny records. In addition, the number of dams in total was relatively small and the number of single connection parents relatively large compared to the other breeds (Table A2 – Appendix). Single connection parents are animals, which usually provide no information. The missing or small number of animal relationships might be the reason why estimates are different than expected or could not be obtained at all.

#### 4.7.4 Nubian

Table 33. Variance components and resulting parameter estimates for Nubian

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	14728.37	2.64	369.29	17630.38	0.51	214.22
$\sigma^2_M$	-	16991.28	14375.94	-	17889.33	16150.85
$\sigma_{AM}$	-	-	2300.33	-	-	1857.01
$\sigma^2_E$	42825.46	41221.79	41161.49	41786.29	41677.47	41520.21
$\sigma^2_P$	57553.84	58215.72	58207.07	59416.67	59567.31	59742.28
$h^2 = \sigma^2_A / \sigma^2_P$	0.2559	0.0000	0.0063	0.2967	0.0000	0.0036
s.e.	0.2157	0.2736	0.2763	0.2276	0.2926	0.0507
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.2919	0.2469	-	0.3003	0.2703
s.e.	-	0.1605	0.2952	-	0.1625	0.3875
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0395	-	-	0.0311
s.e.	-	-	0.3013	-	-	0.4715
Log L	-2405.73259	-3193.837862	-3193.81049	-2351.909154	-3139.884979	-3139.868222
Fat yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	69.46	19.9	8.97	75.72	18.22	7.80
$\sigma^2_M$	-	46.86	31.89	-	51.05	39.46
$\sigma_{AM}$	-	-	16.91	-	-	12.51
$\sigma^2_E$	89.36	91.84	99.56	87.75	94.46	100.11
$\sigma^2_P$	158.82	158.6	157.33	163.47	163.74	159.88
$h^2 = \sigma^2_A / \sigma^2_P$	0.4373	0.1255	0.0570	0.4632	0.1113	0.0488
s.e.	0.1973	0.2176	0.3349	0.2124	0.2482	0.3826
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.2955	0.2027	-	0.3118	0.2468
s.e.	-	0.1289	0.3210	-	0.1354	0.3307
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.1074	-	-	0.0783
s.e.	-	-	0.3547	-	-	0.3793
Log L	-1638.97518	-2426.999572	-2426.89184	-1608.597984	-2396.421798	-2396.401496
Protein	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	21.05	0.0001094	0.11	25.18	0.0035	0.27615
$\sigma^2_M$	-	25.6	27.31	-	26.93	29.90
$\sigma_{AM}$	-	-	-1.73	-	-	-2.87
$\sigma^2_E$	62.83	59.24	59.1	61.31	59.75	59.45
$\sigma^2_P$	83.87	84.83	84.78	86.49	86.68	86.75
$h^2 = \sigma^2_A / \sigma^2_P$	0.2509	0.0000	0.0013	0.2911	0.0000	0.0032
s.e.	0.1963	0.2521	0.8702	0.2121	0.2634	0.4146
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.3017	0.3221	-	0.3106	0.3446
s.e.	-	0.1452	0.5777	-	0.1443	0.3876
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	-0.0205	-	-	-0.3306
s.e.	-	-	0.8389	-	-	0.4311
Log L	-1563.37809	-2350.806034	-2350.79734	-1535.572401	-2322.905296	-2322.894702

Variance and covariance components, resulting parameter estimates and maximum log likelihood values for Nubian are given in Table 33. **LogL** values were generally smaller for basic model 2.

### **Cumulative milk yield**

Fitting phantom groups in the model (BM2) increased estimates for  $\sigma^2_A$  by 19.7 % and  $\sigma^2_P$  just slightly. Estimates for  $h^2$  were 25.6 % without phantom group coefficients and 29.7 % with coefficients included. Fitting maternal genetic effects in the model changed the importance of direct and maternal effects totally. Direct heritability had estimates close to zero and for  $m^2$  the results were 29.2 and 30 % of the total variation. Including the covariance between maternal and direct effects increased direct heritability and decreased  $m^2$  slightly. The covariance was small (4 and 3.1 %) and in both cases it was not statistically significant. Fitting phantom groups did not change the estimates for  $h^2$  and  $m^2$ . **LogL** values changed very little with the covariance included as an additional effect.

### **Cumulative fat yield**

Results for fat yield showed similar trends than for milk yield. Direct heritability estimates of 43.7 (BM1) and 46.3 % (BM2) seem to be reasonable. Standard errors were relatively large, but were expected because of the small number of animals in the data set. Including maternal effects in the models resulted in small estimates for  $h^2$  and large ones for  $m^2$ . Adding  $\sigma^2_A$  and  $\sigma^2_M$  together yielded almost the same value for  $\sigma^2_A$  when  $\sigma^2_A$  fitted alone in sub-model1. The estimates for the covariance fitted in the models were positive and counted for 10.7 and 7.8 % respectively. **LogL** values changed very little when  $\sigma_{AM}$  was added as an in the model, but decreased significant when maternal effects were included in addition to direct effects.

### **Cumulative protein yield**

The direct genetic effect accounted for 25.1 (BM1) and 29.1 % (BM2) of the total variation. Including maternal effects reduced  $\sigma^2_E$  but increased  $\sigma^2_P$  in both basic models. Direct heritability estimates were again close to zero, and maternal heritability estimates

were high (30.2 and 31.1 %). Including the covariance between the two effects in the model changed values for  $\sigma^2_A$  and  $\sigma^2_M$  very little. Estimates for the covariance were small and negative for BM1, high and negative for BM2 and were not statistically significant. Log likelihood values indicate, for all traits, that Model 1 (just fitting direct genetic effects in addition to fixed effects) described the data set best for Nubians.

Genetic correlations between direct and maternal genetic effects for cumulative milk, fat and protein yields are given in Table 34.

**Table 34. Genetic correlation between direct and maternal genetic effects - Nubian**

	Basic Model 1	Basic Model 2
Cumulative milk yield	0.9984	0.9984
Cumulative fat yield	0.9995	0.7131
Cumulative protein yield	-1.0000	-0.9982

The genetic correlations between direct and maternal effects were very high and positive for milk and fat yield. For protein yield, the correlations were also very high but negative. Fitting phantom group effects in the model reduced estimates just slightly.

The proportions between direct and maternal heritability, estimated for Nubians, are very unlikely and it may be that maternal and direct effects should be seen as two random effects, which are very closely related to explain these results. Genetic correlations indicated that increase in  $\sigma^2_A$ , also caused an increase in  $\sigma^2_M$ , but maybe the second random effect will be just a constant part of the other animal effect.

As with other breeds, the best models to describe the data set are, models just fitting direct effects in addition to the fixed effects. The covariance between direct and maternal effects was not statistically significant in both basic models. Estimates for maternal effects were statistically significant for milk and fat yield on a probability level of 5 % and for protein yield on a 2.5 % probability level (Appendix Table A19).



### 4.7.5 Combined data set - ALL BREEDS

Table 35. Variance Components and resulting parameter estimates for combined data set (all breeds).

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	17065.17	10504.21	8425.78	18721.49	12458.69	10966.02
$\sigma^2_M$	-	5607.15	3766.79	-	5230.88	3853.92
$\sigma_{AM}$	-	-	2302.7	-	-	1773.81
$\sigma^2_E$	81332.06	82196.83	83045.66	80184.91	80892.71	81862.59
$\sigma^2_P$	98397.23	98308.19	97540.93	98906.41	98582.28	98456.34
$h^2 = \sigma^2_A / \sigma^2_P$	0.1734	0.1068	0.0864	0.1893	0.1264	0.1114
s.e.	0.0667	0.0800	0.1025	0.0676	0.0817	0.0976
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0570	0.0386	-	0.0531	0.0391
s.e.	-	0.0461	0.0697	-	0.0457	0.0717
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0236	-	-	0.0180
s.e.	-	-	0.0653	-	-	0.0684
Log L	-14171.83008	-17333.56262	-17333.49547	-14123.03122	-17284.88984	-17284.84849
Fat yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	26.82	12.12	7.37	28.84	13.94	9.15
$\sigma^2_M$	-	12.95	7.59	-	12.98	7.80
$\sigma_{AM}$	-	-	6.23	-	-	6.16
$\sigma^2_E$	103.9	104.99	108.27	102.55	103.99	107.16
$\sigma^2_P$	130.72	130.06	129.47	131.39	130.91	130.26
$h^2 = \sigma^2_A / \sigma^2_P$	0.2052	0.0932	0.0569	0.2195	0.1065	0.0702
s.e.	0.0665	0.0767	0.0802	0.0664	0.0784	0.0818
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0996	0.0586	-	0.0992	0.0599
s.e.	-	0.0474	0.0638	-	0.0486	0.0634
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0481	-	-	0.0473
s.e.	-	-	0.0528	-	-	0.5381
Log L	-8479.511076	-11639.73877	-11639.38255	-8457.259255	-11617.56213	-11617.22787
Protein yield	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
$\sigma^2_A$	14.34	4.76	3.75	15.83	6.20	5.41
$\sigma^2_M$	-	8.35	7.18	-	8.29	7.30
$\sigma_{AM}$	-	-	1.38	-	-	1.15
$\sigma^2_E$	76.09	76.77	77.6	75.11	75.84	76.70
$\sigma^2_P$	90.43	89.88	89.91	90.94	90.34	90.56
$h^2 = \sigma^2_A / \sigma^2_P$	0.1586	0.0529	0.0417	0.1741	0.0687	0.0597
s.e.	0.0655	0.0760	0.0801	0.0678	0.0779	0.0907
$m^2 = \sigma^2_M / \sigma^2_P$	-	0.0929	0.0799	-	0.0918	0.0806
s.e.	-	0.0467	0.0165	-	0.0475	0.0696
$c^2 = \sigma_{AM} / \sigma^2_P$	-	-	0.0153	-	-	0.0127
s.e.	-	-	0.0511	-	-	0.0618
Log L	-8171.690092	-11332.12783	-11332.09453	-8151.420213	-11312.00710	-11311.98594

The estimates of (co) variance components and genetic parameters for cumulative milk, fat and protein yield, for the combined data set, are presented together with the maximum (log) likelihood values, for each analysis in Table 35.

For all traits and both basic models, ignoring maternal effects (Model 1) resulted in substantially higher estimates of  $\sigma^2_A$  and  $h^2$ . Estimates of  $\sigma^2_A$  and log likelihood values were higher using models in which phantom groups were fitted.

### **Cumulative milk yield**

Fitting maternal effect (Model 2) decreased values of  $\log L$  markedly over those for Model 1. Heritabilities of 17.3 (BM1) and 18.9 % (BM2) were reduced to 10.7 and 12.6 % respectively when maternal effects were included. Maternal effects accounted for 5.7 and 5.3 % of the total variation in cumulative milk yield. Values of  $\sigma^2_A$  and  $\sigma^2_E$  were reduced correspondingly. Estimates of the genetic covariance between direct and maternal effects were very small (2.3 and 1.8 %) and changed the likelihood values little compared to models ignoring  $\sigma_{AM}$ . Fitting phantom groups resulted in a slightly smaller value for  $\sigma^2_M$  and  $\sigma_{AM}$ .

### **Cumulative fat yield**

Heritabilities of 20.5 and 21.9 % were obtained with both basic models, fitting just additive direct genetic effects in addition to the fixed effects (M1). Including maternal effects resulted in 10 and 9.9 % of the total variation being contributed by  $m^2$ , which reduced  $h^2$  to 9.3 and 10.6 % respectively. These results suggested that  $m^2$  constituted a bigger portion of the total heritability for cumulative milk yield than  $h^2$ . Allowing for maternal effects (Model 2) decreased  $\log L$  by 27%. On the other hand, including  $\sigma_{AM}$  in the model increased  $\log L$  values just a little compared to models ignoring the covariance between direct and maternal effect.

Estimates of the genetic covariance, were small (4.8 and 4.7 %) compared to  $\sigma^2_P$ , but were of similar size to  $h^2$  (5.6 and 7.0 %) and  $m^2$  (5.9 and 6.0 %).

