DESIGN AND IMPLEMENTATION OF A GENETIC IMPROVEMENT PROGRAM FOR COMISANA DAIRY SHEEP IN SICILY

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Introduction.

In Italy, the Comisana is the second most important dairy breed of sheep, after the Sarda. The breed is native to Sicily and mostly raised in the marginal Central and Southern areas of the country. The importance of the breed is related to its high genetic potential to produce milk in the extreme environmental conditions of the Mediterranean. Its resistance to diseases and heat is very high. Milk from Comisana sheep is mostly processed on-site to produce a variety of traditional high quality homemade cheeses of which the most popular is Pecorino Siciliano. High fertility and prolificacy makes the Comisana an excellent dual-purpose breed with about 1/3 of the total income coming from meat. These products represent a precious economic resource for the marginal areas where they are produced.

There is growing interest in dairy sheep production systems in Europe, where present CE agricultural policy is actively supporting development of sustainable agricultural production systems to ensure the longevity and economic vitality of marginal rural communities. Moreover, the potential for expanding the dairy products market within and beyond the European Community is very high.

Genetic improvement of local dairy sheep breeds and populations is an important component of the development of a viable dairy sheep industry. At present, the genetic progress for milk production in the population of Comisana sheep is very small, probably close to zero, and the observed phenotypic change in milk production, if any, is mostly environmental. Poor animal identification, a very small proportion of animals and flocks enrolled in a production recording system and small flock size hamper the opportunity for genetic improvement. Though artificial insemination with fresh semen and induced estrus is possible in dairy sheep, there is no infrastructure to facilitate its utilization in the Comisana breed. Consequently, the only tool available for genetic improvement is within-flock selection. The within-flock selection that is occurring is not effective for the following reasons:

- The selection practiced is of a very low intensity and accuracy. This is true especially for rams, which are selected from the "best" ewes without adjusting for non-genetic effects. The accuracy of estimated genetic merit of a ram from the production of his mother is only $\sqrt{1/4h^2} = 0.25$ (if $h^2 = 0.25$);
- Multiple rams are generally used simultaneously in the flock, so paternity is not known;
- The criteria used in selection are different from farm to farm;

- Much attention is given to morphological traits, which have unknown (probably low) genetic correlation with milk production;

Last but not least, at the present time there is no genetic structure in the population to facilitate the dissemination of genetic progress, even if it was somehow generated. Under these conditions, an effective genetic improvement program needs to be developed within the framework of a pyramidal management of the population (Barillet, 1997). With such a structure, breeders are divided into at least two groups: the selection breeders of the nucleus flocks and the breeders of the commercial flocks. The tools required by the breeding program, such as animal identification, control of production, data collection and storage, progeny testing, elite mating, etc., could be concentrated in the nucleus flocks. Such a program has been developed and is being implemented for the Comisana breed by the Istituto Sperimentale Zootecnico per la Sicilia and Cornell University. The characteristics of the program as well as the results of the last three years of activity are presented in this paper.

Breeding program.

Objective: Genetically improve the dairy traits (milk yield and composition) for the entire population of the Comisana breed in Sicily. To accomplish this objective a pyramidal breeding program is needed. In such a program, the population is divided in several strata with a nucleus, where the genetic progress is generated, and a mechanism to ensure the dissemination of the genetic progress through the rest of the pyramid.

A dairy sheep breeding program to be effective must be based on progeny test, must be able to accurately evaluate the genetic merit (breeding value) of males and females, select the superior males and females to be parents of the next generation and disseminate the genetic superiority to the entire population. The major components of the breeding program are:

1. Create a nucleus flock (top of the pyramid) in which the genetic improvement is generated via intense selection of males and females to be parents of the next generation.
2. Implement a good on-farm animal identification and production recording system for the nucleus.
3. Implement a progeny-testing program for young rams produced by elite matings in the nucleus.
4. Implement an evaluation program to estimate the genetic merit of all males and females in the nucleus and use it to identify genetically superior individuals as parents for the next generation.
5. Create a multiplication flock to produce young rams for the next cycle (best 100 ewes mate with best 2 proven rams) and breeding rams to be used to disseminate the genetic superiority to the whole breed (all other ewes in the multiplication flock mate with top 6 proven rams).
6. Develop a strategy to ensure the gene flow from the apex (nucleus) through the rest of the genetic pyramid.

Nucleus flocks. The Comisana nucleus was started in 1994 when Istituto Sperimentale Zootecnico per la Sicilia purchased about 600 ewes from the expansion area of the breed (Sicily,

Lazio, Toscana, and Abruzzo). The nucleus was expanded in 1998. Today it consists of seven flocks of which one flock of about 450 milking ewes belongs to the Istituto Sperimentale Zootecnico, five flocks of 600, 500, 220, 150 and 120 milking ewes are typical commercial farms, and one flock of 100 milking ewes belongs to an agro-tourist farm.

