GENETICS OF LINEAR TYPE TRAITS IN LOCAL

DUAL PURPOSE BREEDS AND

RELATIONSHIPS WITH PRODUCTIVE TRAITS

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RIASSUNTO GENERALE

I caratteri morfologici lineari descrivono gli estremi biologici di un intervallo di caratteristiche visive di un animale e una delle principali ragioni per cui vengono raccolti è quella di permettere gli allevatori e le associazioni di razza di selezionare gli esemplari più funzionali e produttivi. Seguendo questo obiettivo, ogni anno le Associazioni Nazionali di Razza formano e preparano specifici esperti che avranno poi il dovere di valutare i caratteri morfologici lineari di diversi gruppi di bovine. Servendosi dei dati derivanti dalle valutazioni morfologiche di due razze italiane autoctone a duplice attitudine, sono stati elaborati i punteggi di ciascun carattere lineare, con lo scopo di stimare gli aspetti genetici di tali caratteri e le correlazioni con quelli produttivi. Gli obiettivi selettivi delle razze indigene a duplice attitudine prese in considerazione in questo studio sono molto simili e hanno come scopo principale quello di mantenere l'attitudine sia alla produzione di latte che di carne. Per questa ragione, le associazioni di razza danno molta importanza alla definizione dei pesi dei caratteri inclusi nell'indice di selezione, e per questo è fondamentale capire e comprendere appieno gli aspetti genetici sia dei caratteri morfologici che di quelli produttivi.

I primi due studi del presente lavoro di tesi sono stati condotti per due differenti razze bovine a duplice attitudine, ma seguendo all'incirca lo stesso tipo di analisi e prendendo in considerazione nei modelli statistici gli stessi effetti: l'effetto fisso dell'allevamento-anno-esperto, i giorni in lattazione e l'età al parto divisi in classi e infine l'effetto genetico dato dall'animale. Per il primo studio, i dati riguardanti 20 diversi caratteri lineari morfologici appartenenti a 10,735 bovine al primo parto di razza Rendena (principalmente allevata in Trentino Alto Adige, Italia) sono stati analizzati attraverso un modello single-trait per la stima dei valori di ereditabilità, mentre per la stima delle correlazioni fenotipiche e genetiche tra i caratteri morfologici, è stato utilizzato un modello multi-trait. Il valore di ereditabilità più elevato è risultato essere quello per la statura (0.52), mentre il più basso è rappresentato dai piedi (0.12). I caratteri individuali morfologici appartenenti allo stesso gruppo morfologico hanno riportano correlazioni genetiche elevate: sono risultate tutte ≥0.69 tra i caratteri individuali riguardanti la taglia dell'animale, ≥0.87 tra i caratteri riguardanti la muscolosità, da -0.39 a 0.22 tra quelli appartenenti alla forma dell'animale, e infine un range più ampio di valori di correlazione genetica sono stati trovati tra i caratteri

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individuali della mammella (da -0.39 a 0.91). Inoltre, quasi tutte le correlazioni genetiche tra i caratteri individuali della muscolosità e della mammella sono risultate negative (da un minimo di -0.53 di correlazione tra la vista anteriore delle spalle e l'attacco posteriore della mammella, fino ad un massimo di -0.15 di correlazione tra dorso, lombi, groppa e la vista laterale dei capezzoli), fatta eccezione per il carattere inerente la profondità della mammella e quello della lunghezza dei capezzoli che hanno presentato valori leggermente positivi di correlazione genetica (da 0.07 a 0.31) con tutti e quattro i caratteri individuali della muscolosità. In questo primo step, sono stati calcolati anche i trend genetici dal 2000 al 2009 dei caratteri morfologici analizzati. Il risultato di maggiore rilievo è dato dall'aumento del merito genetico dei caratteri mammari durante gli anni, a discapito del merito genetico dei caratteri muscolari, che ha presentato un leggero decremento. Questo significa che le bovine di razza Rendena negli ultimi anni stanno diventando sempre più specializzate per la produzione di latte, perdendo lentamente le caratteristiche necessario alla duplice attitudine. Il secondo studio è stato condotto con lo scopo di valutare i parametri genetici dei caratteri lineari morfologici in un'altra razza autoctona italiana a duplice attitudine: la Valdostana (principalmente allevata in Valle d'Aosta, Italia). Per stimare i valori di ereditabilità e di correlazioni genetiche tra i 26 diversi caratteri morfologici punteggiati per questa razza, sono state prese in considerazioni le valutazioni effettuate su 25,183 primipare del ceppo di Valdostana Pezzata Rossa (ARP) e 14,701 primipare del ceppo di Valdostana Pezzata Nera e Castana (ABP-CHES). Le stime di ereditabilità ottenute attraverso una serie di analisi single-trait hanno mostrato valori che andavano da un minimo di 0.03 (carattere della finezza per entrambi i ceppi) a un massimo di 0.32 (ARP) e di 0.29 (ABP-CHES) per il carattere della statura. Riguardo le correlazioni genetiche tra i caratteri, il valore più elevato per il ceppo di ARP è risultato essere quello della correlazione tra la vista laterale e la vista posteriore del dorso, dei lombi e della groppa (0.97), mentre per ABP-CHES la correlazione maggiore è stata calcolata tra la statura e la lunghezza corporea (0.98), indicando che la selezione per i due caratteri è direttamente proporzionale. Anche per la razza Valdostana, la maggior parte delle correlazioni genetiche tra i caratteri muscolari e quelli mammari sono risultate negative, specialmente quelle che prendevano in considerazione i caratteri volumetrici della mammella. Questi risultati hanno dimostrato un sostanziale comportamento

antagonistico dei caratteri morfologici riguardanti l'attitudine alla produzione di latte e quelli inerenti la produzione di carne.

Lo studio successivo ha avuto come scopo principale quello di valutare un modo più semplice di elaborare l'elevato numero di caratteri morfologici punteggiati dagli esperti ogni anno. Per evitare la ridondanza delle informazioni presenti negli indici di selezione, le associazioni di razza dovrebbero utilizzare nelle valutazioni morfologiche solo un numero limitato di caratteri, preferibilmente quelli che presentano relazioni biologiche note con i caratteri produttivi. L'analisi fattoriale si è dimostrata essere una valida procedura di raggruppamento dei caratteri individuali, in quanto permette il loro raggruppamento nel medesimo fattoriale, e quindi che ogni fattoriale possa a sua volta includere caratteri morfologici con caratteristiche biologiche simili. In questa ottica, è stata applicata l'analisi fattoriale a 20 diversi caratteri lineari morfologici punteggiati su 11,399 bovine di razza Rendena, e a 22 caratteri individuali valutati su 36,168 bovine di razza Valdostana Pezzata Rossa (ARP). A seguito di questa procedura, sono stati trovati 6 fattoriali latenti per ciascuna razza, che presentavano valori di eigenvalue ≥ 1 e che ricoprivano il 63% (Rendena) e il 58% (ARP) della varianza totale. Per entrambe le razze prese in considerazione, il fattoriale 1 (F1) comprendeva caratteri morfologici principalmente legati alla muscolosità e il fattoriale 2 (F2) quelli legati alla taglia dell'animale. I fattoriali 3 (F3) e 4 (F4) rispecchiavano invece i caratteri individuali legati rispettivamente alle misure volumetriche e alla conformazione mammaria. I caratteri morfologici individuali di arti e piedi venivano invece inclusi nel fattoriale 5 (F5), mentre per l'ultimo fattoriale (F6) non era stato trovato un significato biologico preciso. Le stime di ereditabilità maggiori, calcolate attraverso analisi REML single-trait, sono risultate quelle di F2 (0.52 per la Rendena; 0.37 per ARP) e di F1 (0.40 per la Rendena; 0.32 per ARP). Le correlazioni tra i valori genetici stimati (EBV) sui caratteri morfologici individuali e quelli stimati sui sei diversi fattoriali, hanno mostrato coefficienti molto simili a quelli osservati dai risultati dell'analisi fattoriale. Da questo studio è quindi risultato evidente che, per entrambe le razze, il numero di caratteri morfologici punteggiati può essere facilmente rappresentato da un numero più limitato di fattoriali, evitando di ridurre l'accuratezza della descrizione della conformazione degli animali valutati. L'uso dell'analisi fattoriale nelle valutazioni genetiche potrebbe infatti rappresentare un valido aiuto per la definizione dei valori genetici individuali.

L'ultimo studio del presente lavoro di tesi, ha riguardato la stima delle relazioni esistenti tra i caratteri morfologici lineari e quelli inerenti la produzione di latte. L'analisi fattoriale è stata applicata ai caratteri morfologici muscolari e mammari punteggiati su 33,206 bovine al primo e al secondo parto appartenenti alla razza Valdostana Pezzata Rossa, ottenendo 3 diversi fattoriali. F1 rappresentava i caratteri di muscolosità, F2 includeva i caratteri legati alle dimensioni della mammella, e infine F3 rappresentava una buona attitudine lattifera della bovina. Oltre a questo, sono stati presi in considerazione anche 169,008 valutazioni giornaliere riguardanti la produzione di latte, e il contenuto di grasso e proteine (kg/giorno) nello stesso, appartenenti a 16,605 bovine valutate fino alla terza lattazione compresa. Attraverso una serie di analisi AIREML single-trait, sono stati stimati i parametri genetici sia dei fattoriali morfologici che dei caratteri inerenti la produzione di latte. Per analizzare i fattoriali sono stati inseriti nel modello l'effetto fisso dell'allevamento-anno-esperto, le classi di età al parto e quelle di giorni in lattazione al momento della valutazione, e infine l'effetto casuale dell'animale. Le produzioni di latte, grasso e proteine sono state invece elaborate attraverso un modello a ripetibilità, che prendeva in considerazione l'effetto dell'allevamento-giorno di controllo entro lattazione, le classi di gestazione, le classi di età al parto e il mese di parto, entrambi entro lattazione, e infine l'effetto permanente ambientale entro e tra lattazione. Tutti gli effetti sopra citati per i due differenti dataset, sono stati poi uniti in un unico modello per analizzare le correlazioni genetiche e fenotipiche tra i caratteri, attraverso una serie di analisi AIREML bi-trait. I valori di ereditabilità ottenuti sono stati moderati per entrambi i gruppi di caratteri (morfologici e produttivi). I tre fattoriali hanno mostrato valori di 0.31 (F1), 0.17 (F2) e 0.20 (F3), mentre la produzione di latte, grasso e proteine hanno riportato stime di ereditabilità rispettivamente di 0.20, 0.13 e 0.17. Inoltre, le correlazioni genetiche sono risultate elevate e positive tra F2 (dimensioni mammarie) e i tre caratteri produttivi (tutte ≥0.83). Sono state invece calcolati valori di correlazioni genetiche negative per i caratteri produttivi sia con F1 (muscolosità) che con F3 (conformazione mammaria), con un intervallo di valori da -0.23 a -0.53. Infine, le correlazione fenotipiche sono risultate più basse di quelle genetiche per tutti i quattro studi precedentemente presentati.

I risultati derivanti da questi studi potrebbero essere di notevole interesse nella definizione dei pesi adeguati da attribuire ai caratteri analizzati contemporaneamente nella selezione di queste due razze bovine autoctone a duplice attitudine. Infatti, sia

nella razza Rendena che in quella Valdostana la selezione per la duplice attitudine gioca un ruolo molto importante negli obiettivi selettivi e rappresenta il principale obiettivo delle associazioni di razza. E' per questo motivo che una comprensione sempre maggiore e più profonda delle relazioni presenti tra i caratteri morfologici antagonistici della muscolosità e della mammella e anche tra di essi e i caratteri produttivi dovrebbe essere di primaria importanza per i piani di selezione futuri di queste due razze italiane autoctone.

GENERAL ABSTRACT

Linear type traits describe biological extremes for a range of visual characteristics of an animal and one of the primary reason for collecting them is to allow breeders to select the most functional and profitable cows. Following this main objective, every year the National Breeders Associations train specific classifiers with the purpose to evaluate linear type traits in cows. Using data from the morphological evaluations on two Italian dual-purpose autochthonous breeds, the scores for each type trait has been investigated aiming to assess their genetic aspects and their correlations with the productive traits. Selection goals among the dual-purpose and indigenous breeds used in the study are very similar and lead to maintain both milk and meat production aptitudes. For this reason, the Associations give great emphasis to detect the correct weights to attribute to traits included in the indexes. The understanding of the genetics of both morphological and productive traits is therefore fundamental.

The first two steps of the study have been conducted for two different dual-purpose breeds, but following almost the same analysis and taking into account in the model the same effects: the fixed effect of herd-year-classifier contemporary group, the days in milk and age at calving accounted into different classes and the genetic effect of the animal. For the first study, data regarding 20 different type traits from 10,735 first parity cows of the Italian Rendena breed (mainly raised in Trentino Alto Adige region, Italy) were analysed through single trait animal model for the heritability estimates evaluation and using a multi-trait animal model to assess the genetic and phenotypic correlations between type traits. The most heritable type trait was stature (0.52), whereas the lowest was feet (0.12). The same group of type traits showed strong genetic correlations: ≥0.69 among the individual body size traits, ≥0.87 among the individual muscularity traits, from -0.39 to 0.22 among the individual body shape traits, whereas a wider range were found among the individual udder traits (from –0.39 to 0.91). Furthermore, almost all the genetic correlations between the individual muscularity and individual udder traits resulted negative (from -0.53 between shoulder fore view and rear udder attachment, to -0.15 between back, loins and rump and teat placement side view), with only few exception represented by genetic correlations of udder depth and teat length with all the four individual muscularity traits that showed slightly positive correlations (from 0.07 to 0.31). In this first step, also the genetic trends from 2000 to

2009 of type traits have been analysed. The most important result was that the genetic merit for muscularity traits decreased, whereas the genetic merit of the individual udder traits slowly increased over time, meaning that the dual-purpose characteristics of the Rendena cows are becoming more like specialized in milk production. The second step of the study was carried out with the aim to evaluate the genetic parameters of linear type traits in another dual-purpose indigenous breed: the Valdostana breed (mainly raised in Valle d'Aosta region, Italy). Morphological evaluations on 25,183 cows of the Aosta Red Pied (ARP) strain and 14,701 cows of the Aosta Black Pied and Chestnut (ABP-CHES) strain were used to analyse heritability and genetic correlations of 26 different type traits within strain. Heritability estimates obtained from the single-trait animal model analysis ranged from 0.03 (thinness for both strains) to 0.32 (ARP) and 0.29 (ABP-CHES) of stature. Regarding the genetic correlations between the individual type traits, for ARP strain the strongest correlation was between thigh, buttocks side and rear view (0.97), whereas for the ABP-CHES strain the highest correlations were observed between stature and body length (0.98), meaning that selecting for one trait lead to the simultaneous improvement of the other. Also for the Valdostana breed, most of the genetic correlations between muscularity and udder traits resulted negative, especially those involving udder volume. These results indicate a substantial antagonistic behaviour of type traits related to dairy and beef characteristics of animals.

The following step has been addressed to the analysis of a simpler way to manage the large number of information given by the type traits scored on animals and managed by the Breeders Associations. To avoid redundant information in selection indexes, only a limited number of type traits with a known biological relationship with production should be used in the morphological evaluation. Factor analysis resulted to be a useful procedure to group type traits, so that correlated traits could be isolated in the same factor, and therefore each factor could include traits with common biological characteristics. In this study, a factor analysis was applied to 20 individual linear type traits evaluated on 11,399 Rendena cows, and to 22 individual linear type traits evaluated on 36,168 ARP cows. From this procedure, six latent common factors, for each breed, with eigenvalues ≥1 were obtained, explaining 63% (Rendena) and 58% (ARP) of the total variance. For both breeds, factor 1 (F1) included type traits mainly related to muscularity and factor 2 (F2) to body size traits. Factor 3 (F3) and factor 4 (F4) accounted for udder size and udder conformation type traits, respectively. Type

traits regarded feet and legs were included in factor 5 (F5), whereas factor 6 (F6) did not show any biological meaning. The greatest heritability estimates trough the REML single-trait animal model for factor scores were 0.52 in the Rendena and 0.37 in the ARP, respectively for F2. Heritability for F1 resulted 0.40 for the Rendena, and 0.32 for the ARP. Rank correlations between Estimated Breeding Value (EBV) of the individual type traits and of factors showed strongly similar coefficients than those observed in factor analysis. From this study, it was appreciable that for both breeds the number of linear type traits could be easily represented by few factors without reducing in accuracy in describing the conformation of animals evaluated from classifiers. Therefore, the use of factor analysis in genetic evaluation could be taken into account for the morphological evaluation aimed at obtaining individual EBVs.

The final step of the study was to estimate the relationships between linear type traits and milk production traits. Factor analysis was applied to muscularity and udder individual type traits for 33,206 first and second parity cows belonging to the Aosta Red Pied strain of the Valdostana breed, obtaining three latent factors. The F1 reflected the individual muscularity traits, F2 included dimensional udder traits, and finally, F3 represented a good dairy conformation. Furthermore, data from 169,008 test-day (TD) yield records, regarding milk, fat and protein content (kg/day), belonging to the first 3 lactations of 16,605 cows were analysed. Through a series of AIREML single-trait analysis, genetic parameters of both morphological factors and milk related traits were obtained. The models for the two datasets accounted for different effects: for the morphological information, herd-year-classifier, classes of age at calving and of days in milk as fixed effects, and the random additive effect of cow were taken into account. For milk traits, herd-TD within lactation, classes of gestation, classes of age at parity and of month of parity both within lactation, and permanent environment effect were considered for the repeatability TD model, together with the additive genetic component. All the previous effects were jointly retained for the AIREML bi-trait analysis, to assess the phenotypic and genetic correlations among and between traits. Heritability estimates were moderate for both group of traits. F1, F2 and F3 showed heritability values of 0.31, 0.17 and 0.20, whereas milk, fat and protein content presented values of 0.20, 0.13 and 0.17, respectively. Strong and positive genetic correlations were found between all the three milk production traits and F2 (udder dimension traits; $\hat{r} \geq 0.83$). On the other hand, negative genetic correlations were

obtained between milk yield traits and both F1 (muscularity traits) and F3 (udder conformation traits), ranging from -0.23 to -0.53. Phenotypic correlations resulted lower than the genetic ones in all the four steps analysed.

Results from this study could be of great interest in planning the correct weights to give to analysed traits in case of simultaneous selection, as possible for dual purpose breeds like those taken into account. Indeed, in both the Rendena and the Valdostana breeds the selection for purposes play an important role, and represent the main selection goal in both Breeders Associations. Therefore, a deep understanding of the relationships between the antagonistic muscularity and udder type traits and also between them and the productive traits should be of the primary interest for future breeding plans in the two breeds.

# CHAPTER 1

GENERAL

INTRODUCTION

1.1 OVERVIEW ON EVALUATION OF MORPHOLOGICAL TRAITS

The implementation of functional type traits appraisal systems represents a great innovation in the development of morphological evaluation in livestock species. Prior to 1980, cows were rated on how closely they approached the "ideal" of the trait evaluated. In many cases, each trait considered was a combination of two or more biological characteristics and, frequently, little specific evidence was available to support a definition of the ideal for traits (Norman et al., 1988). In those years, lot of studies involved parameter estimation of descriptive morphological traits (Atkeson et al., 1969; Cassel et al., 1973; Rennie et al., 1974) and their relationships with other variables important for the herd life of livestock (Wilcox et al., 1959; Hanson et al., 1969; Laben et al. 1982). Soon, the deficiencies in the old classification procedure (Wilson, 1979; Norman et al., 1983) contributed to the development of the linear functional type traits appraisal and to the introduction, in 1976, of the concept of linear analysis of type traits (Freeman, 1982). Thompson et al. (1983) gave advantages of linear scoring over categorical system to evaluate type traits: 1) the traits are scored individually; 2) the scores cover the biological range; 3) a wide range of numerical scores can be used; and 4) the degree rather than the desirability is recorded. In other terms, the linear evaluation resulted immediately simpler than the previous classification system. Specific traits were designed to score specific conformational traits from one extreme to the other on a continuous biological scale (Short et al., 1991), and they were described with numerical points. Linear scores usually approximate a normal distribution, and, therefore, more accurate genetic evaluation can be calculated. In addition, the linear type classification allows the evaluation of individual rather than complex traits and the use of a broader numerical scoring range as compare to the traditional system allow the improvement of type traits (Norman et al., 1988). Linear scoring of type is usually carried out routinely for first lactation cows or, sometimes, for groups of offspring of test bulls in many breeds and countries. One reason for characterising offspring through a morphologically system is to present a "picture" of the conformation of cows that breeders might expect when using semen of a particular sire. Another important use of linear type score is to detect deficiencies in the body conformation of animals which could result in severe problems to cope with their environment (e.g., leg problems) or present troubles to the farmer (e.g., milking cows with very loose udders or wrong teats positions; Sölkner and Petschina, 1999).

Selection for type traits has been practised for many years and currently represents a major part of most livestock improvement programmes around the world (Figure 1), due to the economic value recognised to some measurements (Mantovani et al., 2005). Different type traits evaluations for different breeds are today used in many countries. Some literature has reported, over years, studies conducted on dairy and beef cattle. For example in the Holstein Friesian dairy population, United States of America (Thompson et al., 1981; Foster et al., 1989; Short and Lawlor, 1992; Wiggans et al., 2006), Iran (Sanjabi et al., 2003; Toghiani et al., 2009) and Italy (Cassandro et al., 2014) used a 1 to 50 scale system. The same breed has been also considered in other countries, but through a different scoring approach of type classification. In United Kingdom, Brotherstone et al. (1990, 1991) used a range from 1 to 9 points to evaluate the conformation of cows, as well as in Ireland (Berry et al., 2004), in Switzerland (Kadarmideen and Wegmann, 2003) and in the Czech Republic (Němcová et al., 2011). Also for the Brown Swiss cattle, studies reported different scale systems: from 1 to 50 points in the USA (Wiggans et al., 2006) and Italy (Samoré et al., 2010), or a 9-points scale in Switzerland (Moll and Casanova, 1999).

Figure 1. Different type classifications [a] around the world.
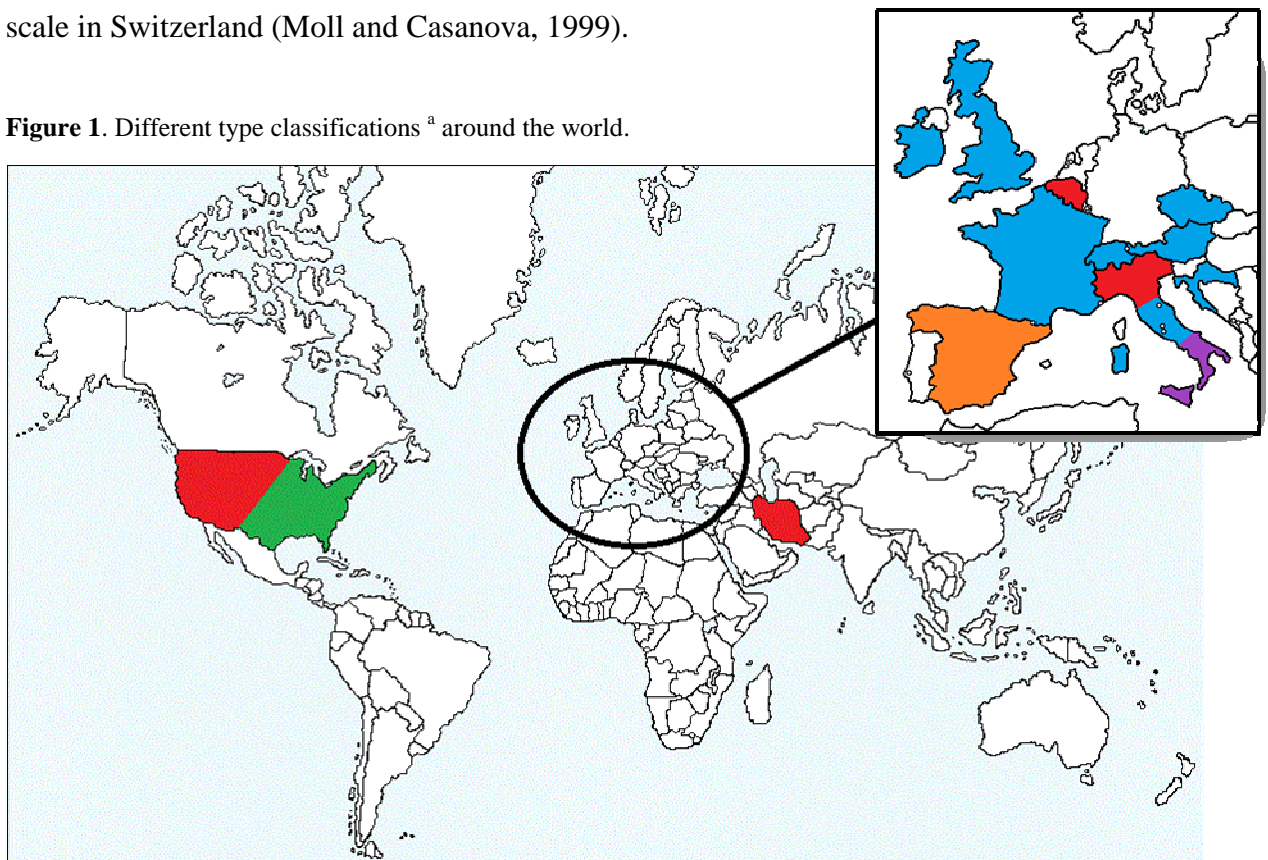
[a] **1-50 points** (Holstein-Friesian, Brown Swiss, Belgian Blue and Milking Shorthorn breeds); **50-99 points** (Jersey, Ayrshire and Guernsey breeds); **1-5 points** (Chianina, Rendena and Valdostana breeds); **1-9 points** (Piemontese, Holstein-Friesian, Brown Swiss, Simmental and Charolais breeds); **5-9 points** (Asturiana de los Valles breeds).