### **Cumulative protein yield**

Results for cumulative protein yield showed same trends as cumulative milk and fat yield. Ignoring maternal effects resulted in higher estimates for  $h^2$ . For both basic models, values for  $m^2$  of 9.2 % of the total variation reduced  $h^2$  from 15.9 to 5.3 % for BM1 and from 17.4 to 6.9 % for BM2. These results suggest again that maternal heritability contribute a bigger part to the total heritability than the direct heritability. Allowing for covariance between maternal and direct effects reduced estimates for  $\sigma^2_A$  and  $\sigma^2_M$ . The estimates for  $\sigma_{AM}$  of 1.5 and 1.3 % were just a small part of the total variance  $\sigma^2_P$ .

Genetic correlations between direct and maternal genetic effects for cumulative milk, fat and protein yields are given in Table 36.

**Table 36. Genetic correlation between direct and maternal genetic effects**

	Basic Model 1	Basic Model 2
Cumulative milk yield	0.4087	0.2729
Cumulative fat yield	0.8330	0.7290
Cumulative protein yield	0.2653	0.1826

The genetic correlations between direct and maternal effects were positive and small to high for all traits.

As with the single breed analyses, the best model to describe the data set is the one fitting just direct genetic effects in addition to the fixed effects. Included maternal effects and covariance between direct and maternal effects decreased maximum likelihood values and decreased the goodness of fit. Maternal effects were not statistically significant for milk yield, but significant ( $p < 0.05$ ) for fat and protein yield.

### **4.8 Best estimates**

“Best estimates”, are results calculated with the most appropriate model. Within models the best model to describe the data set is just fitting additive genetic variance. The F-test was used to determine if phantom groups have an effect or not. Calculated F-values are given in appendix Table A21. Results demonstrated clearly, that just for the multiple breed

analysis, phantom groups had an effect and the null hypothesis could be rejected. Parameter estimates and calculated standard errors from the 'best' model for each breed and trait are summarised in Table 37.

**Table 37. Heritabilities for milk, fat and protein yield by breed**

<b>Breed</b>	<b>Trait</b>	<b><math>h^2 \pm s.e</math></b>
<b>Alpine</b>	Milk yield	0.303 $\pm$ 0.125
	Fat yield	0.187 $\pm$ 0.128
	Protein yield	0.212 $\pm$ 0.126
<b>Toggenburg</b>	Milk yield	0.171 $\pm$ 0.153
	Fat yield	0.201 $\pm$ 0.139
	Protein yield	0.166 $\pm$ 0.148
<b>Saanen</b>	Milk yield	f*
	Fat yield	0.094 $\pm$ 0.162
	Protein yield	0.040 $\pm$ 0.184
<b>Nubian</b>	Milk yield	0.256 $\pm$ 0.216
	Fat yield	0.437 $\pm$ 0.197
	Protein yield	0.251 $\pm$ 0.196
<b>All breeds</b>	Milk yield	0.189 $\pm$ 0.068
	Fat yield	0.220 $\pm$ 0.066
	Protein yield	0.174 $\pm$ 0.068

\*f = estimation failed

Estimated heritabilities are well within the range of estimates from the literature summarised in Table 6. Boldman et al. (1984) found a similar heritability (0.25) using Alpine, Saanen, Toggenburg, Nubian and LaMancha goats with the BLUP method. Even Garcia (1971) who used a small number ( $\Rightarrow$  high standard errors) of the same dairy breeds, found similar results for milk ( $0.17 \pm 0.20$ ) and fat production ( $0.22 \pm 0.20$ ). Kennedy et al (1982) divided genotypes into dairy breeds and dual purpose breeds and analysed the data separately with the MINQUE method. They reported very high estimates for milk and fat yield (0.69 and 0.62) for the dairy breeds, whereas estimates for Nubian (0.32 and 0.51) correspond with the results obtained in this study. A study with Canadian dairy goats on first lactation reported heritabilities of  $0.38 \pm 0.10$  for milk yield,  $0.29 \pm 0.14$  for fat yield and  $0.31 \pm 0.10$  as an average for all breed (Sullivan, 1988). A study using only Alpine does reported very high heritabilities for milk yield, fat and protein yield (0.60, 0.47 and 0.47). Possible reasons for different results can have many explainable. For example

management, number of lactation, age at first kidding and/or through different statistical methods used etc.

Alpine results are in this study the most appropriate estimates for the single breed analyses. The distribution of animals per flock was good and they had the largest number of flocks. Sire and dam distribution per flock was similar to Toggenburg, but the Toggenburg data had one weak point, i.e. that 34 % of the animals with records came out of one flock.

In general, each heritability estimate is based on the degree of resemblance among related animals vs. non-related animals in a population. If relationships exist between animals and are not recorded, estimates will be biased downwards (Massey, 1993), which explains why heritability estimates for all traits for Saanen are unexpectedly low. In this study, Saanen and Nubian data sets were very small, but Nubians had the advantage of a more complete (bigger) pedigree file, which resulted in more acceptable results than Saanen. Also a failure to account for environmental contributions might reduce the estimates of heritability.

The estimation of variance components for the combined data set was made under the assumption that all breeds have the same genetic variation. Results of the single breed analyses showed that there are differences concerning variance components, which might result in a bias, when all breeds are combined together. Genetic evaluation in Canada is undertaken with a data set containing all registered breeds, only as breed as an additional fixed effect. For future evaluations and when more data are available, we should consider analysing goat data separately by breed, similar to dairy cattle.

#### **4.9 Maternal effects**

Studies show that maternal effects are present in beef cattle, and sheep. Using – twice the log likelihood value and comparing it to the tabulated  $\chi^2$  values, gave the following results; maternal effects for Alpine, for all traits and for both basic model were not statistically significant (Appendix Table A16).

Same results for Toggenburg, maternal effects for all traits and both basic models were not statistically significant (Appendix Table A17).

For Saanen maternal effects were not statistically significant for all traits and both basic models (Appendix Table A18).

Nubian is the only breed where the estimates for maternal effects on milk, fat and protein yields were highly significant (milk and fat  $p < 0.05$  and protein  $p < 0.025$ ) (Appendix Table A19). The significance levels found, indicate that there are maternal effects in Nubian, but the high estimates for  $m^2$  obtained in this study are doubtful and further investigation based on large numbers is warranted.

The combined data set containing all breeds indicates similar results. Maternal effects on milk yield for both basic models are not significant ( $p < 0.25$ ), but maternal effects on fat and protein yield are significant at a 5 % probability level (Appendix Table A20).

Van Vleck and Bradford (1966) using Holstein data found within-flock estimates of heritabilities from records expressed as deviations from flock-mate averages of 0.37, 0.30, and 0.24 from daughter-dam regressions for the first three lactations, and corresponding estimates from half-sib correlation of 0.24, 0.21, and 0.23. Differences between these results suggested a large maternal effect in first lactation, a smaller one in second lactation and almost no effect in third lactation.

A second study made by Van Vleck and Hart (1966) used covariances among first lactation milk records expressed as deviation from flock mate averages of Holstein cows related as cousins of varying degree, as daughter-dam, as full and maternal sibs, and as aunt-niece of varying degrees, to examine whether maternal genetic effects are important. Results suggested that only additive genetic effects were important for milk yield.

Kirkpatrick et al. (1988) agreed with Reed and Van Vleck's (1987) conclusion, i.e. that there is no influence of cytoplasmic genes on lactation traits, therefore assuming no maternal influence on lactation.

More complicated models, which include maternal genetic effects and persistent environmental effects, could have been used to account more adequately for source of variation (Riska et al, 1985). Using such models would have complicated the analyses without changing the results, since maternal genetic effects would have contributed equally to heritability estimates (Kirkpatrick et al, 1988).

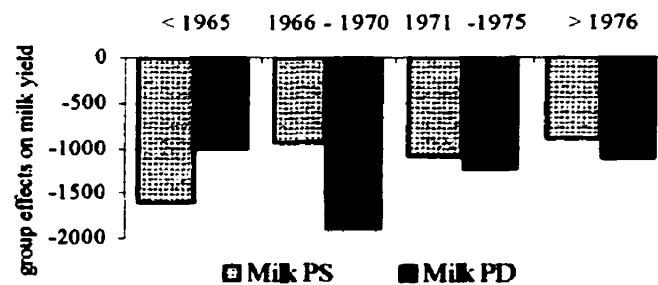
Critical for this kind of analysis is that, the data set is large with relationships among the animals. Willham (1963) stated that cousins are the best relationships to test for maternal effects.

In this study, insufficient numbers of records were available to give reliable results. These results indicate that further research, is necessary to find reliable estimates for maternal heritability.

#### **4.10 Phantom groups**

Including coefficients for phantom parents in the model resulted in general slightly higher results. This was a somewhat expected result, because of small data sets and the short-recorded time period (18 years) for Canadian dairy goats.

In this study the missing parents were grouped by assigned birth dates calculated using the four different pathways for genetic intervals. The small number of animals and the fact that milk recording for Canadian dairy goats started in 1980 and just a few phantom parents had to be assigned after 1980 led to the decision of using 4 groups for sire and 4 groups for dams. Reports of rules on how many groups should be assigned without over parameterisation were not found. Calculations done earlier with 23 sire and 23 dam groups, each of the 23 groups representing one year, gave fixed effects solutions for the groups which were unrealistically high (200000 kg for milk yield). Westell (1984) using a data set of 1,074,971 animals in her study assigned 12 sire and 12 dam groups. The point is that grouping phantom parents might be sensible only in a large population, so that groups can represent the population mean in their time period more accurately.



**Figure 17. GLS solution for sire and dam phantom groups for Alpine**

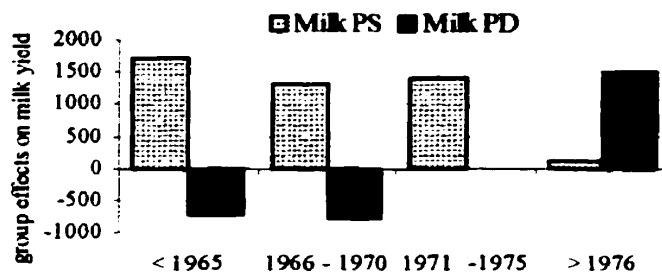


Figure 18. GLS solution for sire and dam phantom groups for Toggenburg

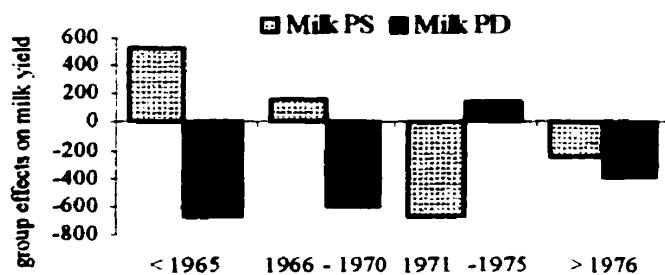


Figure 19. GLS solution for sire and dam phantom groups for Saanen

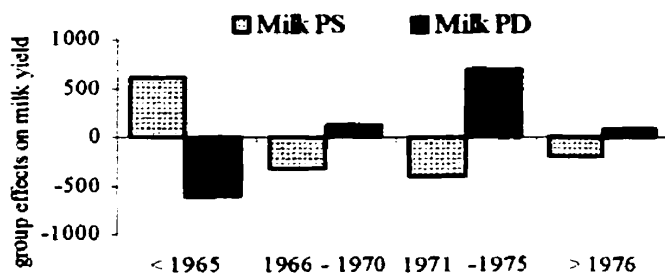


Figure 20. GLS solution for sire and dam phantom groups for Nubian

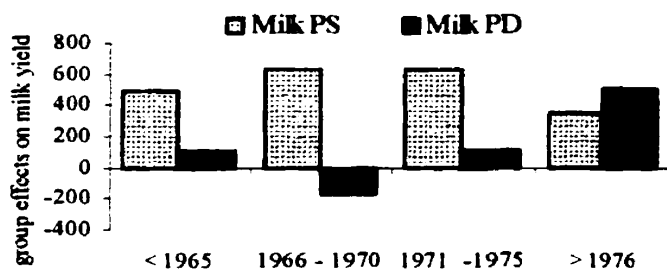


Figure 21. GLS solution for sire and dam phantom groups for all breeds



A good agreement between solutions for groups and the mean yield would indicate that the group accurately reflects the mean genetic merit of the animals constituting them. (Golden et al., 1994)

Group solutions plotted for milk yield and by breed in Figures 17 to 21 indicate no particular trend, but show the effect of each group on the milk yield. Values plotted for fat and protein yield are not included in the results, because they show a similar pattern though on a lower level (Appendix). Further studies have to be made to investigate the connection between the number of assigned groups and the accuracy of the resulting estimates.