Animal identification and milk recording. Initially, a standard A_4 testing program (ICAR nomenclature) consisting of monthly recording of the two daily milkings for milk quantity and composition was adopted. Individual milk samples were collected at each milking and milk composition (fat %, protein %, lactose % and somatic cells count) was determined by the Istituto Zooprofilattico Sperimentale della Sicilia "A. Mirri". Starting with fall 2000 a hybrid system consisting of A_4 testing for milk yield and AC testing for milk composition (corrected monthly test with individual samples for morning milking corrected for evening/morning differences in milk composition using bulk tank samples from morning and evening milk produced by the whole flock) has been adopted. Records are collected and stored using "Progecom" software package developed by A. Carlucci from the Associazione Allevatori di Matera, Italy. The package consists of a data base management program, an electronic animal identification system and a filed interface program that interrogates the animal identification system and facilitates the collection of records on farm and their transfer to the data base management program. The electronic animal identification system consists of a microchip type ISOHCX stored in a passive, battery less device named "rumen bolus". The rumen bolus is orally introduced and resides permanently in the animals' reticulum. This system should greatly simplify and improve the accuracy of the control of production activity.

Genetic theory tells us that the genetic change we can achieve through selection depends on selection intensity, accuracy of selection and the amount of genetic variation present in the population. Selection intensity, i, is a prediction of the superiority of selected parents, expressed in units of standard deviation, and is a function of the proportion selected. The accuracy of selection, $r_{BV,EBV}$, is an indicator of how well we can estimate true genetic merit and is measured by the correlation between true and estimated breeding value. Therefore:

ΔG = (selection intensity) (accuracy of selection) (Additive Genetic Standard Deviation)
$= (i)\ (r_{BV,EBV})\ \sigma_{BV}$

In a program with 4-pathways structure, each path contributes to the total genetic change and, because selection intensity, accuracy of selection and generation interval are different for each path, they need to be considered simultaneously in order to optimize the entire program. The expected genetic change per year, Δg, is:

$$\Delta g = (\Delta G_{SS} + \Delta G_{SD} + \Delta G_{DS} + \Delta G_{DD})/(L_{SS} + L_{SD} + L_{DS} + L_{DD})$$

Progeny testing of young rams. A progeny test based program was designed to optimize the rate of genetic progress in the nucleus given its size and the biological parameters of the population (pregnancy rate, survival rate from birth to milking string, prolificacy, etc.). Such a breeding program has a 4-pathway structure:

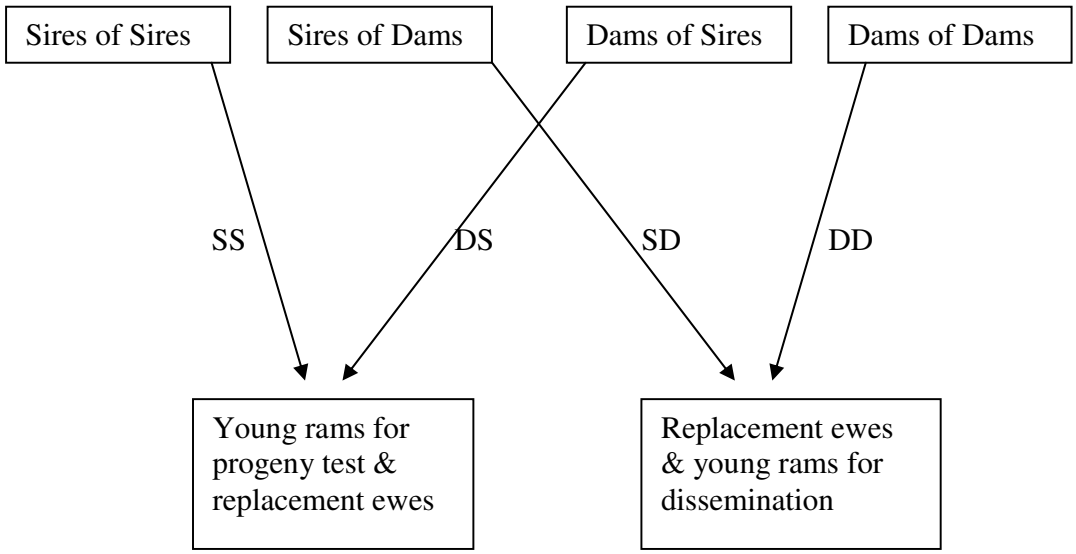

Figure 1. Gene flow diagram in 4 pathways breeding program.

With breeding restricted to natural mating and higher prolificacy in sheep, the sire-son and sire-daughter pathways are not as dominant and the dam-daughter pathway is not as negligible as in dairy cattle.

The first step in the design of a breeding program is to determine the testing capacity of the nucleus, i.e., the number of daughters completing the first lactation that can be generated. To determine it we need to consider the production system and its management practices. In commercial flocks there are two breeding seasons each year. Spring breeding is in March, April and May when all pluriparous ewes are covered and Fall breeding is in September, October and November when all primiparous ewes born the previous fall and pluriparous ewes still open are covered. Ewes pregnant from fall breeding are lambing in February, March and April, have a short lactation of about 150 days, are re-bred the next spring and all lambs are sold for meat at Easter. Ewes pregnant from spring breeding are lambing in September, October and November, have a long lactation of about 250 days, are re-bred the following spring and the female lambs born are kept as replacements while the male lambs are sold for meat at Christmas. With this production system, young rams in progeny test should be used only during spring breeding season to ensure that their daughters are kept as replacements for the milking flock. Breeding is limited to natural mating and, because the production system is based on natural pasture, it is difficult to create and maintain isolated small breeding groups. To be able to produce groups of daughters with known paternity needed for progeny test, we had to resort to sequential estrus synchronization and breeding of groups of ewes. Given these limitations, the testing capacity of the nucleus is about 400 daughters.

