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*SELECTION METHODOLOGY FOR A
DAIRY BREED IN A TROPICAL
ENVIRONMENT*

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ABSTRACT

Aim of this thesis is to evaluate the genetic and racial structure of a dairy cattle breed reared in Tropics, joint to the investigation of the best selection methodology for productive traits adapted to low/medium input production system.

The genetic and racial structure of the Carora Breed, a Venezuelan dairy cattle population, was studied through the analysis of the whole pedigree. The database included 4324 living animals (including culled bulls used for AI), born from 1983 to 2010. The racial composition of Carora breed was studied clustering the current population into 5 racial groups, identified on the basis of the individual racial proportion, in order to detect the breed composition in this synthetic breed.

The Carora pedigree resulted quite complete, and the inbreeding level is below the level of 1%, even if the size of this breed is reduced. From this study an increase in the Brown Swiss genes proportion was detected, indicating the possibility of a reduction in adaptability linked to the features of this breed, typically suitable for temperate climates.

Genetic parameters of weight at 18 months (W18) and milk yield (MY) of 1781 Venezuelan cows were estimated with a Multiple Trait Animal Model, including the direct breed effects and the epistatic loss.

Results showed that direct breeds effects and epistatic loss affected milk trait, while they seemed not important for weight. An high percentage of *European* genes positively influenced milk production.

Four random regression models were used on 95606 test day records to obtain genetic parameters for test day yield and persistency. Akaike's information criterion (AIC) and minus twice log likelihood ($-2\log L$), were used to compare the models and to choose the best one

fitting the data.

Estimated heritability for milk yield ranged from 0.21 to 0.30, while repeatability ranged from 0.50 to 0.56.

Five persistency measures were calculated taking in account different point of the lactation. In general, heritability values for the five measures of persistency ranged from low to moderate (from 0.18 to 0.26), indicating the possibility of new selection opportunities.

The use of persistency indexes accounting for milk yield, may allow the selection of individuals able to express their potential genetic values in tropical environment, without incurring in excessive heat stress losses

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CHAPTER 1

GENERAL INTRODUCTION

1. General introduction

In developing countries the demand for dairy products has been increasing and has resulted in growth in livestock production through increased animal population rather than productivity (Thornton, 2010).

The livestock population has increased dramatically in tropical areas in recent years. Rangeland in tropical areas includes tree, bush and grass savannah, steppes in temperate zones, and high pastures in arid areas. Nomadic pastoralists graze pastures extensively over large areas, whereas sedentary smallholder farmers use pastureland intensively over smaller areas. This kind of exploitation of the soil presents many challenges:

- Overgrazing, burning and increase in undesirable plants;
- Insufficient soil organic carbon;
- Soil degradation: erosion, compaction, crusting;
- Free grazing, no clear land use rights.

The consequences are reduced vegetation cover and loss of valuable fodder species, resulting in reduced biodiversity, as only species unattractive to animals survive. Reduced cover also leads to accelerated decomposition of soil organic matter and increased aridification.

Sustainable agricultural practices have the potential to reverse this trend. They can help to improve local livelihoods, reduce hunger, and restore natural ecosystems. Also, sustainable land management practices can contribute significantly to climate change adaptation and mitigation.

Furthermore, sustainable farming must be socially, biologically, environmentally and economically viable over a foreseeable period of time and thereby contribute to the well-being of all stakeholders. Therefore the technologies providing these solutions must be

appropriate, and they must be technically feasible, cost-effective and publicly acceptable. Among the strategies that could be executed, good management of livestock production can contribute to the achievement of this goal.

This study considers genetic aspects and the role of information technology in aiding the implementation of genetics, management, control and the definition of future target areas that may contribute to a sustainable livestock production systems.

When considering genetic solutions to sustainable livestock production, genetic management strategies that utilize indigenous animal genetic resources and reduce the reliance on external chemical inputs are those most likely to be successful and sustainable.

A wide variety of genetic technologies potentially provide partial or full solutions to the issue of developing sustainable livestock production systems. These range from simple issues of the appropriate choice of breed for given environmental constraints, through to high technology solutions utilizing molecular genetics.

The choice of the appropriate genotype or breed, is the first step in defining a sustainable livestock production system. There are two components to this choice: the actual breed(s) used and crossbreeding strategies that might exploit favorable characteristics of two or more breeds or lines and also exploit hybrid vigor (heterosis) observed when breeds are crossed (Bishop and Woolliams, 2004)

The use of conventional livestock breeding techniques, such as selection within breeds and crossbreeding, aided by appropriate breeding scheme design and application of statistical technologies, can result in rapid improvement of livestock production in terms of quantity and quality.

Rapid genetic changes in one generation or per year can be mainly

achieved by selection within breeds and are determined by genetic variability, intensity and accuracy of selection.

The environment molded local breeds, making them specifically adapted to their habitat. This genetic diversity was exploited by local breeders to obtain well-adapted and productive breeds. Furthermore, local breeders knew how to handle these breeds, and consequently they established different production system compatible with the environment.

In the recent years, with the expansion of globalization, breeders imported germplasm from other countries to increase productions. A widely used strategy to improve the dairy potential of tropical cattle is the introduction of genetic material from dairy breeds of the European (*Bos taurus*) type, either by importing stock of both sexes in large numbers, or by acquiring bulls (or semen) for crossbreeding with indigenous females. Even if this importation can be positively considered in terms of productivity, it might be associated to the loss of genetic variability and adaptability of the new crosses (Syrstad and Ruane, 1998).

Importation of genetic material from temperate countries is one of the main reasons for erosion of the genetic resources of tropical cattle (Hall and Ruane, 1993).

For this reason, local breeds, generally represented by a limited number of animals, deserve a special treatment when selecting for higher productions, since an inappropriate management of genetic resources could lead to the appearance of undesired traits.

In general, local breeds do not benefit from modern breeding techniques as much as they should. Selection programs may increase genetic ability for productivity and consequently profitability of local breeds. However, three major considerations have to be forwarded:

- Breeding goals should take into account the conservation values of the breed. Traits proposed for selection should be accurately evaluated for their genetic correlations with those traits that determine the conservation value of the breed, in order to avoid their deterioration. These might include adaptation to harsh environment or to low-input production systems or traits like longevity, fertility and quality of meat and milk.
- Breeding schemes should be adapted to the farming environment.
- Selection schemes should take in account maintenance within the breed and risk associated with high rates of inbreeding (Gandini and Oldenbroek, 2007).

Inbreeding is inevitable, since a large number of not related ancestors is required to avoid it.

In a closed population, like local breeds, it is quite easy to have a constant increase of inbreeding, but genetic variability is maintained by natural mutations, that remove potentially harmful inbreeding depression.

So, inbreeding alone cannot be enough to explain the loss of genetic variability, but it is necessary to understand how fast the inbreeding level increases (ΔF). For this reason, an important parameter for management is the evaluation of ΔF per generation.

The progress of inbreeding, in particular when ΔF is high, is associated with inbreeding depression, in which traits show a steady decline in performance as inbreeding progresses. These traits are often those associated with fitness, such as reproductive ability, and survival to breeding maturity, but many other physical traits such as growth rate or mature size will also show depression (Woolliams, 2007).

The genetic variability is expressed by the additive genetic standard deviation and is estimated as the phenotypic standard deviation times the square root of heritability. The estimate of additive genetic standard deviation of traits in tropical cattle is often biased due to high variability of environmental conditions and to low quality of recording systems.

Improvement in accuracy of additive genetic standard deviation, and consequently of heritability, can be achieved by the use of random regression methodology that is extensively used in developed country for analyzing productive traits. An advantage of test-day random regression methodology is the ability to account for environmental effects on each test day, which reduces residual variance components, thus increasing estimated heritability and the accuracy of predicting breeding values (Santellano-Estrada *et al.*, 2008). Also, this methodology allows an efficient use of all information available, and the prediction of genetic merit from daily milk records of early lactation. Therefore, this methodology may result in the costs' reduction of breeding programs in tropical countries characterized by both poor data collection and animals with short lactations (Ilatsia *et al.*, 2007).

Aim of this thesis is to evaluate the genetic and racial structure of a dairy cattle breed reared in Tropics, joint to the investigation of the best selection methodology for productive traits adapted to low/medium input production system.

CHAPTER 2

GENETIC VARIABILITY AND POPULATION STRUCTURE IN THE CARORA DAIRY BREED

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2. Genetic variability and population structure in the Carora dairy breed

ABSTRACT

The genetic and racial structure of the Carora Breed, a Venezuelan dairy cattle population, was studied through the analysis of the whole pedigree. The database included 4324 living animals (74 bulls and 4250 cows), plus their ancestors, for a total of 11012 animals (886 bulls and 10126 cows) born from 1954 to 2010 and reared in 75 herd in Venezuela.