Solutions for phantom groups with standard errors for milk, fat and protein yield are given in Table A-15 (Appendix).

## **5. CONCLUSIONS**

- Results on estimates of variance components indicate that estimates of the covariance between direct additive and maternal additive genetic effects are small and not statistically significant for cumulative milk yield, cumulative fat yield and cumulative protein yield in all Canadian dairy goats used in this study. Maternal effects seem to be significant for Nubian and the all breed combined data set. Heritabilities are moderate to high for Alpine (0.23 to 0.31) and Toggenburg, (~ 0.19), and high for Nubian. (0.29 to 0.46). Information on Saanen dairy goats was not sufficient to provide useful estimates. If maternal genetic effects exist heritability would be biased.
  
- Genetic evaluation for dairy goats in Canada is made under the assumption that genetic variances are the same in all breeds. This study reveals that the variances are different for each breed and future evaluation, when more data are collected should be done separately.
  
- Appropriate statistical models should be used to account for all known important environmental effects like, age at first kidding, flock-year or even genetic trends to get unbiased estimates for genetic parameters such as heritabilities. Phantom groups are an efficient way to make results more accurate through accounting for selection. For effective genetic improvement, and more reliable databases, more data on dairy goats and their pedigree has to be collected.
  
- Before using phantom parent grouping in genetic evaluation in dairy goats, further studies should ensure that the grouping does not introduce systematic errors (such as over parameterisation) into current analyses. Milk recording for dairy goats started 1980 and the last animal assigned to a group was from 1986. It is doubtful that there was a lot of genetic progress to account for in six years, and maybe genetic grouping based on phantom parents was not necessary.

- Estimates of maternal effects and covariance between direct and maternal effects were not statistically significant. Further studies have to be carried out to investigate these uncertain trends in this study. If evidence for negative correlation between direct and maternal effects were to be found, methods of selection accounting for both direct and maternal effects would result in greater economic response to long term selection than selection based only on direct genetic effects.

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## **APPENDIX**

### **I. Phantom Groups**

**Table A1. Number of animals assigned per phantom group per breed**

Phantom group		Number of Animals assigned per group				
Sire	Year	Alpine	Toggenburg	Saanen	Nubian	All breeds
PS1*	1957-1965	202	153	142	164	462
PS2*	1966-1970	307	197	194	214	763
PS3*	1971-1975	205	88	128	184	541
PS4*	> 1975	60	37	72	101	277
Dam	Year	Alpine	Toggenburg	Saanen	Nubian	All breeds
PD1*	1957-1965	249	199	177	191	587
PD2*	1966-1970	315	186	210	230	779
PD3*	1971-1975	162	73	102	166	483
PD4*	> 1975	84	48	91	101	331

\*PS = Phantom Sire groups

\*PD = Phantom Dam groups

## II. Data Structure

Table A2: Data Structure: Offspring-Parent combinations

	ALPINE	TOGGENBURG	SAANEN	NUBIAN	ALL BREEDS
NO. OF RECORDS IN DATA	691	641	439	433	2204
NO. OF PEDIGREE RECORDS	3871	2642	2472	2901	11012
AVERAGE INBREEDING COEFFICIENT	1.01873	1.02117	1.01819	1.01986	1.02059
NO. OF INBRED ANIMALS	1378	1095	863	832	4120
... WITH AVERAGE INBREEDING COEFFICIENT	1.05262	1.05108	1.0521	1.06924	1.05504
no. of animals with great-grand parent(s)	2548	1876	1576	1746	7549
no. of "base" animals	772	471	532	663	2034
no. of animals in the data	691	641	439	433	2204
<b><u>no. of sires :</u></b>					
... in total	1166	722	783	967	3223
... with progeny in the data	180	153	123	150	606
... which are also grand sires	1099	662	738	904	2988
... which also have grandprogeny records	106	90	73	76	345
... paternal half-sib record pairs	5422	5048	2586	1686	14742
... av. no. progeny recs./sire	3.84	4.19	3.57	2.89	3.64
<b><u>no. of dams :</u></b>					
... in total	2135	1440	1340	1584	6040
... with progeny in the data	517	455	328	320	1617
... with own record as well	106	146	78	75	405
... dam-offspring record pairs	134	177	122	108	542
... which are also grand dams	1802	1184	1141	1388	5061
... which also have grandprogeny records	162	190	118	109	579
... with own record as well	19	29	24	18	90
... maternal half-sib record pairs	474	524	312	304	1626
... av. no. progeny recs./dam	1.34	1.41	1.34	1.35	1.36
<b><u>no. of paternal grand sires :</u></b>					
... in total	547	334	386	462	1514
... with progeny in the data	111	93	80	101	385
... quarter-sib record pairs	7628	8276	3882	2312	22098
... av. no. progeny recs./grand sire	6.23	6.89	5.46	4.29	5.72
<b><u>no. of maternal grand sires :</u></b>					
... in total	811	517	526	655	2276
... with progeny in the data	257	197	179	204	831
... quarter-sib record pairs	3166	4200	1506	1318	10244
... av. no. progeny recs./grand sire	2.68	3.19	2.39	2.12	2.62
<b><u>no. of grand sires together :</u></b>					
... in total	1358	851	912	1117	3790
... with progeny in the data	368	290	259	305	1216
... quarter-sib record pairs	10794	12476	5388	3630	32342
... av. no. progeny recs./grand sire	3.75	4.38	3.34	2.84	3.6

**Table A2: Data Structure: Offspring-Parent combinations .....continuation**

<b><u>no. of paternal grand dams :</u></b>					
... in total	727	455	481	608	2042
... with progeny in the data	150	128	108	137	523
... with own record as well	7	12	9	8	36
... grand dam-offspring record pairs	38	42	44	16	140
... quarter-sib record pairs	6196	5770	2924	1928	16818
... av. no. progeny rec.s/grand dam	4.61	5.01	4.05	3.16	4.21
<b><u>no. of maternal grand dams :</u></b>					
... in total	1279	870	790	940	3649
... with progeny in the data	417	350	257	264	1283
... with own record as well	27	32	28	21	108
... grand dam-offspring record pairs	36	48	41	36	161
... quarter-sib record pairs	906	1172	554	444	3162
... av. no. progeny rec.s/grand dam	1.61	1.78	1.55	1.54	1.64
<b><u>no. of grand dams together :</u></b>					
... in total	2006	1325	1271	1548	5691
... with progeny in the data	567	478	365	401	1806
... with own record as well	34	44	37	29	144
... grand dam-offspring record pairs	74	90	85	52	301
... quarter-sib record pairs	7102	6942	3478	2372	19980
... av. no. progeny rec.s/grand dam	2.4	2.64	2.29	2.09	2.38

### III. GLS - solutions and standard errors for age at first kidding BMI

Table A3: GLS - solutions for age at first kidding – Alpine – cumulative milk, fat and protein yield (Basic Model 1).

Milk yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	444.71	4.6879	-395.3713302	261.4500886
10	17	533.24	11.593	-187.283166	238.5301443
11	45	630.38	31.6005	-230.4385425	227.2719436
12	116	685.42	71.8651	-240.9856469	219.5724469
13	123	768.83	75.7636	-234.4358537	223.8126935
14	55	670.47	36.1687	-227.8119984	227.3364079
15	49	751.53	33.326	-230.4119588	227.0660465
16	34	843.38	23.2526	-186.4309312	229.6279602
17	37	828.00	25.2072	-242.475595	228.7979024
18	25	731.12	17.6137	-247.0086723	231.8094311
19	17	731.76	12.0243	-102.9783631	237.9992074
20	16	722.06	11.2347	-108.2006034	238.5937709
21	19	700.74	13.7305	-77.82426799	235.727549
22	35	850.29	24.5031	-104.6272978	229.9617658
23	48	768.31	33.0324	-106.4811983	228.1710899
24	25	780.68	17.9658	-95.11664387	232.9697945
25	13	870.46	9.1318	-122.8316663	243.760182
26	4	1296.50	2.9953	380.9430242	275.0751161
27	3	997.00	2.2041	202.3209974	284.3025362
28	2	868.50	1.988	-51.53754644	305.2117524
29	1	743.00	0.7222	-227.634366	375.0676253

Fat yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	13.43	5.4485	-17.74735654	9.41964989
10	17	18.50	13.4211	-10.2715227	8.57597944
11	45	21.27	35.8982	-11.70527527	8.1577048
12	116	24.11	83.1511	-11.94196197	7.85977535
13	123	26.35	87.5301	-11.94559162	8.0267812
14	55	23.67	41.5074	-11.40210596	8.1577091
15	49	26.87	38.1	-11.39971706	8.16878188
16	34	28.62	26.587	-10.19154965	8.24096638
17	37	29.51	28.7883	-11.01670658	8.21206788
18	25	27.62	20.0139	-9.4405736	8.32444286
19	17	24.55	13.7165	-6.51583819	8.56472254
20	16	23.47	12.8211	-7.85270351	8.57927735
21	19	23.74	15.5243	-6.6166339	8.47866684
22	35	30.47	27.9402	-7.02007765	8.24602629
23	48	27.02	37.7913	-6.19541697	8.19229111
24	25	26.26	20.3751	-5.93870996	8.37244737
25	13	29.08	10.409	-8.44075294	8.77858309
26	4	45.61	3.3598	10.56020476	9.96467602
27	3	33.29	2.4945	3.00795901	10.31856325
28	2	28.70	1.669	-5.77122763	11.13226954
29	1	29.78	0.8264	-9.43263482	13.62240342

Protein yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	12.34	5.2807	-13.43500944	7.88364869
10	17	16.10	13.0215	-7.06622218	7.18061511
11	45	18.75	34.9678	-8.86135597	6.83275432
12	116	20.86	80.621	-9.08676088	6.58722046
13	123	23.33	84.8947	-8.8025611	6.72435579
14	55	20.35	40.3244	-8.26698888	6.83334212
15	49	23.54	37.0592	-8.23551034	6.84273498
16	34	25.82	25.858	-6.57821148	6.90289674
17	37	26.23	28.0017	-7.64833442	6.87851
18	25	23.10	19.4941	-8.05949004	6.97176825
19	17	21.53	13.3501	-5.3268962	7.16960352
20	16	21.32	12.4777	-5.07297026	7.18311081
21	19	20.45	15.1384	-4.62632921	7.09844803
22	35	25.67	27.1954	-4.78232621	6.90846843
23	48	22.98	36.7542	-4.70146462	6.86125837
24	25	23.76	19.8575	-3.40943915	7.01083094
25	13	25.56	10.132	-6.05914741	7.34755629
26	4	39.48	3.2819	10.07607002	8.3300569
27	3	28.93	2.4326	2.98790789	8.62198312
28	2	25.00	1.6304	-3.05995169	9.29178288
29	1	25.72	0.8043	-5.73870644	11.38057579



**Table A4: GLS - solutions for age at first kidding – Toggenburg – cumulative milk, fat and protein yield (Basic Model 1).**