The nucleus is structured in a multiplication group of about 500 ewes and a progeny-testing group consisting of all other pluriparous ewes in the nucleus. We need 6 rams each year to cover the multiplication group of 500 ewes; best 2 rams for elite mating to produce the next batch of young rams for progeny test (Sires of Sires, SS) and all 6 rams to produce the replacements for the multiplication group (Sires of Dams, SD) and the rams to be used to disseminate genetic superiority through the rest of the population (breeding rams for the second stratum of the genetic pyramid). With 6 proven rams needed and the testing capacity of 400 daughters, an optimum program needs to balance the number of young rams progeny tested (selection intensity) and the number of daughters per ram (accuracy) to maximize the genetic superiority of the rams selected. In Table 1 the magnitude of ΔG_{SS} and ΔG_{SD} is presented for various selection intensities.

Table 1. Genetic superiority of the best 6 rams to be used as sires of dams (ΔG_{SD}) and the best 2 rams to be used as sires of sires (ΔG_{SS}) calculated as a function of selection intensity[1] and accuracy[2], given a testing capacity of 400 daughters.

			Top 6 ♂ as Sires of Dams SD			Top 2 ♂ as Sires of Sires SS		
Nr. Rams tested	Nr. Daughters per ram	Accuracy	% selected (p)	Selection intensity (i)	ΔG_{SD}	% selected (p)	Selection intensity (i)	ΔG_{SS}
10	40	.853	.600	0.646	$0.551\sigma_{BV}$	.200	1.399	$1.193\sigma_{BV}$
16	25	.791	.375	1.012	$0.800\sigma_{BV}$	.125	1.647	$1.303\sigma_{BV}$
20	20	.756	.300	1.156	$0.874\sigma_{BV}$	.100	1.754	$1.326\sigma_{BV}$
25	16	.718	.240	1.298	$0.932\sigma_{BV}$	.080	1.854	$1.331\sigma_{BV}$
30	13	.681	.200	1.399	$0.953\sigma_{BV}$	.067	1.939	$1.320\sigma_{BV}$
40	10	.632	.150	1.557	$0.984\sigma_{BV}$	.050	2.059	$1.301\sigma_{BV}$
50	8	.600	.120	1.663	$0.998\sigma_{BV}$	.040	2.154	$1.292\sigma_{BV}$

[1] $i = z/p$ where p is the proportion of rams selected and z is f(x=p) when f(x) ~ N(0,1)

[2] $r_{BV,EBV} = \{nh^2/[4+(n-1)h^2]\}^{½}$

Table 1 shows that ΔG_{SS} and ΔG_{SD} are highest when 25 and 50 young rams are tested, respectively. Our objective is to maximize ($\Delta G_{SS} + \Delta G_{SD}$) and its value is essentially equal if 40 or 50 young rams are tested each year. The cost of progeny testing is high and it depends entirely on the number of rams tested. Therefore, implementing a program in which 40 rams are progeny tested each year makes genetic as well as economic sense.

With the nucleus made up of 7 separate flocks, an effective progeny-testing program has to be carried out between flocks and this is possible only if genetic ties between all flocks of the nucleus are created. Using rams uniformly across all flocks is the best way to create genetic connections between flocks. Short of using AI, this is impossible to achieve. A strategy was developed to create genetic ties between flocks with natural mating by assigning a limited number of rams to have daughters in two flocks. The diagram in Figure 2 illustrates this strategy.

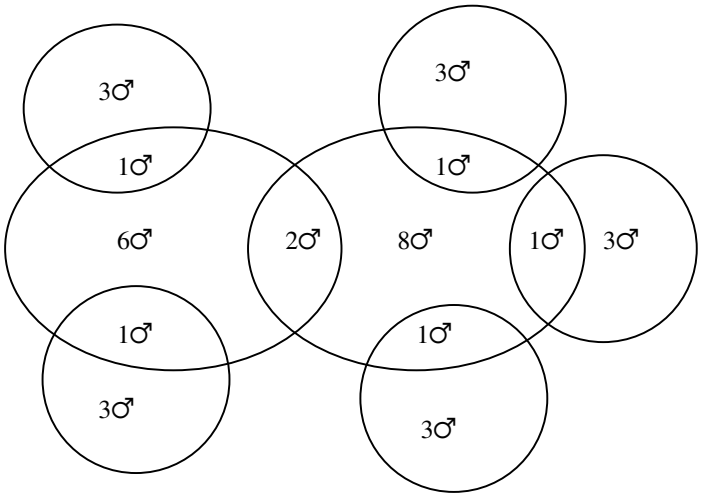

Figure 2. Design of breeding groups in the nucleus to create the genetic ties needed to perform between-flocks genetic evaluation for the young rams in progeny test. Each circle represents a different flock.

The sequence of events and the time scale for progeny testing young rams is illustrated in Table 2.

Table 2. Time line for the progeny testing of young rams.