Other dairy breeds were considered by different authors but less frequently. In the USA, a 50 to 99 points scale of evaluation were taken into account at the end of 80's for three different breeds: Jersey (Thomas et al., 1985), Ayrshire and Guernsey (Norman et al., 1988). From reported studies, it results evident that breeders and researchers pay lot of attention on linear type classification of dairy cattle, but little has known about the morphological evaluation on beef and even less about dual purpose breeds. Regarding beef cattle, literature reports that for many breeds the associations use a 1 to 9-point scale system. This has been reported for example for the Austrian and Croatian Simmental (Sölkner and Petschina, 1999; Jovanovac and Raguž, 2011), for the Charolais cattle (Norris et al., 2008) and also for the Italian Piemontese breed (Albera et al., 2001; Mantovani et al., 2010). Other beef breeds use different scales: 1 to 50-points the Belgian Blue breed (Hanset et al., 1998), 1 to 5-points the Italian beef cattle breeds (i.e., Chianina, Marchigiana, Romagnola, Maremmana, and Podolica), and 5 to 9-points the Asturiana de los Valles beef cattle (Gutiérrez et al., 2002). Finally, regarding dual purpose breeds, Norman et al. (1988) reported a range from 1 to 50 points for the Milking Shorthorn cattle, whereas for the Czech Fleckvieh a 1 to 9-point scale system was used (Zavadilová et al., 2009). Moreover, for the Italian Rendena (Mantovani et al., 2005) and Valdostana (Mazza et al., 2013) dual purpose breeds a 5-points scale was took into account for the evaluation of type.

Methods for evaluating cows through type traits are continuously updated and developed to increase the accuracy and objectively of the description of the functional aspects of cow's conformation (Short et al., 1991; Shannon et al., 1993). Type traits can have a good effect on the general appearance of herds, but they cannot be measured objectively and they are more difficult to quantify in monetary values than productive traits (Hinks, 1983). In addition, one of the problems associated with the type classification is the subjective scores that classifiers assign to animals. Classifiers differ in their mean score, and unofficially in the age adjustment method, but also in the range of the scale that they use (Bowden, 1982; Fleuren, 1988). For breeding value estimation, most of these factors can be fixed in the model or, before, by the editing of records process. However, classifier effects still remain a problem for animal breeders (Veerkamp et al., 2002) and a regular training is necessary to homogenise classifier's scoring process. Following this objective, in all countries in which type evaluation is undertaken, classifiers follow specific training organized by the breeder associations.

Despite this, lot of studies carried out in recent years reported adjustments methods for classifier's effects (Brotherstone, 1994; Koenen et al., 2001; Berry et al., 2004). This aiming at reducing possible bias in the estimates of genetic parameters for linear type traits. For each breed and country, classifiers score a very huge number of individual type traits, mainly in the first lactation cows. However, various type traits are scored on the basis of the different selection goals (Table 1). In dairy cattle, most of the type traits recorded regard the dairyness of cows and the body conformation. In these situations, breeder associations evaluate the genetic parameters of body size and udder related traits, such as strength, angularity or even udder height. Type traits associated with feet and legs are also accounted for selection, because of a cow with straighter rear legs is expected to walk with less sideways motion, which would reduce udder contacts and damages, as well as joint impacts and injuries (Wiggans et al., 2006).

Table 1. Overview on the individual type traits evaluated in dairy, beef and dual purpose breeds.

TYPE TRAIT	DAIRY	BEEF	DUAL PURPOSE
Stature	X	X	X
Strength	X		
Angularity	X		
Rump angle/width	X	X	X
Shoulder		X	
Top line		X	
Thighs and Buttocks		X	X
Loins		X	X
Bone thinness		X	
Thorax width/depth		X	X
Feet and Legs	X	X	X
Pasterns	X	X	X
Fore/Rear udder attach	X		X
Suspensory ligament	X		X
Teat placement	X		X
Teat length	X		X

In beef cattle, where the main selection goal is related to the expression of meat performances (Veselá et al., 2005), type traits associated with milk production are of limited interest, and individual type traits highlighting thighs, buttocks and thorax dimensions are the major important descriptors. The morphological evaluation for the dual purpose breeds seems a completely different matter, as compared to the specialized breeds. Indeed, evaluating animals through the morphological type traits could be very difficult when indirect improvement of both milk and meat production are required. A lot of studies reported strong genetic correlations between some udder related traits and milk yield (Mrode and Swanson, 1994; DeGroot et al., 2002; Berry et al., 2004), but also antagonistic behaviour between muscularity traits and dairyness (Mantovani et al., 2010;). From these negative genetic correlations between linear type traits associated with milk and meat production it is evident that breeders associations, in order to maintain the dual purpose attitude, have to take a careful choice of traits to be selected.

Today, all breed associations and virtually all the breeding companies use some form of linear analysis to score the conformation of cattle. Early analyses of these programs involved mainly genetic parameter estimates (Lucas et al., 1984), others (Vinson et al., 1982; Thomas et al., 1984) investigated the relationship of linear scores with other type measurements. One of the primary reasons for collecting and implementing information on type in genetic evaluations is to help breeders in selecting profitable and functional cows so that early culling for causes unrelated to yield (involuntary culling) can be avoided (Misztal et al., 1992). Furthermore, selection emphasis on type associated with longer herd life may be beneficial to increase profitability (Rogers and McDaniel, 1989). Many studies have examined, over years, the relationships between longevity and type traits (Rogers and McDaniel, 1989; Burke and Funk, 1993; Cruickshank et al., 2002; Vacek et al., 2006), showing a certain degree of correlations (Vollema and Groen, 1997; Bouška et al., 2006). However, only a low to moderate genetic relationship between various type traits and the functional longevity (i.e., yield-corrected lifetime) have been reported (Shapiro and Swanson, 1991; Sölkner and Petschina, 1999; Strapák et al., 2005). Besides, Forabosco et al. (2005) suggested that the use of the indirect measures for longevity increases the reliability of proof (Estimating Breeding Value, EBV) in young bulls, and thus stimulates the use of them, aiming also at decreasing the generation interval. Given the nature of type traits as descriptors of cow's physical appearance, there is also an interest in knowing if these

traits are related genetically with calving ease. However, only one study showed that some type traits deal directly with aspects of the animal that might be considered to be related to factors affecting calving ease (Cue, 1990). Finally, researches from different countries indicate the usefulness of linear type traits as predictors of body weight (Veerkamp and Brotherstone, 1997; Koenen and Groen, 1998), health (Rogers et al., 1991; Pryce et al., 1998; Rupp and Boichard, 1999) and fertility (Pryce et al., 1998; Royal et al., 2002).

1.2 GENETIC PARAMETERS: HERITABILITY ESTIMATES AND CORRELATIONS BETWEEN TYPE TRAITS

An important question in many scientific fields is whether observed variation in a particular trait is due to environmental or to biological factors. Heritability is a concept that summarizes how much of the variation in a trait is due to genetic factors (Wray and Visscher, 2008) and it is obtained by the ratio between the genetic variance and the phenotypic variance. From this statement, it is evident how important is the estimation of heritability values even for type traits, particularly when they are included in the selection goals of a given breed. However, findings of zero or close to zero heritability do not demonstrate that genes are irrelevant; rather, it demonstrates that, in the particular population studied, there is no genetic variation for the studied traits (Griffiths, 2000). Various studies reported different heritability estimates for linear type traits, but generally the type associated with body size tend to show the largest heritability values (0.07 to 0.59; Brotherstone, 1994; Koenen and Groen, 1998) followed by the udder traits (0.11 to 0.44; Short and Lawlor, 1992; Veerkamp and Brotherstone, 1997). Heritability values for the feet and legs traits tend to be the smallest (0.07 to 0.27; Brotherstone, 1994; Berry et al., 2004). Almost the same results were showed for beef cattle in which the udder traits are of a less magnitude (Gutiérrez et al., 2002). Regarding dual purpose breeds, despite the poor literature, the heritability estimates reflect the previous values reported in specialized dairy or beef breeds. Indeed, height at withers and body depth are the most heritable trait (0.39 and 0.63, respectively), followed by muscularity, by udder related traits (0.30 and 0.19 respectively) and finally, the less heritable traits are those regarding feet and legs, ranging from 0.09 to 0.19 (Zavadilová et al., 2009).

Selection on one specific trait produces inevitably consequences on the others. This is demonstrated by lot of studies on phenotypic and genetic correlations between type traits evaluated, but it is also evident in specialized dairy cattle that have been widely selected for milk and have today encountered the problem of a short or very short herd life (Essl, 1998; Vukasinovic et al., 1995). Generally, traits regarding the same region of the body represent strong genetic correlations among them both in dairy and in beef cattle, and also in dual purpose breeds. For example, Mantovani et al. (2010) found a genetic correlation of 0.97 between two body size measurements and also from 0.60 to 0.92 between withers, shoulder, loins and thighs traits (body shape related traits) in the Italian Piemontese beef cattle. Strong genetic correlations were also reported among the udder size related traits (from 0.35 to 0.91; Berry et al., 2004; Němcová et al., 2011). Between type traits of different body region, the range of correlations estimated is very large, starting from negative (e.g., between some body size and body shape related traits; Meyer et al., 1987) towards positive correlations (e.g., 0.54 between stature and udder; Berry et al., 2004). Regarding the dual purpose breeds, a special focus has to be place on the genetic correlations between the antagonistic muscularity and udder related traits. The little literature found reports negative relationships between lot of the individual type traits associated with milk and meat production (Degano, 2014) These findings are very relevant for the dual aptitude of breeds, as an improvement of one group could lead to a detriment in the other, causing the loss of both milk and meat productions. Finally, phenotypic correlations result lower than the genetic ones in most of the considered studies (De Lorenzo and Everett, 1982; Mrode and Swanson, 1994; Wiggans et al., 2006).

1.3 FACTOR ANALYSIS AS A USEFUL VARIABLE REDUCING PROCEDURE

Examining carefully all the literature previously mentioned, it is evident that a great number of type traits is currently evaluated in many cattle breeds. Therefore, a major problem associated with linear type scores is, as a matter of fact, the huge amount of traits that classifiers have to score every year. In addition, a strong degree of interrelationships can occur among the traits scored. Indeed, type referring to the same part of the body usually show high genetic correlations (Sieber et al., 1987). Furthermore, the aggregation of all important traits for selection in a global index is

often a complex matter (Macciotta et al., 2012). Over years, many dairy conformation systems have been developed over time, and each one involve usually a number of highly correlated traits that could be simplified. For example, Schaeffer et al. (1985) found strong genetic correlations among udder traits in Holstein, although ranging from 0.27 between rear height and teat placement to 0.75 between udder support and teat placement. Similarly, Short and Lawlor (1992) reported strong correlations of fore udder attachment with both udder depth (r_g = 0.79) and udder width (r_g = 0.90) in Holstein cattle. High genetic correlations were also found among non-udder related traits by Lin et al. (1987) and Misztal et al. (1995) that showed strong values between stature, body depth and strength, ranging from 0.75 to 0.95. Furthermore, the shortcoming of using a large number of type traits in genetic evaluation could lead to a severe overestimation of the accuracy of EBV for herd life (Visscher, 1994). To avoid this, and also to reduce the amount of traits managed by breeder associations, only a limited number of type traits with a known biological relationship should be used. A general statistical approach which properly accounts for dependencies among variables is the factor analysis (Linder and Berchtold, 1982). This procedure is aimed to remove redundant information from correlated variables and represents the "new" traits with a smaller set of derived variables called "factors". Nowadays the factor procedure is available in many statistical program packages such as SAS (Statistical Analysis System), BMDP (BioMeDical Package) and SPSS (Statistical Package for Social Science; Russel, 2002) and it is used in many fields. Ali et al. (1998) reported that applying the factor analysis to type trait data is important for different reasons. Indeed it allows:

1- to summarize information from the observed type traits into a few unobserved and relatively uncorrelated derived factors;

2- to partition each trait response into a covariant and therefore the variances of each component can be estimated;

3- to group type traits, such that correlated traits (i.e., controlled by same genes) could be isolated in the same factor and each factor will include traits with common biological characteristics.

In other words, what factor analysis provides is a method for examining the structure of phenotypic, genetic and environmental variation in a population of individuals. The interpretation of the outputs requires an understanding of the sources of correlations between traits loaded into factors. Different studies (Thompson, 1957;

Anastasi, 1970) have investigated these arguments. Correlations may be generated through the action of the pleiotropic effect (the involvement of the same gene, or genes, in the development of two or more traits), genetic linkage, selection or environmental processes. The principal component analysis (PCA) and factor analysis (FA) are both variable reduce techniques that reduces the number of observed traits to a smaller of principal components which account for most of the variance of the observed variables, but they are sometimes mistaken as the same statistical method (Suhr, 2003). Generally, PCA decomposes a correlation matrix with ones on the diagonals and the amount of variance is equal to the trace of the matrix, whereas FA starts from an adjusted matrix in which also the diagonals have been adjusted for the unique factors. The total amount of variance in PCA is equal to the number of observed variables being analysed, in FA observed variables are a linear combination of the underlying factors (estimated factor and a unique factor; Suhr, 2003). The components accounting for the maximal variance are usually retained following the eigenvalues criterion in both methods (Cattell, 1978). According to this criterion, only components with eigenvalues more or equal than 1 is used for the analysis. Macciotta et al. (2012) reported another difference between PCA and FA: in FA the partitioning of explained variance between extracted factors is quite balanced, with an expected slight predominance of the factor 1 (0.29), whereas the eigenvalues of the other factors ranged between 0.1 and 0.19. This is recognized as a peculiarity of FA in comparison with PCA, in which the magnitude of the differences between the first component and the other variables is greater (Jombart et al., 2009).

In Table 2 are reported the results of factor analysis conducted by Vukasinovic et al. (1997) on linear type traits of Swiss Brown cattle. The individual type traits scored were 18, but with the use of PCA, they reduce the number of variables into 5 phenotypic factors that accounted for 58% of the total variation of type traits.

Table 2. Phenotypic factor patter coefficients for factors. Coefficients ≥|30| are in bold.

Type traits		Phenotypic factors				
		P1	P2	P3	P4	P5
1	Wither height	0.01	**0.83**	0.02	0.05	-0.02
2	Heart girth	0.00	**0.56**	-0.02	0.60	0.02
3	Body length	0.12	**0.81**	0.03	0.13	0.06
4	Body depth	0.26	**0.52**	-0.01	**0.39**	0.05
5	Body width	0.00	**0.30**	0.02	**0.73**	0.14
6	Muscularity	0.01	0.07	-0.02	**0.86**	0.16
7	Hocks	0.02	**0.33**	0.08	**-0.46**	**0.47**
8	Pasterns	0.00	0.08	0.05	0.00	**0.69**
9	Front leg position	0.10	-0.06	0.01	0.14	**0.56**
10	Rear leg position	0.11	0.00	0.01	0.12	**0.75**
11	Fore udder	**0.70**	0.05	0.19	0.04	0.07
12	Rear udder	**0.69**	0.14	0.24	-0.04	0.04
13	Udder attachment	**0.73**	-0.04	0.10	0.08	0.10
14	Udder quality	**0.73**	0.11	0.09	-0.01	0.04
15	Teat form	0.09	-0.03	**0.80**	0.03	0.01
16	Teat length	0.06	-0.07	**0.80**	0.10	0.00
17	Teat placement	0.27	0.12	**0.62**	-0.08	0.06
18	Teat position	0.22	0.04	**0.63**	-0.11	0.06

Table modified from Vukasinovic et al. (1997)

Finally, retaining only traits with a given pattern coefficients, for example≥|30| (patterns indicate the contribution of an individual type trait to the particular phenotypic factor), they were able to drive into a subjective description of each factor (Table 3). A more detailed discussion on factor analysis is reported in Chapter 3.

Table 3. Subjective description of phenotypic factors.

Phenotypic factors	Description
P1	Good udders
P2	Tall, long and deep animals with good hocks
P3	Proper teats
P4	Compacted well-musculated animals with rather poor hocks
P5	Good feet and legs

Table modified from Vukasinovic et al. (1997)

1.4 GENETIC CORRELATIONS BETWEEN LINEAR TYPE TRAITS AND MILK YIELD

The primary emphasis in dairy cattle selection is for milk yield traits because highest productive cows usually are more profitable (Bertrand et al., 1985). Various efforts have been tried to clarify the relationships between conformation and production. Producing ability has long been the main objective for dairy farmers and researchers. Copeland (1941) suggested, since the '40s, that if quality conformation and performance cannot be combined in one individual, then breeding goals with respect to type could have been reconsidered later. Indeed, one of the main purposes of type evaluation and selection include development of dairy cattle with longer and more productive lives, but also more appreciated by farmers for their aspect. Lot of studies were conducted on genetic correlations of milk, fat, protein yield and somatic cell scores with type traits (Norman et al., 1988; Misztal et al., 1992). Some researchers report that traits associated with body size have a positive relationship with milk yield. On the other hand, fore udder attachment, udder cleft, and udder depth present a negative association with milk yield, whereas rear udder height and width have a small positive genetic interaction (Foster et al., 1989; Short and Lawlor, 1992). Other studies report correlations between type traits related to udder and somatic cell score (Rogers et al., 1991; Boettcher et al., 1998). DeGroot et al. (2002), for example, reported genetic correlations between traits associated with body size and milk yield ranging from -0.10 (strength) to 0.91 (dairy form). In the same study, negative genetic correlations were found between fore udder attachment, udder depth, teat length and milk yield. These estimates between udder type and yield traits were generally similar to those reported from earlier studies (Misztal et al., 1992; Short and Lawlor, 1992), but in disagreement with Berry et al. (2004) that reported positive and quite strong genetic correlations between fore and rear udder attachments, teat positions and milk yield (from 0.32 to 0.51) in Holstein Friesian. These latter moderate correlations indicate that selection on milk yield alone will result in teats that are closer together from the rear view, but further away from a side view, the latter probably reflecting udder capacity (Berry et al., 2004). Jagtenberg and Scheppingen (1994) reported that cows with poor teat placement are unlike to be compatible with robotic milking system. All the previous statements reflect the high importance that type traits evaluation give to the milk production and milk ability.

Genetic evaluation of dairy sires and cows has evolved immensely over the years. From the initial stages when simple dam-daughter comparisons were made, rapid advances in computer hardware and improvements in computing algorithms have made it possible to implement modern methods for analysis (Dzomba et al., 2010). During years different methods of milk yield evaluation have been developed. One of the firsts was the 305-day lactation model, used to analyse the genetic merit of sires and cows in traditional evaluation (Ali and Schaeffer, 1987). Nowadays, the most used method to analyse milk production is the test day model (TDm), which can account for factors specific for each test-day, such as management groups within a herd on a TD, day of the year (including weather conditions), and, for each cow, days in milk, pregnancy state or even number of times milked on the TD. Many of these effects can change for a cow from different test-day records, and would be difficult to model for 305-day yield (Jamrozik et al., 1997). The most diffused TDm is the random regression (RR-TDm) that allows the fitting of lactation curves to individual lactation. The best known application of RR-TDm has been to genetic evaluation of dairy cattle using test-day production records (Schaeffer et al., 2000). Anyway, for smaller and indigenous populations, a repeatability TD model (RP-TDm) is considered more useful (Dal Zotto et al., 2005; Guzzo et al., 2009). Under this model, consecutive TD samples from the same lactation are considered as repeated observations on the same trait, and a permanent environmental effect accounts for environmental similarities between different TD within the same lactation (Bilal and Khan, 2009).

Linear type traits evaluation represents in lot of breeds a very useful method to indirectly analyse productive traits and also many other functional traits, as fertility, longevity and health. Therefore, it is evident the extreme importance of a correct scoring system and of an accurate management of the data collected by specialized classifiers. Analysis of correlations with milk yield analysed by random TDm have not been already carried out widely, and this could be a field of interest for both breeders and researchers.

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CHAPTER 2

AIMS OF THE THESIS

The present thesis has been carried out with the final intent to evaluate the genetic parameters of the linear type traits in different autochthonous Italian dual purpose breeds and in next steps to investigate a possible method to simplify the management of the data and to assess the relationships between morphological evaluation and production traits. The studies included arise from the collaboration between the University of Padua, Department of Agronomy, Food, Natural resources, Animals and Environment, and two national breeders associations: A.N.A.Re. (National Association of Rendena breeders) based in Trento, Italy, and A.N.A.Bo.Ra.Va. (National Association of Valdostana breed) based in Aosta, Italy. Results from the present work have addressed to define a new global selection indexes in both Rendena and Valdostana breeds and to implement different and more useful methods to manage the data and to evaluate the production traits. In particular, the thesis has been structured in four chapters with the following specific aims:

i. to investigate the environmental effects associated with linear description and to estimate genetic parameters, as heritability values and both phenotypic and genetic correlations between linear type traits describing carefully the body regions in the Rendena primiparous cows. Moreover, the genetic merit of type traits has been quantified to assess the changes over time;

ii. to investigate the influence of some environmental effects, such as the age at calving, days in milk, herds and classifier incidences, in the indigenous Valdostana dual purpose breed. In addition, to investigate the presence of heterogeneity of variance between the two different strains of the breed (Aosta Red Pied and Aosta Black Pied-Chestnut) and also to estimate genetic parameters of linear type traits included in the selection index of dual purpose aptitude: muscularity and udder related traits;

iii. to evaluate the use of factor analysis to simplify and reduce the number of the individual type traits and to clarify the relationships between type and factor traits in the Rendena and in the Aosta Red Pied breed, both selected for the dual purpose;

iv. to estimate, by focusing on the Aosta Red Pied breed, genetic parameters and correlations between linear type traits, obtained thorough the factor analysis, and the milk yield traits, including fat and protein contents, analysed via a repeatability test-day model.

Finally, the thesis ends with a general conclusion about the application of the linear type classification in the genetic improvement of these two autochthonous dual purpose breeds.

CHAPTER 3

GENETIC PARAMETERS FOR LINEAR TYPE TRAITS IN THE RENDENA DUAL-PURPOSE BREED

Part of the results have been presented at the 20th International Symposium "Animal Science Days", Kranjska gora, Slovenia, 2012. *Acta Agriculturae Slovenica*, Supp.3:161-165.

3.1 SUMMARY

The aim of the study was to estimate the genetic parameters of five composite traits and 20 individual type traits on 10,735 first parity cows of the Italian Rendena dual purpose breed. Data were analysed by a single trait animal model for heritability estimates, and using a multi-trait animal model with canonical transformation for correlation estimates. The unique model used accounted for the following effects: herd-year-classifier, days in milk, age at first calving and the genetic additive cow effect. The most heritable trait was the stature (0.52), whereas the lowest values was found for feet (0.12). Genetic correlations were almost all negative, with only few exceptions, for fleshiness with body size and udder traits, and slightly positive (from 0.04 to 0.21) with body shape. Individual body size traits showed weak genetic correlations with body shape and udder. Genetic trends showed that body size, body shape and udder traits increased during the last 10 years, whereas the genetic merit for fleshiness traits decreased. These results suggest that the characteristics of the dual purpose Rendena cattle are becoming more like specialized milk producing animals. Further investigation will be required to analyse the genetic correlations between type traits and productive ones.