<b>Milk yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	807.00	1.7114	-391.2917858	427.2726539
10	7	639.57	5.6385	-210.8592323	381.1738299
11	30	632.10	24.1932	-171.2867344	360.375272
12	48	633.85	35.6142	-97.55257611	355.5266637
13	65	598.28	49.7293	-202.8812033	353.5664385
14	56	675.95	43.4956	-176.0475173	353.2833735
15	44	912.70	34.5434	-160.9377487	354.4610172
16	45	812.07	35.1264	-165.4415125	353.3062552
17	39	857.95	28.8624	-205.4611471	355.3688512
18	33	832.33	26.5323	-278.1145338	356.8031578
19	36	890.33	29.0794	-129.4420734	355.6885568
20	27	788.48	22.3065	-187.4022325	357.9367071
21	32	932.47	26.1804	-10.15630822	356.4198732
22	36	1024.25	29.1283	91.1895712	355.1936884
23	46	844.33	36.5231	12.62989447	343.8535307
24	51	857.71	39.1412	66.00583568	353.7896046
25	19	1031.95	15.4544	-3.43046683	360.5655829
26	11	688.09	9.1433	-94.64848461	370.2136553
27	8	767.13	6.7478	-264.1949931	372.552618
28	4	773.00	3.3915	-81.9657411	405.901437
29	1	892.00	0.8576	66.50028588	508.4169387
30	1	640.00	0.856	-150.0453375	506.634657
<b>Fat yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	25.48	1.664	-13.9721067	13.9214216
10	7	19.72	5.466	-8.80039945	12.42587751
11	30	20.66	23.3932	-7.41347075	11.75456297
12	48	19.57	34.2677	-5.86175661	11.59245235
13	65	18.95	48.041	-8.80720164	11.53069131
14	56	22.00	42.0141	-6.96170469	11.51756899
15	44	29.24	33.3906	-7.25665466	11.55866844
16	45	25.14	33.9539	-8.66005482	11.52128929
17	39	27.63	27.7631	-8.55876753	11.59049197
18	33	27.45	25.6817	-10.55281629	11.63626596
19	36	30.21	28.2367	-5.50532848	11.59927187
20	27	25.83	21.629	-7.13191406	11.67443354
21	32	29.53	25.3793	-2.40701351	11.62161709
22	36	31.15	28.1706	-1.05755286	11.58248426
23	46	26.59	35.2678	-1.75167627	11.21483489
24	51	27.47	37.7423	-3.95300936	11.53721027
25	19	34.00	14.9764	-0.56568946	11.75558761
26	11	21.99	8.8549	-4.61063809	12.07131673
27	8	24.51	6.5563	-11.17993546	12.14423691
28	4	23.88	3.2902	-5.06927401	13.2335939
29	1	27.96	0.8344	-2.32057773	16.57859491
30	1	20.84	0.833	-8.04314596	16.51178228
<b>Protein yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	21.60	1.7183	-12.57193186	12.06799371
10	7	19.30	5.667	-7.35610799	10.76522011
11	30	18.62	24.3113	-5.97455332	10.17694814
12	48	17.64	35.8167	-4.81005841	10.04051547
13	65	16.91	49.9809	-7.43585151	9.98490376
14	56	19.48	43.716	-6.56370894	9.47740782
15	44	25.96	34.7139	-5.94915636	10.01031519
16	45	22.57	35.2997	-6.47961079	9.9776767
17	39	24.21	29.0273	-7.47895286	10.03565144
18	33	23.66	26.6576	-9.02415666	10.07630162
19	36	25.76	29.2033	-5.09757265	10.04490892
20	27	22.44	22.4059	-7.09504547	10.10816055
21	32	26.58	26.2984	-2.13325497	10.06575112
22	36	29.32	29.2694	0.85265574	10.03101866
23	46	23.75	36.7087	-1.01453819	9.71049246
24	51	24.58	39.3495	-3.08958062	9.99129246
25	19	29.12	15.5248	-1.42864983	10.18297595
26	11	19.75	9.1856	-3.79163227	10.45530706
27	8	21.57	6.7758	-9.13496411	10.52178241
28	4	21.88	3.4063	-3.73262437	11.46335225
29	1	22.58	0.861	-2.00950095	14.35808199
30	1	19.28	0.8593	-4.44146061	14.30886775

**Table A5: GLS - solutions for age at first kidding – Saanen\* – cumulative milk, fat and protein yield (Basic Model 1).**

<b>Milk yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS	
9	4	637.75	3.9126	-191.6243593	334.7012749	
10	10	727.69	15.5423	-172.4834385	281.7392481	
11	36	668.39	34.388	-54.58685765	277.6362111	
12	71	692.17	66.9168	-176.7976161	267.6023693	
13	51	792.47	48.4931	-37.3331266	261.5196254	
14	54	755.81	51.8728	-81.92905627	261.6555731	
15	31	839.32	29.9959	36.83975445	272.3701625	
16	18	926.83	17.3541	-64.18783139	286.8697998	
17	26	1030.92	25.1631	45.79205881	279.0112375	
18	15	896.80	14.6161	56.89121482	284.6747853	
19	8	681.50	7.8236	-125.2980492	300.3517607	
20	19	942.95	18.3809	9.54485536	281.3705533	
21	18	875.44	17.5426	-118.6119798	282.2396675	
22	24	1034.42	23.1776	101.8760297	280.1128314	
23	24	963.42	23.2335	-84.36266718	281.0090128	
24	12	1050.33	11.7216	32.64741472	301.2256958	
25	9	984.22	8.7964	-122.1978501	308.5368664	
26	2	553.00	1.9607	268.0487125	583.9288689	
36	1	1245.00	0.9797	59.46333148	486.1482219	
<b>Fat yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS	
9	4	19.62	3.6119	-4.78672295	11.62430401	
10	10	22.81	14.1958	-5.46150324	9.8320126	
11	36	21.29	30.2252	-2.21758376	9.68169831	
12	71	21.00	57.9952	-6.29838604	9.34850956	
13	51	25.77	42.9019	-2.06024643	9.1493856	
14	54	23.79	46.1367	-3.13862331	9.16405204	
15	31	28.62	27.1948	2.18423904	9.52726863	
16	18	32.63	15.9667	-2.06072532	10.01376142	
17	26	33.73	22.585	2.84057353	9.75202191	
18	15	29.18	13.4668	1.907538	9.93968624	
19	8	22.29	7.2035	-3.1409562	10.47406098	
20	19	29.18	16.7354	-0.05893534	9.82089188	
21	18	28.10	16.0847	-3.10226137	9.84676805	
22	24	34.38	20.8997	6.19870411	9.79599774	
23	24	33.15	21.0307	0.0096412	9.80069414	
24	12	36.00	10.7216	3.40941088	10.49867032	
25	9	31.22	8.0673	-2.69796411	10.73844725	
26	2	21.01	1.8169	9.54625004	20.05168089	
27	1	35.45	0.9179	-2.62220599	16.91558782	
<b>Protein yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS	
9	4	18.56	3.8188	-3.52541529	10.11661457	
10	10	21.12	15.0939	-4.25015266	8.52895344	
11	36	20.10	32.9572	-0.58368724	8.40347357	
12	71	20.47	63.6256	-4.27922486	8.1039478	
13	51	24.01	46.5074	-0.3554086	7.92485625	
14	54	22.38	49.7954	-1.45712098	7.93046669	
15	31	25.57	29.0509	2.50791614	8.2510104	
16	18	27.54	16.965	-0.36653934	8.67974777	
17	26	30.73	24.2739	2.80614532	8.44889875	
18	15	26.95	14.2094	2.48663334	8.61994035	
19	8	21.17	7.6269	-1.55585832	9.08840754	
20	19	27.47	17.8697	1.36305458	8.51432739	
21	18	25.53	17.0523	-2.60803944	8.54173164	
22	24	30.96	22.4342	5.35651359	8.48540863	
23	24	29.00	22.4914	-0.61278371	8.50207418	
24	12	31.56	11.3963	2.92758254	9.11193511	
25	9	29.09	8.5663	-1.91999423	9.32998725	
26	2	17.59	1.9188	10.4813359	17.55149618	
27	1	43.18	0.9627	8.65043233	14.69375872	

\* values of GLS solutions and standard errors for milk are obtained using model 2, because model 1 did not yield in estimate results.

**Table A6: GLS - solutions for age at first kidding – Nubian – cumulative milk, fat and protein yield (Basic Model 1).**

Milk yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS
10	4	595.25	3.1401	-120.1052615	205.5797454
11	20	485.55	15.0486	76.41095554	134.2023422
12	58	508.14	38.5328	94.24617987	120.3776677
13	64	454.05	43.401	43.47458442	119.1266348
14	52	476.58	36.6656	49.31971185	119.160063
15	28	471.89	20.441	78.34586074	127.2282248
16	20	537.20	14.8756	123.2163902	123.0556708
17	17	464.24	11.9666	16.28153801	146.9993114
18	13	503.31	9.6242	167.0878245	146.6781865
19	15	575.13	11.2642	145.1671024	137.2691673
20	20	674.50	14.9041	220.4232811	132.7517816
21	25	435.08	18.5749	21.7179338	121.8455785
22	28	471.86	20.3162	117.423428	113.6029703
23	27	573.96	19.5223	144.0694328	124.657946
24	17	455.88	12.6826	40.65512149	131.4243271
25	9	573.89	6.9017	192.1162466	149.9640843
26	8	496.63	6.1421	187.0434402	156.1045263
27	5	570.60	3.8168	-43.77476015	214.2763268
29	3	507.67	2.1283	209.3485604	263.482596

Fat yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS
10	4	28.66	2.5668	-3.65345336	10.75400976
11	20	22.12	12.1336	4.35752691	7.34365368
12	58	24.11	29.9604	4.44692159	6.72265913
13	64	22.07	33.7404	2.99935789	6.65735844
14	52	23.40	28.6313	3.78006442	6.65086083
15	28	22.99	16.2623	4.92464645	7.03216065
16	20	25.09	11.7742	6.75817085	6.803313
17	17	23.45	9.1501	1.92928812	8.02735026
18	13	24.37	7.5211	9.1628796	8.01555361
19	15	27.05	9.0543	7.42332205	7.51549178
20	20	30.38	11.8474	9.23561731	7.29313389
21	25	18.61	14.7341	0.48720276	6.78057777
22	28	22.85	16.1092	6.47360039	6.41552036
23	27	17.30	15.2817	8.09609558	6.91605339
24	17	21.24	10.0274	2.15962165	7.24458089
25	9	28.46	5.5916	13.1977828	8.11033461
26	8	24.18	4.8923	10.19184421	8.39365334
27	5	21.75	3.0397	-5.37619319	11.25042985
29	3	20.11	1.6257	8.48134055	13.85328796

Protein yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SEERRORS
10	4	21.71	3.1556	-7.04687635	7.84811325
11	20	17.11	15.1285	0.7125846	5.11660809
12	58	18.60	38.7841	1.38680339	4.5866139
13	64	17.07	43.6808	-0.16787463	4.53883765
14	52	17.80	36.8938	0.28561226	4.54030982
15	28	17.83	20.5582	1.68593296	4.8492126
16	20	19.70	14.9613	3.38666287	4.69019645
17	17	18.27	12.0479	0.29210692	5.66489841
18	13	19.28	9.6828	5.07334102	5.59243916
19	15	20.83	11.3255	3.28283664	5.23341179
20	20	24.26	14.9891	5.75828237	5.06067452
21	25	15.57	18.6812	-1.07166436	4.64311844
22	28	17.31	20.4345	2.69097906	4.32690244
23	27	21.48	19.6417	4.14155685	4.75070364
24	17	16.27	12.7558	-0.83592082	5.00955153
25	9	20.16	6.9373	5.59255431	5.71957241
26	8	18.96	6.176	4.98001469	5.9548326
27	5	20.84	3.8381	-2.68418206	8.1793966
29	3	18.25	2.1428	6.93652274	10.05736717

**Table A7: GLS - solutions for breed – All breeds – cumulative milk, fat and protein yield (Basic Model 1)**

<b>Milk yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	740.01	164.83	-373.799	250.8489
Saanen	439	825.68	118.56	-278.0114	254.0316
Toggenburg	641	796.29	124.24	-350.0127	254.9251
Nubian	433	500.61	149.52	-600.0804	252.89
<b>Fat yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	25.74	142.85	-14.96744	9.173017
Saanen	439	26.74	103.65	-12.24453	9.289337
Toggenburg	641	25.46	107.3	-16.03895	9.321726
Nubian	433	23.74	131.89	-16.74097	9.245225
<b>Protein yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	22.48	177.14	-12.10844	7.592172
Saanen	439	24.65	126.83	-9.275795	7.688577
Toggenburg	641	22.64	133.81	-12.05526	7.715746
Nubian	433	18.48	159.12	-16.0279	7.655001