AGE OF THE RAM	EVENT
Month 0	The ram is born
Month 18	Start of breeding activity
Month 23	Daughters are born
Month 33	Daughters are covered
Month 38	Daughters are starting first lactation
Month 42	Daughters complete first lactation
Month 43	Genetic evaluation of the ram
Month >43	Superior proven ram used for breeding

After progeny test breeding, the young rams are kept in waiting until their daughters complete first lactation and their breeding value is estimated.

Genetic evaluation program. Best linear unbiased prediction (BLUP) applied to an animal model (AM) is the standard procedure for genetic evaluation. It has the advantage that all known information is optimally taken into account and selection or special mating has a small or no effect on the evaluation. This procedure is even more valuable in dairy sheep because, with natural mating, the number of progeny per ram is relatively small, which makes information from other relatives more important.

Control of production occurs on a monthly basis and milk yield as well as milk composition information are recorded on the day of control. Recent work on milk yield performance has indicated that additional information (and accuracy) is obtainable by analyzing test day records with an animal model (TDAM) for genetic evaluations of the parents of future generations of dairy ewes. More milk yield records per ewe (up to 10 per lactation instead of one record per lactation), permits a more unique definition of the contemporary groups (CG) of animal cohorts (the TD effect). Consequently, the accuracy of genetic evaluations using TDAM models is greater than using cumulative milk yield information.

An autoregressive test day animal model (TDAM) developed by J. Carvalheira (Carvalheira et al., 1998) is being used for the genetic evaluation of the animals in the nucleus. The computer software is based on a series of programs that build the incidence matrices according to the structure of the data, and compute the inverse of the genetic additive relationship matrices to be incorporated into the coefficient matrix of the BLUP mixed model equations.

Multiplication flock. The flock located at the Istituto Sperimentale Zootecnico performs this function. Elite mating of the 100 best ewes with the top 2 proven rams is used to produce the young rams for progeny test. The top 6 proven rams covers the remaining ewes to produce the replacement ewes for the multiplication flock and the breeding rams for disseminating genetic progress trough the rest of the population. A diagram describing the production of young rams for progeny testing and of breeding rams for dissemination of the genetic progress is in Figure 3.

Dissemination of genetic progress from the nucleus. All males produced in the multiplication flock by the 6 best proven rams that can be registered in the Genealogic Book of Comisana breed, i.e., conform to established breed standards, are used for breeding. The best 40 based on pedigree index represent the young rams to be progeny tested in the nucleus and the rest, approximately 200 young rams each year, are made available as breeding rams for the flocks in the second stratum of the genetic pyramid. After one cycle of the program is completed, approximately 400 young rams representing the sons of the 40 rams undergoing progeny testing will also be made available as breeding rams for the third stratum of the genetic pyramid.