3.2 INTRODUCTION

The Rendena breed is an indigenous Italian dual purpose breed (milk and meat) that belongs to the "European federation of cattle breeds of the alpine system", an organization that includes 10 mountain breeds that are the link between the resources naturally found in the mountain areas and production, such as milk and meat and their transformation products (FERBA). The breeding goal for the Rendena is a combination of improved quality and quantity of meat and milk. The Rendena population is mainly raised in Trentino Alto Adige (i.e., the region of origin) and in Veneto, north-east of Italy, particularly in the provinces of Trento, Padova, Vicenza and Verona (Bittante et al., 1993). Rendena cattle are characterised by small to medium size, good fertility and longevity. The coat is characterized by different shades of dark brown, almost black in males, with a white ring around the black muzzle. Studies on genetic diversity have reported a great genetic distance between this breed and other alpine breeds (Del Bo et al., 2001). An important characteristic of the Rendena is its suitability to grazing

pastures both in the valleys and on the high pastures (Alps) of the mountain (Mantovani et al., 1997). Selection in this breed is based on a two-step process in which candidate young bulls obtained from mating bull sires and dams, are selected for beef attitudes during the first year of life in a genetic centre. Selection account for both realized average daily gain coupled with in vivo fleshiness and dressing percentage scored by skilled operators at the end of test (Mantovani et al., 1997). Young candidate bulls are then sent to progeny testing to evaluate their milk attitude. Due to the reduced population size (i.e., a population of about 4,000 registered cows), young bulls are also used as bull sires, to limit the inbreeding in the population and to speed up the genetic change. In addition, Rendena primiparous cows yearly undergone to a morphological evaluation carried out since 1994. This evaluation account for both fleshiness and dairy traits (i.e., mammary traits mainly), and it could become a useful instrument to select bull dams.

Genetic parameters of linear type traits have been documented extensively in Holstein populations (Short & Lawlor, 1991; Veerkamp & Brotherstone, 1997; Berry et al., 2004; Zavadilová & Štípková, 2012). In general, the heritability of traits describing body size (from 0.24 to 0.43) were larger than heritability estimates for traits describing the mammary system (from 0.11 to 0.38) which in turn were larger than feet and legs related traits (from 0.14 to 0.19; Biscarini et al., 2003; Berry et al., 2004; Němcová et al., 2011). Contrasting results were, however, reported in Italian Piemontese cows; heritability estimates for dairyness traits (0.03) were slightly lower than feet and legs traits (0.08; Mantovani et al., 2010), although Piemontese has only few areas in which cows are still milked and the breed is mainly selected for beef attitude. Similar heritability estimates were found for other beef cattle breeds, such as for example for Asturiana de los Valles beef cattle (Gutiérrez & Goyache, 2002). Weak to strong genetic correlations exist among the range of type traits assessed in Holstein and Jersey populations with generally strong correlations evident among traits that describe similar morphological characteristic (Mrode & Swanson, 1994; DeGroot et al., 2002).

No genetic parameters, however, have been published for linear type traits in Rendena cattle. The objective, therefore, of the present study was i) to estimate genetic parameters for a series of type traits describing the body and udder conformation of the breed and ii) to analyse how genetic merit for these traits have changed over time. Results from this study will be useful to quantify the impact of previous breeding

strategies on the morphological characteristic of the Rendena breeds and what potential exists to alter these genetic trends.

3.3 MATERIALS AND METHODS

Data

Linear type classification records on 12,864 primiparous Rendena cows scored between the years 1994 to 2012 were available. The linear type classification system consists of 20 linear description traits and 5 composite traits (Table 1). The individual type traits describe specific body regions of an animal including the thorax, rump, feet, legs, thigh and udder conformation (Table 1). The composite traits summarise body size, fleshiness, body shape, and udder as well as an overall score of animal conformation.

Only animals calving for the first time between 22 and 48 months of age and scored between 10 and 305 days post-calving were retained. Data from herd-year-classifier contemporary groups with <2 records were discarded. After editing 10,735 records remained for subsequent analysis. All available pedigree information (17,180 animals) was used to set up the relationship matrix among animals; the birth date of all animals was also available.

Statistical Analysis

A fixed effects model in PROC GLM (SAS, 2009) was firstly undertaken to quantify the factors associated with each of the 25 traits. Genetic and residual variance components were estimated for each trait separately in a series of univariate animal linear mixed model analyses in the REMLf90 program (Misztal, 2008) and applying the EM-REML algorithm.

The animal linear mixed model for the single trait analysis was:

$$y_{ijkl} = HYC_i + DIM_j + AFC_k + u_l + e_{ijkl} \, ,$$

where y_{ijkl} is the type score or linear description for cow l, HYC_i is the fixed effect of the herd-year-classifier of evaluation i (1,380 different levels), DIM_j is the fixed effect of days in milk j (8 classes from 10 to 30 d after calving and from 31 to 210 d after calving using 30-d intervals, or for later evaluation >210 d), AFC_k is the fixed effect of age at first calving k (9 classes: < 24 mo, from 25 to 38 using 2-mo intervals, and ≥ 39 mo for

the last class), u_l is the random additive effect of cow l, and e_{ijkl} is the random residual term. Co-variance components were estimated using a multi-trait animal model in the REML estimation of variance components program with canonical transformation and equal model for all analysed traits (Misztal et al., 2002).

The standard errors of the heritability estimates were approximated as (Falconer, 1989):

$$SE_{\hat{h}^2} = 4\sqrt{\frac{2(1-t)^2[1+(k-1)t]^2}{k(k-1)(s-1)}},$$

where t is intra-class correlation obtained by (h²/4) for paternal half-sib estimates, k is the average number of offspring per sire, and s is the number of sires. The standard error of the estimated genetic correlations was obtained as (Falconer, 1989):

$$SE_{\hat{r}_g} = \frac{1-\hat{r}_g}{\sqrt{2}}\sqrt{\frac{SE_{\hat{h}_1^2}SE_{\hat{h}_2^2}}{\hat{h}_1^2\hat{h}_2^2}},$$

where $\hat{r}_g$ is the estimated genetic correlation between trait 1 and 2, $\hat{h}_1^2$ and $\hat{h}_2^2$ are the estimated heritability values, $SE_{\hat{h}_1^2}$ and $SE_{\hat{h}_2^2}$ are the SE of the estimated heritability values for the 2 considered traits.

Breeding values of all animals in the pedigree for all traits were estimated and annual genetic trends were generated as the mean of all animals by a fictitious year of birth ,i.e., considering a birth year as the time between 1st of August of a given year and the 31st of July of the subsequent one. This in order to accomplish the strong seasonality of the breed toward the management of the summer gazing on alps and to analyse trends among groups of contemporaries. Due to a paucity of animals born prior to 2000 and in 2010, only genetic trends from 2000 to 2009 onwards are presented.

3.4 RESULTS

The herd-year-classifier contemporary group effect explained a significant ($P < 0.001$) proportion of the variation in all type traits. Furthermore, both DIM and AFC were associated ($P < 0.05$) with almost all traits with the exception of body shape, rump angle and rear legs side view which were not associated with DIM (data not shown); rump angle and teat placement side view were not associated with AFC. All the fleshiness traits increased (P<0.001) with days in milk, whereas all the body size traits increased (P<0.001) with age at first calving. Of the body shape traits, only rump width

increased significantly (P<0.001) with age at first calving. Of the udder traits, fore udder attachment increased (P<0.001) with age at first calving and decreased (P<0.001) with days in milk; rear udder attachment, udder width and teat placement side view decreased (P<0.001) with days in milk. Suspensory ligament decreased with age at first calving, while teat length increased with the same fixed effect. The coefficient of determination (R^2) of the multiple regression model for each type trait ranged from 0.19 (thinness) to 0.36 (shoulder-fore view). Moreover, more than 0.30 of the variance in all of the fleshiness traits (i.e., shoulder, back, loins and rump, thigh and buttocks), was explained by the model.

Table 1. Descriptive statistics, mean, additive genetic standard deviation (σ_g) and heritability (h^2), standard error in parenthesis.

	Descriptor				
Trait	Minimum (1)	Maximum (5)	Mean	σ_g	h^2 (SE)
Composite traits					
Overall score	Poor	Excellent	2.99	0.41	0.26 (0.03)
Body size	Little	Large	3.11	0.54	0.45 (0.03)
Fleshiness	Poor	Excellent	2.96	0.38	0.31 (0.03)
Body shape	Fine	Heavy	2.91	0.41	0.18 (0.02)
Udder	Poor	Excellent	3.06	0.53	0.37 (0.03)
Linear type traits					
Body size					
Stature	Short	Tall	3.13	0.68	0.52 (0.04)
Body length	Short	Long	3.17	0.55	0.41 (0.03)
Thorax depth	Very thin	Very large	3.19	0.44	0.30 (0.03)
Thorax length	Short	Long	3.01	0.29	0.18 (0.02)
Fleshiness					
Shoulder, Fore view	Scarce	Developed	2.79	0.38	0.29 (0.03)
Back, Loins and Rump	Scarce	Developed	2.93	0.38	0.27 (0.03)
Thigh, Buttocks side view	Hollow	Rounded	3.01	0.41	0.32 (0.03)
Thigh, Buttocks rear view	Hollow	Rounded	2.85	0.41	0.32 (0.03)
Body shape and feet and legs					
Thinness	Heavy	Fine	3.25	0.46	0.33 (0.03)
Rump angle	Back-inclined	Counter-inclined	2.68	0.39	0.36 (0.03)
Rump width	Narrow	Broad	3.15	0.38	0.27 (0.03)
Rear legs side view	Straight	Sickle	3.10	0.34	0.21 (0.02)
Feet	Weak	Straight	2.89	0.23	0.12 (0.02)
Udder					
Fore udder attach	Loose	Tight	3.25	0.49	0.32 (0.03)
Rear udder attach	Short	Tall	2.98	0.49	0.31 (0.03)
Udder width	Narrow	Broad	3.03	0.61	0.43 (0.03)
Udder depth	Deep	Shallow	3.35	0.36	0.27 (0.03)
Suspensory ligament	Weak	Strong	3.21	0.33	0.18 (0.02)
Teat placement side view	Close	Far	2.97	0.40	0.30 (0.03)
Teat length	Short	Long	3.05	0.47	0.34 (0.03)

Variance components

Univariate variance components for the different type traits are in Table 1. Heritability estimates varied from 0.12 (feet) to 0.52 (stature). The heritability of all five composite type traits varied from 0.18 (body shape) to 0.45 (body size). Heritability of the body size traits varied from 0.18 (thorax length) to 0.52 (stature), the fleshiness traits varied from 0.27 (back, loins and rump) to 0.32 (thigh, buttocks side and rear view), and the body shape traits ranged from 0.12 (feet) to 0.36 (rump angle). The heritability of the udder traits varied from 0.18 (suspensory ligament) to 0.43 (udder width). The standard errors of estimates for heritability of all traits ranged from 0.02 to 0.03. The coefficient of genetic variation for all 25 traits varied from 0.08 (feet) to 0.22 (stature) and was greatest for the udder traits (0.10 for suspensory ligament to 0.20 for udder width) and lowest for the fleshiness traits (0.13 for back, loins and rump to 0.14 for thigh, buttocks rear view) (data not presented).

Genetic correlations among the type traits

Genetic and phenotypic correlations among type traits are in Table 2. Genetic correlations among the individual body size traits were all ≥ 0.69 while the genetic correlations between each of the individual body size traits and body size composite varied from 0.79 (thorax length) to 0.99 (stature). Genetic correlations among the individual fleshiness traits were all ≥ 0.87. Furthermore, the genetic correlations between the fleshiness composite and the individual fleshiness traits ranged from 0.92 (with shoulder, fore view) to 0.99 (with thigh, buttocks side and rear view). Genetic correlations between individual body size traits with the fleshiness traits were all negative, with the exception of thorax length which was positively (0.36 to 0.44) correlated with all individual fleshiness traits. Genetic correlations among the individual body shape, feet and legs traits were weak and varied from -0.39 (rear legs with feet) to 0.23 (rump angle with feet). The genetic correlations between body size composite and individual traits were all positive, with the exception for rear legs side view (-0.14). The genetic correlations between the individual body size traits and the body shape, feet and legs traits were all weak; the exception was the genetic correlations between rump width and the individual body size traits (r = 0.62 to 0.77).

Table 2. Genetic (above the diagonal) and phenotypic (below the diagonal) correlations for composite and linear type traits of Rendena primiparous cows. Standard error of genetic correlations ranged from 0.001 to 0.124.

| Trait | Composite Traits | | | | | Linear Type Traits | | | | | | | | | | | | | | | | | | | |
	Ty	Bs	Fl	Bh	Ud	ST	BL	TD	TL	SF	BLR	TBS	TBR	TH	Ran	RW	RL	FE	FA	RA	UW	UP	SL	TP	TeL
Composite Traits																									
Overall score (Ty)		0.12	-0.09	0.63	0.92	0.06	0.11	0.27	0.08	-0.16	-0.10	-0.12	-0.08	0.45	0.46	0.03	-0.14	0.18	0.72	0.79	0.86	-0.16	0.13	0.34	-0.28
Body size (Bs)	0.18		-0.18	0.47	0.06	0.99	0.97	0.85	0.79	-0.13	-0.21	-0.20	-0.22	-0.01	-0.08	0.76	0.07	0.20	-0.10	0.14	0.09	0.23	0.07	-0.02	0.09
Fleshiness (Fl)	0.21	0.13		-0.05	-0.41	-0.25	-0.26	-0.22	0.40	0.92	0.98	0.99	0.99	-0.32	0.09	0.16	-0.31	0.19	-0.26	-0.49	-0.40	0.29	-0.26	-0.18	0.11
Body shape (Bh)	0.56	0.26	0.06		0.43	0.43	0.48	0.45	0.43	-0.05	-0.05	-0.10	-0.06	0.53	0.62	0.31	-0.14	0.25	0.21	0.46	0.44	0.10	0.06	0.15	-0.03
Udder (Ud)	0.82	0.08	-0.13	0.30		0.03	0.08	0.25	-0.16	-0.47	-0.42	-0.43	-0.39	0.46	0.28	-0.09	-0.03	0.07	0.78	0.89	0.92	-0.28	0.19	0.38	-0.34
Linear Type Traits																									
Stature (ST)	0.14	0.88	0.03	0.25	0.06		0.96	0.79	0.73	-0.19	-0.27	-0.26	-0.28	0.01	-0.15	0.70	0.07	0.18	-0.13	0.12	0.05	0.28	0.08	-0.05	0.05
Body length (BL)	0.15	0.83	0.06	0.25	0.07	0.76		0.80	0.72	-0.20	-0.30	-0.28	-0.29	0.02	0.02	0.77	0.18	0.23	-0.07	0.14	0.10	0.20	0.06	-0.02	0.11
Thorax depth (TD)	0.21	0.67	0.13	0.24	0.12	0.53	0.56		0.69	-0.25	-0.25	-0.24	-0.25	0.04	-0.01	0.62	0.14	0.05	0.09	0.28	0.27	0.00	0.16	0.12	0.12
Thorax length (TL)	0.21	0.60	0.44	0.21	0.02	0.48	0.46	0.51		0.44	0.38	0.36	0.36	-0.17	0.03	0.73	-0.08	0.26	-0.20	-0.17	-0.14	0.36	-0.01	-0.10	0.10
Shoulder,fore view (SF)	0.12	0.09	0.72	0.04	-0.14	0.00	0.03	0.08	0.43		0.94	0.88	0.87	-0.36	0.12	0.17	-0.23	0.10	-0.28	-0.53	-0.44	0.31	-0.25	-0.24	0.14
Back,loins and rump (BLR)	0.17	0.10	0.82	0.06	-0.12	0.00	0.02	0.09	0.43	0.73		0.96	0.94	-0.30	0.11	0.08	-0.33	0.13	-0.28	-0.47	-0.41	0.27	-0.20	-0.15	0.09
Thigh,buttocks side view (TBS)	0.17	0.10	0.89	0.04	-0.14	0.01	0.04	0.10	0.41	0.65	0.75		0.98	-0.32	0.04	0.15	-0.29	0.19	-0.27	-0.51	-0.42	0.26	-0.26	-0.19	0.07
Thigh,buttocks rear view (TBR)	0.17	0.10	0.85	0.05	-0.12	0.00	0.04	0.11	0.39	0.63	0.70	0.79		-0.33	0.10	0.14	-0.32	0.21	-0.26	-0.46	-0.38	0.26	-0.27	-0.17	0.10
Thinness (TH)	0.24	-0.04	-0.20	0.34	0.26	-0.01	-0.03	-0.04	-0.11	-0.19	-0.19	-0.20	-0.19		0.16	-0.19	-0.04	0.07	0.32	0.42	0.44	-0.20	0.09	0.18	-0.19
Rump angle (RAn)	0.23	-0.06	0.03	0.33	0.16	-0.11	-0.01	-0.01	0.00	0.04	0.05	0.00	0.03	0.10		0.06	0.05	0.23	0.26	0.27	0.22	0.01	-0.01	0.13	-0.03
Rump width (RW)	0.20	0.53	0.28	0.27	0.05	0.47	0.48	0.45	0.50	0.23	0.24	0.26	0.26	-0.12	0.01		0.15	0.22	-0.15	-0.08	-0.09	0.21	0.01	-0.14	0.10
Rear legs side view (RL)	-0.12	-0.01	-0.15	-0.10	-0.05	-0.03	0.03	0.01	-0.08	-0.12	-0.15	-0.15	-0.15	0.00	0.05	0.00		-0.39	0.00	-0.11	0.03	-0.13	0.06	0.07	0.04
Feet (FE)	0.14	0.09	0.11	0.22	0.06	0.08	0.08	0.06	0.10	0.09	0.09	0.11	0.10	0.00	0.05	0.10	-0.19		0.02	0.09	-0.02	0.25	-0.06	0.12	-0.11
Fore udder attach (FA)	0.59	0.04	-0.02	0.22	0.68	0.01	0.04	0.10	0.03	-0.05	-0.04	-0.03	-0.03	0.17	0.12	0.04	-0.02	0.03		0.48	0.56	-0.16	0.08	0.16	-0.31
Rear udder attach (RA)	0.60	0.07	-0.18	0.27	0.73	0.08	0.06	0.08	-0.04	-0.19	-0.17	-0.20	-0.17	0.24	0.18	0.00	-0.07	0.05	0.40		0.91	-0.23	0.09	0.36	-0.13
Udder width (UW)	0.65	0.10	-0.11	0.28	0.77	0.08	0.08	0.14	0.03	-0.13	-0.11	-0.12	-0.11	0.23	0.12	0.07	-0.03	0.05	0.43	0.61		-0.39	0.09	0.32	-0.14
Udder depth (UP)	-0.04	0.04	0.05	0.00	-0.06	0.10	0.03	-0.09	0.03	0.04	0.05	0.05	0.05	-0.04	0.00	-0.02	-0.08	0.04	-0.02	-0.03	-0.17		0.11	-0.36	-0.10
Suspensory ligament (SL)	0.16	-0.01	-0.11	0.08	0.21	0.01	0.00	0.01	-0.05	-0.12	-0.10	-0.11	-0.10	0.09	0.04	-0.03	0.01	0.01	0.11	0.15	0.12	0.10		0.03	-0.31
Teat placement side view (TP)	0.24	0.03	-0.03	0.11	0.26	0.01	0.04	0.07	0.03	-0.05	-0.02	-0.04	-0.03	0.07	0.07	0.03	0.02	0.03	0.13	0.21	0.22	-0.17	0.08		-0.17
Teat length (TeL)	-0.16	0.09	0.06	-0.02	-0.21	0.08	0.08	0.08	0.07	0.06	0.06	0.06	0.06	0.05	-0.09	-0.03	0.09	-0.01	0.00	-0.16	-0.08	-0.08	-0.12	-0.12	-0.15

Genetic correlations between individual fleshiness traits with the body shape, feet and legs traits were slightly positive (r = 0.04 to 0.21) with the exception of thinness and rear legs side view which were negatively genetically correlated with all individual fleshiness traits (0.23 to 0.36). Genetically deeper udders were associated with tighter and taller udder attachments, with broader udders and also associated with more distant teat placement. Genetically deeper udders with stronger suspensory ligament as well as shorter teats was associated with greater genetic merit for udder composite. The genetic correlations between individual udder traits and the individual body size traits were all weak (≤ 0.36). Genetic correlations between the individual udder traits with the individual fleshiness traits were negative (0.15 between teat placement side view and back, loins and rump to 0.53 between rear udder attach and shoulder fore view), with the exception of the positive genetic correlations with both udder depth (0.26 with thigh, buttocks side and rear view to 0.31 with shoulder fore view) and slightly positive correlations with teat length (0.07 with thigh, buttocks side view to 0.14 with shoulder fore view). Genetic correlations between individual udder traits and individual body shape traits were all weak, ranging from -0.19 (teat length and thinness) to a maximum of 0.44 (udder width and thinness). Of the four composite traits the udder composite (0.92) was most strongly correlated with overall conformation followed by body shape (0.63) and body size (0.12). Negative correlations existed between overall score and the composite fleshiness trait (-0.09). Standard errors for genetic correlation resulted in the range of 0.063, i.e., from 0.001 to 0.124 (data not shown).

Genetic trends

Annual genetic trends in the body size traits are in Figure 1, with the exception of thorax length, which did not change across time (P>0.05). All traits increased almost consistently with year of birth indicating that animals were getting taller, longer and larger with time; linear regression fitted through the annual genetic trends clearly shows that body size composite increased by 0.012 units (thorax depth) to 0.019 units (body length) annually in the last 10 years. In direct contrast, genetic merit for fleshiness decreased with time, with the exception for thigh, buttocks side view. Linear regression fitted through the mean annual genetic merit showed that all individual fleshiness traits decreased, on average, by 0.013 units per year over the last 10 years (Figure 2). Genetic trend in thigh, buttocks rear view is not presented (P>0.05).

Annual genetic merit for the body shape traits are in Figure 3; genetic trend in feet is not presented as it did not change (P>0.05) with time. Linear regression fitted through the mean annual estimated breeding values showed that all body shape traits increased, on average, by 0.005 units (rump width) to 0.017 units (thinness) per year over the last 10 years. This means that cows are getting finer and more sickle. Annual genetic merit for the udder traits are shown in Figure 4, with the exception of udder depth and teat length, which did not vary (P>0.05) with time. Linear regression fitted through the mean annual estimated breeding values showed that all udder traits increased, on average, by 0.006 units (suspensory ligament) to 0.031 units (udder width) per year over the last 10 years. These trends indicate that udders of Rendena cattle are progressively getting stronger and larger.