All the analyses were carried on with ENDOG V4.8. The effective number of founders (f_e), the effective number of ancestors (f_a), individual inbreeding (F), average relatedness (AR) and the rate of inbreeding (ΔF) per generation were analysed to describe the genetic variability of the population.

The racial composition of this breed was studied dividing the current population in 5 racial groups in order to detect the breed proportions in this synthetic breed.

The groups were identified on the basis of the individual racial composition, with the letters: *C*, for pure Carora, *Cr*, for Creole cattle, *B*, for the Brown Swiss, *H* for Holsteins, and those with zebu genes were classified with the letter *Z*.

The Carora pedigree resulted quite complete; the percentage of known ancestors was higher (95%) in the first generation and decreased from 91 to 65 in the following four generations. The maximum number of traced generation, the mean maximum generation, the mean complete

generation, and the mean equivalent generation were respectively 13, 8.75, 2.72, and 4.93. The number of founders was 1665, 39 of which may be considered effective founders, while the effective number of ancestors was 28 but those that contributed to the 50% of the total variability were only 10.

In the living population the average relatedness coefficient (AR) was 5% while the mean inbreeding coefficient (F) was 3.17% and the rate of inbreeding (ΔF) was 0.75%. The generation interval, calculated following the four gametic pathways: sire to son, sire to daughter, mother to son and mother to daughter, on average resulted 5.91 years.

Results about the racial composition showed an increase in the Brown Swiss genes proportion, indicating the possibility of a reduction in adaptability linked to the features of this breed, typically suitable for temperate climates.

Correct management strategies should be implemented to maintain levels of ΔF lower than 1% and to avoid the increase of Brown Swiss genes in the racial composition of this breed.

Keywords: Genetic variability, population structure, tropical dairy breed.

INTRODUCTION

The Carora Breed is a *B. taurus* breed raised Venezuela and other Southern American countries, mainly for milk production. This synthetic breed has been selected starting from the Quebrada Arriba Creole Cattle, now extinct, that was a tropical local cattle with good milk production and well adapted to the tropical environment, crossed with Brown Swiss cattle.

This process started in the 1930s, with semen coming from Europe and North America.

Later, crossbred bulls were used in order to control the fertility and adaptability problems of those animals too much similar to Brown Swiss Cattle, and for this reason less adapted to the tropical environment (Cerutti *et al.*, 2006).

The selection was also driven by the tropical environment, in fact the fitness of that animals with creole genes was higher than the others, leading to a breed with the morphology and the adaptability suitable for tropical conditions, but with a production level comparable to European breed reared in the same conditions (Perotto *et al.*, 2010)

Carora cattle are breed in a tropical environment with a large range of temperatures, from 22 to 38°C and relative humidity up to 90%.

Also the production systems may vary a lot among herds, Carora cattle can be found both in extensive and in intensive systems.

The former system is characterized by grazing, hand milking in the presence of calf, while the latter consists in an intensive exploitation of the cows with machine milking and high energy level rations.

The breeders' association (Asociación Venezolana de Criadores de Ganado Carora - ASOCRICA) was created in 1979 and Carora dairy

cattle were officially recognized in 1982 (Caroli *et al.*, 2008). Since 1995, Carora bulls have been used in Holstein herds to obtain a crossbred and more productive animal adapted to the tropical climate. In addition, Carora bulls are mated today to *Bos indicus* cows with the aim of obtaining “*doble proposito*” animals (Cerutti *et al.*, 2006; Caroli *et al.*, 2008). “*Doble proposito*” cows are intend to produce good quantities of milk, but also can wean calves with a good muscular development, suitable for meat production.

The primary selection object is improving milk in terms of quantity and quality. A second objective is uniformity of morphology to breed standards, considering that several types of crosses are included in the herdbook. Particular attention is given to improving the reliability of genetic evaluations in the tropical farming conditions.

Ideal type

The ideal type should have a light colored coat with short, smooth and glossy hairs. The color of the coat may vary from the white to the bay, but also light or dark grey are allowed and animal with light brown coat with dark eye sockets are accepted.

The skin should be thick, black and greasy, with the presence of skin fold around the neck, the pigmentation should be homogenous.

The udder of the ideal type should be well developed and well balanced with symmetric quarters, with a strong mammary ligament and big and developed veins.

Figure 1: Carora cow



Figure 2: Carora bull.



This breed presents a set of characteristics that makes it different from other breeds reared in the same conditions and defines its high level of adaptation to tropical conditions.

The most important features of this breed are:

- Light thick hair coat and dark mucosa, that allow the sunlight reflection and protect the skin from burning;
- Nutritional requirements that can be easily fulfilled by the exploitation of available pastures, that implies low cost productions;
- Rusticity and good adaptation to harsh climatic and soil conditions.

Carora breed also presents other characteristics that make it a good breed from a productive point of view, those features are:

- Good development of the udder that allows the machine milking;
- Good fertility level with one calf per year;
- Easy management due to its meekness.

The Carora breed presents a distinctive trait that assures the heat tolerance: the presence of the *slick* hair gene.

This gene codes for the *slick* hair coat that is one of the most effective defense from heat. Many studies demonstrated the increased heat resistance of animals with this kind of coat that experienced lower body temperatures in heat stress conditions. The superior thermoregulatory ability associated with the *slick* phenotype is apparently the result of increased convective and conductive heat loss and decreased absorption of solar radiation (Olson *et al.*, 2003).

Animals with this feature present better fertility, due to increased

embryo survival, and greater milk production during periods of heat stress than cosmopolite breeds reared in same conditions. This trait shows its importance especially in tropical conditions where pastures are largely exploited.

The physiological basis for improved body temperature regulation in *slick*-haired cows involve lower metabolic rate, increased sensible or evaporative heat loss, more efficient transfer of heat to the animal surface (determined largely by blood flow and anatomical characteristics of the respiratory tract), or a combination of these adaptations (Dikmen *et al.*, 2008).

Stayability of Carora cows is significantly higher than in Brown Swiss, Holstein and Jersey Venezuelan herds (Cerutti *et al.*, 1995; Rizzi *et al.*, 2002) and Holstein Venezuelan herds are more prone to fertility problems and mastitis than Carora herds (Cerutti and Rizzi, 1995).

Due to this set of features, suitable for harsh conditions, Carora cows are able to produce relatively great quantities of milk even in grazing systems, with average production approximately of 3500 kg. Furthermore its Brown Swiss derivation entails the presence of those genes codifying for the G variant of the α_{s1} -Casein, that is involved in the milk clotting and in the ripening in cheese produced by rennet coagulation (Caroli *et al.*, 2008).

Herdbook

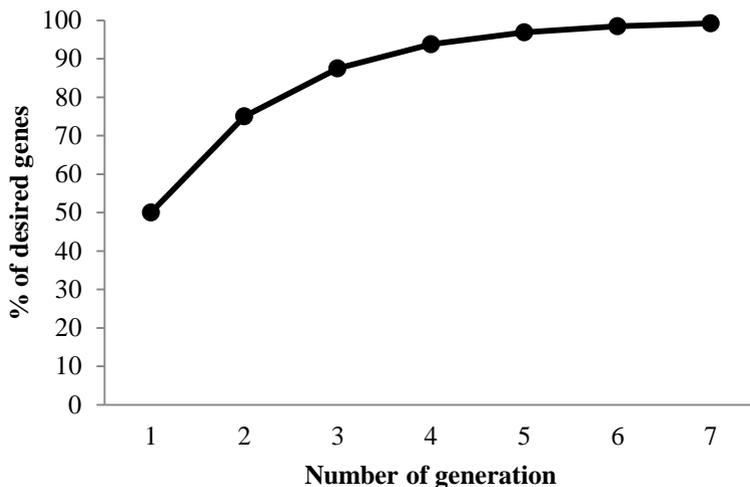
In 1992, the Carora Cattle Breeders Association of Venezuela (ASOCRICA) launched a long term breeding programme. Before 1992 animal registration was restricted to herds considered to have founded the breed.

In 1992 a new register was started from local registers of Caroran

Creole herds and of those herds undergoing grading up programmes with Caroran Creole bulls. For genetic evaluation the Breeders Association defines "Carora" as those animals with 87.5% or higher cumulative genetic contribution from Caroran Creole, Brown Swiss and Creole, with a minimum of 12.5% from Caroran Creole founders.

Carora breed herdbook contains records of around 165000 animals, of which only 4300 still living. The current population is composed by pure and grading-up animals and bulls, that, even if culled, are still used for AI. Grading-up animals are the result of cross-breeding with the aim of gradually substituting the older breed with the new breed, increasing the desired gene proportion in new animals. After the systematic use of Carora bulls for 5 or 6 generation, it is possible to obtain animals which breed composition tend to be completely Carora, as shown in Figure 3.

Figure 3: Trends in genes proportion in 7 generation of grading-up.



In the herdbook, information relative to the breeds proportion are recorded; since this breed has been obtained by several crosses between local and cosmopolite breeds.