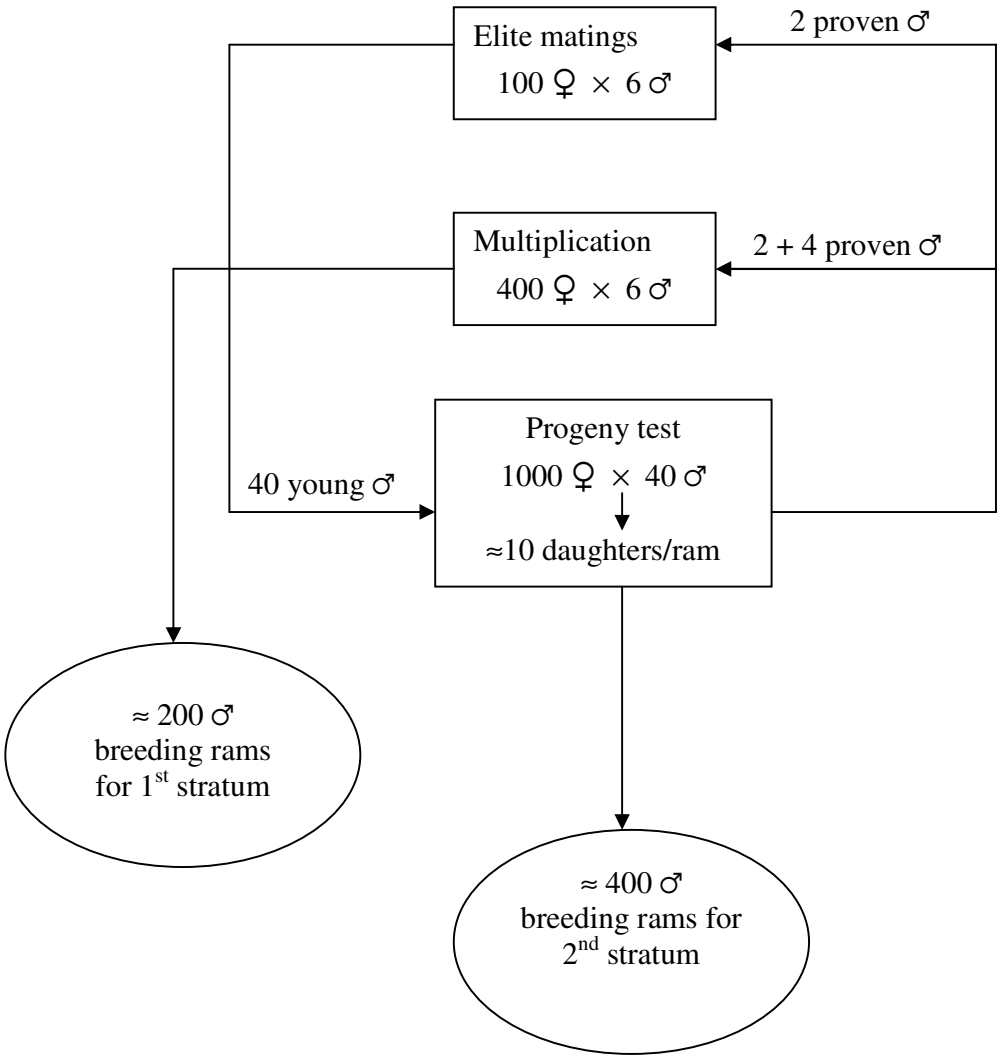

Figure 3. Production of young rams for progeny test and for dissemination of genetic progress through the population.

The genetic pyramid has a simple structure, with the nucleus group at its apex and two strata of flocks. The first stratum is represented by flocks enrolled in the National Production Recording program that also have good animal identification systems, adequate management, and with at least 50% of their animals registered in the Genealogical book of the breed. With these requirements, these flocks should be able to produce breeding rams, which we expect to be sold for use in the third stratum of the pyramid consisting of all other commercial flocks in Sicily. A diagram of the genetic pyramid is shown in Figure 4.

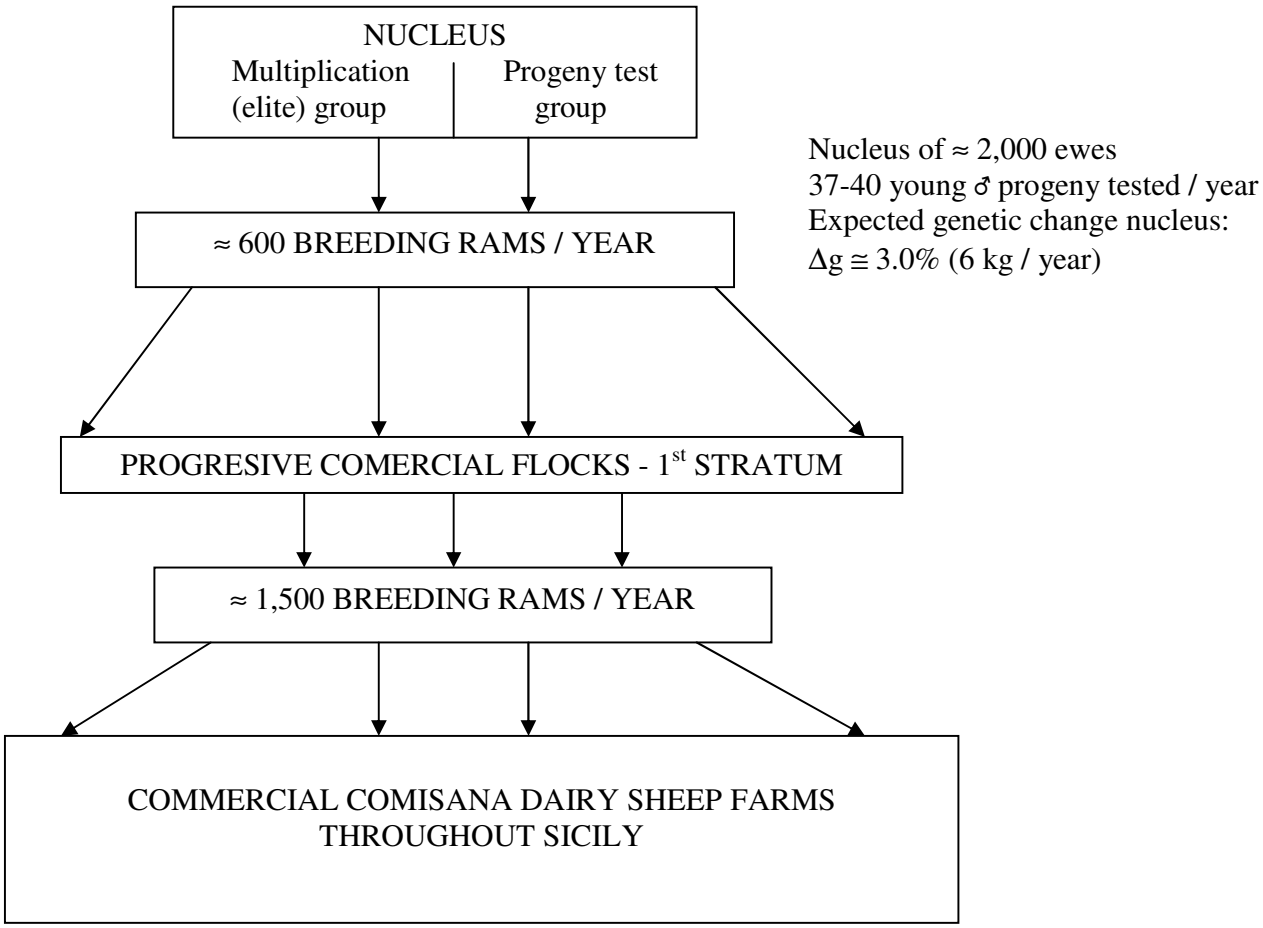

Figure 4. Diagram of the genetic pyramid

Results and Discussion.