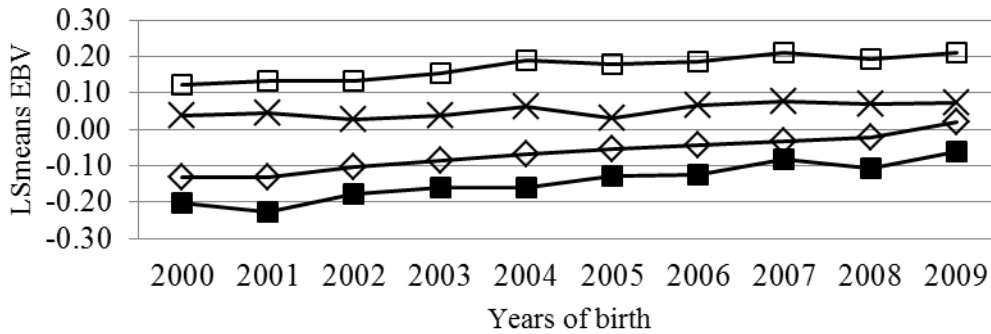**Figure 1**. Genetic trend of individual body size traits: stature (□), body length (×), thorax depth (▲).
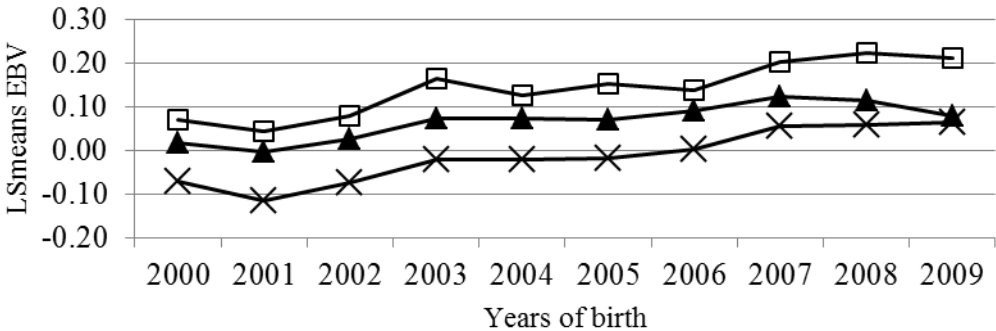
Figure 2. Genetic trend of individual fleshiness traits: shoulder, fore view (+), back, loins and rump (▲), thigh, buttock side view (×).
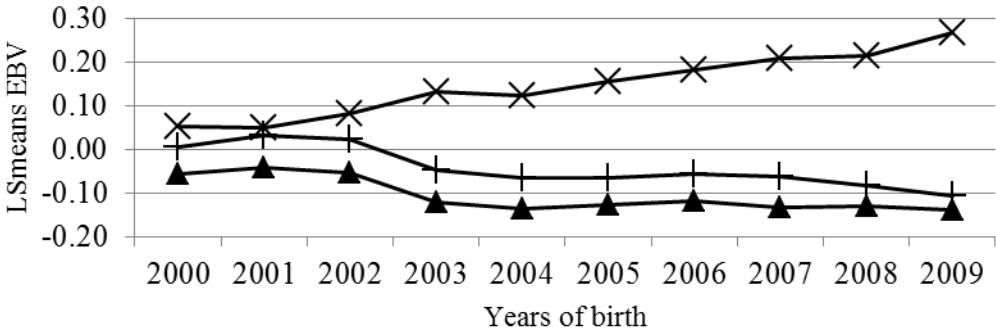
Figure 3. Genetic trend of individual body shape traits: thinness (■), rump angle (◊), rump width (×), rear legs side view (□).

Figure 4. Genetic trend of individual udder traits: fore udder attach (■), rear udder attach (▲), udder width (○), suspensory ligament (●), teat placement side view (+).
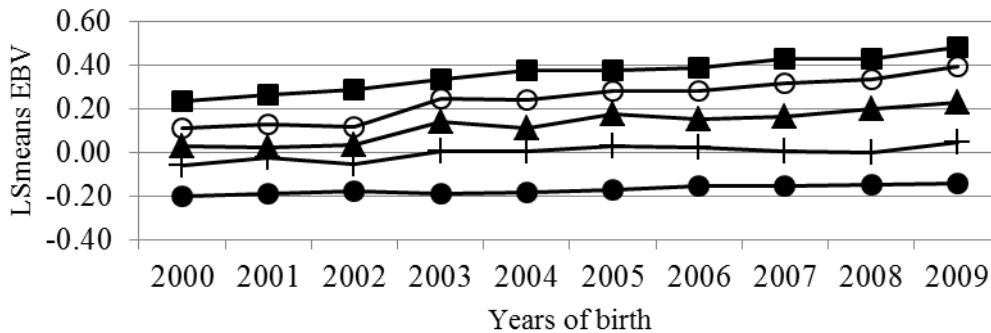
3.5 DISCUSSION

This study represent a first analysis of genetic parameters on linear type traits describing morphological characteristics of Rendena cows. In addition, this is a first analysis on the impact of past breeding programs on genetic trends in animal morphological characteristics in Rendena cattle.

Heritability

The greater heritability estimates for the body size traits (0.18 to 0.52) compared to the udder traits (0.18 to 0.43), which in turn were greater than fleshiness traits (0.27 to 0.32) and finally body shape and feet and legs traits (from 0.12 to 0.36), corroborates most other studies in Jersey (Gengler et al., 1997; Biscarini et al., 2003) and Holstein-Friesian (Veerkamp & Brotherstone, 1997; Berry et al., 2004). Different results were showed in beef cattle: dairyness traits showed the lowest heritability values, whereas

body size and fleshiness the highest heritability values (Gutiérrez & Goyache, 2002; Mantovani et al., 2010). However, heritability estimates in the present study were, on average, greater than reported in most other population studies based on field data (Theron & Mostert, 2004; Wiggans et al., 2006). Irrespective, considerable genetic variation existed in all linear traits and the coefficient of genetic variation for the type traits reported in the present study (0.08 to 0.22) were within the range reported (or calculated from provided data) in other dairy cattle (Brotherstone et al., 1990; Berry et al., 2004; Toghiani, 2011) and slightly lower than coefficient of variations in beef populations (Forabosco et al., 2004). Coefficient of genetic variation for milk yield generally range from 0.06 to 0.08 (Veerkamp & Brotherstone, 1997; Berry et al., 2003) while the coefficient of genetic variation for body weight or body condition score are 0.06 to 0.12 (Berry et al., 2003; Tsuruta et al., 2004). Greater coefficient of variation for milk yield was found for Italian Brown Swiss (0.24; Samoré et al., 2010).

Genetic correlations and genetic trend

About genetic correlations, the study has shown that many traits scored by the Rendena breeders society have a strong genetic correlation. This is the lear evidence of a great redundancy in many traits under evaluation, suggestiong that the number of traits to be evaluated could be reduced with minimal loss in accuracy. For example, the high correlations (0.98) between some fleshiness traits (thigh, buttocks side and rear view) and also between stature and body length (0.96), suggest that one of these traits could be removed from the classification scheme. Moreover, most of the genetic variation (>90%) in body size, fleshiness and udder composite traits could be explained by the individual type traits. In total 99% of the genetic variation in both the body size and fleshiness composite traits could be explained by the stature, body length and thorax depth (body size) and by three traits for fleshiness (shoulder fore view, back, loins and rump, and thigh, buttocks side view). Similarly, also for the udder composite, 99% of genetic variation could be explained by fore and rear udder attachments, udder width, udder depth and suspensory ligament. The exception was the body shape composite trait where only 76% of the genetic variation could be explained by the set of all individual traits. The ability of the individual linear type traits to explain almost all of the genetic variation in most of the subjectively scored composite traits suggests that these composite traits could actually be derived from genetic regression equations. Definitions

of some composite traits can vary across time resulting in non-unity genetic correlations for the same trait across years. This phenomenon could be minimised by developing the genetic regression equations from the individual linear type traits using recent data and applying to all animals in retrospect.

The genetic trends observed for the type traits, estimated using breeding values from the univariate analysis, are corroborated by the genetic correlations estimated in the multi-traits analysis. The negative genetic correlation between body size and fleshiness, interpreted as greater body size was associated with reduced fleshiness, disagrees with previous studies in beef cattle (Gutiérrez & Goyache, 2002). Negative correlations generally existed between fleshiness and udder traits and this means that a major improvement of one of these traits consequently leads to a decrease of others. Negative genetic correlations between these traits are also reported by Mantovani et al. (2010) in a study conducted on hypertrophic Piemontese cows. General positive correlations between udder and body size traits suggest the consequently increase of animal size, which is becoming an indirect selected trait. These positive genetic correlations between body size, especially stature, and udder traits are in agreement with previous report on Holstein-Friesian (Berry et al., 2004), on Jersey population (Gengler et al., 1997) and also in beef cattle (Gutiérrez & Goyache, 2002) and with other studies that showed positive correlations between body size and milk yield (Tsuruta et al., 2004). More developed udders, in fact, need a major surface to increase in size.

Furthermore, body size and udder are both positive correlated with body shape, which in turn is negative correlated with fleshiness, as reported also by Berry et al. (2004). The observed increase in genetic merit for body size over the past decade in the Rendena breed is mostly likely an artefact of selection for milk yield but also increased meat yield. Several studies have documented that selection for milk production alone will result in greater body size, especially for stature (Mrode et al., 1994; Veerkamp & Brotherstone, 1997; Cruickshank et al., 2002; Berry et al., 2004). Furthermore, animals of greater body size yield more carcass weight (Pabiou et al., 2012). Increased body size is likely to result in greater dry matter intake and could have implications for animal feed efficiency and therefore cost of production. Restricting further increases in body size may be particularly important for Rendena cattle which are a mountain breed, with good grazing ability both in the valleys and on the high level pastures of the alps (Mantovani et al., 1997). However restricting increasing in body size may have

implications for the (beef) revenue attainable from the sale of carcasses from cull cow and surplus animals. The observed decline in genetic merit for fleshiness is also a likely artefact of selection for milk production since many studies have documented negative genetic correlations between milk yield and body condition score (Berry et al., 2003; Loker al., 2012). This consistent decline in shoulder and in back, loins and rump is despite the breeding goals that A.N.A.R.E (*Associazione Nazionale Allevatori razza Rendena,* breeders association) have implemented for this indigenous dual purpose breed, which selection pressure on both milk and meat production, as well as fertility and longevity (Forabosco & Mantovani, 2011). The deterioration in genetic merit for fleshiness though suggests that greater selection pressure should probably be placed either directly or indirectly on fleshiness because of the known genetic (Berry et al., 2003; Berry et al., 2004) and phenotypic (Roche et al., 2009) relationships between fleshiness or body condition score with fertility and health. Furthermore, reduced genetic merit for fleshiness may have implications for achieving sufficient subcutaneous fat cover of the animal carcass to obtain a high value for the carcass.

The genetic trends of all traits suggest that the characteristics of the dual purpose Rendena cattle are becoming more like specialized milk producing animals (i.e., a large thorax, long legs, developed udder and reduced muscle development). If the Rendena breeders association want to maintain the dual purpose characteristics of this breed, breeding goals will have to be altered to include selection pressure, either directly or indirectly, on type traits characteristics of beef cattle. Results from this study indicate that genetic gain in all type traits is indeed possible given the relatively high heritability and large genetic variation present. The rate of genetic gain in these traits will be dictated by their genetic correlation with other traits already included in the breeding goal.

3.6 CONCLUSIONS

Results of this study indicate that herd-year-classifier, days in milk and age at first calving were the most significant effects and they most affect linear type traits in Rendena breed. Furthermore estimates of heritability indicate that body size is the most hereditable trait, with the except of thorax length. However all analyzed traits showed good heritability values considering that data were obtained from field condition. The low heritability estimates for feet, thorax length and suspensory ligament (0.12, 0.18 and

0.18 respectively) suggest little response to direct selection for these traits. Genetic trends for stature, body length and all the udder traits (except suspensory ligament) should result in greater heritability values with time. Genetic correlations between type traits showed favourable and moderate genetic correlations between body size and udder, and negative and quite high genetic correlations between udder and fleshiness traits. Because of the breeding goal for this breed is to improve both quality and quantity of milk and meat. However, considering result of both genetic trends and the correlations between fleshiness and udder traits, it is evident that, during years, the selection in this breed is going to the improvement of dayriness traits, at the expense of fleshiness traits.

The results obtained will be used to better redefine the current selection index of the Italian Rendena breed. Further investigation is required to analyse the genetic correlations between type traits and productive ones (i.e., milk yield, health, and fertility traits).

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CHAPTER 4

GENETIC PARAMETERS OF TYPE TRAITS IN PRIMIPAROUS DUAL PURPOSE AUTOCHTHONOUS POPULATIONS: AN ACROSS STRAIN COMPARISON WITHIN THE VALDOSTANA BREED

Part of the results have been presented and published in:

Under submission

4.1 SUMMARY

The main objectives of this study were i) to investigate the best model that could explain the total variance and ii) to estimate the genetic parameters of 4 composite (body size; muscularity; body shape; and udder) and 22 individual type traits between and within the two strains of the Valdostana dual purpose breed: the Aosta Red Pied (**ARP**; n = 25,183 records) and the Aosta Black Pied and Chestnut (**ABP-CHES**; n = 14,701 records). All type traits were scored from 2000 to 2012 on primiparous cows using a 1 to 5-point scale system. A model comparison was undertaken by considering the Akaike Information Criterion values obtained from the analysis, producing a final model that took into account the effects of herd-year-classifier, days in milk, age at calving as fixed and the animal additive genetic effect as random. Heritability estimates obtained through single trait animal model analysis varied from 0.03 for thinness (in both strains) to 0.32 (ARP) and 0.29 (ABP-CHES) for stature. Medium-low heritability estimates were obtained for individual muscularity traits (0.22 for ARP and 0.13 for ABP-CHES, respectively), and for individual udder type traits (0.12 on average in both Valdostana strains). The greatest genetic correlations between composite traits were for muscularity with body shape in both Valdostana strains (0.55 for ARP and 0.52 for ABP-CHES, respectively). Different and opposite values of genetic correlations were found for the composite body shape and the composite udder traits (0.13 for ARP and -0.25 for ABP-CHES, respectively), probably due to the different breeding purposes set up for the two Valdostana strains. Regarding the individual type traits, for ARP strain the highest genetic correlation was 0.97 (between thigh, buttocks side and rear view), whereas for the ABP-CHES strain was 0.98 (between stature and body length), meaning that improving one trait of each pair led to a positive variation in the other one. Most of the genetic correlations between the individual muscularity traits and the individual udder traits were negative, especially those involving udder volume (from -0.19 to -0.42 in ARP, and from -0.17 to -0.41 in ABP-CHES, respectively), indicating a substantial antagonistic situation of type traits related to dairy and beef traits. In conclusion, the selection for the dual purpose in local breeds such as in Valdostana cattle implies a thorough consideration of opposite morphological traits.

4.2 INTRODUCTION

Today, only few cattle breeds can be defined as "dual purpose" because the current economic system pushes towards increasing specialization. In addition, the improvement of dual purpose is complicated by the simultaneous improvement of both milk and meat. Limits to selection for dual purpose are also due to the opposed morphology, e.g., muscle development in correspondence to the finest cuts lead to less space for a capacious udder. Thus, an efficient morphological evaluation in dual purpose cattle should account mainly for muscularity and udder traits. However, the worth morphological evaluation is controversial, because it deals with traits not directly linked to the production. On the other hand, many farmers and breeders give a high value to animals' morphology. Type traits were first introduced at the beginning of '80 (Vinson et al., 1982; Lucas et al., 1984) aiming at describing the biological extremes of animals' visual characteristics (Berry et al., 2004). A primary practical reason for collecting the linear type other than for body description was the indirect selection for traits expressed late in life, such as longevity (Forabosco et al. 2004). Genetic parameters of type traits have been widely studied in specialized dairy (Misztal et al., 1992; Samoré et al., 2010) and beef breeds (Norris et al., 2008; Mantovani et al., 2010). However, they have been investigated also in some European local dual purpose breeds (Mazza et al., 2014), in a contest in which the morphological evaluation represents an important tool for both selection and the maintenance of the breeds under the typical farm conditions in which they are reared, thus preserving the local environment and the local culture (Gandini and Villa, 2003). Within this framework, the aim of the study was to analyze the genetic aspects of linear type traits in the local Valdostana breed. In particular, the study set out to: i) investigate different combinations of fixed and random effects to identify the model with the best fit, and ii) estimate heritability and genetic correlations between linear type traits within the two strains of Valdolstana cattle. This as part of a bigger project aimed at introducing genetic evaluation for type in the selection of these cattle strains together with other productive traits already considered as selection goals for the strains.

4.3 MATERIAL AND METHODS

Subject of the study

The Valdostana is an indigenous dual purpose Italian breed accounting for three strains with different coat color, production, morphology and temperament. The three strains are widespread in the Aosta Valley region (northwest of Italy) and managed in two separated herd books. The first herd book of Valdostana cattle was established in 1985 and it is dedicated to the Aosta Red Pied (**ARP**), which is particularly docile and strong, highly adapted to harsh climates and more readily selected for milk yield. The ARP strain derives from Red and White cows of central Europe and moved to Italy at the end of the 5th century. After an expansion in the mid-20th century, the number of animals slowly decreased in the subsequent 50-year period, and the decline was mostly observed in valleys and flats, particularly in the neighboring Piedmont region. The second herd book, also founded in 1985, is dedicated to the Aosta Black Pied and Aosta Chestnut strains (**ABP-CHES**), considered to be a unique group because of common characteristics and the practice of crosses that occurred in the past. Aosta Black Pied and Aosta Chestnut have indeed shown strict and genetic relationships (Del Bo et al., 2001), probably attributable to repeated crossbreeding between Hérens cattle from Switzerland and Aosta Black Pied that have originated the Aosta Chestnut (Forabosco and Mantovani, 2011). The similarities between these two strains have led to their management in the same herd book. However, because of the present endangered status of the ABP as compare to the CHES, today there is an attempt at avoiding further crosses between these 2 strains, to prevent the complete ABP substitution with CHES. The ABP-CHES strain is characterized by a lower milk production than ARP, but it is well-developed and very strong, lively and quite aggressive with counterparts on summer pasture. For these reasons, the strain has been empirically selected mainly for the traditional battle contest called "*Batailles de Reines*", where cows fight to assess dominance relationships (Sartori and Mantovani, 2010, 2012). At present, ABP-CHES selection goals are fighting ability, milk and meat; on the other hand, ARP selection goals are milk and meat production, but with greater emphasis to milk than ABP-CHES. These latter two strains are less numerous than the ARP population, which is the more consistent within the Valdostana breed.

Data editing

Type records were provided by the National Breeders Association of Valdostana cattle (A.N.A.Bo.Ra.Va.), and consisted in 26 linear type evaluations (Table 1) carried out on primiparous cows, once in their life, by different trained classifiers between 2000 and 2012. For both ARP and ABP-CHES, only animals that presented the first calving between 22 and 48 months of age were retained. Records referred to days in milk <10 d or >350 d, and with missing information on classifiers, herds or analyzed scores were discarded. After this first editing, only data belonging to herd-year-classifier contemporary groups with at least two animals per group were taken into account. The remaining data consisted in 25,183 records for ARP and 14,701 records for ABP-CHES.

Table 1. Descriptor and statistics (mean and standard deviation within brackets) of 26 type traits scored on 25,183 Aosta Red Pied (ARP) and 14,701 Aosta Black Pied and Chestnut (ABP-CHES) primiparous cows

Type traits	Descriptor		Valdostana strain	
	Minimum (1)	Maximum (5)	ARP	ABP-CHES
Composite				
Body size	Undeveloped	High developed	3.07 (0.83)	3.20 (0.81)
Muscularity	Poor	Excellent	3.01 (0.85)	3.31 (0.82)
Body shape	Fine	Heavy	2.97 (0.84)	3.11 (0.81)
Udder	Poor	Excellent	3.13 (0.89)	2.62 (0.82)
Individual				
Stature	Short	Tall	3.05 (0.91)	3.10 (0.87)
Body length	Short	Long	3.19 (0.88)	3.36 (0.87)
Thorax depth	Shallow	Very deep	3.17 (0.80)	3.25 (0.77)
Thorax width	Close	Wide	2.93 (0.84)	3.19 (0.81)
Front muscularity	Scarce	Developed	2.87 (0.86)	3.29 (0.86)
Back, Loins and Rump	Scarce	Developed	2.95 (0.87)	3.22 (0.83)
Thigh, Buttock side view	Hollow	Rounded	3.07 (0.87)	3.35 (0.83)
Thigh, Buttock rear view	Hollow	Rounded	3.04 (0.90)	3.23 (0.84)
Thinness	Heavy	Fine	3.37 (0.93)	3.19 (0.84)
Rump angle	Back inclined	Forward inclined	3.06 (0.73)	2.89 (0.70)
Rump width	Narrow	Broad	3.17 (0.77)	3.21 (0.71)
Rump length	Short	Long	3.27 (0.82)	3.42 (0.77)
Rear legs	Straight	Sickle	3.05 (0.78)	3.06 (0.71)
Foot angle	Low	High	2.83 (0.69)	2.85 (0.63)
Fore udder attach	Short	Long	3.12 (0.98)	2.63 (0.92)
Rear udder attach	Low	High	3.29 (0.88)	2.59 (0.83)
Udder width	Narrow	Broad	3.28 (0.90)	2.59 (0.86)
Udder depth	Deep	Shallow	3.18 (0.80)	3.67 (0.85)
Suspensory ligament	Weak	Strong	2.99 (0.80)	2.77 (0.80)
Teat placement rear view	Diverging	Converging	2.84 (0.64)	2.69 (0.65)
Teat placement side view	Close	Far	2.95 (0.68)	2.48 (0.70)
Teat length	Short	Long	2.94 (0.77)	2.65 (0.82)

Estimation of variance components

Both preliminary and final analyses were carried out separately for ARP and ABP-CHES strains. First, to investigate the non-genetic effects to be fitted in the final model, preliminary analyses were undertaken on datasets, through the generalized linear model procedure of SAS software (PROC GLM; SAS Inst. Inc., Cary, NC). The non-genetic factors retained for the subsequent genetic analysis were the effect of the herd-year-classifier (**HYC**, 5,613 different levels for ARP and 4,119 different levels for ABP-CHES), the effect of days in milk (**DIM**, 7 classes for both ARP and ABP-CHES: from 10 to 30 d after calving for the first class, from 31 to 181 d after calving using 30 d intervals, and an open last class ≥181 d after calving), the effect of age at calving (**AC**, 5 classes for both ARP and ABP-CHES and divided in 5 classes for first parity cows – from 22 to 29 mo, from 30 to 34 mo, from 35 to 36 mo, from 37 to 41 mo, and from 42 to 48 mo). All available pedigree information (51,980 animals for ARP, 9.16 maximum generations tracked back; and 28,227 animals for ABP-CHES, 5.08 maximum generations tracked back) was used to set up the relationship additive matrix among animals. The relationship matrix was built using the method of Henderson (1976), accounting for the 2 genetic groups of unknown male parents and unknown female parents (Gutiérrez and Goyache, 2005). The effect of DIM and AC were always considered as fixed, whereas the effect of HYC was alternatively taken into account as a fixed or random effect in a series of single trait analysis accounting for the 22 individual and the 4 composite traits.

Therefore, the most complete matrix notation of the models can be expressed as:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Wq} + \mathbf{Zu} + \mathbf{e,}$$

where y is an $N \times 1$ vector of observations, $\mathbf{\beta}$ is the vector of systematic fixed effects of order p, $\mathbf{q}$ is the vector of HYC when considered as a random effect, $\mathbf{u}$ is the vector of animal effects with order m, and $\mathbf{e}$ is the vector of residual effects. Furthermore, $\mathbf{X}$, $\mathbf{W}$, and $\mathbf{Z}$ are the corresponding incidence matrices with the appropriate dimensions.

Single-trait linear model analyses in the AIREMLF90 program (Average Information REML; Misztal, 2008) were carried out to estimate the variance components and the heritability for each composite and individual trait within ARP and ABP-CHES. The Akaike Information Criterion values (**AIC**; Akaike, 1973) were also

investigated to define which of the two models to select (i.e., with HYC fixed or random), as it is the one that minimizes the Kullback-Leibler (1951) discrepancy between the model and the truth. The AIC is defined as:

$$\text{AIC}_i = -2\log L_i + 2V_i,$$

where L_i is the maximum likelihood for the candidate model i, determined by adjusting the V_i free parameters in such a way as to maximize the probability that the candidate model has generated the observed data (Wagenmakers and Farrel, 2004).

After these analyses only the model that accounted the HYC as fixed effect was retained to estimate the (co)variance components among 26 type traits (4 composite and 22 individual traits) within strains, through a multi-trait animal model with a canonical transformation REML method and unique incidence matrix (Misztal, 2008).

The assumptions about the structure of phenotypic variance were as follows:

$$\text{Var} \begin{vmatrix} u \\ e \end{vmatrix} = \begin{vmatrix} G \otimes A & 0 \\ 0 & E \otimes I \end{vmatrix},$$

where **G** and **E** are the (co)variance matrices among the 26 traits for the animal and residual effects, respectively; **A** is the additive genetic relationship among the animals; **I** is an identity matrix; and $\otimes$ is the Kronecker product operator.