Racial groups mainly represented are Creole breeds, Cosmopolite breeds (Holstein, Brown Swiss, Ayrshire, Guernsey and Jersey), Zebu breeds (Brahman, Guzerat, Gyr and Nellore) and Carora, represented by a 59% of pure animals and 41% of crossbreeds.

In addition to the information about relationships and breeds proportion, information for the genetic evaluations of the Carora animals is reported.

The first aim of the genetic improvement is to create and maintain a database with all productive and reproductive records and information about each animal recorded in it.

Genetic evaluations regard both productive (305-days milk yield) and morphological traits (especially traits related to the udder and legs) and recently also milk quality and growth. In addition, records for coat type phenotypes are reported.

To obtain genetic improvement, the breeding value of the animals must be estimated from the phenotypes (which can be observed or measured) of the animals themselves and (or) those of their relatives.

Bulls are chosen on the basis of the breeding values resulting from genetic evaluations, performed each six months on the whole Carora population, and on the relationship index, in order to obtain the best compromise between genetic progress and inbreeding control.

The object of this study was to evaluate the genetic and racial structure of this breed through the analysis of the pedigree of the actual living population reared in Venezuela.

MATERIALS AND METHODS

For this study, 4324 Carora individuals reared in 75 herds of Venezuela were considered including 74 bulls, either alive or used for AI, born between 1983 and 2010. Additionally their relatives (11012 individuals, including 886 sires) were included in the analysis.

Two software were utilized to analyze the genetic structure of this population; the first was ENDOG V4.8, (Gutiérrez and Goyache, 2005) that was used to evaluate the genetic diversity of this population and the completeness of the pedigree, and PEDIG software (Boichard, 2002) was used to evaluate the accuracy of the resulting inbreeding coefficient for different generations (3, 5, 8) through the pedigree completeness index (PEC).

Genetic variation measurement

The effective numbers of founders (f_e) and ancestors (f_a) joint with the individual inbreeding coefficient (F), the average relatedness (AR) and the rate of increase of inbreeding (ΔF) per generation were investigated to describe the genetic variability of this dairy cattle population.

The number of equally contributing founders that would be expected to produce the same genetic diversity in the population (effective number of founders - f_e), was calculated as:

$$f_e = \frac{1}{\sum_{k=1}^f q_k^2}$$

Where q_k is the probability of the gene origin of the k th ancestor (Lacy, 1989).

The parameter f_a , represents the minimum number of ancestors, not

necessarily founders, explaining the complete genetic diversity of the population object of study (Boichard *et al.*, 1997) and was calculated as:

$$f_a = \frac{1}{\sum_{j=1}^a q_j^2}$$

Where q_j is the marginal contribution of ancestor j in the population, which is the contribution explained only by that ancestor.

The inbreeding coefficient (F), defined as the likelihood that an individual has 2 identical alleles by descent; was computed according to Meuwissen and Luo (1992) and was also used to calculate the increase of inbreeding for each generation.

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

Where F_t and F_{t-1} are the average inbreeding at the i_{th} generation (Falconer and Mackay, 1989).

In a breeding program, the rate of inbreeding (ΔF) is more important than the actual inbreeding level (F) because it measures how many more generations a population can be kept before reaching the critical inbreeding level.

While the F coefficient is the probability that an individual has two identical alleles by descent, the average relatedness (AR) is the probability that an allele randomly chosen in the population belongs to a given animal and explain how much this animal is represented in the whole pedigree. It was calculated using the algorithm proposed by Gutierrez and Goyache (2005).

Pedigree completeness

To understand the depth and the completeness of this pedigree, the mean and maximum number of traced generations and the mean complete and mean equivalent generations were calculated. The maximum number of traced generations represents the maximum number of generation that is possible to trace back from an individual to its furthest ancestor and it is useful to calculate the complete number of equivalent generations, that explains the portion of known ancestors across the generations and is the result of the summation of $(0.5)^n$, where n is the number of generation separating the individual from the most distant known ancestor.

Pedigree completeness index (PEC)

The pedigree completeness index was calculated with PEDIG for each individual and was obtained according to the equation of MacCluer *et al* (1983):

$$PEC_{Individual} = \frac{4C_{sire}C_{dam}}{C_{sire} + C_{dam}}$$

where C is the contribution from both paternal and maternal lines and

was calculated as $C = \frac{1}{d} \sum_{i=1}^d a_i$, in which a_i is the proportion of ancestor present in the i generation, while d is the complete number of generations taken in account, in this study 3, 5 and 8 generations, respectively.

Generation interval

Generation intervals were calculated considering the four selection paths: sire-son, sire-daughter, dam-son and dam-daughter, and represent

the average age of parents at the birth of their offspring that will be parents too.

Racial composition

On the basis of historical information and on the racial makeup of founder herds, a breed or a breed composition were assigned to a founders and hypothetical founders. From the founder population down the pedigree, for each animal (j) the probabilities of gene origin (k) from each breed (i) was computed as $k_{ij} = \frac{k_{is} + k_{id}}{2}$, where s and d are respectively the sire and the dam of animal j .

The breeds recorded into the herdbook were grouped in 5 racial groups, to underline the importance of the breeds that mostly influenced the living population. The groups were identified with the letters: C , for pure Carora, Cr , for Creole cattle, B , for the Brown Swiss, H for Holsteins, and those with zebu genes were classified with the letter Z .

Those breed percentages were joined with the number of animals born in each year to evaluate the trends of the probability of gene origin in the living population, and relative ancestors.

RESULTS AN DISCUSSION

The whole Carora pedigree comprehended 13 generations and resulted quite complete, in fact the average proportion of known ancestors in the parental (P) generation exceeded the 95%, and until the fifth generation (GGGGP) this proportion remained above the 65% (Table 1, Table 2)

The generation intervals resulted on average 5.91 years, and are reported in Table 3:

Table 1: Traced generations in Carora population.

Parameter	Mean \pm SD
Maximum No. of traced generation	8.75 \pm 2.21
Maximum No. of complete generation	2.72 \pm 1.18
No. of complete equivalent generation	4.93 \pm 1.42

Table 2: Pedigree completeness in the Carora Population.

Percentage of known ancestors:	
P generation	95.2
GP generation	91.0
GGP generation	86.5
GGGP generation	81.0
GGGGP generation	65.1

Table 3: Generation intervals (mean \pm SD) for the 4 parent-offspring pathways.

	N	Years
Sire-Son	57	6.76 \pm 4.20
Sire-Daughter	966	6.32 \pm 4.03
Dam-Son	56	6.97 \pm 2.57
Dam-Daughter	957	5.38 \pm 2.59

This average generation interval is easily comparable to Reyna cattle in Nicaragua, (Corrales *et al.*, 2010) and to the four breeds studied by Martínez *et al.*(2008), small creole population living in condition similar to those in which the Carora is reared.

The number of founders (ancestor without known parents) was 1665, 39 of which may be considered effective founders, namely, those founders that are expected to produce the same genetic diversity in the

population.

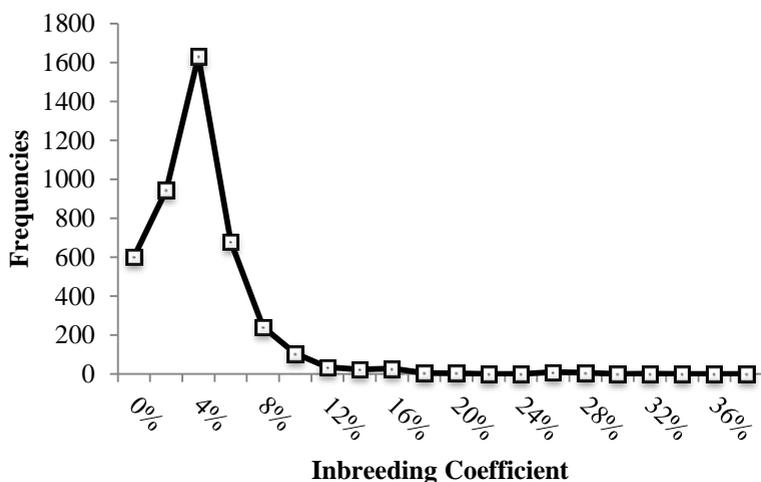
The complete genetic diversity of the Carora living population was explained by an effective number of 28 ancestors, but only 10 were those who contributed to the 50% of the total variability of the population.

The ratio between effective founders and effective ancestors (f_e/f_a) resulted 1.4, indicating a bottleneck in the population, that probably occurred in the past years (Boichard *et al.*, 1997).

The inbreeding coefficient (F) varied from 0 to 38% but on average resulted 3.17%, as shown in Figure 4.

The accuracy of the resulting values of inbreeding was confirmed by the PEC (pedigree completeness index) taking in account 3, 5 or 8 generation back in the pedigree; that resulted 91, 84 and 61%, respectively.

Figure 4: Frequencies of the inbreeding (F) coefficient in the Carora living population.