The first cycle of progeny testing was carried out in a single flock in 1996 – 1998, with 30 rams being ultimately evaluated. The best 4 rams were used to cover the best 60 ewes (elite mating) and produced the second batch of young rams. In January 1999, the nucleus was expanded to include 6 new commercial flocks. A new group of 36 young rams started the progeny testing cycle in Spring 1999. This group consisted of 20 young rams from the previous cycle of elite mating and the others were rams from inside the new flocks added to the nucleus. The program has the sequence of activities well structured now and it is expected to reach the steady state by Spring 2002. A time diagram of the expected events and activities in the nucleus for the 4-year period between 1999 and 2003 is shown in Table 3.

March & April 1999	Breeding groups for 1st batch of 36 young rams
Sept. & October 1999	1st crop of Daughters are born
March & April 2000	Breeding groups for 2nd batch of 36 young rams
Sept. & October 2000	1st crop of Daughters are bred
Sept. & October 2000	2nd crop of Daughters are born
Feb. & March 2001	1st crop of Daughters are lambing
March & April 2001	Breeding groups for 3rd batch of 36-40 young rams
June & July 2001	1st crop of Daughters complete first lactation
July 2001	Genetic evaluation of the 1st batch of tested rams
Sept. & October 2001	2nd crop of Daughters are bred
Sept. & October 2001	3rd crop of Daughters are born
Sept. & October 2001	First round of elite mating for 1st batch of proven rams
Feb. & March 2002	2nd crop of Daughters are lambing
Feb. & March 2002	First crop of sons from 1st batch of proven rams are born
March & April 2002	Breeding groups for 4th batch of 36-40 young rams
March & April 2002	Second round of elite mating for 1st batch of proven rams
June & July 2002	2nd crop of Daughters complete first lactation
July 2002	Genetic evaluation of the 2nd batch of tested rams
Sept. & October 2002	3rd crop of Daughters are bred
Sept. & October 2002	4th crop of Daughters are born
Sept. & October 2002	Second crop of sons from 1st batch of proven rams are born
Sept. & October 2002	First round of elite mating for 2nd batch of proven rams

Table 3. Time line of events and activities in the nucleus.

The first genetic evaluation of the animals in the nucleus using a test-day animal model (TDAM) was performed in August 2000 using production data collected from the ewes in the nucleus flock between October 1998 and June 2000. The first objective was to estimate the (co)variance components and genetic parameters for test day records of the Comisana ewes using an autoregressive test day model. The second objective was to perform a genetic evaluation for ewes and rams in the nucleus flock using all sources of information in an animal model using BLUP methodology.

The following model was used to describe the data:

$$Y_{ijkmnpqr} = YM_i + AGE_j + DIM_k(L_m) + A_n + LTE_p + STE_q + E_{ijkmnpqr}$$

where:

Y is test day observation,
YM is fixed effect of year-month ,
AGE is fixed effect of age at lambing,
DIM(L) is the fixed effect of days in milk nested within lactation,
A is the random effect of the animal,
LTE is the random long-term environmental effects accounting for the autocorrelations generated by the ewe across lactations,
STE is the random short-term environmental effects accounting for the autocorrelations due to the ewe within each lactation, and
E is the random residual effect assumed normally distributed.

Table 4 shows the size of the data set used in this study and the number of levels for each fixed effect in the model.

No. of animals with records	398
Total no. of animals	1228
Total no. of test day records	2439
No. of year-month levels	18
No. of age levels	10
No. of lactation-days in milk levels	62
Lactation 1:	
No. ewes with records	181
No. test day observations	751
Lactation 2:	
No. ewes with records	181
No. test day observations	857
Lactation >2:	
No. ewes with records	140
No. test day observations	831

Table 4. Number of observations and levels of fixed effects for the test day milk data.

The number of individuals in the pedigree file was 1228. In the pedigree file we had 111 sires of which 61 were foundation rams with unknown birth date, 596 dams of which 375 ewes were foundation ewes with unknown birth date, and 521 offspring. Foundation sires and dams were considered unrelated and were given arbitrary birth dates 3 years prior to the birth date of the first offspring. Year-month fixed effects consisted of year 1998, October to December, year 1999 January to April and August to December, and year 2000, January to June, for a total of 18 year-month levels. Age at lambing fixed effects consisted of < 15 mo., 15 to 16 mo., 17 to 18 mo., 19 to 20 mo., 21 to 22 mo., 23 to 26 mo., 27 to 30 mo., 31 to 36 mo., 37 to 42 mo., and > 42 mo., for a total of 10 levels. Days in milk by lactation fixed effects consisted of 10 day-intervals between 20 and 180 days for first lactation and between 20 and 240 days for second and for third or greater lactation, for a total of 62 levels.