The standard errors of the heritability values were calculated as (Lynch and Walsh, 1998):

$$\text{SE}(\frac{\sigma_n^2}{\sigma_d^2})^2 = (\frac{\sigma_n^2}{\sigma_d^2})^2 (\frac{Var(\sigma_n^2)}{\sigma_n^4} + \frac{Var(\sigma_d^2)}{\sigma_d^4} + \frac{2Cov(\sigma_n^2, \sigma_d^2)}{\sigma_n^2 \sigma_d^2}),$$

where n and d are integers pointing to components vn and vd that are to be used as the numerator and denominator respectively in heritability calculation.

The standard errors of the genetic correlations were approximated as in Falconer (1989):

$$\text{SE}_{\hat{r}_g} = \frac{1 - \hat{r}_g^2}{\sqrt{2}} \sqrt{\frac{\text{SE}_{\hat{h}_1^2} \text{SE}_{\hat{h}_2^2}}{\hat{h}_1^2 \hat{h}_2^2}},$$

where $\hat{r}_g^2$ is the square of the estimated genetic correlation between trait 1 and 2, $\hat{h}_1^2$ and $\hat{h}_2^2$ are the heritability estimates for trait 1 and 2, respectively, $\text{SE}_{\hat{h}_1^2}$ and $\text{SE}_{\hat{h}_2^2}$ are the standard errors of the heritability estimates of each pair of considered traits.

4.4 RESULTS

Descriptive statistics for all considered type traits are summarized in Table 1. Mean values for ARP dataset presented a range from 2.83 (foot angle) to 3.37 (thinness), whereas for APB-CHES the 26 linear type traits ranged from 2.48 (teat placement side view) to 3.67 (udder depth). Standard deviations were very similar for the two strains with an average of 0.83 for ARP and 0.80 for ABP-CHES. Regarding the analysis of variance, due to a high computational demand, the effect of HYC was not directly analyzed, but treated with the ABSORB statement of the GLM procedure (SAS, 2009). Both the fixed effects of DIM and AC were significant ($P<0.001$; data not shown) for almost all considered traits and for both Valdostana strains considered, with only few exceptions, i.e., not significant ($P>0.05$) for the effect of DIM for rear legs in ARP, and for thinness and rump angle in ABP-CHES (data not shown). Furthermore, considering only ABP-CHES, neither DIM nor AC were significant effects ($P>0.05$) for rear legs, foot angle and teat placement rear view (data not shown).

Model comparison

The AIC values obtained from AIREMLF90 analysis considering alternatively HYC as fixed or random are reported in Table 2. From an inspection of the AIC values calculated on ARP and on ABP-CHES datasets, the differences between the averages of AIC values of the two models are 21.3 x 10^3 for ARP and 8.9 x 10^3 for ABP-CHES. The lowest AIC values for all considered type traits and in both Valdostana strains were obtained by considering the HYC as a fixed effect rather than as a random effect. The trait that always showed the lower fitting, both considering HYC fixed or random and in both Valdostana strains was the fore udder attach (Table 2).

Departing from these results, the subsequent analyses focused only on the model that included the fixed effect of HYC, the fixed effect of DIM and AC, and the random additive effect of cow and the residual term.

Table 2. Akaike Information Criterion values (x10^3; Akaike, 1973) obtained by investigating different models accounting for the Herd-Year-Classifier effect (HYC) as fixed or random for all type traits scored on Aosta Red Pied (ARP) and Aosta Black Pied and Chestnut (ABP-CHES) cows.

| Type traits | Valdostana strain | | | |
| | ARP | | ABP-CHES | |
	fixed HYC	random HYC	fixed HYC	random HYC
Composite				
Body size	22.803	26.677	35.461	44.543
Muscularity	23.395	45.733	35.362	44.892
Body shape	23.908	45.852	36.668	45.415
Udder	24.520	46.865	36.137	45.641
Individual				
Stature				
Body length	23.536	46.156	37.787	47.672
Thorax depth	22.312	44.339	34.000	42.706
Thorax width	22.740	45.342	35.084	44.667
Front muscularity	23.333	45.838	36.758	46.869
Back, Loins and Rump	23.687	46.150	36.384	45.841
Thigh, Buttock side view	23.747	46.237	36.055	45.862
Thigh, Buttock rear view	24.307	46.854	36.414	46.255
Thinness	25.606	48.220	38.242	47.805
Rump angle	21.445	42.848	33.453	40.600
Rump width	21.796	43.686	32.892	40.785
Rump length	22.439	44.817	35.343	44.179
Rear legs	23.169	44.623	34.577	41.521
Foot angle	20.819	41.774	31.498	37.086
Fore udder attach	26.012	48.923	39.724	50.290
Rear udder attach	24.059	46.584	36.503	46.290
Udder width	24.876	47.279	37.730	47.747
Udder depth	22.055	44.372	36.982	47.185
Suspensory ligament	23.288	45.009	35.315	44.780
Teat placement rear view	19.852	40.194	31.334	37.906
Teat placement side view	19.836	40.910	33.213	40.704
Teat length	22.781	43.981	37.884	46.505

Heritability estimates

Heritability estimates and their standard errors from the single-trait AIREML analysis for all type traits and for both Valdostana strains are presented on Table 3. Generally, regarding composite traits, the lowest heritability value was for body shape (0.08 for ABP-CHES and 0.09 for ARP) and the greater was for body size (0.26 for ABP-CHES and 0.29 for ARP). Across the individual type traits, the heritability

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estimates for ARP ranged from 0.03 (thinness) to 0.32 (stature), whereas for ABP-CHES they varied from a minimum of 0.01 (suspensory ligament) to a maximum of 0.29 (stature).

Table 3. Estimated variances and heritability for 26 type traits scored on Aosta Red Pied (ARP) and Aosta Black Pied and Chestnut (ABP-CHES) cows.

| Type traits | Valdostana strain | | | | | |
| | ARP[1] | | | ARP[1] | | |
	σ^2_a	σ^2_r	$\hat{h}^2\ (SE_{\hat{h}}^2)$	σ^2_a	σ^2_r	$\hat{h}^2\ (SE_{\hat{h}}^2)$
Composite						
Body size	0.162	0.402	0.29 (0.03)	0.126	0.363	0.26 (0.02)
Muscularity	0.158	0.442	0.26 (0.03)	0.074	0.401	0.16 (0.02)
Body shape	0.055	0.559	0.09 (0.02)	0.043	0.471	0.08 (0.02)
Udder	0.090	0.574	0.14 (0.02)	0.068	0.431	0.14 (0.02)
Individual						
Stature	0.225	0.486	0.32 (0.04)	0.173	0.428	0.29 (0.03)
Body length	0.146	0.461	0.24 (0.03)	0.110	0.458	0.19 (0.02)
Thorax depth	0.077	0.441	0.15 (0.02)	0.075	0.357	0.17 (0.02)
Thorax width	0.090	0.455	0.17 (0.03)	0.064	0.400	0.14 (0.02)
Front muscularity	0.122	0.466	0.21 (0.03)	0.057	0.463	0.11 (0.02)
Back, Loins and Rump	0.130	0.484	0.21 (0.03)	0.066	0.442	0.13 (0.02)
Thigh, Buttock side view	0.136	0.482	0.22 (0.03)	0.058	0.437	0.12 (0.02)
Thigh, Buttock rear view	0.159	0.504	0.24 (0.03)	0.071	0.439	0.14 (0.02)
Thinness	0.023	0.716	0.03 (0.01)	0.018	0.553	0.03 (0.01)
Rump angle	0.071	0.398	0.15 (0.03)	0.050	0.361	0.12 (0.02)
Rump width	0.043	0.440	0.09 (0.02)	0.030	0.362	0.08 (0.02)
Rump length	0.040	0.479	0.08 (0.02)	0.030	0.436	0.07 (0.02)
Rear legs	0.032	0.530	0.06 (0.02)	0.018	0.422	0.04 (0.01)
Foot angle	0.026	0.404	0.06 (0.02)	0.013	0.340	0.04 (0.01)
Fore udder attach	0.113	0.675	0.14 (0.02)	0.099	0.549	0.15 (0.02)
Rear udder attach	0.103	0.530	0.16 (0.03)	0.077	0.437	0.15 (0.02)
Udder width	0.070	0.617	0.10 (0.02)	0.088	0.474	0.16 (0.02)
Udder depth	0.039	0.458	0.08 (0.02)	0.058	0.470	0.11 (0.02)
Suspensory ligament	0.033	0.537	0.06 (0.02)	0.007	0.456	0.01 (0.01)
Teat placement rear view	0.032	0.354	0.08 (0.02)	0.025	0.326	0.07 (0.02)
Teat placement side view	0.059	0.331	0.15 (0.03)	0.051	0.354	0.13 (0.02)
Teat length	0.108	0.443	0.20 (0.03)	0.103	0.468	0.18 (0.02)

[1] σ^2_a is the additive genetic variance, σ^2_r is the random residual variance, $\hat{h}^2$ is the estimated heritability and $SE_{\hat{h}}^2$ values within brackets is the standard error of the estimated heritability.

Furthermore, the four individual body size traits showed the greatest mean heritability estimates (0.20 for ABP-CHES and 0.22 for ARP), followed by the individual muscularity traits (0.13 for ABP-CHES and 0.22 for ARP), and then by the individual udder type traits (0.12 for both Valdostana strains). Finally, the lowest mean heritability values were for the individual body shape traits: 0.06 (ABP-CHES) and 0.08 (ARP). Standard errors of heritability estimates were in general very low (i.e., ≤ 0.03), with the only exception for stature in ARP (i.e. = 0.04).

Within strain genetic correlations

Genetic correlations (r_g; Table 4) in ARP ranged from -0.55 (between thinness and front muscularity and between rump width and thinness) to 0.99 (between tight, buttocks side view and composite muscularity), with a mean of 0.13 and a standard deviation of ± 0.37 considering all 26 traits. Regarding the second strain (ABP-CHES; Table 4) the genetic correlations varied from -0.76 (between udder depth and fore udder attach) to 0.98 (stature and body length with composite body size, and body length with stature), with a mean of 0.18 and a standard deviation of ± 0.39 considering all 26 scored traits. Among the composite type traits, the genetic correlations were negative for udder with body size and muscularity in ARP (-0.25 and -0.26, respectively) and positive with body shape (0.13); on the other hand, in ABP-CHES, the same correlations were -0.01 (between udder and body size), -0.35 (between the udder and muscularity), and -0.25 (between udder and body size).

In both Valdostana strains, genetic correlations were positive and substantial between the individual body size traits and their corresponding composite trait ($r_g \geq$ 0.82) and the individual muscularity traits and the corresponding composite ($r_g \geq 0.93$). Regarding the correlations between the individual body shape traits and their composite, they ranged from negative values for rear legs (-0.28 in ARP and -0.18 in ABP-CHES, respectively) to medium positive values for rump width, rump length, and foot angle (from 0.36 to 0.46 for ARP, and from 0.34 to 0.47 for ABP-CHES, respectively). Thinness and rump angle showed in both strains a correlation with body shape close to zero. Furthermore, both ARP and ABP-CHES showed high genetic correlations between the composite udder trait and the individual traits related to udder size, i.e., fore udder attach, rear udder attach, and udder width (from 0.80 to 0.83 in ARP, and from 0.86 to 0.89 in ABP-CHES).

Table 4. Estimated genetic correlations for 26 type traits scored on Aosta Red Pied (ARP; above diagonal) and Aosta Black Pied and Chestnut (ABP-CHES; below diagonal) cows[1].

Type traits	Composite				Individual																					
	Bs	Fl	Bh	Ud	ST	BL	TD	TW	FM	BLR	TBS	TBR	TH	RAN	RW	RL	RLEG	FA	FUA	RUA	UW	UP	SL	TPR	TPS	TL
Composite																										
Body size (Bs)		0.42	0.29	-0.25	0.96	0.95	0.95	0.82	0.46	0.42	0.37	0.32	-0.31	-0.05	0.70	0.64	0.09	0.19	-0.17	-0.15	-0.07	-0.13	-0.06	-0.17	-0.13	0.04
Muscularity (Fl)	0.47		0.55	-0.26	0.20	0.35	0.49	0.79	0.97	0.96	0.99	0.98	-0.53	-0.15	0.78	0.58	-0.06	0.18	-0.20	-0.38	-0.33	0.20	0.12	-0.15	-0.30	0.03
Body shape (Bh)	0.49	0.52		0.13	0.17	0.20	0.33	0.41	0.51	0.53	0.51	0.49	0.08	-0.09	0.40	0.46	-0.28	0.36	0.04	0.05	0.13	0.03	-0.28	0.20	0.10	-0.05
Udder (Ud)	-0.01	-0.35	-0.25		-0.17	-0.29	-0.20	-0.28	-0.27	-0.31	-0.26	-0.27	0.46	0.12	-0.31	0.03	-0.24	0.24	0.83	0.81	0.80	0.17	0.20	0.48	0.38	-0.19
Individual																										
Stature (ST)	0.98	0.34	0.45	0.02		0.93	0.88	0.68	0.25	0.20	0.16	0.11	-0.26	-0.02	0.57	0.54	0.05	0.25	-0.11	-0.05	0.03	-0.15	-0.08	-0.17	-0.09	0.03
Body length (BL)	0.98	0.38	0.43	-0.01	0.98		0.88	0.73	0.36	0.38	0.31	0.27	-0.29	-0.04	0.67	0.66	0.09	0.19	-0.18	-0.18	-0.13	-0.17	-0.09	-0.24	-0.16	0.01
Thorax depth (TD)	0.90	0.62	0.44	-0.13	0.85	0.85		0.83	0.52	0.48	0.47	0.40	-0.26	-0.09	0.73	0.65	0.20	0.18	-0.18	-0.03	0.05	-0.15	-0.07	-0.16	-0.03	0.00
Thorax width (TW)	0.84	0.82	0.54	-0.14	0.75	0.76	0.89		0.83	0.79	0.76	0.72	-0.51	-0.02	0.88	0.70	0.09	0.23	-0.24	-0.27	-0.20	0.17	0.11	-0.16	-0.30	0.04
Front muscularity (FM)	0.59	0.93	0.59	-0.37	0.48	0.49	0.74	0.89		0.93	0.96	0.92	-0.55	-0.12	0.75	0.59	0.01	0.12	-0.23	-0.42	-0.34	0.25	0.12	-0.20	-0.38	0.10
Back, Loins and Rump (BLR)	0.50	0.96	0.48	-0.36	0.39	0.40	0.65	0.83	0.92		0.94	0.95	-0.52	-0.08	0.81	0.59	-0.09	0.12	-0.28	-0.37	-0.36	0.21	0.15	-0.11	-0.26	0.00
Thigh, Buttock side view (TBS)	0.43	0.96	0.39	-0.18	0.30	0.33	0.53	0.76	0.86	0.91		0.97	-0.53	-0.20	0.75	0.54	-0.03	0.17	-0.19	-0.37	-0.33	0.16	0.10	-0.20	-0.32	0.09
Thigh, Buttock rear view (TBR)	0.34	0.96	0.50	-0.23	0.22	0.24	0.47	0.71	0.86	0.91	0.96		-0.51	-0.18	0.73	0.51	-0.08	0.20	-0.21	-0.37	-0.37	0.19	0.14	-0.12	-0.26	-0.04
Thinness (TH)	0.01	-0.15	0.12	0.37	0.03	0.03	-0.04	-0.08	-0.09	-0.18	-0.07	-0.13		-0.02	-0.55	-0.12	0.24	-0.20	0.43	0.56	0.55	-0.28	-0.16	0.36	0.47	-0.20
Rump angle (RAN)	0.00	-0.15	-0.02	-0.02	0.00	0.06	0.08	0.04	-0.08	-0.08	-0.23	-0.19	0.32		-0.01	0.17	0.20	0.01	0.00	0.14	0.19	0.36	-0.08	0.05	0.03	-0.17
Rump width (RW)	0.68	0.81	0.47	-0.25	0.59	0.67	0.75	0.85	0.81	0.81	0.75	0.69	-0.09	0.07		0.70	-0.10	0.12	-0.37	-0.17	-0.13	0.21	0.15	-0.02	-0.24	0.01
Rump length (RL)	0.78	0.62	0.42	-0.10	0.71	0.73	0.84	0.83	0.70	0.65	0.55	0.50	0.12	0.09	0.72		-0.03	0.14	-0.08	-0.01	0.06	0.28	0.09	0.04	-0.08	-0.09
Rear legs (RLEG)	0.05	-0.15	-0.18	0.14	0.07	0.09	0.08	-0.09	-0.14	-0.22	-0.16	-0.15	0.21	0.07	-0.10	0.21		-0.37	-0.11	-0.08	-0.01	-0.35	-0.30	-0.28	-0.06	-0.14
Foot angle (FA)	0.17	0.29	0.34	-0.22	0.16	0.14	0.23	0.35	0.29	0.31	0.25	0.28	-0.09	0.27	0.38	0.10	-0.39		0.27	0.07	0.03	0.21	-0.04	-0.10	0.00	-0.11
Fore udder attach (FUA)	-0.08	-0.31	-0.25	0.87	-0.04	-0.08	-0.13	-0.18	-0.31	-0.31	-0.17	-0.21	0.30	-0.03	-0.33	-0.16	0.11	-0.49		0.58	0.56	-0.14	0.08	0.30	0.18	-0.01
Rear udder attach (RUA)	0.06	-0.30	-0.14	0.86	0.08	0.06	0.02	-0.03	-0.31	-0.33	-0.19	-0.23	0.29	0.12	-0.20	0.00	-0.06	0.04	0.68		0.96	-0.08	0.00	0.53	0.54	-0.13
Udder width (UW)	-0.04	-0.36	-0.15	0.89	-0.02	-0.05	-0.10	-0.12	-0.35	-0.41	-0.25	-0.26	0.28	0.06	-0.29	-0.10	-0.02	0.01	0.72	0.96		-0.03	-0.07	0.46	0.43	-0.08
Udder depth (UP)	-0.02	0.12	0.22	-0.75	0.00	-0.02	-0.08	0.00	0.11	0.22	-0.01	0.05	-0.19	0.09	0.07	-0.06	-0.23	0.23	-0.76	-0.71	-0.74		0.54	0.08	-0.30	-0.21
Suspensory ligament (SL)	0.03	-0.15	0.05	0.78	0.05	-0.01	0.00	0.00	-0.12	-0.17	-0.03	-0.07	0.55	-0.09	-0.07	0.12	0.11	0.09	0.55	0.75	0.75	-0.61		0.31	0.04	-0.27
Teat placement rear view (TPR)	0.08	-0.04	-0.06	0.51	0.03	0.10	-0.04	0.02	-0.08	-0.15	0.08	0.01	0.43	-0.01	-0.01	-0.11	0.09	-0.26	0.41	0.41	0.39	-0.27	0.35		0.43	-0.41
Teat placement side view (TPS)	-0.10	-0.40	-0.22	0.76	-0.07	-0.07	-0.11	-0.29	-0.40	-0.43	-0.32	-0.32	0.38	0.02	-0.20	-0.05	0.29	-0.29	0.62	0.68	0.70	-0.66	0.69	0.33		-0.19
Teat length (TL)	0.34	0.03	0.03	0.31	0.30	0.38	0.30	0.23	0.09	-0.06	0.09	0.05	0.04	0.12	0.28	0.35	0.19	0.08	0.19	0.39	0.41	-0.63	0.25	0.00	0.44	

[1] *SE values for genetic correlations with a mean of 0.113 and standard deviation of 0.054, i.e., ranging from 0.002 to 0.373.*

A positive medium high genetic correlation was observed between the composite udder and the teat placement rear view in both Valdostana strains (i.e., 0.48 and 0.51 for ARP and ABP-CHES, respectively).

However, individual udder depth, suspensory ligament, teat placement side view, and teat length showed genetic correlations with the composite udder trait in opposite or different magnitude, depending on the strain considered. Indeed, the genetic correlation between udder depth and composite udder was 0.17 in ARP, and -0.75 in ABP-CHES; the genetic correlation between suspensory ligament and teat placement side view with composite udder were 0.20 and 0.38 in ARP, but 0.78 and 0.76 in ABP-CHES, respectively; the genetic correlation between teat length and composite udder was -0.19 in ARP, and 0.31 in ABP-CHES. Among the individual body size group and the individual muscularity traits, both strains showed high positive genetic correlations. Indeed, in ARP genetic correlations within the body size group traits ranged from 0.68 to 0.93, while in ABP-CHES the same correlations ranged from 0.75 to 0.98; on the other hand, considering the individual muscularity group traits the genetic correlations ranged from 0.92 to 0.97 in ARP, and from 0.86 to 0.96 in ABP-CHES. Also the genetic correlations between the individual body size traits and individual muscularity traits were all positive, but the range of r_g was wider than r_g estimated within body size or muscularity group traits. The greatest genetic correlations observed when comparing individual body size and muscularity traits were those between thorax width and individual muscularity scores, that ranged from 0.72 to 0.83 in ARP, and between 0.71 and 0.89 in ABP-CHES, respectively. Considering the group of individual body shape traits, the genetic correlations estimated varied in ARP from -0.55 (between rump width and thinness) to 0.70 (between rump width and rear legs) and from -0.39 (between foot angle with rear legs) to 0.72 (between rump length with rump width) in ABP-CHES. In ARP, considering the individual udder traits, genetic correlations ranged from -0.41 (between teat placement rear view and teat length) to 0.96 (between rear udder attach and udder width), and correlations between teat length and all the other individual type traits were all negative. However, in spite of a general different magnitude of genetic correlations among individual udder traits in ABP-CHES as compared to ARP, the greatest r_g value was estimated between rear udder attach and udder width (i.e., r_g = 0.96). In this strain all the genetic correlations were negative between udder depth and the other individual udder traits. Other high values of r_g were observed between the

rump width and the thorax width (0.88 and 0.85 for ARP and ABP-CHES, respectively) and between these traits and all the individual muscularity traits in both Valdostana strains, i.e., $r_g \geq 69$ for rump width and individual muscularity traits, and $r_g \geq 71$ for thorax width and individual muscularity traits, respectively. Furthermore, most genetic correlations between individual muscularity traits and udder traits were negative, especially those involving the fore and rear udder attach, and udder width, that ranged from -0.19 to -0.42 in ARP, and from -0.17 to -0.41 in ABP-CHES. Standard errors for all analyzed type traits ranged from 0.002 (between composite muscularity trait and thigh, buttocks side view) to 0.235 (between foot angle and suspensory ligament) in ARP, and from 0.002 (between composite body size trait and stature) to 0.373 (between rear legs and suspensory ligament) in ABP-CHES, respectively. Finally, phenotypic correlations (data not shown) among type traits estimated ranged from -0.22 to 0.83, with a mean of 0.10 (±0.18) in ARP, and from -0.23 to 0.81, with a mean of 0.10 (±0.17) in ABP-CHES.

4.5 DISCUSSION

The linear type classification for the dual purpose cattle considered in this study, covering 4 composite and 22 individual traits, gives a fairly comprehensive assessment of the appearance of the animals belonging to the 2 different strains of Valdostana cattle. Model comparison is a very useful method to define which are the effects that most influence the considered type traits and to choose the better way to analyze data. The objective of the AIC model selection is to estimate the information loss when the probability distribution associated with the true (generating) model is approximated by probability distribution associated with the model that is to be evaluated (Wagenmakers and Farrel, 2004). Akaike (1973), and later Bozdogan (1987), have shown that choosing the model with the lowest expected information loss (i.e., the model that minimizes the expected Kullback-Leibler discrepancy) is asymptotically equivalent to choosing a model that has the lowest AIC value. In this study and in both Valdostana strain, the best fitting was observed by treating the main environmental effect, i.e., the herd-year-classifier as fixed, which is in agreement with other previous findings on these breeds, although for different traits (Sartori and Mantovani, 2010).