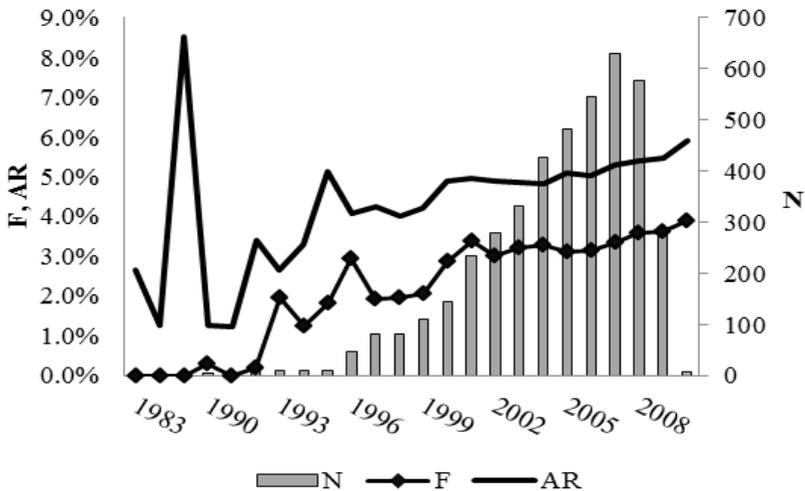


PEC values of the first five generation in the past can easily fall in to the limit of at least 80%, suggested by MacCluer *et al.*, (1983) as good indicator of the accuracy of the inbreeding coefficient in a population, since less complete pedigrees give clearly underestimated inbreeding coefficients, and consequently the rate of inbreeding may be overestimated.

The average relatedness resulted 5.91%.

In the last years, the trends, even if increasing, in average inbreeding (F) and average relatedness (AR) seemed to be more stable, also in relation to the number of individual born in the period of the study, as shown in Figure 5.

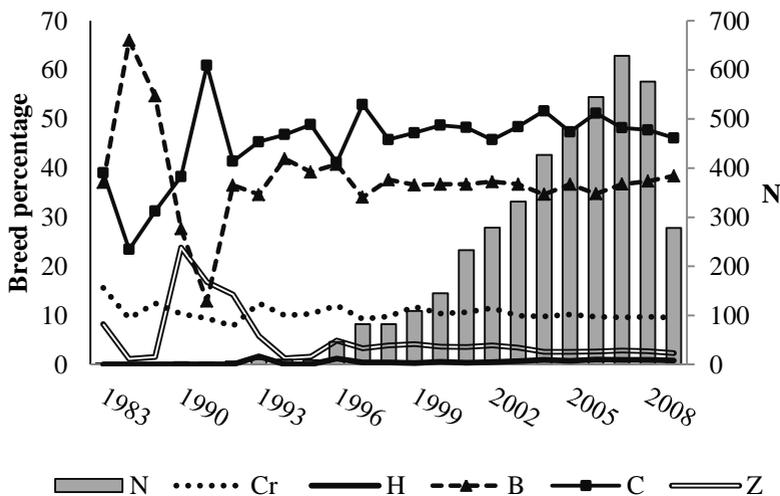
Figure 5: Trends in level of average inbreeding (F), average relatedness (AR), and number of individuals born (N) by year of birth in the period 1983- 2009.



Starting from the inbreeding coefficient (F), was possible to calculate the ΔF , the increase in inbreeding per generation; that resulted 0.75%, and consecutively the effective number of the population N_e , that resulted 67, two parameters useful when estimating the endangerment of

a population.

Figure 6: Trends in the genes proportion in the actual living population in relation to the number of individuals born (N) by year of birth in the period 1983-2009.



These values were comprised in the limit of maximum 1% (ΔF) per generation and an effective size of at least 50 animals, below of which the fitness of a population steady decreases (Meuwissen and Woolliams, 1994).

Regarding the trends in breed proportion, as shown in Figure 6, indicated that the two prevalent breeds were represented by the Brown Swiss and the Carora breeds, while the other breeds had just a marginal contribution in the current population, especially in the last years.

Considering the breed proportion among effective ancestors (f_a) of the living population, results showed an high percentage of Brown Swiss genes in those ancestors that contributed to the 100% and 50% of the total genetic variability of the actual population.

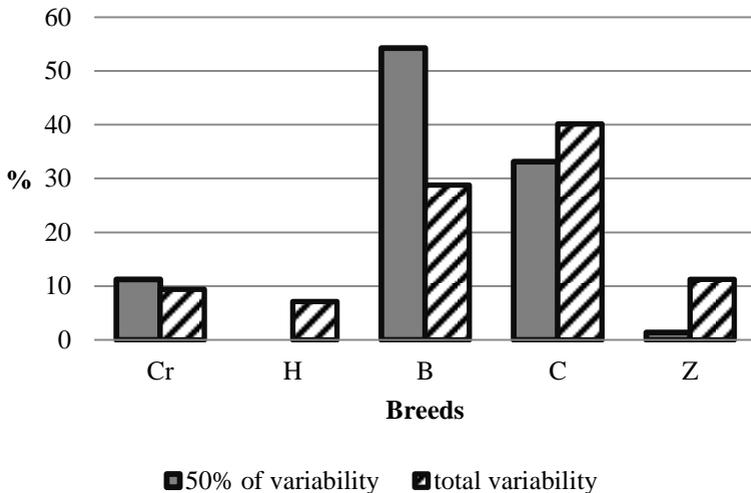
It is noteworthy the slight increase of the Brown Swiss genes proportion

in the breed; this could be related to the selection strategy carried out until now and focused on the improvement of milk production, since higher yields are associated to the presence of “European genes” as reported by Tullo *et al.* (2010).

Figure 7 reports the mean probabilities of gene origin of those ancestors that contributed to the total genetic variability (dashed bars) and of those ancestors that contributed to the 50% of the genetic variability of the population under study (solid bars).

Even if in the 1665 ancestors that contributed to the total variability the prevalence of the genes was represented by Carora genes, in the small number of the effective ancestors, contributing to the 50% of genetic variability of the current population ($f_a=10$), an high percentage of Brown Swiss genes (>50%) was found, confirming the trend reported in Figure 6.

Figure 7: Breed proportion of the ancestor contributing to the 50% and the total genetic variability in the actual Carora population.



These results could be relevant, because the increase of Brown Swiss genes could be positively linked to high milk production, but on the other hand could be also linked to the presence of the long furry hair coat typical of the Brown Swiss, an undesirable trait when breeding in tropical conditions (Olson *et al.*, 2003).

CONCLUSIONS

The completeness of the Carora breed pedigree is index of the goodness of the management in the recording genealogical data in the Carora Breeders' Association.

Despite the small size of the Carora population, this breed is not endangered. The average inbreeding coefficient is not alarming, even if a correct breeding strategy is required to maintain this coefficient at this level.

The awareness of the limit that shouldn't be exceeded, combined with the correct data management could be the right tools for the conservation, and the development of this breed.

Regarding the breed proportion in the current population, the Carora Breeders Association should account for the racial composition of those animals involved in the reproduction, since a lack of attention in this aspect, aiming only to the increase of milk production, could lead to the proliferation of animals less adapted to the harsh environment, with all those consequences of heat stress and reduced productivity typical of temperate breeds reared in Tropics.

CHAPTER 3

*GENETIC EFFECTS ON MILK
PRODUCTION AND WEIGHT
IN A CATTLE POPULATION IN
TROPICS*

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3. Genetic effects on milk production and weight in a cattle population in Tropics

ABSTRACT

Genetic parameters of weight at 18 months (W18) and milk yield (MY) of 1781 Venezuelan cows were estimated with a Multiple Trait Animal Model, that included the random genetic additive effect, the fixed effects of the herd, the year, the season of weighting/calving, the direct breed effects and the epistatic loss, calculated as $1-\Sigma p^2$, where p is the breed proportion.

Heritability estimates were 0.32 ± 0.03 for W18 and 0.23 ± 0.03 for MY, and the genetic correlation between the two traits resulted 0.50 ± 0.08 . Direct breeds effects and epistatic loss affected milk trait, while they seemed not important for weight. A high percentage of *Bos Taurus* genes positively influenced milk production.

Keywords: Genetic variability, milk production, weight at first insemination, tropical dairy breed.

INTRODUCTION

Carora is a short-horned *Bos taurus* cattle breed raised in Venezuela and other Southern American countries, mainly for milk production (ASOCRICA, 2007). It is a synthetic breed developed in west-central Venezuela by using Brown Swiss semen on the local Creole population (Ganado Creole de Quebrada Arriba). Its origins can be traced back to the 1930's and it was declared to be a breed by the Venezuelan Government in 1975 (Morales *et al.*, 1989). Carora cattle are bred in a tropical environment with a large range of average temperatures, with relative humidity up to 90%, and under different production systems, from extensive systems, characterized by grazing and manual milking in the presence of the calf, to intensive systems with high yields, machine milking, and feed supplementation. The primary selection objective is improving milk production in terms of quantity and quality. Since 1995, Carora bulls have been used in Holstein herds to obtain a crossbred and more productive animal adapted to the tropical climate. In addition, Carora bulls are mated today to *Bos. indicus* cows with the aim of obtaining dual-purpose animals.