The lactation curves for first, second, and third and greater lactation for the first 140 days of lactation are shown in Figure 5. These curves are constructed using the solutions for days in milk by lactation fixed effects. These solutions represent test day production adjusted for all effects in the model, including genetic differences, so what remains is almost entirely nutritional management. It is interesting to note lower production and higher persistency for first lactation relative to lactation 2 or greater, very similar to what occurs in dairy cattle. The production system is based on a seasonal pattern of lambing, with most of first lactation ewes lambing in February, March and April and most of second or greater lactation ewes lambing in September, October and November. Consequently, the differences in milk yields and shape of lactation curves between first lactation and second or greater lactation for the Comisana ewes are due to biological factors associated with maturity as well as nutritional factors associated with different seasons of lambing. The 140 days cumulative milk yield for first, second and third and greater

lactation is 83 kg, 225 kg and 200 kg, respectively. These yields are in line with average production for the Comisana ewes in Sicily.

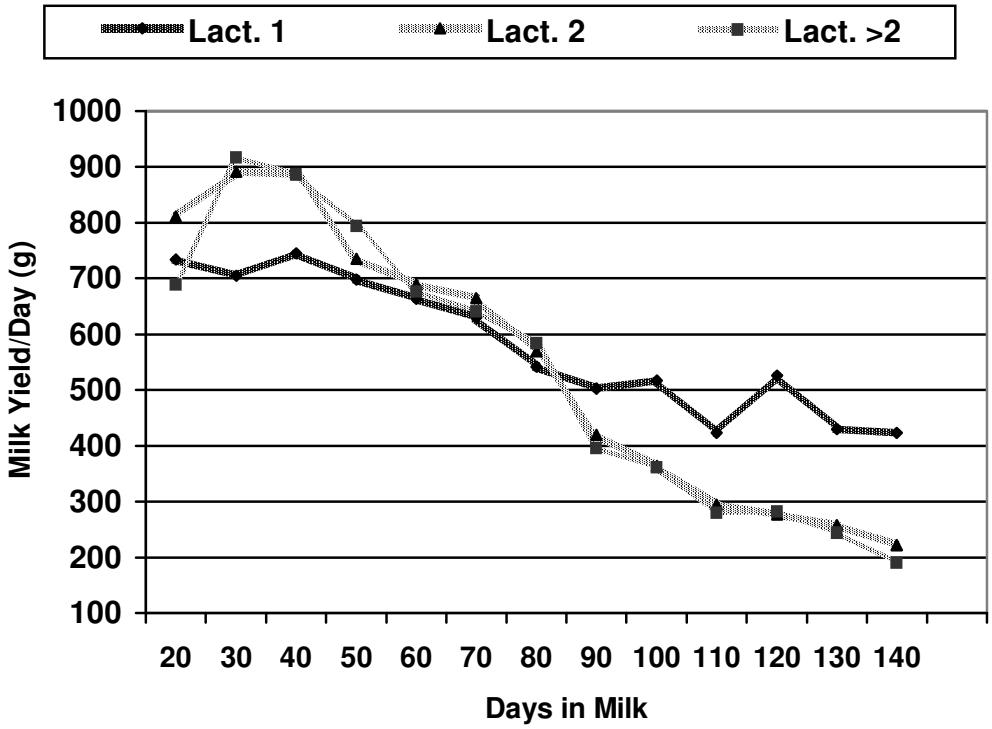

Figure 5. Lactation curves for first, second, and third and greater lactation for Comisana ewes in the breeding nucleus, 1998-2000 data.

The variance components and the genetic parameters were also estimated and are presented in Table 5. The estimated variance components are used as inputs for subsequent genetic evaluation analysis, which includes the genetic ranking of all individuals in the data set. The genetic variance is small relative to phenotypic variance, resulting in heritability values lower then 0.2 for each parity considered. These values are somewhat lower then other estimates for heritability of milk yield for dairy sheep, which are in the 0.25 to 0.3 range, similar to heritability for milk production dairy cattle. These lower estimates are data related and a direct consequence of a relatively small data set with many animals in the population genetically unrelated. With the expansion of the size of the nucleus and a better genetic structure, we expect to obtain higher estimates of heritability in the next evaluation.

The size of the estimated short term environmental variance for each lactation indicates that an important part of the non-genetic variation due to the repeated effect of ewe within lactation was accounted for by this effect. The test day records were highly correlated within lactation, with STE autocorrelation of 0.47, 0.59 and 0.5 for first, second, and third or greater lactation, respectively. Long-term environmental effects had a negligible impact on milking performance with long-term environmental autocorrelation of essentially zero.

Table 5. Variance components and genetic parameters for daily milk yield (g) for the Comisana breed.

Genetic variance	14148.11
Error variance	10576.40
Long term environmental variance	8858.68
Long term environmental autocorrelation	0.0007
Short term environmental variance (Lact.1)	42966.82
Short term environmental autocorrelation (Lact.1)	0.47
Short term environmental variance (Lact.2)	66414.70
Short term environmental autocorrelation (Lact.1)	0.59
Short term environmental variance (Lact.>2)	55271.13
Short term environmental autocorrelation (Lact.>2)	0.50
Phenotypic variance (Lact. 1)	76550.02
Phenotypic variance (Lact. 2)	99997.90
Phenotypic variance (Lact. >2)	88854.33
Heritability (Lact. 1)	0.19
Heritability (Lact. 1)	0.15
Heritability (Lact. 1)	0.16

In the second stage of the analysis the breeding values (EBV) and accuracy of EBV were estimated for all animals in the data set. Using BLUP methodology, these estimates are pre adjusted for all other effects included in the model.