**Table A8: GLS - solutions for age at first kidding – All breeds – cumulative milk, fat and protein yield (Basic Model 1).**

<b>Milk yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	St. ERRORS	
9	13	559.85	0	0	0	
10	44	626.50	35.7115	104.9988841	113.1533001	
11	131	619.11	103.937	140.3621679	103.6097522	
12	293	643.52	214.9626	129.1342407	101.539911	
13	303	669.73	225.7473	127.8323484	102.0810757	
14	217	646.06	167.9759	124.4440885	102.9691289	
15	152	764.58	120.4933	169.8494735	103.8779308	
16	117	791.84	92.9539	186.0862266	104.3342298	
17	119	830.18	91.8389	158.3141177	104.848675	
18	86	764.42	69.714	140.8613215	107.1389257	
19	76	770.67	61.8537	210.1651496	107.3668934	
20	82	783.51	66.8938	219.3012113	107.6762711	
21	94	742.43	77.0638	220.2304077	105.9690547	
22	123	850.98	98.7391	317.3079124	104.5116383	
23	145	788.53	115.5372	259.7774263	104.4394817	
24	105	796.32	83.3922	240.4025032	105.5647202	
25	50	898.92	40.8675	280.9080583	111.9284396	
26	25	713.36	20.9008	340.2520886	124.9464313	
27	16	748.81	13.4331	141.627033	134.8038676	
28	6	804.83	5.0731	238.721936	162.9980251	
29	5	762.20	4.0687	321.9942036	180.7336956	
30	2	766.00	1.6726	310.8628847	269.8264602	
<b>Fat yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	St. ERRORS	
9	13	17.19	0	0	0	
10	44	21.19	34.4576	3.49831273	4.1110276	
11	131	21.27	100.2409	4.16787657	3.76233336	
12	293	22.61	206.4049	3.48747563	3.68757068	
13	303	23.76	217.183	3.54177658	3.70691947	
14	217	23.21	161.804	3.95902816	3.73917288	
15	152	27.20	116.301	5.67726866	3.77224128	
16	117	27.30	89.7539	5.60794915	3.78895203	
17	119	28.95	88.357	5.68751762	3.80718478	
18	86	27.33	67.3703	5.61682467	3.89049607	
19	76	27.49	59.8716	7.39885976	3.89805596	
20	82	27.25	64.6468	6.98155083	3.91027031	
21	94	25.18	74.5529	6.30984589	3.84795044	
22	123	29.70	95.2793	10.04115191	3.79535233	
23	145	27.95	111.4109	9.25316735	3.79242523	
24	105	27.15	80.4404	8.28943357	3.83380077	
25	50	31.22	39.521	10.00844443	4.06465528	
26	25	26.39	20.2239	12.27367613	4.53575303	
27	16	25.29	13.0149	3.37041837	4.89399118	
28	6	25.49	4.9173	7.62016687	5.91393271	
29	5	25.11	3.9176	9.95741502	6.57597795	
30	2	24.40	1.6222	8.72019153	9.80608316	
<b>Protein yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	St. ERRORS	
9	13	15.68	0	0	0	
10	44	18.94	36.3107	2.83147287	3.43513551	
11	131	18.84	105.7154	3.72683457	3.14617171	
12	293	19.79	219.1673	3.155936	3.08315299	
13	303	20.75	229.9325	3.17359483	3.09971295	
14	217	20.02	170.9662	3.33028305	3.12667482	
15	152	23.60	122.5069	4.87926287	3.15423757	
16	117	23.79	94.4901	5.34296322	3.16803117	
17	119	25.41	93.5269	4.84233652	3.18383293	
18	86	23.41	70.8323	4.42626892	3.25332896	
19	76	23.36	62.7993	6.03236752	3.26053289	
20	82	23.83	67.9661	6.05131743	3.2695396	
21	94	22.21	78.2611	5.60017191	3.21783231	
22	123	25.87	100.3977	9.12290797	3.17344543	
23	145	23.94	117.517	7.56839457	3.17137118	
24	105	23.84	84.8092	7.17500028	3.20534135	
25	50	26.57	41.5098	7.94070541	3.39865976	
26	25	22.48	21.2212	10.20255649	3.79463806	
27	16	22.72	13.6309	3.58108251	4.09381283	
28	6	22.92	5.1465	6.89250461	4.95147043	
29	5	24.73	4.1407	11.75953103	5.4830237	
30	2	20.93	1.6967	8.33455886	8.18996763	

#### IV. GLS - solutions and standard errors for age at first kidding BM2

Table A9: GLS - solutions for age at first kidding – Alpine – cumulative milk, fat and protein yield (Basic Model 2)

Milk yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	444.71	4.6487	-401.9812552	264.3391377
10	17	533.24	11.4975	-185.8872128	241.2184201
11	45	630.38	31.3725	-213.8213583	230.1831548
12	116	685.42	71.2899	-223.0562144	222.5263652
13	123	768.83	75.1627	-217.742924	226.6005094
14	55	670.47	35.893	-207.8221231	229.9095706
15	49	751.53	33.0748	-221.8616074	230.3472105
16	34	843.38	23.078	-172.0185182	232.1583685
17	37	828.00	25.0204	-207.616946	231.6304641
18	25	731.12	17.4866	-233.2326285	234.7640456
19	17	731.76	11.9348	-85.49590134	241.1609843
20	16	722.06	11.1506	-92.68110502	241.5556591
21	19	700.74	13.6347	-44.25577289	238.293154
22	35	850.29	24.3211	-79.66367966	232.6227979
23	48	768.31	32.7821	-90.8984461	230.817999
24	25	780.68	17.837	-82.24803049	235.4369849
25	13	870.46	9.0642	-107.7218827	246.6952666
26	4	1296.50	2.9757	-400.9128247	277.4036381
27	3	997.00	2.1885	235.5974046	287.3178856
28	2	868.50	1.4782	-45.43428404	308.0613996
29	1	743.00	0.7165	-176.4512446	380.8609519
Fat yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	13.43	5.1466	-18.51761492	9.65833015
10	17	18.50	12.7007	-10.72430566	8.80227678
11	45	21.27	34.218	-11.7853604	8.39151435
12	116	24.11	78.6224	-12.1171674	8.09849979
13	123	26.35	82.8127	-12.13655007	8.25690094
14	55	23.67	39.3836	-11.42272205	8.38150786
15	49	26.87	36.2238	-11.66110048	8.39564848
16	34	28.62	25.2734	-10.6328847	8.46237223
17	37	29.51	27.3729	-10.92396754	8.44606778
18	25	27.62	19.0752	-9.55029387	8.56137008
19	17	24.55	13.0547	-6.85166231	8.80490905
20	16	23.47	12.2008	-8.01627729	8.8172867
21	19	23.74	14.8263	-6.48669836	8.69788686
22	35	30.47	26.5953	-7.03117912	8.47468502
23	48	27.02	35.9213	-6.49676606	8.41529431
24	25	26.26	19.4385	-6.16642982	8.58911579
25	13	29.08	9.9089	-8.70804697	9.00667896
26	4	45.61	3.2186	10.30796123	10.16998853
27	3	33.29	2.3823	3.36837662	10.55213614
28	2	28.70	1.599	-6.45190486	11.34430489
29	1	29.78	0.7862	-9.09616641	13.98849673
Protein yield					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	7	12.34	5.1015	-14.06333225	8.02519839
10	17	16.10	12.5923	-7.42822585	7.31469518
11	45	18.75	33.9638	-8.85233125	6.97392118
12	116	20.86	77.952	-8.98974735	6.73146185
13	123	23.33	82.1142	-8.71497386	6.86234967
14	55	20.35	39.0669	-8.04213721	6.96562338
15	49	23.54	35.9411	-8.32089682	6.97752336
16	34	25.82	25.0759	-6.56606983	7.03294354
17	37	26.23	27.1607	-7.05829217	7.01914079
18	25	23.10	18.9332	-8.09658825	7.11489094
19	17	21.53	12.9545	-5.30089837	7.31651342
20	16	21.32	12.1069	-4.98702983	7.32695432
21	19	20.45	14.7203	-4.05635163	7.22775644
22	35	25.67	26.3919	-4.46844855	7.0435289
23	48	22.98	35.6395	-4.66724881	6.99364764
24	25	23.76	19.2961	-3.43260756	7.13771215
25	13	25.56	9.8333	-6.1162289	7.48423839
26	4	39.48	3.1971	10.1491612	8.44782775
27	3	28.93	2.3652	3.55669314	8.76375427
28	2	25.00	1.5883	-3.3025576	9.41943694
29	1	25.72	0.7801	-5.04756756	11.61765512

**Table A10: GLS - solutions for age at first kidding – Toggenburg – cumulative milk, fat and protein yield (Basic Model 2).**

<b>Milk yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	807.00	1.6853	-311.6846997	428.6998724
10	7	639.57	5.5323	-101.5943068	383.3615281
11	30	632.10	23.7513	-105.1188357	362.4880319
12	48	633.85	34.8652	-36.99047433	357.7302825
13	65	598.28	48.7934	-149.0928848	355.3108252
14	56	675.95	42.6748	-107.681022	354.4786436
15	44	912.70	33.9061	-98.11557215	356.1827552
16	45	812.07	34.4791	-120.9978702	355.1738795
17	39	857.95	28.2514	-148.8173132	357.0614225
18	33	832.33	26.0627	-219.8999287	358.7652491
19	36	890.33	28.6145	-66.19669385	357.6121982
20	27	788.48	21.9331	-161.0188251	359.283163
21	32	932.47	25.7382	39.54502555	357.8523709
22	36	1024.25	28.5995	153.269577	357.199099
23	46	844.33	35.8293	65.86124908	345.6336915
24	51	857.71	38.3658	5.17119403	356.0859474
25	19	1031.95	15.1905	62.87441176	362.2352708
26	11	688.09	8.9844	7.21229305	374.3303929
27	8	767.13	6.6424	-168.732349	375.4511619
28	4	773.00	3.3358	-48.21035389	408.4759554
29	2	766.00	1.6504	88.96317008	456.3398412
<b>Fat yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	25.48	1.6747	-11.11202903	13.95839038
10	7	19.72	5.4896	-5.04138904	12.48346131
11	30	20.66	23.5732	-5.23010812	11.80517403
12	48	19.57	34.5672	-4.18791006	11.64928394
13	65	18.95	48.4187	-7.12844076	11.57110609
14	56	22.00	42.3458	-4.82213585	11.54336576
15	44	29.24	33.6497	-5.24832939	11.59927833
16	45	25.14	34.2188	-7.45278619	11.5664998
17	39	27.63	28.0079	-6.72813745	11.62830635
18	33	27.45	25.8734	-8.78211658	11.68350252
19	36	30.21	28.4268	-3.37804422	11.64588083
20	27	25.83	21.7821	-6.53433761	11.70075702
21	32	29.53	25.5598	-0.8045539	11.65343033
22	36	31.15	28.3863	0.75301042	11.63238376
23	46	26.59	35.55	-0.21102309	11.25624971
24	51	27.47	38.0553	-1.67375454	11.59613423
25	19	34.00	15.0841	1.70545333	11.79607166
26	11	21.99	8.9201	-1.39857084	12.18986839
27	8	24.51	6.5997	-8.30245407	12.22552777
28	4	23.88	3.3132	-3.63325003	13.30162913
29	2	24.40	1.6396	-0.98066685	14.86156636
<b>Protein yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTIONS	ST. ERROR
9	2	21.60	1.6832	-10.30635861	12.12778468
10	7	19.30	5.5237	-4.4798783	10.84540025
11	30	18.62	23.7152	-4.12650368	10.25513175
12	48	17.64	34.8048	-3.23242752	10.12036431
13	65	16.91	48.7174	-5.96264615	10.05202402
14	56	19.48	42.6082	-4.73421597	10.02836853
15	44	25.96	33.8542	-4.19857607	10.07665258
16	45	22.57	34.4264	-5.19686993	10.04812375
17	39	24.21	28.202	-5.87841491	10.1015842
18	33	23.66	26.0244	-7.45174713	10.14973484
19	36	25.76	28.5766	-3.3519796	10.11710172
20	27	22.44	21.9026	-6.29503268	10.16445515
21	32	26.58	25.7021	-0.84968423	10.12384841
22	36	29.32	28.5564	2.39831597	10.10540682
23	46	23.75	35.7728	0.37766169	9.77830116
24	51	24.58	38.3029	-1.13662973	10.07391558
25	19	29.12	15.169	0.49217708	10.24782853
26	11	19.75	8.9714	-1.05471607	10.58999255
27	8	21.57	6.6338	-6.54121268	10.62155221
28	4	21.88	3.3312	-2.37520351	11.5559581
29	2	20.93	1.6482	0.62500988	12.91026848