The object of this study is to evaluate both the additive and non-additive genetic effects on the milk production and on weight at 18 months and the genetic parameters for the two traits in Carora and dual purpose cows in tropical environment.

MATERIAL AND METHODS

1781 weights at 18 months (W18), for 1245 Carora and 356 crossbred cows were collected from 1992 to 2006 on 21 herds of the central-west part of Venezuela. For these cows, 4844 milk yields (MY) at 305 days were collected in the same period, but the number of herds increased to 27.

For each animal, information relative to the herd, the year and the month of calving/weighting, and the proportion of breed genes were available.

Months were pooled in three seasons: the dry season from December to March, the wet season from May to August and the transition season that included the remaining months.

Breeds involved in the sample composition were Carora (CAR), Creole (CRI), Holstein Fresian (HOL), Brown Swiss (BRO) and Zebu (ZEB) breed.

For each animal the epistatic loss was calculated as $1 - \Sigma p^2$, where p is the breed proportion, according to Kinghorn (1980, 1983) who defined 'epistatic loss' as 'proportional to the probability that two non-allelic genes in the diploid individual are of different breeds'.

The crossbreds averaged between 0 to 54.69% of CRI breed genes, from 0 to 75% for HOL and BRO and from 0 to 100% for CAR and ZEB (Co)variance components for W18, and MY, were estimated by a Multiple Trait Animal Model, that included the random genetic additive effect, the fixed effects of the herd, the year, the season of weighting/calving, the direct breed effects, considered as the deviation from Carora breed, the epistatic effects (Kinghorn, 1980) and only for the MY model the permanent environmental as random effect and the age of calving as fixed effect. Pedigree information for these analyses

included 203 sires and 1479 dams for a total of 4432 animals. All analyses were performed with VCE6 software (Groeneveld *et al.*, 2008).

RESULTS AND DISCUSSION

Descriptive statistics for weight at 18 months and milk yield are in Table 1

Table 1: Means, standard deviations and coefficients of variation for weight at 18 months (W18) and milk yield (MY)

TRAIT	N	Mean	ST.DEV	Coefficient of Variation
W18 (kg)	1781	293.45	48.09	16%
MY (kg)	4844	3011.93	1157.00	38%

Their heritabilities, genetic and phenotypic correlation with the relative standard errors are reported in Table 2.

Table 2 Heritability (diagonal), genetic (upper) and phenotypic (lower) correlations of weight at 18 months (W18) and milk yield (MY) with relative standard errors in parenthesis.

	W18	MY
W18	0.32 (0.03)	0.50 (0.08)
MY	0.14	0.23 (0.03)

Results from the analysis relative to weight at 18 months and milk are similar to those found in literature for dairy cattle in tropical environments: heritability of body weight (0.32 ± 0.06) is in agreement with values reported by Araguren-Mendéz *et al* (2006), who found values of 0.38 ± 0.10, while the heritability of the milk (0.23 ± 0.03) is close to value of 0.25 found by Syrstad *et al* (1993).

Genetic and phenotypic correlations differed from those ones reported elsewhere in the literature. Genetic correlation, 0.50 ± 0.08 , was higher than value of 0.34 reported for dual purpose cows (Salgado *et al.*, 2008). Vercesi Filho *et al* (2006) found a negative correlation (-0.22 ± 0.22) between milk and weight in crossbred dairy cattle in Brazil.

The phenotypic correlation (0.14) is positive and higher than that reported by Vercesi Filho *et al* (2006), who found a negative phenotypic correlation (-0.13).

Repeatability for milk, 0.37, can be included in the range of repeatability of tropical breeds reported by Syrstad (1993).

Heterozigosity and breed effects for weight and milk yield are reported in table 3.

Table 3 Heterozigosity and breed effects for weight and milk yield

	W18	MY
Epistatic loss	-3.28	490.05
Breed effect:		
CRI	-0.034	-10.623
HOL	-0.013	3.711
BRO	-0.003	3.331
ZEB	-0.016	-2.849

Results of the analysis show an important difference between the W18 and the MY. The value of -3.28 for weight indicates that for an increase of 1% of epistatic loss, there is an expected decrease in W18 of 0.03 kg., while, in the opposite way, for milk the increase in epistatic loss corresponds to an increase of 4,9 kg of milk. In other words, if an animal is not purebred milk yield is expected to increase up to 490 kg.

Breed effect plays a more important role on the milk yield than on the weight at 18 months. In general, the breed of the animal have a small effect on weight and these results could be due to the small differences

in the size of the animals involved in this analysis. However, when the direct effects of the breed are not considered, the epistatic loss value falls to -9.04 kg and this suggests that the direct effects, even if small, affect the variability of the trait.

In contrast, for milk yield, there is an important breed effect. In fact, the substitution of 1% of Carora with Creole genes leads to a decrease of 10.6 kg of milk. Direct Zebu breed effects were similar in sign but the decrease is smaller, 2 kg instead of 10, for an increase of 1% of Zebu genes.

The two European breeds (HOL and BRO) show similar results (3.711 and 3.331), that is, the substitution of 1% of CAR with HOL or BRO genes leads to an increase of milk production of about 3 kg. That is not surprising, because Holstein and Brown Swiss breeds are specialized in milk production and have been selected towards this objective for many years. Results are in agreement with those ones found by Kahi *et al* (2000) and Montaldo *et al* (2006) that reported the positive effects of the HOL breed in selection programs to improve milk yields in local populations.

CONCLUSIONS

Heritability both for weight and for milk yield were in the ranges previously reported for these two traits. Furthermore, a positive and average to high correlation between these two traits was found, indicating that selection for cows reared in tropical environments with high weight at 18 months, which corresponds to age at first insemination, may improve milk yield. Positive additive direct effects for milk yield were found for European breeds, but direct effects on

weight were very small. Results relative to non-additive genetics effects suggested that crossbreeding effects would be important to milk yield improvement.

CHAPTER 4

GENETIC EVALUATION OF THE CARORA DAIRY CATTLE BREED USING TEST DAY RANDOM REGRESSION MODELS

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4. Genetic evaluation of the Carora dairy cattle breed using test day random regression models

ABSTRACT

In tropical environments, lactation curves with lower peaks and higher persistency might be desirable from both an economical and a physiological standpoint. The objective of this study was to obtain genetic parameters for test day yields (TD), and persistency (PS) for the tropical breed Carora and to compare these with results from a standard 305-yield animal model. Four random regression models (RRM) were used on a dataset composed of 95606 test day records collected in Venezuela from 1992 to 2010, and tested to find the best fitting the data. Milk TD yields (kg), comprised between 5 and 400 DIM, were analyzed with four model that included fixed effects of class of age, year and month of calving, herd and the Legendre polynomials of days in milk, from third to fourth order, for additive and permanent environmental effects, respectively. Random effects were fitted for the interaction herd-year-month-of-test and for the additive genetic and permanent environmental effects.

Akaike's information criterion (AIC) and minus twice log likelihood (-2logL), were used to compare the models and to choose the best one fitting the data.

Estimated daily heritabilities for milk yields ranged from 0.21 to 0.30, with the lowest values around the peak of the lactation. Within lactation

repeatabilities ranged from 0.50 to 0.56. Correlation values between the BVs obtained with the RRM and the lactation model currently used in Venezuela (stAM), are quite high and positive (Pearson correlation=0.71 and Spearman correlation=0.72). Correlations between persistency and 305d milk yield EBV ranged from -0.18 (PS as the deviation of daily productions in the interval 50-279 DIM from a point in the end of lactations) to 0.52 (PS as EBV difference between the second and the first stage of lactation).

In general, heritability values for the five measures of persistency resulted on average (from 0.18 to 0.26), indicating the possibility of new selection opportunities.

The use of persistency indexes accounting for milk yield, may allow the selection of individuals able to express their potential genetic values in tropical environment, without incurring in excessive heat stress losses

Keywords: Random Regression Models, Persistency, Dairy Cattle, Tropics

INTRODUCTION

Current systems of genetic evaluation for dairy cattle productive traits (milk yield, fat and protein percentage) are based on the analysis of data relative to the cumulative production of the lactation, estimated by the sum of test day record data.

Test day (TD) records are represented by record of the production taken along the lactation, usually at well-defined time intervals (generally every 3, 4 or 6 weeks).

The current system of ranking, focused on the whole lactation yield, is based on the Animal Model (AM), that is a genetic evaluation where all animals, male and female, are evaluated at the same time. In this kind of analysis, the cow's milk record is considered the result of the sum of the cow's genetic ability and management and environmental effects.