Heritability estimates

Objectively scored linear type traits showed medium-low heritability in both Valdostana strains. Simple appreciation of heritability values estimated indicates a generally greater magnitude of the genetic component for the ARP strain than for the ABP-CHES. Compared with the other studies on dual purpose breeds, heritability estimates of Valdostana cattle resulted lower, for example, than in the Rendena breed (Mazza et al., 2014) and slightly lower than in the Milking Shorthorn breed (Wiggans et al., 2004) for traits similar to those considered in this study. However, as the literature reported very few studies on dual purpose breeds, the type traits analyzed in Valdostana cattle can be compared mainly to specialized dairy and beef breeds. In accordance with other studies on dairy cattle (Biscarini et al., 2003; Berry et al., 2004; Zavadilová et al., 2009), heritability estimates in both strains of Valdostana breed were greater for the individual body size traits than for the udder traits, and the lowest values were for those traits associated with feet and legs. As regards the udder traits, heritability values in Valdostana breed ranged from 0.06 to 0.20 for ARP and from 0.01 to 0.18 in ABP-CHES. Slightly higher values were found for specialized dairy breeds, such as Holstein-Friesian and Brown Swiss. Thompson et al. (1981) and Toghiani (2011) reported heritability estimates for dairyness-related traits on Holstein population from 0.10 (rear udder attach) and 0.19 (teat placement), to 0.25 (udder depth), and 0.28 (fore udder attach). Samoré et al. (2010) have reported heritability values for udder traits in Brown Swiss cattle from 0.14 (udder cleft) to 0.33 (teat length). Similar values of heritability estimates for udder traits in this study were found for the Jersey population (i.e., from 0.07 for fore udder attach to 0.27 for teat length; Theron and Mostert, 2004). In specialized beef cattle dairyness-related traits were most lowly heritable, whereas body size and muscularity traits had the greatest heritability values (Gutiérrez and Goyache, 2002; Mantovani et al., 2010), as reported also in this study. Furthermore, some studies in the Belgian Blue breed showed higher heritability values than in the Valdostana breed, especially in some muscularity traits, such as thigh side and rear view (0.39 and 0.31, respectively; Hanset et al., 1994), probably attributable to the large diffusion of the myostatin mutation within this breed. As a matter of fact, autochthonous breeds, as the Valdostana cattle, could be more affected than cosmopolitan breeds by genetic drift and by increased homozygosity due to the smaller population size (Falconer, 1989). These

effects could be responsible of the lower heritability estimates obtained for some traits in Valdostana cattle as compare to breeds diffused worldwide (Falconer, 1989).

Within strain correlations between type traits

In both Valdostana strains genetic correlations were greater than the phenotypic ones, in agreement with many other studies carried out on beef cattle, such as in Charolais (Norris et al., 2008) and in the Piemontese breed (Mantovani et al., 2010), or on the Holstein dairy breed (Berry et al., 2004) or, furthermore, on dual purpose breed like the Rendena (Mazza et al., 2014). In accordance to our findings, negative genetic correlations between foot angle and rear legs were reported also by Van der Waaij et al. (2005) and Němcová et al. (2011) for the Holstein population. Medium to high genetic correlations between thinness and rear udder attach and between thinness and udder width were in agreement with correlations estimated by Wiggans et al. (2004) in Brown Swiss, Jersey, Guernsey and Milking Shorthorn. This genetic correlation indicates that thinner cows are more likely to have broader and taller udder, and consequently more supported, voluminous and productive udder too.

Focusing on individual udder traits, fore and rear udder attach and udder width showed a medium-high positive genetic correlations, whereas negative to zero genetic correlations were observed between these three traits and udder depth. A possible explanation of this result could be related to the fact that while fore and rear attach and udder width are volumetric traits of the udder, the udder depth describes the position in respect to the hock, being desirable when the score is in the middle of the scale system (i.e., three in the present system). In addition, an increase in the size of udder, as fore, rear udder attach and udder width, lead to a lower value of the udder depth or, from a functional point of view, a move down of the udder that can negatively affect milking labor and mastitis, as reported in Holstein by Rogers (1993). However, these correlation are in agreement with genetic correlations estimated in the Rendena dual purpose breed considering the same traits (Mazza et al., 2014), but in disagreement with those estimated by Biscarini et al. (2003) for Jersey breed and by Berry et al. (2004) for Holstein, probably due to a detriment in genetic variability in milk-related traits after a strong selection for volumetric parameters as in the latter two dairy breeds. Different genetic correlations between the two strains of Valdostana breed were found between the composite body shape and the composite udder traits: ARP showed a positive

genetic correlation (r_g = 0.13), whereas ABP-CHES demonstrated a higher negative correlation (r_g = -0.25). This difference is probably due to the different breeding purposes for the two strains, as the ARP is more selected for milk production and closer to a good dairyform, i.e., enough space for the development of the udder. On the other hand, ABP-CHES is a fighting strain, so the selection has led to animals with greater muscle formation, but with narrower rumps, and consequently to a less voluminous and productive udders. Finally, being both Valdostana strains dual purpose oriented, a special focus must be placed on the genetic correlations between muscularity and udder traits. In this study almost all the genetic correlations between the muscularity and udder individual type traits showed medium-high negative genetic correlations in both strains, especially considering the four individual muscularity traits and the first three individual udder traits related to the mammary size, i.e., r_g from -0.19 to -0.42 in ARP, and from -0.17 to -0.41 in ABP-CHES. Therefore, in this scenario, the selection for the dual purpose implies a need of taking into account both muscularity and udder traits as selection goals. Indeed, avoiding one of two group-traits could inevitably lead to a detrimental loose in the other group. These negative genetic correlations between muscularity and udder traits are in agreement with studies conducted on some specialized breeds in which these traits are recorded, even if they are not as important as in dual purpose breed. For example, in the Asturiana de los Valles beef cattle, the genetic correlation between thighs and udder development was reported at -0.20 (Gutiérrez and Goyache, 2002), and in the Piemontese breed the genetic correlations between dairyness and thigh thickness and profile were -0.15 and -0.19, respectively (Mantovani et al., 2010). Similar results were found also in some dairy breeds: in the Swiss Brown cattle, muscularity trait showed negative genetic correlations with all the individual udder traits (from -0.07 with teat length to -0.61 with rear udder; Vukasinovic et al., 1997). Also in the Ayrshire breed the genetic correlation between beef shape and fore and rear udder attach were -0.12 and -0.41, respectively (Mrode and Swanson, 1994). In dual purpose breeds, the problem related to the simultaneous improvement of antagonistic trait like muscularity and udder is not presented in specialized breeds, where the emphasis on morphological traits may be related only to those that are more related to beef or milk traits. As a matter of fact, most of the dairy and beef cattle breeds did not present specific muscularity or udder traits whatsoever in the scoring system, and this is the case, for example, of the Holstein-Friesian (Berry et al., 2004) or the

Jersey dairy cattle (Rogers et al., 1991); similarly, among beef breeds, the Belgian Blue cattle (Hanset et al., 1994) and the Charolais breed (Norris et al., 2008) could be considered as an example of breeds in which muscularity type traits are not coupled with udder trait in morphological evaluation form. On the other hand, dual purpose breeds, as they cannot be excessively specialized, do not need to account for functional selection traits as for example feet and legs or calving ease related traits. Furthermore, on dual purpose breeds, it is very important to consider the different economic weights of the traits under selection, that is milk and meat production attitudes. The possible introduction of linear type related to milk and meat production traits could be of further benefit to select antagonistic traits as in dual purpose breeds. In conclusion, results from this study indicate that genetic variation exists for type traits evaluated in both strains of Valdostana cattle. The strong genetic correlations between some individual type traits of the same region of the body indicate that they are controlled by the same genes, suggesting the possibility of reducing the number of traits under evaluation. The genetic parameters obtained from this study have been used to update the evaluation of the breeding value in the two strains of Valdostana breed. Further investigations into genetic and phenotypic associations between type traits and milk yield could help to improve selection for dual purpose within Valdostana cattle.

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CHAPTER 5

FACTOR ANALYSIS FOR GENETIC EVALUATION OF LINEAR TYPE TRAITS: A COMPARISON BETWEEN THE RENDENA AND THE AOSTA RED PIED AUTOCHTHONOUS BREEDS

Under submission

5.1 SUMMARY

Factor analysis was applied to individual type traits (**TT**) scored in primiparous cows belonging to 2 dual purpose Italian breeds, Rendena (**REN**; 20 TT, n = 11,399), and Aosta Red Pied (**ARP**; 22 TT, n = 36,168). Six common latent factors (F1-F6; eigenvalues≥1) which explained 63% (REN) and 58% (ARP) of the total variance were obtained. F1 included TT mainly related to muscularity, and F2 to body size. The F3 and F4 accounted for udder size and conformation, respectively. F5 included rear legs and feet. No easy biological meaning was obtained for F6. Moderate to low heritability were estimated via REML from factor scores (from 0.22 to 0.52 in REN, and from 0.08 to 0.37 in ARP). The greatest h^2 were estimated for size and muscularity (0.52 and 0.37 for size; and 0.40 and 0.32 for muscularity in REN and ARP, respectively). As expected, rank correlations between individual TT EBV's and factors' EBV showed similar coefficients than those observed in the factor analysis as loading of TT within each latent factor. These results suggest the possible use of factor analysis to simplify the linear TT information into new variables useful for breeding in dual purpose cattle.

5.2 INTRODUCTION

In the past, morphological evaluation has been one of the pillars of cattle selection, because it made possible an immediate evaluation of the animal conformation and a relatively simple classification (Forabosco et al. 2005). During years, the economic and genetic relevance of type traits in dairy cows has become secondary as respect to the productive traits. However, morphology is still important in many specialized dairy and beef breeds, and the global index use for selection in many breeds often includes also morphological traits. In addition, the morphological evaluation represents a key contact moment between the farmer and the breeding organizations. Morphology is today obtained in a well-organized scoring system of many traits using a linear scale. The use of morphological traits in selection programmes requires the knowledge of both their genetic parameters and their relationship with the main productive traits. The traditional approach to analyse the relationship between type traits and production data has been based on the use of a multiple regression method. This approach, however, has limitations because there are often a large number of traits that are interrelated. Indeed, some traits refer to the same part of the body are characterized by a high genetic correlation (Foster 1985), reflecting the expression of the same genes.

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For example, VanRaden et al. (1990) and Mazza et al. (2014), found high genetic correlations between rear udder height and rear udder width, ranging from 0.85 to 0.95, in some cattle breeds. High genetic correlations were also found among non-udder traits; for example, Klei et al. (1988) and Misztal et al. (1992) identified high genetic correlations between body depth and strength (from 0.85 to 0.93) in Holstein cows. Furthermore, using a large number of traits containing common information in multiple regressions can also lead to biased estimates of their relationship with productive traits due to collinearity (Sieber et al. 1987; Macciotta et al. 2012). To avoid redundant information in selection indexes, only a limited number of type traits with a known biological relationship with production and/or herd life should be used in the indirect estimation. A general statistical approach which properly accounts for dependencies variables is the factor analysis (Linder and Berchtold 1982). This procedure removes redundant information from correlated variables and represents the original variables with a smaller set of derived variables called 'factors' (Vukasinovic et al. 1997). Basically, factor analysis can be regarded as an analytical linear model that is much less restrictive than a traditional linear model with one or a few dependent variables (Enevoldsen et al. 1996). Ali et al. (1988) presented 4 reasons for which applying factor analysis to type trait data is consider as an important innovation: (1) summarizing information from the observed type traits into a few unobserved and relatively uncorrelated derived factors; (2) partitioning each trait response into a covariant and a specific part and the variance of each component can be estimated; (3) grouping type traits such that correlated traits could be isolated in the same factor and each factor will include traits with common biological and/or physiological characteristics; (4) the magnitude of each loading in the factor pattern reflects the importance of each type trait within the derived factor. Previously, factor analysis has been applied in scientific disciplines during most of the 20th century, like in socio-biology (Crawford and DeFries 1978; Crawford and Anderson 1989) and it has been also used in animal science to find indicators of management and production levels for dairy cattle herds (Enevoldsen et al. 1996), to evaluate relationships between longevity and type traits (Vukasinovic et al. 1997), to model the shape of the lactation curve (Macciotta et al. 2004; Aspilcueta-Borquis et al. 2012), and to study the structure of relationships between milk yield, milk composition and milk coagulation properties (Macciotta et al. 2012). Applications in animal and veterinary science, however, are few and in most of the cases outdated, but

these and other examples confirm the usefulness of the analytical approach (Schwabe et al. 1977; Korver et al. 1987; Sieber et al. 1988). However, only few studies dealing with factor analysis applied to linear type traits in dual purpose breeds are available in the literature. In such breeds, the study of relationship between different type traits reflecting both milk and meat characteristics could be of further interest for addressing appropriately the selection for both these traits. Therefore, the aim of the present study was to investigate the use of the factor analysis as a method to investigate the relationships between type traits in two Italian local dual purpose populations characterized by a similar morphological evaluation chart and identical scoring system. Both these breeds, the Rendena and the Aosta Red Pied, have been previously investigated for the genetics of the individual linear type traits and analytically described (Mazza et al., 2013a, 2013b, 2014). This study, as part of a bigger project aimed at implementing a global selection index in these dual purpose breeds, was also aimed at investigating the use of factor scores as a tool to obtain breeding values to be implemented in animal breeding. For this reason the genetic parameters of factors obtained were also estimated.

5.3 MATERIALS AND METHODS

Subjects of the study and morphological evaluation

The Rendena (REN) and the Aosta Red Pied (ARP) cattle are indigenous Italian dual purpose breeds (milk and meat production) that belongs to the "European federation of cattle breeds of the alpine system", an organization whose main purpose is the preservation and the promotion of the breeds raised in the Alps (FERBA 2014). Both breeds are diffused in northern Italy (east Alps and Veneto Region the REN and west Alps the ARP) are small medium size cattle with good fertility and longevity. Their main characteristics is the rusticity, i.e., the ability of living and producing in harsh climates and environments with low quality forages, such the alpine pasture where cows grazes during the summer season (Forabosco and Mantovani, 2011). The two breeds are linked by a comparable milk production (3,700 kg/lactation/cow in ARP and 5,200 kg/lactation/cow in REN) and similar milk characteristics (about 3.5% of fat and 3.3% of protein in both breeds). The two breeds have also a similar chart used for linear type evaluation, accounting for 20 and 22 linear type traits, for REN and ARP, respectively, and the same 4 composite traits. i.e., body size, muscularity, body shape and udder (see

for description Mazza et al., 2013a and Mazza, 2014). The main differences between the 2 charts (Mazza et al., 2013a and Mazza, 2014) are the addition of rump length and teat placement side view in ARP as respect to REN, and a different expression of one trait within the group of body size (thorax width in ABP is changed with the thorax length in REN) and in the group of muscularity traits (front muscularity in ABP is replaced by the shoulder fore view score in REN). Last, the thinness score in the 2 breeds has opposite biological extremes, i.e., the minimum is fine in ABP and heavy in REN, and vice versa for the maximum score (Mazza et al., 2013a, 2014). All traits for both breeds were scored from 1 to 5-point scale system by specialized classifiers within annual rounds of evaluations (approximately from February to May) that are aimed at scoring all primiparous cows after calving (usually falling between October and December due to the strong seasonality).

Data editing and statistical analysis

Data available for this study consisted of type classification records on 11,933 first parity Rendena cows evaluated between 1994 and 2014, and on 36,168 primiparous Aosta Red Pied cows evaluated from 1997 to 2014. Classifications of conformation traits considered in this study were the 20 (REN) and 22 (ARP) individual linear type traits collected once in the life of each cow by the two National Associations of Breeders (A.N.A.RE., National Association of Rendena Breeders; and A.N.A.Bo.Ra.Va., National Association of Valdostana Breeders). The final datasets were obtained from an editing process in which cows with incomplete measurements or with mission information on the age at parity, the stage of lactation at morphological evaluation or belonging to a herd-year-classifier contemporary group with less than 2 animals were excluded. The choice of maintaining at least 2 observation within each herd-year-classifier was due to the great amount of environmental cells with 2 or 3 records, i.e., about 33% in REN and about 51% in ARP. Remaining observation included in the study belonged to daughters of 730 sires (15.4 avg. daughter/sire) for REN and to daughters of 2,169 sires (15.5 avg. daughter/sire) for ARP. All available pedigree information (18,610 animals from 1,309 sires for REN; 63,015 animals from 4,951 sires for ARP) was used to set up the relationship matrix among animals in the genetic analysis.

A preliminary factor analysis was separately computed for the 2 breeds using the raw data (Chu and Shi 2002; SAS Institute, 2009). Factor analysis with the Varimax rotation as described by Kaiser (1958) was carried out to obtain latent factors accounting only for the traits with large absolute value of loadings (Ali et al. 1998, Macciotta et al. 2016, 2012). Phenotypic factor score from standardized type traits were then calculated for each animal using the factor pattern coefficients kept from the eigenvalues criterion (Cattel 1978). According to this criterion, only components with eigenvalues ≥1 were kept for the analysis (i.e., Kaiser criterion; Russel 2002) and interpreted from the biological point of view by looking at the loading coefficients of the individual linear type traits (i.e., the correlation with the factor).

Generalizing Russel (2002), the classic factor analysis equation specifies that a measure being factored can be represented by the following equation accounting n factors:

$$x_m = w_{m1}F_1 + w_{m2}F_2 + \ldots w_{mn}F_n + w_{mn}U_n + e \, ,$$

where the F_n represent the common factors that underlie the measures being analysed and the U_n represent the factors that are unique to each measure. Furthermore, the w_{mn} represent the factor coefficients or loadings of each measure on the respective factors (i.e., correlation between the nth common factors), whereas the e reflect random measurement error in each item. Note that each measured trait has its own unique factor, reflecting systematic variance in the item that is not shared with the other measures being analysed. On the basis of this equation, the variance in the measure being factored can be separated into three parts. The first part of the variance in the measure reflects the influence of the common factors, the second part reflects the influence of the factor unique to the measure, and the third random error variance (Russel 2002).

Finally, genetic and residual variance components were estimated for each factor separately using a series of univariate animal linear model analysis in the REMLf90 program (Misztal 2008) and applying the EM-REML algorithm.

The model considered for the REML single-trait analysis was as follow:

$$y_{ijkl} = HYC_i + AFC_j + DIM_k + u_l + e_{ijkl} \, ,$$

where y_{ijkl} is the type factor trait for cow l, HYCi is the fixed effect of herd-year-classifier of evaluation i (1,718 different levels for REN; 8,068 different levels for

ARP), AFC_j is the fixed effect of age at first calving (9 classes for REN; 5 classes for ARP), DIM_k is the fixed effect of days in milk (8 classes for REN; 7 classes for ARP), u_l is the random additive effect of cow l and e_{ijkl} is the random residual term.

In the matrix notation, the model can be expressed as:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ is an N×1 vector, $\mathbf{\beta}$ is the vector of systematic effects of order p, $\mathbf{u}$ is the vector of animal additive effects with order q, and $\mathbf{e}$ is the vector of residual effects. Furthermore, $\mathbf{X}$ and $\mathbf{Z}$ are the corresponding incidence matrices with the appropriate dimensions.

The resulting assumptions about the structures of (co)variance were:

$$V\begin{vmatrix} a \\ e \end{vmatrix} = \begin{vmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_e^2 \end{vmatrix},$$

where σ_a^2 is the direct additive genetic variance, and σ_e^2 the residual variance, $\mathbf{A}$ the numerator relationship matrix and $\mathbf{I}$ an identity matrix. The standard errors of the heritability estimates were calculated following the formula proposed by Falconer (1989). A rank correlation analysis (SAS Institute, 2009) was carried out considering EBVs derived from BLUP univariate analysis on factor score and the EBVs from BLUP univariate analysis obtained for the individual linear type traits (20 for REN and 22 for ARP). Each BLUP run was carried out by accounting for the appropriate estimates of (co)variances previously obtained via REML analysis. EBVs belonging to each factor score were correlated with EBVs obtained for all individual traits. Rank correlation analyses were carried out within breed by considering animal with records, which had a homogeneous mean accuracy both within and across breeds.

5.4 RESULTS

Phenotypic factor analysis

Rotated factor patterns coefficients (multiplied by 100 and rounded), communalities and eigenvalues of original variables are reported in Table 1 (REN) and in Table 2 (ARP). Only coefficients ≥|30| are reported. Six latent common factors were extracted for each breed (eigenvalues from 4.59 to 1.04 for the Rendena breed, and from 5.20 to 1.05 for the Aosta Red Pied) and presented. The 6 latent factors explained 63%

and 58% of the total variance, respectively for the REN and the ARP, among the type traits considered in each breed.. In both breeds Factor 1 (F1), the one with accounting for the bigger proportion of variance and with the greatest eigenvalues, results meanly related to cow's muscularity traits, including shoulder fore view (loading coefficient of 0.86 for REN) and front muscularity (loading coefficient of 0.81 for ARP), back, loins and rump and thigh, buttocks side and rear view. Other type traits not related to muscularity and mainly associated to body or rump size are also included in F1, but with much lower magnitude (i.e., lower loading coefficient) as compare to muscularity traits, i.e., thorax length (0.52) and rump width (0.34) in Rendena breed, and thorax depth (0.36), thorax width (0.56), rump width (0.56) and rump length (0.35) in Aosta Red Pied breed.. Factor 2 (F2) clearly describes the size of the cows in both breeds, including the four individual body size type traits (stature, body length, thorax depth and thorax length or thorax width depending on the breed considered), that are included in F2 with a loading coefficient greater than 60% in both breeds. This factor presents 16% and 13% of the total variance explained for Rendena and Aosta Red Pied breed, respectively. Again, the rump size traits enter in this factor in both breeds, although only in the REN the loading coefficient resulted greater than 60%. On the other hand, rump size traits results highly correlated: from 0.69 to 0.96 in REN breed, and from 0.68 to 0.93 in ARP breed (data not shown).

Table 1. Phenotypic factors, loading of individual type traits (coefficients ≥|30|), communality and eigenvalues obtained after Varimax rotation of 20 linear type traits for the Rendena breed.

Traits	F1	F2	F3	F4	F5	F6	Communality	Eigenvalues
				Varimax phenotypic factors				
Stature		88					0.80	4.588
Body length		89					0.79	2.757
Thorax depth		78					0.66	1.990
Thorax length	52	65					0.70	1.327
Shoulder fore view	86						0.75	1.084
Back, Loins and Rump	90						0.83	1.037
Thigh, Buttocks side view	89						0.82	0.952
Thigh, Buttocks rear view	87						0.79	0.867
Thinness			38				0.25	0.851
Rump angle			35			66	0.65	0.748
Rump width	34	68					0.59	0.673
Rear legs side view					80		0.67	0.560
Feet					-63		0.42	0.482
Fore udder attach			69				0.50	0.438
Rear udder attach			77				0.66	0.396
Udder width			81				0.69	0.353
Udder depth				73			0.68	0.309
Suspensory ligament				61			0.41	0.218
Teat placement side view			46			-46	0.47	0.210
Teat length				-55		52	0.64	0.160
Variance explained (%)	0.18	0.16	0.12	0.06	0.06	0.05		

Table 2.Phenotypic factors, loading of individual type traits (coefficients ≥|30|), communality and eigenvalues obtained after Varimax rotation of 22 linear type traits for the Aosta Red Pied breed.

Traits	Varimax phenotypic factors						Communality	Eigenvalues
	F1	F2	F3	F4	F5	F6		
Stature		88					0.79	5.197
Body length		85					0.75	2.530
Thorax depth	36	71					0.65	1.512
Thorax width	56	60					0.68	1.261
Front muscularity	81						0.71	1.219
Back, Loins and Rump	86						0.76	1.046
Thigh, Buttocks side view	85						0.76	0.967
Thigh, Buttocks rear view	88						0.78	0.925
Thinness			30			33	0.21	0.893
Rump angle						82	0.69	0.798
Rump width	56	40					0.52	0.762
Rump length	35	44				35	0.44	0.730
Rear legs					79		0.63	0.715
Foot angle					-76		0.60	0.615
Fore udder attach			68				0.46	0.516
Rear udder attach			80				0.67	0.442
Udder width			80				0.66	0.393
Udder depth				73			0.58	0.340
Suspensory ligament			49	39			0.39	0.322
Teat placement rear view			45	43			0.41	0.299
Teat placement side view			46	-34			0.35	0.274
Teat length				-48			0.27	0.243
Variance explained (%)	0.17	0.13	0.11	0.06	0.06	0.05		

The third and the fourth factors (F3 and F4) both accounted for trait belonging to the mammary system in both analysed breeds; Particularly, on the basis of the loading coefficient into the F3, the traits mostly accounted for are those related to the udder size, such as fore and rear udder attachments and udder width (loading coefficient ≥0.68 considering the 2 breeds); on the other hand, F4 includes mainly udder conformation traits, as noticeable on the basis of the high positive loading coefficients of the udder depth (0.73 in both breeds) and suspensory ligament (0.61 in REN and 0.39 in ARP), and negative coefficients for teat length (-0.55 for REN; -0.48 for ARP). In this factor, positive value of loading for teat placement rear view (0.43) and a negative coefficient for teat placement side view (-0.34) were observed in the for the Aosta Red Pied breed. In spite of the low amount the total variance explained (6% in REN and ABP), Factor 5 (F5) is related to feet and rear legs individual type traits, with high and positive loading coefficients for rear legs (0.80 and 0.79 for REN and ARP, respectively) and negative coefficients for feet (-0.63 for REN; -0.76 for ARP). The last latent factor (F6), which explained about 5% of the total variance, shows different loadings in the two breeds; for the Rendena population, it involves rump angle and two individual udder conformation traits, such as teat placement side view (with a negative loading coefficients of -0.46) and teat length (0.52). Regarding the Aosta Red Pied breed, Factor 6 includes three individual traits only related to body shape of cows, such as thinness (0.33), rump angle (0.82) and rump length (0.35). In both analysed breeds, thinness is the individual trait with the lowest communality (i.e., 0.25 and 0.21 in REN and ABP, respectively). In ABP, also teat length resulted characterized by a low communality with factors, indicating an almost complete independence from factors and the other individual traits.