**Table A11: GLS - solutions for age at fist kidding – Saanen – cumulative milk\*, fat and protein yield (Basic Model 2).**

<b>Milk yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	ST. ERRORS	
9	4	637.75	3.886	-160.0833005	372.9799019	
10	10	727.69	15.4139	-151.2908533	323.0575719	
11	30	608.39	33.9501	-66.47834972	306.5343156	
12	71	692.17	65.8906	-168.0520666	304.5238606	
13	51	792.47	47.8562	-37.54138785	300.343294	
14	54	755.81	51.3098	-66.60464515	301.3446187	
15	31	839.32	29.7223	34.97574906	309.9055441	
16	18	926.83	17.1793	-80.60845059	319.6323591	
17	26	1030.92	24.9247	19.75901849	314.6219084	
18	15	896.80	14.5073	68.50468624	323.3216175	
19	8	681.50	7.7713	-107.8553063	345.3638302	
20	19	942.95	18.2021	4.13600227	319.0501747	
21	18	875.44	17.4124	-117.3900562	317.7196096	
22	24	1034.42	22.9469	101.7354561	317.3941239	
23	24	963.42	23.0139	-88.74824768	319.5356977	
24	12	1050.33	11.637	31.95328076	337.5201918	
25	9	984.22	8.7351	-108.8056678	340.9243224	
26	2	553.00	1.9484	276.5150718	599.6846001	
29	1	1245.00	0.9732	109.8960994	519.7762990	

<b>Fat yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	ST. ERRORS	
9	4	19.62	3.544	-7.07577368	12.91032227	
10	10	22.81	13.9109	-8.44990241	11.22934799	
11	30	21.29	29.408	-5.26285036	10.66590808	
12	71	21.00	56.4146	-9.04173847	10.66305603	
13	51	25.77	41.8603	-5.14738292	10.44936739	
14	54	23.79	45.0437	-5.76220865	10.4931093	
15	31	28.62	26.6161	-0.70932458	10.78787923	
16	18	32.63	15.6531	-5.1156252	11.10274578	
17	26	33.73	22.059	-0.33358007	10.94334437	
18	15	29.18	13.1487	-0.6714084	11.24046876	
19	8	22.29	7.0634	-5.78808251	11.975903	
20	19	29.18	16.3777	-2.98699274	11.0723575	
21	18	28.10	15.774	-6.73454398	11.04915892	
22	24	34.38	20.4203	3.42699391	11.03460075	
23	24	33.15	20.5736	-3.18625706	11.08864296	
24	12	36.00	10.4997	0.33736321	11.72257076	
25	9	31.22	7.9023	-5.29852846	11.83486781	
26	2	21.01	1.7821	8.12186831	20.56350488	
27	1	35.45	0.9026	-3.95619873	18.00465075	

<b>Protein yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	ST. ERRORS	
9	4	18.56	3.6026	-3.86032849	11.32010117	
10	10	21.12	14.1569	-5.12319912	9.83827408	
11	30	20.10	30.1124	-2.10379776	9.34384207	
12	71	20.47	57.7749	-5.27147366	9.2876661	
13	51	24.01	42.7575	-1.70238312	9.15380568	
14	54	22.38	45.9859	-2.28061815	9.19002775	
15	31	25.57	27.1155	1.24503161	9.44946337	
16	18	27.54	15.9238	-1.93034471	9.72609686	
17	26	30.73	22.5129	0.90241045	9.58600076	
18	15	26.95	13.3716	1.30623396	9.8484863	
19	8	21.17	7.1845	-2.49481713	10.49593849	
20	19	27.47	16.6865	0.08174683	9.70259208	
21	18	25.53	16.0423	-3.77069217	9.67994143	
22	24	30.96	20.834	4.15705708	9.66707715	
23	24	29.00	20.9681	-1.96298738	9.71713123	
24	12	31.56	10.6915	1.8368603	10.27119086	
25	9	29.09	8.0449	-2.56046563	10.37123369	
26	2	17.59	1.8122	9.99400815	18.0509649	
27	1	43.18	0.9198	9.22618735	15.78395342	

\* values of GLS solutions and standard errors for milk are obtained using model 2, because model 1 did not yield in estimates.



**Table A12: GLS - solutions for age at fist kidding – Nubian – cumulative milk, fat and protein yield (Basic Model 2).**

<b>Milk yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS
10	4	595.25	3.0133	-156.014924	233.654053
11	20	485.55	14.396	45.21199757	172.9114376
12	58	508.14	36.5208	58.94827095	157.1638844
13	64	454.05	41.1509	9.66868908	154.7520419
14	52	476.58	34.8192	17.85259782	157.0593474
15	28	471.89	19.4899	44.47184112	165.650001
16	20	537.20	14.1772	91.63980707	157.8315571
17	17	464.24	11.3112	-18.29851952	181.8179742
18	13	503.31	9.1473	115.9760754	182.8288572
19	15	575.13	10.7648	108.1949182	172.7632053
20	20	674.50	14.2118	186.9190549	166.4682175
21	25	435.08	17.7084	-3.60267317	159.6851364
22	28	471.86	19.3566	84.25139887	152.9388747
23	27	573.96	18.554	119.2031391	157.4509158
24	17	455.88	12.0848	8.54018304	169.0061534
25	9	573.89	6.6101	180.6750576	184.0776687
26	8	496.63	5.8636	174.0618933	187.2719158
27	5	570.60	3.6426	-59.4836635	239.4962736
29	3	507.67	2.0116	146.1778027	282.5327831

<b>Fat yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS
10	4	28.66	2.4817	-6.54046645	12.19471665
11	20	22.12	11.7069	1.70782851	9.27513195
12	58	24.11	28.7771	1.72801179	8.54140889
13	64	22.07	32.3985	0.33016017	8.41103158
14	52	23.40	27.4986	1.28287754	8.51601928
15	28	22.99	15.6645	2.31577197	8.93571085
16	20	25.09	11.3255	4.37561587	8.5259395
17	17	23.45	8.7616	-0.46045953	9.73705502
18	13	24.37	7.2207	5.59640617	9.82227212
19	15	27.05	8.7346	4.4223705	9.28915806
20	20	30.38	11.4083	6.61342282	8.97612345
21	25	18.61	14.1793	-1.90338076	8.66096413
22	28	22.85	15.5096	3.8813266	8.34997888
23	27	27.30	14.6798	6.0043171	8.5486407
24	17	21.24	9.6437	-0.4386556	9.11972284
25	9	28.46	5.3987	11.69167446	9.82669794
26	8	24.18	4.7093	8.70201911	9.95824732
27	5	21.75	2.9265	-7.6100007	12.51979329
29	3	20.11	1.5563	4.68644058	14.78566139

<b>Protein yield</b>					
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS
10	4	21.71	3.0308	-7.13082694	8.91538601
11	20	17.11	14.486	0.84099863	6.59141441
12	58	18.60	36.7941	1.28814369	5.98823198
13	64	17.07	41.4575	-0.21707565	5.89633556
14	52	17.80	35.0719	0.39655841	5.98480385
15	28	17.83	19.6204	1.73040888	6.3133129
16	20	19.70	14.2733	3.45703413	6.0151126
17	17	18.27	11.4007	0.36366658	6.93140324
18	13	19.28	9.2129	4.44772519	6.96902266
19	15	20.83	10.8335	3.06309839	6.58511987
20	20	24.26	14.307	5.67682249	6.34461595
21	25	15.57	17.8277	-0.83606799	6.08477977
22	28	17.31	19.4882	2.76199546	5.82625301
23	27	21.48	18.6869	4.38703801	5.99942649
24	17	16.27	12.1671	-0.7649315	6.44113093
25	9	20.16	6.6503	6.50212738	7.0182947
26	8	18.96	5.9021	5.69971282	7.14115031
27	5	20.84	3.6667	-2.69772601	9.13793896
29	3	18.25	2.0276	5.10034463	10.77964873

**Table A13: GLS - solutions for breed – All breeds – cumulative milk, fat and protein yield (Basic Model 2).**

<b>Milk yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	740.01	0	0	0
Saanen	439	825.68	110.6955	86.105529	52.36280324
Toggenburg	641	796.29	115.257	17.90404726	59.57778728
Nubian	433	500.61	140.2825	-236.1517426	50.42568071
<b>Fat yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	25.74	0	0	0
Saanen	439	26.74	97.883	2.56282649	1.95832369
Toggenburg	641	25.46	100.861	-1.18516168	2.2203795
Nubian	433	23.74	124.9537	-1.82685791	1.88578661
<b>Protein yield</b>					
<b>BREED</b>	<b>NREC</b>	<b>MEAN</b>	<b>DIAGONAL</b>	<b>GLS - SOLUTION</b>	<b>St.ERRORS</b>
Alpine	691	22.48	0	0	0
Saanen	439	24.65	118.221	2.61136517	1.56598083
Toggenburg	641	22.64	123.8515	-0.08740305	1.78521144
Nubian	433	18.48	149.1345	-4.16368184	1.50804139

**Table A14: GLS - solutions for age at first kidding – All breeds – cumulative milk, fat and protein yield (Basic Model 2).**

<b>Milk yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS	
9	13	559.85	0	0		0
10	44	626.50	35.0812	108.7309431		113.3493888
11	131	619.11	102.0755	147.5725565		103.8166543
12	293	643.52	210.6245	134.0908547		101.7376267
13	303	669.73	221.4136	135.5370466		102.2844494
14	217	646.66	164.8609	133.0992055		103.1970595
15	152	764.58	118.3832	177.6398461		104.0414841
16	117	791.84	91.3436	193.2493943		104.5484779
17	119	830.18	90.081	167.9275703		105.0566716
18	86	764.42	68.5367	149.3436862		107.3949109
19	76	770.67	60.8582	216.8631316		107.5681159
20	82	783.51	65.7651	227.1976913		107.9053091
21	94	742.43	75.8028	227.8742565		106.1793561
22	123	850.98	96.9986	325.7227983		104.7111348
23	145	788.53	113.4608	265.5650454		104.5799961
24	105	796.32	81.9066	249.2267838		105.7704821
25	50	898.92	40.1912	286.4176723		112.0944742
26	25	713.36	20.5616	354.8100012		125.3509054
27	16	748.81	13.2236	156.0186676		135.1013687
28	6	804.83	4.9951	241.30966		163.1263498
29	5	702.20	3.9928	347.3871962		181.8080834
30	2	766.00	1.6473	350.4391041		271.0977378
<b>Fat yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS	
9	13	17.19	0	0		0
10	44	21.19	33.8994	3.63054296		4.11805999
11	131	21.27	98.6045	4.49914418		3.76985178
12	293	22.61	202.683	3.70260071		3.69476231
13	303	23.76	213.4393	3.8514002		3.71432283
14	217	23.21	159.0871	4.32130217		3.74751565
15	152	27.20	114.4417	5.989386		3.778212
16	117	27.30	88.334	5.85904403		3.79670511
17	119	28.95	86.8264	6.04310162		3.81477809
18	86	27.33	66.3252	5.93533264		3.89988293
19	76	27.49	58.9871	7.6808491		3.90540464
20	82	27.25	63.6452	7.24504695		3.91850431
21	94	25.18	73.4323	6.61726785		3.85558829
22	123	29.70	93.743	10.37039108		3.80261109
23	145	27.95	109.5803	9.47378374		3.79762166
24	105	27.15	79.1311	8.6081592		3.84126337
25	50	31.22	38.9204	10.20946273		4.07077563
26	25	26.39	19.9201	12.70022944		4.55054291
27	16	25.29	12.8269	3.87523484		4.9047283
28	6	25.49	4.8472	7.59335		5.9189808
29	5	25.11	3.8502	10.80951234		6.61379342
30	2	24.40	1.5997	9.689078		9.85139041
<b>Protein yield</b>						
AGE	NREC	MEAN	DIAGONAL	GLS - SOLUTION	SE ERRORS	
9	13	15.68	0	0		0
10	44	18.94	35.686	2.93267864		3.44228266
11	131	18.84	103.8615	3.9293164		3.15356893
12	293	19.79	214.7854	3.28376426		3.09023289
13	303	20.75	225.5706	3.38081261		3.10697669
14	217	20.02	167.8493	3.55969729		3.13467205
15	152	23.60	120.4078	5.10246492		3.16030441
16	117	23.79	92.8887	5.55220479		3.17566429
17	119	25.41	91.7674	5.09343039		3.19126509
18	86	23.41	69.6664	4.65113665		3.26221345
19	76	23.36	61.8135	6.22156248		3.26780162
20	82	23.83	66.8482	6.28298067		3.27768586
21	94	22.21	77.0128	5.8143691		3.22536088
22	123	25.87	98.6686	9.35656868		3.18061302
23	145	23.94	115.4531	7.71543791		3.17672184
24	105	23.84	83.332	7.41892842		3.21271601
25	50	26.57	40.8401	8.10085621		3.40486046
26	25	22.48	20.8872	10.59563896		3.80826237
27	16	22.72	13.4246	3.99208342		4.10436501
28	6	22.92	5.0699	6.98501367		4.95709742
29	5	24.73	4.0656	12.49366801		5.51774583
30	2	20.93	1.6716	9.44670094		8.23159835