Sometimes evaluation is performed on a trait that is repeated during the animal's productive life; as lactation for cows or litters in pigs, and for this reason it is possible to use the Repeatability Model (RM) that differs from the AM for the addition of the permanent environmental effect.

This kind of model presents some advantages, like the simplicity and the reduced computation requirements, but the model has some drawbacks, especially when dealing with test day records. TD records are assumed to measure the same trait during the whole lactation length and are used to compute 305 days yield. Those records are actually repeated observations during a trajectory (days in milk-DIM) and the mean and the covariance between measurements changes gradually along the trajectory. Several studies have reported these changes in heritability according to DIM.

In addition genetic correlations between repeated measurements usually tended to decrease as the time between them increased (Pander *et al.*, 1992).

The extension of TD records to compute 305-day yields is unable to account for these changes in the covariance structure.

An appropriate model for the analysis of repeated measurements over time or age (also defined longitudinal data) should account for the mean and covariance structure that changes with time or age and should be feasible in term of estimating the required genetic parameters.

Information relative to single TDs could be directly used for the genetic evaluation, as a replacement for the whole lactation record, even if the amount of data is bigger than those model that use the complete lactation data. For this reason computational requirements are high, but the new information resources allows to overcome this limit and make the use of the TD records for the estimation of the genetic value of dairy animals a routine procedure.

Various methods have been used to analyze this kind of data (Togashi *et al.*, 2004):

- (i) single-trait analysis with a repeatability model, that assume constant genetic variance over ages and genetic correlation of 1 between records taken at different ages;
- (ii) multivariate analysis, that treat each record at different ages as different traits or arbitrarily divide the age range into intervals and treat the measurements of different intervals as different traits;
- (iii) fit a lactation curve to the data and analyze the parameters of the curve as new traits;
- (iv) apply random-regression model (RRM).

Random regression models (RRM) were introduced by Henderson (1982) and Laird and Ware (1982), but only in the 1994 Schaeffer and Dekkers, suggested the use in cattle breeding for the analysis of test day records.

RRM are intended for use on longitudinal data or repeated records situation where observation for a trait are collected several times during the course of the animal's life.

Longitudinal data can be defined as the measurement of the same physical quantity over time on each experimental unit that can be represented by different animals depending on the trait object of the measure.

Repeated measurements deserve a special statistic treatment because of their complex covariance structure: for instance measurements on the same animal are more correlated than records of the same trait on different animals and the correlations between close records, in term of time, may differ from distant records.

Records that are taken along a trajectory, for example time, can be modeled as a function to define this trajectory. The function that describes such a change over time may be of interest since it could explain how and why the characteristics change over time.

Former studies focused the attention for the analysis of longitudinal on Fixed Regression Models (FRM), but, even if they had the advantage of accounting for the shape of the lactation curve for different group of cows, they didn't account for the covariance structure at the genetic level.

Schaeffer and Dekkers (1994) extended the FRM for genetic evaluation by considering the regression coefficient on the same covariates as random, thus allowing for between-animal variation in the shape of the

curve.

Guo and Swalve (1997), found that the genetic differences among animals could be modeled as deviations from the fixed lactation curves by means of random parametric curves, and Brotherstone *et al* (2000) proposed the use of orthogonal polynomials, such as Legendre polynomials, to model the curves.

Areas of animal breeding that have already utilized RRM include conformation traits, body condition scores, feed intake and heart girth measures in dairy cattle; weights and back fat thickness in swine and beef cattle.

Other potential application include wool yield in sheep; sperm production and quality in male reproduction of any species; lifetime milk production in dairy cattle; genotype by environment interactions; survival analysis and female reproduction (Schaeffer, 2004).

An additional benefit of the RRM in dairy cattle is that it provides the possibility of genetic evaluation for persistency of the lactation (Mrode and Thompson, 2005).

Lactation persistency can be defined as the ability of a cow to produce constantly throughout her lactation (Strabel *et al.*, 2001), or the ability of a cow to produce milk at an high level after reaching the peak of her lactation (Jamrozik *et al.*, 1998). Persistency therefore gives an indication of the flatness of the production curve and for ease of interpretation, should be independent of level of production (Jensen, 2001).

Improvement in persistency through selection allows for the possibility of using cheaper food around peak yield (Sölkner and Fuchs, 1987) and may reduce stress due to a high peak production (Mostert *et al.*, 2008). There is an advantageous relationship between flat lactation curves and

a higher disease resistance. It is also often claimed that cows with a high persistency are less susceptible to nutritional disorders and, perhaps as a result of this, more fertile. This could be the result of low energy needs at the onset of lactation, causing these cows to have lower negative energy balances (Mostert *et al.*, 2008). Strabel *et al* (2001), concluded that more persistent lactations are advantageous since they are associated with fewer health problems and reduce feeding and reproductive costs, and also result in a higher yield for longer during the lactation.

The breed object of this study, Carora Cattle breed, is a short-horned *Bos taurus* cattle breed raised in Venezuela and other Southern American countries, mainly for milk production (ASOCRICA, 2007). It is a synthetic breed developed in west-central Venezuela by using Brown Swiss semen on the local Creole population (Ganado Creole de Quebrada Arriba). Its origins can be traced back to the 1930's and it was declared to be a breed by the Venezuelan Government in 1975 (Morales *et al.*, 1989). Carora cattle are bred in a tropical environment with a large range of average temperatures, with relative humidity up to 90% and under different production systems, from extensive systems, characterized by grazing and manual milking in the presence of the calf, to intensive systems with high yields, machine milking, and feed supplementation. The primary selection objective is improving milk production in terms of quantity and quality. Since 1995, Carora bulls have been used in Holstein herds to obtain a crossbred and more productive animal adapted to the tropical climate. In addition, Carora bulls are mated today to *Bos. indicus* cows with the aim of obtaining dual-purpose animals (Cerutti *et al.*, 2006; Caroli *et al.*, 2008)

Since 1992 the genetic evaluation of the Carora dairy breed was carried

on with the single trait AM, using only a part of the available information.

The objective of this study is to infer genetic parameters of lactation and persistency in Carora Dairy cattle through the use of random regression functions for test-day analyses.

MATERIAL AND METHODS

Edited data consisted of 95606 test day records (TD) of 4582 cows in 9543 lactations, were used to evaluate the genetic variability and the variance components of the Carora breed for the daily milk production.

Test day records of the first three lactations (4582 first, 2915 second and 2039 third lactations) were collected in 57 herds located in Venezuela in 19 years from 1992 to 2010. Lactations with the first TD recorded beyond the 40th day and with the first calving lower than 18 months and bigger than 40 months of age were eliminated.

Test day records ranged from the 5th to the 400th day of lactation and on average for each cow 10 controls were available. Average milk daily production was 12.68 ± 5.18 kg. The pedigree file contained 9509 animals, plus 12 phantom groups, in total 9521, to identify animals with missing parent, grouped by a five-year period to avoid problems linked to the lacking of information.

4 random regression models (RRM) were tested to find the best fitting the data. The general structure of the model was:

$$y_{zhijklmnr} = HYM_h + AC_i + NL_j + YOC_k + MOC_r + f_j(t) + \sum_{n=0}^q a_{ln} Z_{mn} + \sum_{n=0}^q p_{ln} Z_{mn} + e_{zhijklmnr}$$

Where $y_{hijklmnr}$ is the z th observation of the l th animal at time t ; HYM is the random effect of herd-year-month of record ($h=6104$ levels), AC_i , NL_j , YOC_k and MOC_r are the fixed effects of age of calving classes ($i=10$ levels), number of lactation ($j=1$ to 3), year of calving ($k=18$ levels) and month of calving ($r=12$ levels). $f_j(t)$ identify the fixed regression function on time that accounts for an average trajectory of yield across all animals within parity j .

$\sum_{n=0}^q a_{ln} z_{mn}$ and $\sum_{n=0}^q p_{ln} z_{mn}$ are respectively the m random regression coefficients for the additive and permanent environmental effect for the l th animal, where z_{mn} are the covariates related to time t and order q (third to fourth order) and $e_{zhijklmnr}$ is the random residual.

Since in this study four models were compared to evaluate the best one fitting the data, the models utilized differed by the order of Legendre polynomials used as covariates for the additive and permanent environmental effects. The models used are reported below:

$$\text{Model 1: } L3L3=L_{\alpha(3)}+Lp(3);$$

$$\text{Model 2: } L3L4=L_{\alpha(3)}+Lp(4);$$

$$\text{Model 3: } L4L3=L_{\alpha(4)}+Lp(3);$$

$$\text{Model 4 } L4L4=L_{\alpha(4)}+Lp(4);$$

where the number in parentheses gives the order of Legendre polynomial for the additive genetic effect (L_{α}) or permanent environmental effect (L_p). Fixed regression function, also in this case were represented by fourth order Legendre polynomials for all the models. Each j -th order polynomial was calculated according to the equation:

$$\varphi_j(t) = \sqrt{\frac{2n+1}{2}} \frac{1}{2^j} \sum_{r=0}^{\frac{j}{2}} \frac{(-1)^r (2j-2r)!}{r! (j-r)! (j-2r)!} t^{j-2r}$$

Where j represented the chosen order for the function (in this study 4) and t was the standardized time interval (from -1 to +1) obtained as follow:

$$w = -1 + 2\left(\frac{\text{DIM} - d_{\min}}{d_{\max} - d_{\min}}\right)$$

where DIM are the days in milk and d_{\min} and d_{\max} are the smallest and the biggest TD recorded ($d_{\min}=5$ and $d_{\max}=400$).