Variance components and factors' heritability

Variance components for the six different factors are in Table 4. Heritability estimates for the Rendena breed presented a mean value of 0.37 with standard errors of 0.02, whereas for the Aosta Red Pied breed the mean value oh heritability was 0.21 with standard errors of 0.01 for all considered factors. In particular, the lowest heritability estimates were for F5 (feet and legs factor) in both breeds (0.22 for REN and 0.08 for ARP, respectively).On the other hand, the highest values of heritability were for F2, factor accounting for the body size individual type traits, and again in both breeds this estimate was the highest observed (0.52 for REN and 0.37 for ARP, respectively).

Factor 1 (i.e., muscularity factor) presented medium heritability values (that is 0.40 for REN and 0.32 for ARP, respectively), whereas factor accounting for mammary size traits (F3) and that considering udder conformation traits (F4) showed higher heritability values in the Rendena population than in the Aosta Red Pied (0.45 vs. 0.17 F3; and 0.31 vs. 0.19 F4, respectively).

Correlations between type EBV's and factor's EBV

Rank correlation analysis (only values ≥|30| reported) between individual type EBV's and factors' EBV are reported in Table 3. As expected, the correlation coefficients showed patterns very similar to the loading patterns of individual traits on each factor accounted. Indeed, EBV's obtained for F1 are highly and positive correlated with the EBV's of the four individual muscularity traits ($0.84 < r < 0.90$ for REN; and $0.82 < r < 0.89$ for ARP, respectively). In addition, rank correlations between EBV's of F2 and EBV's of body size related traits resulted high and positive (from 0.56 to 0.90 for REN, and from 0.54 to 0.90 for ARP, respectively), reflecting results previously reported for the phenotypic loading coefficients between individual traits and the second latent factor. The same findings can be observed also for the other factors taken into account in the present study. For example, rank correlation values between individual traits EBV's and F3's EBV presented greater coefficients for the same individual type traits loaded in the latent F3 scores (mean value of about 0.78 for both breeds). This pattern was observed also for F4 and F5. Finally, correlation analysis between individual type EBV's and F6's EBV indicated the difficult of identifying with precision the latent factor, because of the transient link with a consistent group of individual trait reflecting a single animal aspect.

Table 3. Rank correlation coefficients (only values ≥|30|) between EBV's estimated for individual type traits and EBV obtained from factor score in both breeds considering animals with records (11,933 first parity Rendena, and on 36,168 first parity Aosta Red Pied cows).

Traits	RENDENA (n=11,933)							AOSTA RED PIED (n=36,168)					
	F1	F2	F3	F4	F5	F6		F1	F2	F3	F4	F5	F6
Stature		90							91				
Body length		90							86				
Thorax depth		77							74				
Thorax length	35	56						-	-	-	-	-	-
Thorax width	-	-	-	-	-	-	-	56	56				
Shoulder, fore view	85							-	-	-	-	-	-
Front muscularity	-	-	-	-	-	-		83					
Back, Loins and Rump	90							87					
Thigh, Buttocks side view	90		-31					89					
Thigh, Buttocks rear view	89							90					
Thinness			44							46			
Rump angle			38		69								83
Rump width		64						54	36				
Rump length	-	-	-	-	-	-		34	41				
Rear legs					82							84	
Feet					-57							-80	
Fore udder attach			71							65			
Rear udder attach	-34		81							84			
Udder width			84							84			
Udder depth				70		30					74		
Suspensory ligament				60						36	38		
Teat placement rear view	-	-	-	-	-	-				50	38		
Teat placement side view			43			-47				50	-37		
Teat length				-58		43					-51		

5.5 DISCUSSION

Several studies indicate that the number of traits can be represented by fewer factors without reduction in accuracy in describing the cow's conformation (Sieber et al. 1987; Ali et al. 1998; Forabosco et al. 2005). The primary interest of the present study lies in the algebraic sign and magnitude of the coefficients and in the percentage of the total variance explained by each factor. A trait with a large coefficient contributes more to the factor than a trait with a small one (Sieber et al. 1987). Once the coefficients are determined, with a Varimax rotation in this case, one should try to make an interpretation of the factors trying to give a biological sense at the latent factor (Anderson 1958; Brown et al. 1973). The Varimax rotation criterion was first introduced by Kaiser (1958) and it is so called because it maximizes the sum of variances of the squared loadings (squared correlations between variables and factor). With this procedure, that allow a clear separation between factors, a simpler interpretation of the factors can be undertaken (Russel 2002). In spite of not being considered the best method, the orthogonal rotation is the most diffused method, as reviewed by Russel (2002). A factor score is calculated by multiplying the standardized value of a trait times the trait's factor pattern coefficients and adding these products (Sieber et al. 1987). Ideally, in the factor scores, the coefficient of correlation between each "real" and the obtained factor is maximized (McDonald and Burr 1967). Therefore, the factors can be interpreted and described according to the largest values (coefficients >|30|) of the traits. Regarding the Rendena breed, the first six latent factors, those presenting eigenvalues ≥1, accounted for 63% of the total variance among the 20 type traits, whereas the first six latent factors in the Aosta Red Pied breed accounted for 58% of the total variance among the 22 type traits. Sieber et al. (1988) found that factors with eigenvalues greater than 1 explained 73.6% of the total variance in type score of Holstein dairy cows. A similar value was found for the first five latent factors in a study on Canadian Holstein (Ali et al. 1998).

Table 4. Estimated variance components, heritability values and standard errors for 6 latent factors obtained in Rendena and Aosta Red Pied cows as factor score.

Trait	RENDENA				AOSTA RED PIED			
	σ^2_a	σ^2_r	h^2	SE (h^2)	σ^2_a	σ^2_r	h^2	SE (h^2)
F1	0.314	0.476	0.40	0.02	0.261	0.564	0.32	0.01
F2	0.465	0.422	0.52	0.03	0.305	0.524	0.37	0.01
F3	0.406	0.502	0.45	0.02	0.133	0.636	0.17	0.01
F4	0.278	0.627	0.31	0.02	0.158	0.678	0.19	0.01
F5	0.199	0.721	0.22	0.02	0.076	0.831	0.08	0.01
F6	0.296	0.612	0.33	0.02	0.134	0.710	0.16	0.01

The same value of total variance explained by factors in the Rendena breed was also found in a previous study on factor analysis conducted by Mantovani et al. (2005), but with a smaller dataset. Higher values of explained variance have been reported in a study comparing three Italian beef cattle breeds, i.e. Chianina (91% of total variance explained), Marchigiana (86% of total variance explained), and Romagnola breed (93% of total variance explained; Forabosco et al. 2005). Regarding the single factors obtained in this study in both breeds, the first factors, that explain the greatest part of the total variance, included highly correlated type traits, as reported in previous studies (i.e., from 93% to 95% among individual muscularity traits in REN and ARP, respectively: Mazza et al. 2013b, 2014). Indeed, cows with large values for F1, that resulted highly and positive correlated with muscularity individual traits in both breeds, can be pictured with developed shoulder, back, loins and rump and large buttocks; On the other hand, high values for F2, related to individual body size traits, represent tall and big animals, traits for which high genetic correlations were observed on a previous study carried out on the same breeds (Mazza et al., 2013a, 2014). F3 and F4, were identified in this study as udder traits related factors, giving a definition of the size and the quality of the mammary system, respectively, in both breeds. In other words, high values for F3 lead to tight, tall and broad udder, whereas high values of F4 refer to cows with shallow and strong udders (positive loading coefficient), but also with close and short teats (negative loading coefficient). A negative correlation between teat length and the related factor coefficient was also reported by Mantovani et al. (2005) in the Rendena breed (i.e., -0.70). Factor 5 gives a similar view of REN and ARP cows, presenting high and positive coefficients with rear legs and negative with feet traits, leading to sickle legs and low

foot angle, which have a biological sense in spite of opposite direction of scores (i.e., increasing score for sickle as compare to straight legs, and decreasing score for low as compare to steep foot angle; Mazza et al., 2013a, 2014). Finally, the last factor (F6), showing medium to low coefficients with individual body shape traits, did not give a clear pictures of our dual purpose cows on the basis of different individual trait loaded, particularly in ABP. As in the study of Mantovani et al. (2005), rank correlation analysis between individual type EBV's and factors' EBV shows very similar patterns to the loading coefficients of individual traits on latent factors. For example, rank for EBV's obtained for F1 indicated a high correlation with the individual muscularity traits (0.84<r<0.90 for REN; 0.82<r<89 for ARP, respectively). In addition, also EBV's for mammary size and udder conformation factors (i.e., F3 and F4) show high correlations with EBV's of fore and rear udder attach and udder width (0.70<r<0.83 for REN; 0.65<r<0.84 for ARP, respectively), and with EBV's of udder depth (0.70 and 0.72 in REN and ARP, respectively), suspensory ligament (0.59 and 0.35 in REN and ARP, respectively) and teat length (-0.57 and -0.48 in REN and ARP, respectively). The generally high rank correlations between factor EBVs and the corresponding EBVs for individual type traits with which the factor is associated, indicates the possible use of factor score as a derived variable to be used for animal breeding purposes. However, a careful choice of factors should be considered, because of any further analysis based on the new extracted variable could be attenuated by the random error in the factor score (Russel 2002), Heritability estimates of the six factors showed that in both breeds the most heritable factor resulted linked to the individual body shape traits (i.e., F2), whereas the lowest the result the factor related to feet and legs traits; i.e., F5.

These results reflect findings on heritability estimates of the individual linear type traits obtained on the same breeds in two previous studies (Mazza et al. 2013b 2014). Furthermore, almost the same heritability values of F1 (40% and 37% for REN and ARP, respectively) were found for the individual muscularity traits, with mean values of 30% (REN) and 24% (ARP), showing that factors well reflect the individual muscularity traits with which it is correlated. The same consideration can be carried out for F3 and F4 (udder size and conformation related factors). Mazza et al. (2013b) reported heritability values of fore and rear udder attach and udder width in the Aosta Red Pied breed of 16%, 19% and 14% respectively (mean value of 16%), and heritability values of 9% for udder depth, 7% for suspensory ligament and 20% for teat

length. Heritability estimates for factors in ARP reflect these previous results with values of 17% for F3 and 19% for F4. Also in the Rendena breed heritability estimates of factors are almost the same, but slightly higher, than those reported for the individual type traits: 45% for F3 (mean value of 35% for individual udder size traits; Mazza et al. 2014) and 31% for F4 (mean value of 26% for the individual udder conformation traits; Mazza et al. 2014).

One of the main criticisms about the use of the factor analytic technique has been identified in its vagueness in spite of its possibility of removing redundant information among a set of correlated variables (Crawford and DeFries, 1978; Chu and Shi 2002). From this point of view, considering that genetic correlation in selected population is mainly due to pleiotropic effects of genes, i.e., the involvement of the same genes in the expression of two or more traits, the factor score could become a useful method to remove redundancies among traits of interest for animal selection (Crawford and DeFries 1978). This is particularly interesting when a biological sense could be attributable to single factors on the basis of the loading coefficients of the single factorized traits (Macciotta et al. 2004, 2012)..

5.6 CONCLUSIONS

The present study was aimed at verifying the possibility the use the factor analysis as a tool for the genetic evaluation of morphological type traits by simplifying the information contained in all recorded traits in factors. Compared to the individual linear type traits, some latent factors obtained in this study focussed on dual purpose breed seemed able to represent specific region of the body of animals. Such picture allows a quite good representation of the latent factors, and the use of the factor scores as independent phenotype to be implemented in animal breeding programs for the analysed breeds. Therefore, the multivariate factor approach allows simplifying the analysis using a reduced number of variables, but without excluding any trait, although accounting mainly for the more representative ones loaded in any factor. This study indicates that for both Rendena and Aosta Red Pied dual purpose breeds, the number of type traits can be easily represented by few factors without reducing in accuracy in describing animals' conformation. Results from these analysis suggest a good and efficient possibility to use the latent factors in genetic evaluation, reducing considerably the amount of

elaborations by the Breed Associations, especially for those traits regarding the purposes of the breeds.

Acknowledgments

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CHAPTER 6

GENETIC CORRELATIONS BETWEEN TYPE AND TEST-DAY MILK TRAITS IN LOCAL DUAL-PURPOSE CATTLE POPULATIONS

Under submission

6.1 SUMMARY

Phenotypic and genetic (co)variances between morphological factors regarding specific region of the body and milk yield traits were estimated for the small local population of the Aosta Red Pied dual purpose cows. Factor analysis was applied to muscularity and udder individual type traits (scored linearly in a 1-5 scale) for 33,206 first and second parity cows. Factor 1 (F1) reflected 4 muscularity traits, factor 2 (F2) included 3 dimensional udder traits and factor 3 (F3) represented a good dairy conformation. Data from 169,008 test-day (TD) yield records (milk, fat and protein content) belonging to the first 3 lactations of 16,605 cows were also analysed. The models for the AIREML single-trait analysis accounted for the herd-year-classifier, classes of age at calving and of days in milk as fixed effects, and the random additive effect of cow for the morphological dataset; herd-TD within lactation, classes of gestation, classes of age at parity and of month of parity both within lactation, and permanent environment effect were taken into account for the repeatability TD model (RP-TDm), together with the additive genetic component. In this second model, the shape of the lactation curve was described by the 4th order Legendre polynomials. All the previous effects jointly were used to set up the model for the AIREML bi-trait analysis. The three extracted factors explained about 64% of the total variation among the linear type traits. Heritability estimates resulted 0.17 for F2, 0.20 for F3 and 0.31 for F1, whereas regarding production traits, the most heritable trait was milk yield (0.20), followed by protein (0.17) and fat content (0.13). Negative genetic correlations were found for F2 with both F1 and F3 (-0.38 and -0.12 respectively), and also between all the three milk yield traits and both F1 and F3 (from -0.23 to -0.53). On the other hand, strong and positive genetic correlations were obtained among milk, fat and protein yield, ranging from 0.79 to 0.0.87, and also between F2 and milk production traits (all ≥0.83). Phenotypic correlations resulted lower than the genetic ones, but almost reflecting them. Results from the present study will help the breed association of Valdostana cattle to improve the selection index for both aspects of dual purpose aptitude.

6.2 INTRODUCTION

Increased milk yield is a primary goal in dairy cattle breeding because of its preeminent importance in determining herd profitability (De Lorenzo and Everett, 1982). However, also in dual purpose cattle breeds, milk production is one of the pillars of genetic selection, even if breeders have to maintain equilibrium between selection on milk and meat production, especially in the indigenous cattle, in which the bond between breed, environment and history of the breed is significant (Gandini and Villa, 2003). A part from milk, emphasis on linear type traits classification has been also placed on specialized dairy breeds, and genetic relationships between type traits and yield have been widely studied (Thompson et al., 1981; VanRaden et al., 1990; Short et al., 1991; DeGroot et al., 2002). Linear type traits describe biological extremes for a range of visual characteristics of an animal (Berry et al., 2004). These traits are described with numerical scores following the specific classification system of each breed and they usually approximate a normal distribution, which is fundamental for an accurate genetic evaluations (Norman et al., 1988). On the other hand, the main problem associated with the use of type in genetic programs is the high number of traits scored and their high degree of correlations (Sieber et al., 1987). Indeed, traits referring to the same part of the body usually show a high genetic relationship (Sieber et al., 1987). To overcome this problem, factor analysis has been proposed as useful procedure to remove the redundancy from high correlated traits deriving a new set of less uncorrelated traits called "factors" (Vukasinovic et al., 1997). Factor analysis has been widely studied as a tool for genetic evaluation of type traits in some Italian cattle breed, independently from their attitude. Indeed, in both specialized beef breeds (Chianina, Marchigiana and Romagnola ; Forabosco et al., 2005), and in local dual purpose cattle breed as the Rendena (Mantovani et al., 2005) and Valdostana (Chapter 5 of the present thesis) have been investigated. Generally, traits associated with body size showed positive correlations with 305-day milk yield in Holstein (Foster et al., 1989; Misztal et al., 1992). Some udder related traits, such as fore udder attachment, udder cleft and depth had negative relationships with milk production, whereas rear udder height and rear udder width presented small positive correlations (Foster et al., 1989; Short and Lawlor, 1992; Sanjabi et al., 2003). Studies on association between type and 305-day milk yield and quality traits have been conducted also on some Italian specialized dairy breeds.

Samoré et al. (2010), for example, reported that for the Italian Brown Swiss, a positive genetic correlation among production traits with fore udder attach, rear udder width and rear udder height (from 0.22 to 0.45), indicating that more productive Italian Brown Swiss cows are characterized by a stronger udder attachment. Dwelling on the milk yield, during the past decades one of the most intriguing research topic has been the modelling of lactation curves (Schaeffer et al., 1977; Wilmink, 1987; Vargas et al., 2000) aiming at improving methods to predict 305-day lactation yields. However, during the last decade, records from single test day (TD) have been used in most dairy breeds to enable earlier selection decision (Bilal and Khan, 2009). A TD model is a statistical procedure which considers all genetic and environmental effects directly on a test-day basis (Swalve, 1995).

The use of this particular approach allows a more detailed statistical model, which accounts for environmental variation specific to individual TD yields and genetic effects associated with each animal (Dzomba et al., 2010). Furthermore, the TD milk yields allows to take into account many factors such as breed, herd management (Everett et al., 1994; Jamrozik et al., 1997), day of the year, lactation number (Swalve and Gengler, 1998), age at calving, month of calving, days in milk (Kaya et al., 2003) and many other important effects acting on cows. Different types of TD model have been developed, and many functions describing the shape of lactation curve have been analysed (Silvestre et al., 2006). In Italy, a multi trait-random regression is used for the Italian Holstein (Muir et al., 2007), while a repeatability TD model are applied for the Italian Brown (Dal Zotto, 2000), Italian Simmental (Degano et al., 2003) and for the local dual purpose Rendena breed (Guzzo et al., 2009). Under the repeatability TD model (RP-TD), consecutive test-day samples from the same lactation are considered as repeated observations on the same trait, and a permanent environmental effect accounts for environmental similarities between different TDs within the same lactation (Bilal and Khan, 2009). Therefore, this type of TD model is particularly adaptable to dual purpose indigenous breeds, as the number of cows with evaluation is less than in other specialized cosmopolitan breeds (i.e., Italian Holstein). A further step in classical animal breeding is the analysis of relationship between TD lactation yields and linear type traits, for which literature is scarce, particularly in dual purpose breeds. In this latter case, it is in addition of particular interest the understanding of relationship between TD milk yields and traits related to beef attitude. Within this framework, this study has

aimed to estimate genetic parameters between linear type and TD milk yields using the Aosta Red Pied, a local dual purpose breed, as a case study for other small indigenous breed. A further novelty of this study was due to the attempt of estimating heritability and genetic correlation with TD milk yield traits by using the factorization of some linear type traits scored on primiparous and secondiparous cows by the means of a factor analysis

6.3 MATERIALS AND METHODS

Subject of study

The Aosta Red Pied (ARP) is an indigenous dual purpose breed mainly raised in the Aosta Valley region, in the north-west of Italy, and originated from Red and White animals that lived in central Europe. Those animals, presenting a multi coloured coat (red and white, with white head and light muzzles), were brought by the Burgundy to the northern part of Italy at the end of 5th century (Del Bo et al., 2001). The ARP is one of the most diffused breed of the western Alps, because of its high adaptability to living and producing in the harsh conditions of the alpine areas. Nowadays, this breed is mainly raised as purebred animals. The ARP belong to the "European federation of cattle breeds of the alpine system", together with other 10 breeds raised in the Alpine arc, such as for example the Rendena, the Pinzgauer, the Herens, the Grauvieh, etc. (Forabosco and Mantovani, 2011). In this breed the linear type evaluation is of particular interest to maintain the good beef attitude in the breed. Indeed, the ARP cows are usually characterized by a long and muscular shoulder, which is set closely to the trunk and well covered by muscles, so the back of the animal, the tight and buttocks, which results convex in most part of cows. The thorax is wide and deep, and the rump results broad and long. Finally, the udder is sufficiently developed in order to identify a model of animal with a prevalent aptitude for milk production but good characteristics also for meat (A.N.A.Bo.Ra.Va., 2014). The milk yield of the ARP is mainly used to produce the PDO Fontina cheese. In 2012, the average milk yield per lactation was about 4,000 kilos, with a milk fat and protein percentages of 3.56 and of 3.29, respectively (FAO, 2014). In the same year, the total number of ARP cows, bulls and young animals registered at the Italian Herd Book was 31,665 (250 and 12,834 respectively; FAO, 2014). Up to now, for Valdostana breed the genetic evaluation of milk has been carried out by a traditional lactation model. At present a TD model is

going to be implemented. Therefore, in this study the milk related traits were evaluated through a repeatability TD model, that consider subsequent controls of the same lactation for each cow.

Table 1. Description statistics of individual type and milk yield traits measured in Aosta Red Pied cows used in the study.

Trait	Mean	Standard deviation	Coefficient of variation
Muscularity and udder type traits (score)[1]			
Front muscularity	2.88	0.86	0.299
Back, Loins and Rump	2.95	0.86	0.292
Thigh, Buttocks side view	3.07	0.87	0.283
Thigh, Buttocks rear view	3.05	0.90	0.295
Fore udder attachment	3.09	0.97	0.314
Rear udder attachment	3.24	0.89	0.275
Udder width	3.23	0.91	0.282
Udder depth	3.20	0.80	0.250
Teat placement rear view	2.81	0.65	0.231
Teat length	2.93	0.76	0.259
Test-day yields (kg/day)[2]			
Milk	13.23	4.61	0.348
Fat	0.45	0.17	0.378
Protein	0.43	0.15	0.349

[1] *Obtained from a dataset accounting for 33,206 individual records obtained from primiparous and secondiparous Aosta Red Pied cows;* [2] *Obtained from a dataset accounting for 169,008 test-day belonging to 16,605 Aosta Red Pied cows.*

Data editing

Data were provided by the National Association of Breeders of Valdostana cattle (A.N.A.Bo.Ra.Va.) and included conformation and productive information. Regarding the morphological dataset (**MORPH**), only records with days in milk (DIM) between 10 and 350 days, and with age at calving between 22 and 48 months (for primiparous cows) and between 38 and 60 months (for second parity cows) were retained. Furthermore, only herd-year-classifier contemporary group with less than 2 records were discarded. The final dataset considered of 10 linear type traits belonging to 33,206 first and second

parity cows of the Aosta Red Pied breed evaluated from 1997 to 2012 in 1,090 different herds and by different specialized classifiers. Only traits related to muscularity and udder were retained for the factor analysis, as they are those that mainly are related to beef and milk attitude. Four individual muscularity traits (front muscularity, FMU; back, loins and rump, BLR; thigh, buttocks side view, TBS; thigh, buttocks rear view, TBR) and six individual udder traits (fore udder attach, FUA; rear udder attach, RUA; udder width, UW; udder depth, UP; teat placement rear view, TPR; and teat length, TL) scored on a linear scale from 1 to 5 points were analysed (Table 1).