## V. GLS - solutions for phantom group

Table A15. GLS - solutions for group coefficients by trait and breed

	SOLUTION	S.ERROR	SOLUTION	S.ERROR	SOLUTION	S.ERROR
<b>ALPINE</b>	<b>Milk</b>		<b>Fat</b>		<b>Protein</b>	
<b>Sire</b>						
1	-1602.093072	2506.879034	-41.16992118	90.80570284	-60.99999799	75.51367336
2	-935.1360739	2315.296949	-25.523587055	83.7938149	-44.62911917	69.68885095
3	-1103.023638	2202.385294	-17.86803235	79.807023	-38.94172454	66.36526876
4	-902.8376413	1819.399941	-28.71312126	65.62991219	-24.80064851	54.59890362
<b>Dam</b>						
1	-1008.977752	2155.708152	-14.08188356	78.04722616	-8.272808534	64.90579954
2	-1898.864016	1967.219027	-42.61388948	71.13282421	-32.42499023	59.16210309
3	-1223.514111	1840.490634	-32.44457875	66.02417357	-23.85668172	55.4065179
4	-1128.444935	1524.639344	-22.70524711	54.92718616	-28.96422607	45.70028557
<b>TOGGENBURG</b>	<b>Milk</b>		<b>Fat</b>		<b>Protein</b>	
<b>Sire</b>						
1	1709.799224	2685.010907	47.72472249	87.63078845	38.83305126	75.99457193
2	1334.204675	2366.138268	31.83506671	77.19444011	33.95156975	66.96426248
3	1407.593547	2260.270674	38.18691873	73.72423411	46.43881441	63.96521965
4	111.4322655	1881.973395	20.77796209	61.39153039	19.19160447	53.26059684
<b>Dam</b>						
1	-715.6802882	2247.286433	11.46415101	73.36648409	13.03852804	63.60936524
2	-784.9204342	1826.440113	10.26131331	59.59582518	-1.440212032	51.69176299
3	-23.50374905	1773.60334	24.45859744	57.860796	13.77130174	50.19445254
4	1504.831934	1799.387575	60.18898327	58.69726118	49.2128124	50.92333754
<b>SAANEN</b>	<b>Milk*</b>		<b>Fat</b>		<b>Protein</b>	
<b>Sire</b>						
1	524.6190275	3263.744931	-36.80054714	115.193069	-8.668273888	100.5905034
2	159.7959565	2729.359486	-49.09035783	96.57310604	-11.03503544	84.28537429
3	-671.2682011	2539.652034	-80.80362014	89.88335995	-38.74239077	78.47918671
4	-250.7677239	2279.604735	-44.54442495	81.04780349	-26.99154767	70.72246465
<b>Dam</b>						
1	-672.3801494	2801.045039	-25.30228358	100.0520451	-31.51849157	87.26693278
2	-608.54452	2430.252938	-16.59247049	86.49459318	-33.64081123	75.46331317
3	150.8352978	2327.243778	2.260789949	82.84832579	-13.33224762	72.27396872
4	-387.3936315	2045.78577	-26.05284285	73.02924326	-23.9349857	63.68678195
<b>NUBIAN</b>	<b>Milk</b>		<b>Fat</b>		<b>Protein</b>	
<b>Sire</b>						
1	610.8402887	3235.161708	53.21143114	172.3564645	35.77826672	123.3503438
2	-327.6011111	2703.633834	1.307011673	142.8683736	-17.6080816	103.1179356
3	-400.9499221	2340.808144	-23.87237014	123.6235888	-21.04381487	89.28186648
4	-209.7564226	1791.113187	-18.02793061	94.29281347	-14.15720094	68.32395857
<b>Dam</b>						
1	-622.076635	1832.20517	-66.00544464	98.9541813	-47.50338535	69.82387914
2	115.6706275	1449.778372	-24.05884186	77.22669528	-9.293988346	55.28001506
3	698.9056377	1362.351605	27.37591382	72.06204099	15.12322000	51.95971067
4	85.77920409	1623.105831	-0.174030088	85.8181734	-8.763709815	61.90502984
<b>ALL BREEDS</b>	<b>Milk</b>		<b>Fat</b>		<b>Protein</b>	
<b>Sire</b>						
1	490.3966334	1246.091435	-5.569675152	45.81137414	12.9592568	37.61155983
2	631.5841334	1102.548028	-2.552332555	40.47983426	16.10881604	33.30288039
3	636.7813238	995.8321011	3.297007884	36.52226975	19.64948472	30.09702336
4	352.3785303	771.1481461	-0.513637582	28.31062322	12.52595621	23.29408898
<b>Dam</b>						
1	112.6628674	938.7044249	15.17696679	34.60065229	9.207002376	28.29458865
2	-168.0403338	751.5016205	8.167316346	27.67959787	1.878806008	22.66112706
3	112.7823534	647.9724379	8.280917502	23.86053873	7.045847755	19.54183436
4	506.1819854	688.9707307	16.13690414	25.32848456	16.43769912	20.79674857

\* Estimates for age effects on milk are taken from model 2 of basic model 1 because model 1 did not yield in estimates.

**VI. Estimates for statistically significant test (Goodness of fit for the model)**

**Table A16. Estimates for Model 2,  $\sigma^2_M$  set to zero. Significance test – Alpine**

Milk yield	Basic Model 1			Basic Model 2		
	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	26329.41	19135.87	26329.32	26934.65	15317.57	26934.66
$\sigma^2_M$	-	6831.1	0	-	10002.56	0
$\sigma^2_E$	60521.12	61128.84	60521.19	60124.84	60689.72	60124.83
$\sigma^2_P$	86850.53	87095.81	86850.51	87059.49	86009.85	87059.50
$h^2$	0.3032	0.2197	0.3032	0.3094	0.1781	0.3094
$m^2$	-	0.0784	0	-	0.1163	0
Log L	-4375.160328	-5466.766474	-5467.216161	-4167.172493	-5410.504087	-5411.382603
<b>-2(<math>H_0 - H_A</math>)</b>			<b>0.8994</b>			<b>1.7572</b>
Fat yield	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	21.51	15.79	21.52	27.24	19.86	27.24
$\sigma^2_M$	-	5.58	0	-	7.40	0
$\sigma^2_E$	93.41	92.8	93.41	90.17	89.81	90.17
$\sigma^2_P$	114.92	114.16	114.92	117.41	117.08	117.41
$h^2$	0.1872	0.1383	0.1872	0.2320	0.1697	0.2320
$m^2$	-	0.0488	0	-	0.0632	0
Log L	-2672.44966	-3764.330634	-3764.505499	-2493.673349	-3737.612126	-3737.883459
<b>-2(<math>H_0 - H_A</math>)</b>			<b>0.3496</b>			<b>0.5426</b>
Protein yield	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	16.98	10.1	16.98	19.34	8.89	19.34
$\sigma^2_M$	-	6.9	0	-	10.10	0
$\sigma^2_E$	63.15	62.64	63.15	61.64	61.92	61.64
$\sigma^2_P$	80.13	79.64	80.13	80.98	80.92	80.98
$h^2$	0.2119	0.1268	0.2119	0.2389	0.1099	0.2389
$m^2$	-	0.0887	0	-	0.1249	0
Log L	-2566.942844	-3669.432024	-3669.998677	-2398.888016	-3642.029984	-3643.098125
<b>-2(<math>H_0 - H_A</math>)</b>			<b>1.1332</b>			<b>2.1364</b>

$$\chi^2_{1.0995} = 0.0000393$$

$$\chi^2_{1.0950} = 0.00393$$

$$\chi^2_{1.0500} = 0.455$$

$$\chi^2_{1.0050} = 3.84$$

$$\chi^2_{1.0005} = 7.88$$

$$\chi^2_{1.0990} = 0.000157$$

$$\chi^2_{1.0900} = 0.0158$$

$$\chi^2_{1.0250} = 1.32$$

$$\chi^2_{1.0025} = 5.02$$

$$\chi^2_{1.0975} = 0.000982$$

$$\chi^2_{1.0750} = 0.102$$

$$\chi^2_{1.0100} = 2.71$$

$$\chi^2_{1.0010} = 6.63$$

[from Steel and Torrie, 1980]

Table A17. Estimates for Model 2,  $\sigma^2_M$  set to zero. Significance test – Toggenburg

Milk	Basic Model 1			Basic Model 2		
	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	20323.99	18401.25	20323.98	22268.37	22126.35	22268.31
$\sigma^2_M$	-	1144.79	0	-	9.13	0
$\sigma^2_E$	98765.89	99017.99	98765.91	96604.73	96704.34	96604.78
$\sigma^2_P$	119089.89	118564.03	119089.89	118873.10	118839.82	118873.09
$h^2$	0.1707	0.1552	0.1707	0.1873	0.1862	0.1873
$m^2$	-	0.0097	0	-	0.0001	0
Log L	-3939.714968	-4704.760849	-4704.768404	-3797.473109	-4652.934982	-4652.934864
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>0.0152</b>			<b>0.0002</b>		
Fat	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	25.53	7.59	25.53	24.49	10.79	24.49
$\sigma^2_M$	-	13.59	0	-	10.62	0
$\sigma^2_E$	101.48	104.96	101.48	101.67	103.74	101.67
$\sigma^2_P$	127.01	126.15	127.01	126.16	125.16	126.16
$h^2$	0.2010	0.0602	0.201	0.1941	0.0862	0.1941
$m^2$	-	0.1078	0	-	0.0848	0
Log L	-2271.514742	-3035.649869	-3036.568178	-2153.460898	-3008.412123	-3008.922656
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>1.8366</b>			<b>1.021</b>		
Protein	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	15.78	10.66	15.78	17.96	17.92	17.96
$\sigma^2_M$	-	3.14	0	-	0.061	0
$\sigma^2_E$	79.16	80.07	79.16	77.20	76.97	77.20
$\sigma^2_P$	94.94	93.88	94.94	95.16	94.95	95.16
$h^2$	0.1663	0.1135	0.1663	0.1887	0.1887	0.1887
$m^2$	-	0.0335	0	-	0.0006	0
Log L	-2202.757769	-2967.734426	-2967.811205	-2086.115286	-2941.577182	-2941.577044
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>0.1536</b>			<b>0.0002</b>		

$$\chi^2_{1.0.995} = 0.0000393$$

$$\chi^2_{1.0.950} = 0.00393$$

$$\chi^2_{1.0.500} = 0.455$$

$$\chi^2_{1.0.050} = 3.84$$

$$\chi^2_{1.0.005} = 7.88$$

$$\chi^2_{1.0.990} = 0.000157$$

$$\chi^2_{1.0.900} = 0.0158$$

$$\chi^2_{1.0.250} = 1.32$$

$$\chi^2_{1.0.025} = 5.02$$

$$\chi^2_{1.0.975} = 0.000982$$

$$\chi^2_{1.0.750} = 0.102$$

$$\chi^2_{1.0.100} = 2.71$$

$$\chi^2_{1.0.010} = 6.63$$

[from Steel and Torrie, 1980]