The first six Legendre polynomials for a standardized unit of time w are reported in Table 1.

Table 1: The Legendre polynomial functions of standardized units of time t

Order of fit	Function
0	$0.7071w^0$
1	$1.2247w^1$
2	$-0.7906w^0 + 2.3717w^2$
3	$-2.8062w^1 + 4.6771w^3$
4	$0.7955w^0 - 7.9550w^2 + 9.2808w^4$
5	$4.3973w^1 - 20.5206w^3 + 18.4685w^5$

The Akaike information criterion (AIC) and the minus twice log likelihood ($-2\log L$) were used for model comparison.

Furthermore the best model was compared to the Single Trait Animal Model (stAM) on the same 9543 lactations, and the model was the following:

$$Y_{hijklmn} = H_h + AC_i + NL_j + YOC_k + MOC_m + a_l + pe_l + e_{hijklmn}$$

Where $y_{hijklmn}$ was the n th lactation for the l th animal in the h th herd (57 levels) in the i th class of age at calving (10 levels) in the k th year of calving (18 levels, from 1992 to 2010) in the m th month of calving. The additive genetic effect and the permanent genetic effect were represented respectively by a_i and pe_i .

Daily genetic variances were calculated as:

$$\sigma_{a_i}^2 = t_i G t_i'$$

Where $\sigma_{a_i}^2$ is the genetic variance for DIM i , \mathbf{G} is the genetic variance matrix and where t_i the i^{th} row vector of the matrix containing the Legendre polynomials for standardized day w , for day i , with order of fit k .

The same process was used to calculate the daily permanent environmental variance.

Daily phenotypic variance was calculated as the sum of genetic permanent environmental and residual variances, making possible the computation of daily heritability (h_i^2) and repeatability (r_i).

$$h_i^2 = \frac{\sigma_{a_i}^2}{\sigma_{a_i}^2 + \sigma_{pe_i}^2 + \sigma_{e_i}^2} = \frac{\sigma_{a_i}^2}{\sigma_{y_i}^2}$$

$$r_i = \frac{\sigma_{a_i}^2 + \sigma_{pe_i}^2}{\sigma_{y_i}^2}$$

The total yield genetic and permanent environmental variance were obtained multiplying the G and P matrix by the vector of the coefficients for the whole lactation, obtained summing the 305 daily coefficients.

$$h_{305}^2 = \frac{\sigma_{a_{305}}^2}{\sigma_{y_{305}}^2}$$

$$r_{305} = \frac{\sigma_{a_{305}}^2 + \sigma_{pe_{305}}^2}{\sigma_{y_{305}}^2}$$

Five measures of persistency of lactation were calculated using the results of the RRM, adapting the equations of Jamrozik *et al* (1997), Jakobsen *et al* (2002) and Cobuci *et al* (2004) to the Carora dataset.

The changes only regarded the persistency measures that included the peak of lactation; in fact in this breed, on average, the highest point of the curve is around the 50th day from the calving.

The equations for persistency are reported below:

$$\begin{aligned}
 PS_1 &= (EBV_{270} - EBV_{50}) \\
 PS_2 &= \left(\sum_{t=106}^{205} EBV_t - \sum_{t=6}^{105} EBV_t \right) \\
 PS_3 &= \left(\sum_{t=206}^{305} EBV_t - \sum_{t=6}^{105} EBV_t \right) \\
 PS_4 &= \sum_{t=51}^{270} (P_t - P_{50}) \\
 PS_5 &= \sum_{t=50}^{269} (P_t - P_{270})
 \end{aligned}$$

PS₁ represents the difference between the peak of lactation and a point in the end of the lactation (270th day)

PS₂ and PS₃ represent the differences in EBV between the first third of lactation, and the second third and the last third of lactation, respectively.

PS₄ is the deviation of daily production in the interval 51-270 DIM from the peak production, while PS₅ is the deviation of daily productions in the interval 50-279 DIM from a point in the end of lactations (270th day)

Heritability for each persistency measure was obtained according to the equation of Jakobsen *et al* (2002):

$$h_{(j)}^2 = \frac{\sigma_{a(j)}^2}{\sigma_{a(j)}^2 + \sigma_{pe(j)}^2 + k_{(j)} * \sigma_{e(j)}^2}$$

where ($j= P1, P2, P3, P4, P5$) and $k_{(j)}$ is a constant taking the values 2, 200, 200, 48620, and 48620, for P1, P2, P3, P4, and P5, respectively.

The solutions for RR coefficients for each animals were obtained using the REMLF90 program (Misztal, 2001) with the convergence criterion set to 10^{-12} .

RESULTS AND DISCUSSION

Akaike's information criterion (AIC) and minus twice log likelihood (-2logL), reported in Table 2, were used to compare the models and to choose the best one fitting the data.

Table 2. Akaike's information criterion (AIC), and minus twice log likelihood (-2logL) used for the model comparison.

Model ¹	AIC	-2logL
L3L3	513706.1	513678.1
L3L4	513274	513238
L4L3	518854.2	518818.2
L4L4	518825	518781

The model that resulted the best was the L3L4, in which the order of the coefficients was 3 for the additive genetic effect and 4 for the permanent environmental effect. In a survey on the order of polynomials, Strabel *et al* (2001), reported that the increase of number of parameters for permanent environment (PE) effect could lead to a reduction in the

¹Model L3L3=L $\alpha_{(3)}$ +Lp $_{(3)}$

Model L3L4= L $\alpha_{(3)}$ +Lp $_{(4)}$

Model L4L3=L $\alpha_{(4)}$ +Lp $_{(3)}$

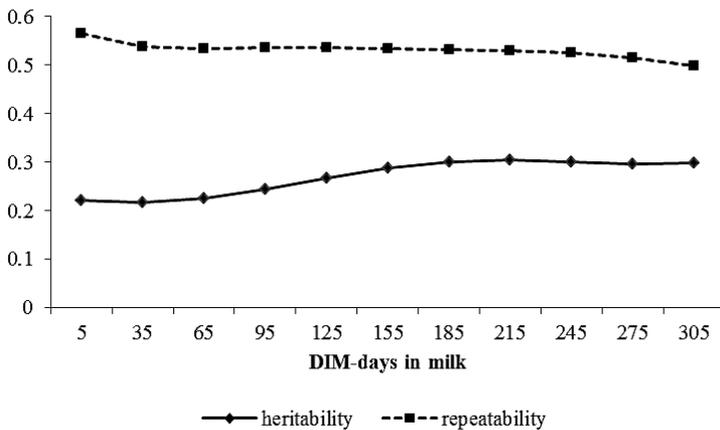
Model L4L4=L $\alpha_{(4)}$ +Lp $_{(4)}$;

where the number in parentheses gives the order of Legendre polynomial for the additive genetic effect (L α) or permanent environmental effect (Lp).

variance of residuals; therefore, the lower order of polynomials for additive genetic (AG) effect than for PE is appropriate and the fourth order of PE and the third order for AG are sufficient.

Starting from the results of this model all the analyses were performed. In Figure 1 are shown the trends for daily heritability and repeatability.

Figure 1: Trends in daily heritability and repeatability for TD model with the best fit to the data.



As it is shown in Figure 1 daily heritability ranged from 0.21 to 0.30 while repeatability ranged from 0.50 to 0.56.

The two trends appear to be in opposition, with an increasing trend during the lactation for the heritability and the opposite situation for the repeatability.

RRM lead to various pattern of daily milk yield heritability (h^2).

The slope of the h^2 curve with lower values at the beginning and at the end of lactation are more desirable as these trends are strongly influenced by non-genetic effects cumulated before calving and associated with the farmer's decision about drying off (Strabel *et al.*, 2001). On the other hand Jamrozik *et al* (1997), asserted that at the

beginning of the lactation heritability could be highest because the daily yields during the first 10 days may be critical to calf survival in terms of volume and content and could lead to a large genetic component.

Reported values agreed with those found in literature, particularly with those obtained by Santellano-Estrada *et al* (2008).

The h_{305}^2 value of 0.33 was quite higher to the value obtained on the stAM on the same lactations data (0.18), and the same situation was found for r_{305} values, 0.53 for the RRM versus 0.39 in the single trait, but this discrepancy between values could be easily explained by the huge amount of information available in a TD-RRM.