The EBV milk yield per day for all 1228 animals in the analysis has a mean of 3.8 g., standard deviation is 50.15 g. and minimum and maximum EBV values are –181.8 g. and + 169.0 g. for a total range of 350.8 g.

When only the 111 sires in the data set are considered, the mean EBV is –1.2 g., standard deviation is 45.05 g. and minimum and maximum EBV values are –121.0 g. and + 126.9 g. for total range of 247.94 g. For 596 dams and for 521 offspring in the data set the values for the same statistics are 3.7 g., 50.0 g., -183.6 g., +190.6 g., 374.2 g. and 4.9 g., 51.4 g., -183.6 g., +190.6 g. and 374.2 g., respectively.

These results indicate that good opportunity exists for selection and, therefore, for genetic progress. For example, the EBV for the top 90% of the dams is between 68.3 and 190.6 g of milk per day. This is equivalent to a genetic superiority between 10.2 and 28.6 kg of milk per 150 days lactation.

In Figure 6, the distribution of EBV for all animals is presented and in Figure 7 the distribution of EBV is presented separately for dams, sires and offspring in the data set.

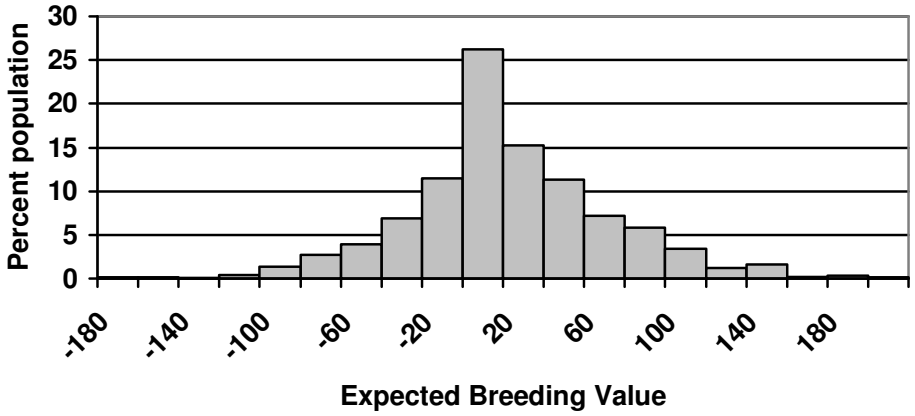

Figure 6. Distribution of EBV for all animals in the data set.

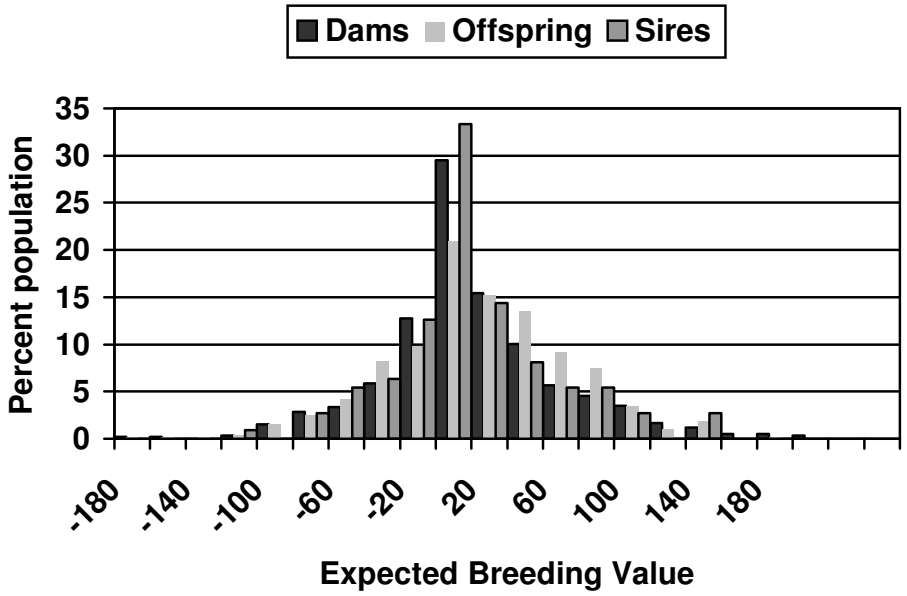

Figure 7. Distribution of EBV for dams, sires and offspring in the data set.

To estimate the genetic trend for the animals in the evaluation, the regression of EBV on the year of birth was evaluated. The estimated regression coefficient was 2 g/day/year, indicating a genetic trend of 300 g of milk for 150 days lactation. This data set reflects the initial phase of the breeding program and a low within flock selection was applied. When the information from the progeny testing of rams becomes available, it will greatly increase the contribution of the SS and SD paths. It is therefore expected that the genetic trend in the nucleus will be 2.5 to 3% of the mean, or about 6 kg of milk per year as indicated in Figure 4.

References

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