**Table A18. Estimates for Model 2,  $\sigma^2_M$  set to zero. Significance test – Saanen**

Milk	Basic Model 1			Basic Model 2		
	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	f*	0.93	f*	f*	1.80	f*
$\sigma^2_M$	-	2307.97	f	-	5861.61	f
$\sigma^2_E$	f	129676.75	f	f	129571.76	f
$\sigma^2_P$	f	131985.65	f	f	135435.16	f
$h^2$	f	0.0000070	f	f	0.000013	f
$m^2$	-	0.0174	f	-	0.0433	f
Log L	f	-3194.788771	f	f	-3139.706979	f
$-2[H_0 - H_A]$			f			f
Fat	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	14.89	0.0065	14.89	18.28	0.04	18.28
$\sigma^2_M$	-	13.96	0	-	16.21	0
$\sigma^2_E$	143.6	143.91	143.6	143.75	145.05	143.75
$\sigma^2_P$	158.49	157.87	158.49	162.03	161.30	162.03
$h^2$	0.0939	0.00004	0.0939	0.1128	0.0002	0.1128
$m^2$	-	0.0884	0	-	0.1005	0
Log L	-1589.723288	-2267.572374	-2267.8223	-1561.013863	-2238.874601	-2239.112875
$-2[H_0 - H_A]$			0.5			0.4764
Protein	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	4.85	0.0021	4.85	12.01	0.0063	12.01
$\sigma^2_M$	-	8.02	0	-	10.08	0
$\sigma^2_E$	115.28	112.47	115.28	112.43	113.57	112.43
$\sigma^2_P$	120.13	120.5	120.13	124.43	123.65	124.43
$h^2$	0.0404	1.77167E-05	0.0404	0.0965	0.00005	0.0965
$m^2$	-	0.0666	0	-	0.0815	0
Log L	-1553.210892	-2231.103234	-2231.309903	-1526.308188	-2204.259897	-2004.407200
$-2[H_0 - H_A]$			0.4134			0.2948

\* = estimation failed

$$\chi^2_{1.0995} = 0.0000393$$

$$\chi^2_{1.0950} = 0.00393$$

$$\chi^2_{1.0500} = 0.455$$

$$\chi^2_{1.0050} = 3.84$$

$$\chi^2_{1.0005} = 7.88$$

$$\chi^2_{1.0990} = 0.000157$$

$$\chi^2_{1.0900} = 0.0158$$

$$\chi^2_{1.0250} = 1.32$$

$$\chi^2_{1.0025} = 5.02$$

$$\chi^2_{1.0975} = 0.000982$$

$$\chi^2_{1.0750} = 0.102$$

$$\chi^2_{1.0100} = 2.71$$

$$\chi^2_{1.0010} = 6.63$$

[from Steel and Torrie, 1980]

**Table A19. Estimates for Model 2,  $\sigma^2_M$  set to zero. Significance test – Nubian**

Milk	Basic Model 1			Basic Model 2		
	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	14728.37	2.64	14727.83	17630.38	0.51	17630.22
$\sigma^2_M$	-	16991.28	0	-	17889.33	0
$\sigma^2_E$	42825.46	41221.79	42825.87	41786.29	41677.47	41786.41
$\sigma^2_P$	57553.84	58215.72	57553.71	59416.67	59567.31	59416.63
$h^2$	0.2559	0.000045	0.2559	0.2967	0.000009	0.2967
$m^2$	-	0.2919	0	-	0.3003	0
Log L	-2405.73259	-3193.83786	-3195.972899	-2351.909154	-3139.884979	-3142.149467
$-2[H_0 - H_A]$			4.27			4.529
Fat	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	69.46	19.9	69.46	75.72	18.22	75.72
$\sigma^2_M$	-	46.86	0	-	51.05	0
$\sigma^2_E$	89.36	91.84	89.36	87.75	94.46	87.75
$\sigma^2_P$	158.82	158.6	158.82	163.47	163.74	163.47
$h^2$	0.4373	0.1255	0.4373	0.4632	0.1113	0.4632
$m^2$	-	0.2955	0	-	0.3118	0
Log L	-1638.97518	-2426.99957	-2429.21549	-1608.597984	-2396.421798	-2398.838296
$-2[H_0 - H_A]$			4.4218			4.8344
Protein	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	21.05	0.0001094	21.05	25.18	0.0035	25.18
$\sigma^2_M$	-	25.6	0	-	26.93	0
$\sigma^2_E$	62.83	59.24	62.83	61.31	59.75	61.31
$\sigma^2_P$	83.87	84.83	83.87	86.49	86.68	86.49
$h^2$	0.2509	1.289E-06	0.2509	0.2911	0.00004	0.2911
$m^2$	-	0.3017	0	-	0.3106	0
Log L	-1563.37809	-2350.80603	-2353.618399	-1535.572401	-2322.905296	-2325.812714
$-2[H_0 - H_A]$			5.6248			5.819

$$\chi^2_{1.0.995} = 0.0000393$$

$$\chi^2_{1.0.950} = 0.00393$$

$$\chi^2_{1.0.500} = 0.455$$

$$\chi^2_{1.0.050} = 3.84$$

$$\chi^2_{1.0.005} = 7.88$$

$$\chi^2_{1.0.990} = 0.000157$$

$$\chi^2_{1.0.900} = 0.0158$$

$$\chi^2_{1.0.250} = 1.32$$

$$\chi^2_{1.0.025} = 5.02$$

$$\chi^2_{1.0.975} = 0.000982$$

$$\chi^2_{1.0.750} = 0.102$$

$$\chi^2_{1.0.100} = 2.71$$

$$\chi^2_{1.0.010} = 6.63$$

[from Steel and Torric. 1980]



**Table A20. Estimates for Model 2,  $\sigma^2_M$  set to zero. Significance test – All breeds**

Milk	Basic Model 1			Basic Model 2		
	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	17065.17	10504.21	17065.14	18721.49	12458.69	18727.77
$\sigma^2_M$	-	5607.15	0	-	5230.88	0
$\sigma^2_E$	81332.06	82196.83	81332.09	80184.91	80892.71	80179.96
$\sigma^2_P$	98397.23	98308.19	98397.23	98906.41	98582.28	98907.73
$h^2$	0.173431	0.10685	0.1734	0.0.1893	0.1264	0.1893
$m^2$	-	0.0570365	0	-	0.0531	0
Log L	-14171.83008	-17333.56262	-17334.39784	-14123.03122	-17284.88984	-17285.59898
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>1.67</b>			<b>1.418</b>		
Fat	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	26.82	12.12	26.82	28.84	13.94	28.84
$\sigma^2_M$	-	12.95	0	-	12.98	0
$\sigma^2_E$	103.9	104.99	103.9	102.55	103.98	102.55
$\sigma^2_P$	130.72	130.06	130.72	131.39	130.91	131.39
$h^2$	0.205166	0.0931989	0.2052	0.2195	0.1065	0.2195
$m^2$	-	0.0995728	0	-	0.0992	0
Log L	-8479.511076	-11639.73877	-11642.07884	-8457.259255	-11617.56213	-11619.82702
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>4.68</b>			<b>4.53</b>		
Protein	Model 1	Model 2 ( $H_A$ )	Model 2 ( $H_0$ ) $\sigma^2_M$ fixed	Model 1	Model 2	Model 2 $\sigma^2_M$ fixed
$\sigma^2_A$	14.34	4.76	14.34	15.83	6.20	15.83
$\sigma^2_M$	-	8.35	0	-	8.29	0
$\sigma^2_E$	76.09	76.77	76.09	75.11	75.84	75.11
$\sigma^2_P$	90.43	89.88	90.43	90.94	90.34	90.94
$h^2$	0.158552	0.0529395	0.1586	0.1741	0.0687	0.1741
$m^2$	-	0.0929023	0	-	0.0918	0
Log L	-8171.690092	-11332.12783	-11334.25785	-8151.420213	-11312.00710	-11313.98797
<b>-2[H<sub>0</sub> - H<sub>A</sub>]</b>	<b>4.26</b>			<b>3.96</b>		

$$\chi^2_{1.0.995} = 0.0000393$$

$$\chi^2_{1.0.950} = 0.00393$$

$$\chi^2_{1.0.500} = 0.455$$

$$\chi^2_{1.0.050} = 3.84$$

$$\chi^2_{1.0.005} = 7.88$$

$$\chi^2_{1.0.990} = 0.000157$$

$$\chi^2_{1.0.900} = 0.0158$$

$$\chi^2_{1.0.250} = 1.32$$

$$\chi^2_{1.0.025} = 5.02$$

$$\chi^2_{1.0.975} = 0.000982$$

$$\chi^2_{1.0.750} = 0.102$$

$$\chi^2_{1.0.100} = 2.71$$

$$\chi^2_{1.0.010} = 6.63$$

[from Steel and Torrie, 1980]

## VII. Estimates for statistically significant test (F-test)

**Table A21. Sums of Squares for residual, additive variance, error variance and calculated F-values**

Breed / Trait							
Alpine	SSR (F)	SSR (R)	$\sigma^2_E$ (F)	$\sigma^2_A$ (F)	df	residual df	F <sub>c</sub> -value
Milk	30543419.84	31228898.39	60521.12092	26329.40902	8	508	0.984209946
Fat	45806.23777	48199.89475	93.41064873	21.513487	8	508	2.548420904
Protein	31311.69951	32584.74617	63.14873288	16.97686676	8	508	1.965058269
Toggenburg	SSR (F)	SSR (R)	$\sigma^2_E$ (F)	$\sigma^2_A$ (F)	df	residual df	F <sub>c</sub> -value
Milk	46370310.44	48098989.52	96604.72943	22268.37369	8	480	1.817777776
Fat	48801.64868	49419.03832	101.6700898	24.48886366	8	480	0.611718018
Protein	37055.89465	38550.02347	77.19976538	17.95579254	8	480	1.962745073
Saanen	SSR (F)	SSR (R)	$\sigma^2_E$ (F)	$\sigma^2_A$ (F)	df	residual df	F <sub>c</sub> -value
Milk	f	f	f	f	f	f	f
Fat	38380.85248	39490.02438	143.7485112	18.27790747	8	267	0.855702969
Protein	30017.79798	31700.83237	112.4262096	12.00739238	8	267	1.690695241
Nubian	SSR (F)	SSR (R)	$\sigma^2_E$ (F)	$\sigma^2_A$ (F)	df	residual df	F <sub>c</sub> -value
Milk	10446573.36	11048969.51	41786.29342	17630.37503	8	250	1.267313041
Fat	21936.4908	23055.27553	87.7459632	75.72180305	8	250	0.85550867
Protein	15328.66025	16209.43941	61.31464098	25.17604029	8	250	1.272939389
All breeds	SSR (F)	SSR (R)	$\sigma^2_E$ (F)	$\sigma^2_A$ (F)	df	residual df	F <sub>c</sub> -value
Milk	137036018	139647150.8	80184.91399	18721.49429	8	1709	3.300004577
Fat	175261.3301	178398.8928	102.5518789	28.84236029	8	1709	2.984874679
Protein	128363.1557	130651.1136	75.11009697	15.83008755	8	1709	3.144866475

F<sub>c</sub> - value = calculated F - value

$$F_{0.100,8,\infty} = 1.67$$

$$F_{0.050,8,\infty} = 1.94$$

$$F_{0.025,8,\infty} = 2.19$$

$$F_{0.010,8,\infty} = 2.51$$

$$F_{0.005,8,\infty} = 2.74$$

[from Steel and Torrie. 1980]