Correlation values between the BVs obtained with the RRM and the stAM are quite high and positive (Pearson correlation=0.71 and Spearman correlation=0.72), indicating a good association between the models.

This result was confirmed also by the results found in literature (Jakobsen *et al.*, 2002).

The breeding values (BVs) obtained with the RRM were first compared to stAM-BVs to evaluate the correlation, and subsequently were used to calculate the persistency values.

Table 3: Mean \pm Standard deviation (SD) minimum (MIN) and maximum (MAX) values of estimated breeding values (EBV) for persistency of lactation (PS₁₋₅).

Persistency	Mean \pm SD	MIN	MAX
PS ₁	0.318 \pm 0.86	-2.85877	4.617
PS ₂	28.46 \pm 58.46	-194.984	288.839
PS ₃	-38.62 \pm 69.93	-300.097	304.69
PS ₄	-582.10 \pm 124.19	-1062	-1.224
PS ₅	-12.32 \pm 82.59	-404.847	353.918

In Table 3 are reported the mean (\pm SD), maximum and minimum values of six measure of estimated breeding values (EBV) of persistency.

Genetic correlations among the five persistency measures and for 305 days milk yield obtained RRM and stAM are reported in Table 4.

The difference could be related to the differences in the amount of information in the two models.

Table 4: Heritability (diagonal) Pearson (above the diagonal) and Spearman (below the diagonal) correlations among persistency values, BV of 305 day obtained with the RRM (BV_{RRM}) and the stAM (BV_{ST})

	PS ₁	PS ₂	PS ₃	PS ₄	PS ₅	BV _{ST}	BV _{RRM}
PS ₁	0.26	0.90	0.97	0.95	-0.87	0.45	0.41
PS ₂	0.88	0.25	0.77	0.99	-0.58	0.56	0.52
PS ₃	0.96	0.73	0.26	0.83	-0.97	0.35	0.30
PS ₄	0.93	0.99	0.80	0.18	-0.66	0.54	0.50
PS ₅	-0.85	-0.53	-0.96	-0.62	0.18	-0.22	-0.18
BV _{ST}	0.44	0.55	0.34	0.54	-0.21	0.18	0.71
BV _{RRM}	0.39	0.53	0.28	0.50	-0.15	0.72	0.33

Different values of persistency were reported by Jakobsen *et al* (2002); Cobuci *et al* (2007); however, it is difficult to compare our values with those ones found in literature, firstly, because day of peak is earlier in Carora breed, and, secondly, because the three persistency measures out of five were reported as EBV.

According to our results and correlations, high values of PS₁, PS₂, PS₃ and PS₄ and low values of PS₅ indicated a high value of persistency of the lactation. Regarding the values of PS₁, this could be explained by the fact that this measure was the results of a difference between a point at

the beginning of the lactation (50th day) and a point in the last part of the lactation (270th day) and a larger positive value of this deviation indicated a higher production in the last part of the lactation, or in other words, a more constant level of production. The average positive correlation with the 305days milk yield (0.41), confirmed the increase in production related to the increase of persistency.

The same consideration could be done for PS₂, PS₃, that were obtained by the difference between the EBV of the yield of second third of the lactation (PS₂-reference period: 106-205 days) and the EBV of the yield of last third of the lactation (PS₃ - reference period: 206-305 days) with the yield of the first third of the lactation (reference period: 6-105 days). Also for these measures, larger positive values were associated to a more constant level of production in the central and final part of the lactation; furthermore the increase of production was confirmed by the correlation with the 305 milk yield EBVs that resulted 0.52 with PS₂, and 0.30 with PS₃, respectively.

Another positive correlation was obtained between the EBVs for total milk yield and the EBVs for PS₄ (0.50).

These measures represented the summation of the daily deviations of the interval 51-279 days from the 50th day.

High values of PS₄ indicated a slight slope of the lactation curve, since these values was obtained as a sum of negative values, more the value is close to 0 more the lactation is constant.

The opposite situation was found for PS₅ values, that were the sum of the daily deviations of the interval 50-269 day from the 270th day of lactation. In this case lower values indicated high persistency since the deviations from the 270th day were smaller when lactation curves presented a less marked slope. For this measure of persistency the

correlation with the 305 days milk yield resulted -0.18, indicating that the values of PS_5 were negatively associated to EBV for the 305 milk yield.

The Pearson correlations between persistency measures confirmed the trend in persistency, especially correlation between PS_5 and the other measures (from -0.66 to -0.98) and this indicated the opposite trend of this measure respect to the others.

The rank correlations (below the diagonal in Table 4) confirmed the Pearson correlation showing the absence of large re-ranking in the population.

Heritability for the five measures of persistency were slightly higher than those reported by Jakobsen *et al* (2002),

The moderate value of heritability of PS_2 (0.25) and the quite high value of correlation with the 305 milk yield (0.52) could be interesting when selecting for quantity of milk yield and persistency

In general these values of heritability are low to moderate and selection for persistency could be included in breeding programs. The negative correlation of PS_5 appeared interesting, since lower values of this measures indicated higher milk yields.

CONCLUSIONS

The use of RRM to analyze longitudinal traits makes it possible to study changes over time, and in a dairy cattle context means a better comprehension of the genetics of lactation.

The correlation between the stAM with the TD-RRM indicates the possibility to use this kind of model instead of the model currently used by the Carora Breeders Association, and based on the lactation records.

The use of a RRM could be useful especially when dealing with records collected in tropical environment, because of the large impact of the environment on daily milk production.

Furthermore, by RRM, genetic merit of animals can be predicted based on daily milk yield records from early lactations.

The five measures of persistency calculated in this study could open new selection opportunities. The importance of these traits should be better investigated, especially considering the moderate heritability and the positive relation with the total milk yield.

However, further studies are needed to evaluate the effectiveness of measures of persistency as selection criteria for the simultaneous improvement of lactation yield and persistency.

CHAPTER 5

SUMMARY

5. Summary

The aim of this thesis was to investigate the most appropriate selection methodology for a tropical dairy cattle breed. Results from this study could be useful for a correct genetic management of this little synthetic breed.

The level of pedigree depth and completeness in the living Carora population, despite its small size, is good and permits the reliable estimation of the parameters defining the genetic variability. Analyses of these parameters indicate that the Carora population is not endangered, since the rate of inbreeding per generation (ΔF) is below of the limit of 1% advised by the Convention on Biological Diversity (CBD, 1992). However, the increase of Brown Swiss gene proportion in the population should be controlled. In fact, these genes are positively associated to milk yield, but can affect negatively the adaptability to the tropical environment, in terms of fertility and survival (Blake, 2004).

The increase of Brown Swiss genes could lead to a decrease of the incidence of short hair type coat. This trait is one of the most effective defenses against heat in tropical environments, since it allows the sun reflection and the maintaining of homeostasis. This could be the object of a more exhaustive study, to understand the complex relation between the increase of productivity and the limitation of the use of Brown Swiss semen. The decrease of *slick* haired coats is also due to presence of heterozygous carriers of that gene, which cannot be distinguished from the normal haired coats. From this point of view, studies should be focused on genetic markers associated to *slick* hair gene, in order to correctly identify genotypes and to include the *slick* hair coat in the breeding program.

The Breeders Association should go on with the genetic management of the breed to monitor inbreeding by selecting calves on the basis of pedigree index and relationship coefficient.

Another important aspect concerns the relation between milk production and persistency. Persistency plays an important role along lactation, and may be more advantageous because of the better use of feed and reduction of stress due to high peak yield.

The good correlation between flatter curves and milk yield, could be a starting point for further studies and for any potential selection strategy. Of course, persistency evaluation could be possible only embracing random regression models for the genetic evaluation of animals.

The RRM presents several advantages in comparison with models using records of complete lactations, because of the larger amount of information that permits to account for temporal environmental effects, to reduce the residual variance component, to increase both estimated heritability and the EBVs accuracy. Random regression models could be also used when few records are available; this permits the reduction of the number of test day records collected during the lactation and the reduction of costs for breeders.

Milk production resulted positively associated to live weight of heifers at 18 months. Heifers with adequate size and body condition could be inseminated earlier and could have higher lifetime production. However, as size increases, also nutrient requirements increase, leading to raise of feed costs, and to reduced incomes especially for smallholders. To handle this problem farmers are stimulate to use more pastures, with negative consequences on the environment, in terms of grazing pressure and land conversion (e.g., forest clearing for pastures).

For these reasons the Association is going to modify the breeding

objectives, giving more emphasis on milk yield per unit of weight or, per unit of metabolic weight rather than on milk yield *per se*, in order to increase the sustainability reducing grazing pressure maintaining the same productive level.

These traits are seldom reported in literature, but their genetic variation is important in tropical dairy production, where variability in feed availability is high.

The Breeders Association is collecting weight data at typical ages during lactation, in order to produce genetic evaluations for this trait and to select for animals with high milk production and reduced size. The use of RRM methodology, could contribute to achieve this target.

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