The initial milk yield traits dataset included 510,870 TD records from national functional controls realized between 1994 and 2009. Data editing was carried out taking into account only the first three lactations and controls with missing milk, fat and protein yields records were discarded. Furthermore, information collected between 5 and 250 DIM and within the range of the mean yield ±3 standard deviations calculated within lactation and 15 d DIM interval classes for milk, fat and protein yield, were retained. The limit of 250 DIM was established because of the strong seasonality of calving in the breed and the practice of the summer alpine pasture, which exclude functional controls during the last part of the lactation for a considerable number of animals. Also cows with days open (DO) period outside the range of 20 and 271 days after calving were discarded. Last, only lactations with at least 4 controls and herd-TD within lactation (HTDL) with at least 2 controls were taken into account in the final dataset. After editing, 169,008 TD belonging to 16,605 cows, evaluated in 833 different herds, remained for further analysis. The pedigree files obtained for genetic analysis included all known ancestors of animal with records up to the 10th generation, and accounted for 59,256 animals for the morphological dataset and 41,991 animals for the TD dataset to carry out single trait analysis.

Finally, for the bi-trait analysis between milk and morphological traits, the two data files described above, were joined into a single dataset accounting 202,214 records belonging to 36,019 animals (13,792 cows with both MORPH and TD information), and in this case the pedigree file contained 61,910 animals tracing back subjects up to 10 generations also in this case.

Statistical analyses and models

In the first step, a factorial analysis was computed using raw linear type data (Kaiser, 1958) belonging to the MORPH dataset. Phenotypic factors scores were calculated for each animal using the factor pattern coefficients kept from the eigenvalues criterion (Cattel, 1978). The Varimax orthogonal rotation method for of coefficients was chosen to obtain a clearer interpretation of each latent factor extracted, i.e., with eigenvalue ≥ 1 Russel (2002). Briefly, following the description of Macciotta et al., 2012, factor analysis encompasses the linear modeling of *n* original observed variables toward a limited set of *p* latent variables (called factors), that could be represented as follows:

$$y_1 = b_{11}X_l + \ldots\ldots + b_{1p}X_p + e_1,$$
$$y_n = b_{n1}X_l + \ldots\ldots + b_{np}X_p + e_n,$$

where X_j is the jth common factor, b_{ij} are the factor coefficients or loadings, that is the correlations between the jth common, e_i is the ith residual specific variable. In other words, the variance of each original variable can be decomposed in a common component that generates (co)variances between variables plus a residual specific variable (Morrison, 1976). In this study, the number of factors retained was identified on the basis of their biological meaning and relationship with the original variables. The individual factor scores obtained for each retained latent new variable were then treated as a new variable to be analyzed (Macciotta et al., 2006). Type factor traits were then analysed in single trait animal model using the AIREML program from the BLUPF90 family (Misztal, 2008), by applying the following model, in accordance with a previous study carried out on the ARP breed (Mazza et al., 2013):

$$y_{ijkl} = HYC_i + AC_j + DIM_k + u_l + e_{ijkl}, \qquad [1]$$

where y_{ijkl} is the type factor score for cow l; HYC_i, AC_j and DIM_k are three fixed systematic effects of herd-year-classifier (7,475 different levels), age at calving (10 classes) and days in milk (7 classes of 30-d intervals), respectively; u_l is the random additive effect of cow l; and e_{ijkl} is the random residual term.

In a second step a repeatability single trait animal model on milk, fat and protein TD was set by the means of the following linear mixed model implemented through the AIREML program from the BLUPF90 family (Misztal, 2008):

$$y_{ijklmnop} = HTDNL_{ij} + GL_k + \sum_{n=1}^{4} \alpha_{j\ln} \times z_n(t) + \sum_{n=1}^{4} \beta_{jmn} \times z_n(t) + u_o + Pe_o + e_{ijklmnop} \qquad [2]$$

where $y_{ijklmnop}$ is the TD record (milk, fat or protein) of the cow, $HTDL_{ij}$ is the fixed effect of the ith the herd-test-day for lactation j (46,722 levels), GL_k is the fixed effect of kth gestation length class (16 classes of 15-d intervals), $\alpha_{j\ln}$ is the nth fixed regression coefficient specific to the lth age at calving and lactation j (42 classes), β_{jmn} is the nth fixed regression coefficient specific to the mth month of parity and lactation j (36 classes), u_o is the random additive genetic effect of the oth cow, Pe_o is the random permanent environmental effect of the oth cow, $z(t)$ is a vector of covariates of size 4 describing the shape of lactation curve of fixed effects evaluated a t DIM, and $e_{ijklmnop}$ is the random residual term. The fixed random regression were fitted with a 4th order Legendre polynomials (Strabel and Misztal, 1999). Last, a series of bivariate analysis considering both within and across lactation TD records (milk, fat and protein one by one) and the factor scores obtained at first step through the MORPH dataset were set up to estimate (co)variance components for the additive genetic, permanent environmental and residual effects specified under the univariate models [1] and [2]. The effects in the previous two models were used jointly in the bivariate model (Kadarmideen and Wegmann, 2003), with the additive genetic component as the unique effect shared by the two traits.

The assumptions on estimated (co)variances for the bi-trait analyses were as follows:

$$Var\begin{vmatrix} u_1 \\ u_2 \end{vmatrix} = \begin{vmatrix} A\sigma_{u1}^2 & A\sigma_{u1u2} \\ A\sigma_{u1u2} & A\sigma_{u2}^2 \end{vmatrix}; \; Var\begin{vmatrix} Pe_1 \\ Pe_2 \end{vmatrix} = \begin{vmatrix} I\sigma_{Pe1}^2 & I\sigma_{Pe1Pe2} \\ I\sigma_{Pe1Pe2} & I\sigma_{Pe2}^2 \end{vmatrix};$$

$$Var\begin{vmatrix} e_1 \\ e_2 \end{vmatrix} = \begin{vmatrix} I\sigma_{e1}^2 & 0 \\ 0 & I\sigma_{e2}^2 \end{vmatrix};$$

where the terms σ_{u1}^2, σ_{u2}^2, σ_{u1u2} indicated the additive genetic (co)variances, σ_{Pe1}^2, σ_{Pe2}^2 σ_{Pe1Pe2} are the permanent environmental (co)variances, and σ_{e1}^2 and σ_{e2}^2 the residual variances of each pair of traits. Finally, **A** and **I** terms are the additive

relationships matrix and an identity matrix, respectively. When estimate of (co)variance components between factor scores and milk traits were carried out, the covariances σ_{Pe1Pe2} and σ_{e1e2} were set at zero, because of the former traits were measured only once in individuals and they did not share the environmental effects.

Genetic and phenotypic correlations between traits were calculated following Searle (1961). The standard error of heritability and correlations were calculated following the formulas proposed by Falconer and Mackay (1996)

6.4 RESULTS

Descriptive statistics of all analysed variables are reported on Table 1. The means of the individual linear type traits approximate the value of 3. The lowest mean value and coefficient of variation (CV) observed for morphological traits were for teat placement rear view (2.81 and 0.231, respectively), whereas the higher mean value was observed for rear udder attachment (3.24). The CV for all the 10 linear type traits considered ranged from 0.231 (teat placement rear view) to 0.314 (fore udder attachment). The individual average daily yield resulted of 13.23 kg for milk, 0.45 kg for fat and 0.43 kg for protein, with a homogeneous CV, that ranged from 0.348 (milk yield) to 0.378 (fat yield). In general, milk traits resulted more variable that morphological scores, with a mean CV that resulted almost 30% greater than for the latter traits. A description of each phenotypic factor based on the traits with pattern coefficients ≥|0.30|, multiplied by 100 and rounded (Mantovani et al., 2005), the eigenvalues and phenotypic variation explained by factors are shown in Table 2. From the factor analysis it was evident that factor 1 (F1) included the four individual muscularity traits (front muscularity, black, loins and rump, thigh and buttocks side and rear view), factor 2 (F2) represented three udder size traits (fore and rear udder attachments and udder width) and factor 3 (F3) included other three udder traits regarding the udder conformation (udder depth, teat placement rear view and teat length). Pattern coefficients ranged from 0.85 to 0.89 (F1), from 0.72 to 0.85 (F2) and finally from 0.47 to 0.71 for F3.

Table 2. Phenotypic factors, loading of individual type traits (coefficients ≥|30|), communality and eigenvalues obtained after Varimax rotation of 10 linear type traits recorded on 33,206 Aosta Red Pied cows.

Type trait	Varimax phenotypic factors			Communality	Eigenvalues
	Factor 1	Factor 2	Factor 3		
Front muscularity	85			0.73	3.082
Back, Loins and Rump	88			0.77	2.155
Thigh, Buttocks side view	88			0.78	1.145
Thigh, Buttocks rear view	89			0.79	0.902
Fore udder attachment		72		0.52	0.840
Rear udder attachment		85		0.73	0.614
Udder width		84		0.73	0.377
Udder depth			71	0.51	0.340
Teat placement rear view			47	0.40	0.296
Teat length			63	0.42	0.249
Variance explained (%)	0.31	0.21	0.12		

The three factors extracted from the analysis explain about 64% of the total variation among the 10 type traits. Factor 1 presented the highest magnitude, accounting for 31% of the total variation, followed by factor 2 (21% of the total variation explained). Heritability estimates from the univariate analysis (Table 3) for morphological factors resulted moderate (0.31 for F1; 0.17 for F2; and 0.20 for F3), and slightly lower for the yield traits (0.20 for milk; 0.13 for fat; and 0.17 for protein). Standard errors of heritability estimates were low, with values between 0.01 and 0.02 for all considered traits. The estimated variances resulted small only for fat and protein yields (Table 2), but a substantial genetic variation was obtained for al factor scores and milk yield.. Finally, in Table 4 are reported the genetic and the phenotypic correlations estimated both within and between morphological factor scores and test-day milk traits. The udder size factor (i.e., F2) showed negative genetic correlations with both muscularity and udder conformation factors (-0.38 with F1; and -0.12 with F3). However, a positive but low genetic correlation was found between muscularity (F1) and udder conformation (F3) factors (0.21). Phenotypic correlations within the 3 factors resulted very low and close to zero (from -0.09 to 0.08). All the three production traits showed positive and high genetic correlations, from 0.79 between milk and fat yield to 0.87 between milk and protein yield. Also in this case, the phenotypic correlations were lower than the genetic ones, but still greater than the phenotypic correlations between factors (from 0.35 to 0.41). Regarding the genetic correlations between morphological factors and milk related traits, muscularity factor (F1) and udder conformation factor (F3) showed medium negative association with all the three productive traits. Indeed, genetic correlations between F1 and yield were -0.53, -0.44 and -0.41 with milk, fat and protein, respectively. Otherwise, F3 showed in genetic correlations of -0.34 with milk, -0.23 with fat and -0.31 with protein yield. The udder size factor (F2) resulted in strong and positive genetic correlations with all the milk yield traits (i.e., 0.89 with milk, 0.83 with fat and 0.86 with protein yield). The phenotypic correlations were lower than the genetic ones, reflecting the negative results between both F1 and F3 with milk, fat and protein (from -0.14 to -0.10), and positive correlations between F2 and milk yield traits (from 0.21 to 0.27). For all the genetic correlations, the standard errors ranged from 0.02 to 0.08, whilst for the phenotypic correlations it resulted generally lower ranging from 0.02 to 0.05.

Table 3. Estimated variances, heritability (h^2) and standard error of heritability (SE) for morphological factor scores and test-day milk yield (single trait analysis).

Trait	Variances[1]			h^2	SE (h^2)
	σ^2_u	σ^2_{Pe}	σ^2_e		
Morphological factor scores[2]					
Factor 1 - Muscularity	0.251	-	0.549	0.31	0.02
Factor 2 - Udder size	0.130	-	0.651	0.17	0.01
Factor 3 – Udder conformation	0.162	-	0.667	0.20	0.01
Test-day yields (kg/day)[3]					
Milk	1.311	3.554	1.740	0.20	0.02
Fat	0.002	0.004	0.006	0.13	0.02
Protein	0.001	0.003	0.002	0.17	0.02

[1] σ^2_u *is the additive genetic variance;* σ^2_{Pe} *is the permanent environmental variance; and* σ^2_e *is the residual variance.* [2] *Estimated from a dataset accounting for 33,206 individual records obtained from primiparous and secondiparous Aosta Red Pied cows.* [3] *Estimated from a dataset accounting for 169,008 test-day belonging to 16,605 Aosta Red Pied cows.*

6.5 DISCUSSIONS

In origin, the linear type system was designed to score specific conformational traits by using a continuous biological scale accounting both extremes (Short et al., 1991). Often the relevance attributed by farmers to the type traits has led to consider as many traits as possible to be evaluated. Although some breeders association have reduced during years the number of type traits worth to be considered at scoring (Sieber et al., 1987), still many traits are taken in to account, particularly in dual purpose breeds, that are characterized by the selection goals that consider both milk and meat attitudes to be improved (Mazza et al., 2013). However, several studies have reported that traits referring to the same region of the body present high genetic correlations among them (Foster, 1985; VanRaden et al., 1990; Mazza et al., 2014). As a result of this and also due to a very huge number of linear type traits scored and managed from the breeders associations, a factor analysis was introduced to remove redundant information from correlated variables representing the original ones with a smaller set of derived traits called "factors". This following example reported also for other breeds (Vukasinovic et

al., 1997; Forabosco et al,, 2005; Mantovani et al., 2005), or referred to similar situation in which a bigger set of variables has been reduced by factor analysis (Russel, 2002; Macciotta et al., 2006). In dual purpose breeds, the equilibrium between meat and milk production is the primary objective, especially in the indigenous cattle for which to maintain the characteristics of the breed is fundamental for breeders. For the ARP breed the individual type traits included in each factor showed high genetic correlations among them and also between them and their morphological factor (unpublished data). Again in the present study a subset of traits, those mainly related to milk and beef characteristics described 3 main factors with a quite clear biological meaning. The relevance of a biological meaning of each latent factor obtained has been highlighted to be fundamental by Macciotta et al. (2006) for obtaining new variables easy to be interpreted. Failing in this could compromise the selection outcome if factor scores are considered as new traits in animal breeding programs. In spite of a general well recognized pleiotropic effect in quantitative traits accounted in selection programs, i.e., the presence of a group of same genes involved in the expression of two or more traits, the use of factors not fully or clearly explainable from a biological point of view, could interfere with a specific selection goal (Macciotta et al., 2012). The heritability estimates of morphological factors obtained in this study were in agreement with previous analysis carried out on the same breed (unpublished data), with the muscularity factor showing the greatest heritability value, followed by the udder conformation factor and by the udder size factor. To compare these results with other studies on heritability of factors is very hard, as literature reports only few researches on factor analysis, but lot of studies on dual purpose breeds show almost the same values of heritability for the individual linear type traits that referred to factors (Wiggans et al., 2004; Zavadilová et al., 2009; Mazza et al., 2013). Regarding the production traits, a brief focus needs to be done on the test day model used.

Lot of studies report milk production traits managed with a random regression model, that allows different shapes of lactation curves for each cow by the inclusion of random regression coefficients for each animal (Schaeffer and Dekkers, 1994; Canavesi et al., 2009).However, when a low number of test day records per cows are evaluated, a repeatability test-day model could be still more appropriate (Swalve, 1995) . The basic assumption of the repeatability TD model is that repeated measurements are regarded as expression of the same trait over time. In other words, a genetic correlation of unity is

assumed between repeat measurements. The main advantages of this model are its simplicity, fewer computations requirements and fewer parameters compared to multivariate (Mrode, 2005) and to random regression model. Independently from the model implemented in this study, the heritability estimates for milk yield traits are in agreement with those reported in literature, although the mean productive level of the ARP cows have to be considered much lower than those observed in specialized breeds (Mostert et al., 2006), where the greater production level are certainly due to the strong selective pressure put on selecting for milk. The single trait heritability estimates obtained for milk, fat and protein content in this study were close to values obtained for specialized Holstein by Swalve (1995), who reported 0.28 for milk0.18 for fat, and 0.19 for protein yield In Guernsey, Mostert et al. (2006), estimated heritability values of 0.24 for milk, 0.13 for fat, and 0.19 for protein yields . Using a similar test-day model, the estimates in the local Italian dual purpose Rendena breed were closer than observations reported for more specialized breeds (i.e., 0.21 for milk, 0.17 for fat, and 0.17 for protein; Guzzo et al., 2009). On the other hand, slightly lower heritability values ranging from 0.10 for fat to 0.18 for milk yield were reported for the Jersey breed by Mostert et al. (2006), and also for the Italian Brown Swiss Dal Zotto et al., 2005 estimated heritability at 0.11. The repeatability TD model has proved to be more conservative than random regression model in relation to the number of animals and herds enrolled in the genetic evaluation system. Use the random regression model can cause, due to an increase in the minimum number of observations per lactation, greater losses of cows and herds (Dal Zotto, 2000), particularly in small local population as in the case of ARP. Genetic and phenotypic correlations within morphological factors observer in this study reflect the correlations between the individual type traits included in each factor. The negative genetic correlation between muscularity and udder size factors observed (-0.38; F1 vs F2) is in accordance with findings on genetic correlations between the individual fleshiness traits and the three individual size traits on the same breed, ranging from -0.41 to -0.31 (unpublished data). In addition, also some analysis carried out on the Italian Rendena dual purpose breeds, which present a similar morphological evaluation chart and scoring system as the ARP, genetic correlations between muscularity traits and udder size traits have resulted negative, ranging from -0.53 to -0.26 (Mazza et al., 2014). Similar negative correlations have been reported also in some specialized dairy and beef cattle, as for example the Ayrshire (from -0.41 to -0.12; Mrode and Swanson, 1994) and

in the Italian Piemontese beef cattle (from -0.19 to -0.15; Mantovani et al., 2010). These results indicates that a too high selective pressure for meat production, and for more developed muscles development, lead to shorter and lower udders. As a consequence, the strong and positive genetic correlations observed in this study between udder size factor (F2) and the three milk yield traits, means that small udders produce less milk, as expected from a biological point of view.

Table 4. Genetic (above the diagonal), and phenotypic (below the diagonal) correlations within morphological factors scores and test-day milk traits, and between factor scores and milk traits. Standard errors of estimates are in brackets[1].

Trait	Morphological factor score[2]			Test-day yields		
	F1	F2	F3	Milk	Fat	Protein
Morphological factor score						
F1		-0.38	0.21	-0.53	-0.44	-0.41
		(0.05)	(0.05)	(0.06)	(0.08)	(0.07)
F2	-0.09		-0.12	0.89	0.83	0.86
	(0.06)		(0.05)	(0.02)	(0.03)	(0.02)
F3	0.06	0.08		-0.34	-0.23	-0.31
	(0.06)	(0.05)		(0.06)	(0.08)	(0.07)
Test-day yields (kg/day)						
Milk	-0.14	0.27	-0.07		0.79	0.87
	(0.04)	(0.03)	(0.04)		(0.05)	(0.03)
Fat	-0.10	0.21	-0.04	0.35		0.86
	(0.05)	(0.04)	(0.05)	(0.03)		(0.03)
Protein	-0.10	0.26	-0.06	0.41	0.37	
	(0.05)	(0.03)	(0.04)	(0.02)	(0.03)	

[1] *Obtained from a dataset accounting for 202,214 records belonging to 36,019 animals (13,792 with both morphological factor scores and test-day milk traits.*
[2] *F1 = factor 1, i.e., muscularity; F2 = factor 2, i.e., udder size; and F3 = factor 3, i.e., udder conformation.*

The positive correlations between udder size traits, especially rear udder attachment and udder width, and milk yield underlie the development of the dairy form of the specialized milk production breeds. Indeed, strong genetic correlations were reported for these traits in Holstein Friesian cattle (Sanjabi et al., 2003; Berry et al., 2004), in the Guernsey breed (Norman et al., 1988; Cruickshank et al., 2002) and also in

the Brown Swiss (Samoré et al., 2010). Finally, regarding the genetic correlations within the group of the milk yield traits the strong and positive genetic correlations are in agreement with literature reported for other breeds. Mostert et al. (2006) described genetic correlations between milk, fat and protein, using a repeatability TD model, ranging from 0.89 to 0.91 in the Ayrshire breed, from 0.85 to 0.92 in the Guernsey breed, from 0.80 to 0.97 in the Holstein and from 0.78 to 0.90 in the Jersey breed. In conclusion, data from this study showed that muscularity factor and milk yield are more heritable than the other morphological and productive traits evaluated. On the basis of the genetic correlation estimated, selection for increasing milk production traits is expected to decrease muscularity and udder conformation factor traits, whereas it increases the udder size factor trait.

These results could be of some interest in planning proper correct weights of the antagonistic traits in a selection index when the primary objective of selection is the maintenance of the dual purpose as in the breed used in this investigation as a case study.

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CHAPTER 7

GENERAL CONCLUSIONS

The thesis have treated various topics on the evaluation and elaboration of linear type traits in different autochthonous Italian dual purpose populations: the Rendena and the Valdostana (Aosta Red Pied, ARP; Aosta Black Pied-Chestnut, ABP-CHES) breeds.

The importance of type classification of cattle populations has been widely investigated through the studies of the present thesis, as they have proved to be, during years, highly correlated with many of the functional traits. Indeed, one of the most important reason to collecting information on morphological conformation of cows is to permit the breeders to select profitable, healthy and more long-lived animals.

The strong influence of different effects on type traits is evident in lot of studies. Among these, the effects of herd-year-classifier, age at calving and days in milk have resulted to be the most significant effects for both considered breeds. From the genetic trends showed in the third chapter, it was proved that the Rendena breed is becoming more specialized for milk production, slightly losing the typical dual purpose aptitude. From these results, breeder association of the Rendena breed (A.N.A.R.E.) has started to redefine the correct weights given in the global selection index for milk traits and consequently for the muscularity type traits. Regarding the Valdostana cattle, a deep importance is given to the origins and the differences between the two strains (Aosta Red Pied and Aosta Black Pied-Chestnut) included in the breed, as they present similar selection goals. As reported from the heterogeneity of variance analysis showed in chapter 4, results indicate that a genetic variation exists for type traits evaluated on both strains, and that genetic correlations found between the two analysed strains provide a useful evidence that ARP and ABP-CHES can be treated with separated breeding programs and so that morphological evaluation must be analysed separately.

Furthermore, to estimate genetic parameters of linear type traits is proved to be a valid method to define the most important traits (most heritable and traits with strong, positive or negative correlations) for which the selection should focused on. Studies conducted on the Rendena and on the Valdostana breed showed that heritable genetic variance exists for all type traits analysed, and that the greatest heritability estimates were for body size related traits (stature, body and thorax conformation), whereas the lowest values were for feet and legs traits. From the results collected in chapter 3 and 4, it is evident the strong genetic correlations between lot of type traits, especially those regarding the same region of the body, pointing out that these traits are controlled by the

same genes and suggesting the possibility to use a method aimed to reduce the number of variables treated.

The possible implementation of the factor analysis as a reduce technique of number of type traits evaluated has been the main topic of the fifth chapter of the present thesis. The conducted factor analysis showed that a considerable amount of the total variance can be explained with the use of latent factors. A reduced number of variables, compared with the use of more than 20 individual type traits, can simplify the calculation of weights. Moreover, the low degree of relationships, showed in chapter 6, could provide the advantage of an independent selection for these variables. Anyway, this approach is sometimes refused by many authors, because of the difficulties on the interpretation of factor composition, that is not completely straightforward, because one trait can contribute to two or more factors and sometimes with opposite signs. Results reported from the studies, led to the implementation of factor analysis on the muscularity and udder related traits in both the considered breeds.

Finally, analysis on the milk production data, showed that the application of the RP-TDm as alternative to traditional lactation model is possible and convenient for the small dual purpose population of the Aosta Red Pied, and consequently it could be taken into account also for other dual purpose and indigenous breeds, that generally present a small population.

The dual purpose aptitude of the local breeds, is one of the most important field for breeders, because of the strong linkage between animals and the environment. To maintain the dual purpose, and so to improve both milk and meat production without pushing too much in only one direction, is very difficult. For this, a deep understanding of the relationships between the antagonistic muscularity and udder type traits is of the primary importance for breeder associations, even considering the high correlations that these traits report with the milk production. Today, A.N.A.R.E. and A.N.A.Bo.Ra.Va. take in serious consideration the results of the present thesis and also with their usefulness, associations are able to better redefine the genetic selection indexes of these two dual purpose breeds, giving more exact weights to the type traits and to the milk yield selection.