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# HERITABILITY OF LINEAR TYPE TRAITS IN THE AUTOCHTHONOUS RENDENA DUAL PURPOSE BREED

Serena MAZZA [1, 2], Roberto MANTOVANI [1]

**ABSTRACT**

The aim of the study was to estimate heritabilities ($h^2$) of type traits and linear description scores in Rendena breed. Five traditional summary traits and 20 linear descriptions were recorded on 9,776 Rendena primiparous cows. All available pedigree information (16,234 animals) was used to set up the relationship matrix among animals. Data were analyzed using a single-trait animal model, accounting 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 ($h^2 = 0.53$), whereas the lowest value was found for feet (0.13). Other considerable values of heritability were found for body size (0.45), body length (0.40), and udder width (0.43). Medium-high heritability estimates were obtained for fleshiness (0.33), and udder (0.35), and regarding linear description for thigh-buttocks traits (0.32, and 0.33), thinness and rump angle (0.36 for both traits), as well as teat length (0.33). On the other hand suspensory ligament (0.17), and thorax length (0.16) showed low heritability values. However, the general good heritability estimates suggest the possibility to use linear description or type traits in genetic evaluation of Rendena cattle.

**Key words:** cattle / autochthonous breeds / dual purpose / Rendena / linear type traits / heritability / Italy

## 1 INTRODUCTION

The Rendena breed is an autochthon dual purpose breed (milk and meat) that belongs to the "European federation of cattle breeds of the alpine system". The Rendena population is mainly raised in Trentino Alto Adige (i.e., the region of origin) and in Veneto, and cows enrolled in functional controls are 70% of total population (ANARE, personal communication). This breed exhibits small-medium size, good fertility and longevity (Mantovani *et al.*, 1997). In Italy the breeding goal for this breed is to improve both quality and quantity of milk and meat. In the past morphological evaluation has been one of the pillars of cattle selection, because it made possible an instant evaluation of the conformation of the animals and a relatively simple classification (Forabosco *et al.*, 2005). Genetic evaluations of type traits in Rendena cows has been implemented since 2004, but no studies have been carried out on genetic evaluation of type traits with other productive traits. In dairy cattle, relationship of type with production (Veerkamp and Brotherstone, 1997; Kadarmideen and Wegmann, 2003) and with longevity (Larroque and Ducrocq, 2001; Vukasinovic *et al.,* 2002) have been widely studied in order to use type traits as predictors of herd life. Studies indicated that dairy cows of moderate size, with functional udders and correct feet and legs were more likely to remain in the herd than cows without these characteristics. In beef cattle, little is known of the relationship between type traits and longevity (Forabosco *et al.,* 2004).

As part of a wider study aimed at analysing genetic structure of type and other productive traits in the Rendena breed, the aim of this study was to estimate heritabilities of type evaluation traits and linear description scores.

1 Dept. of Agronomy Food Natural resources Animal Environment, Agripolis, 35020 Legnaro (PD), Italy
2 Address correspondence to: serena.mazza@studenti.unipd.it

## 2 MATERIALS AND METHODS

### 2.1 TYPE EVALUATION

Records belonging to 11,340 primiparous Rendena cows evaluated from 1994 to 2011 were considered. Morphological evaluation consists in a mixture of different recordings: 5 traditional summary traits (i.e. type traits) and 20 linear descriptions (Table 1). All traits are scored using 1 to 5 point scale system. Type traits include an overall score, which summarizes the general appearance of the animal and 4 different aspects of the animal (i.e. body size, fleshiness, body shape, and udder). On the other hand, linear descriptions include specific body regions regarding thorax, rump, feet, legs, thigh and udder conformation (Table 1).

***Table 1:*** *Descriptive statistics of type traits, and linear description of 9,776 Rendena primiparous cows used in the study*

| | Value | | | | | Descriptor | |
|---|---|---|---|---|---|---|---|
| Trait | Mean | SD | Kolmogorov-Smirnov | Min. | Max. | Minimum | Maximum |
| Type trait | | | | | | | |
| Overall score | 2.986 | 0.846 | 0.237 | 1 | 5 | Poor | Excellent |
| Body size | 3.115 | 0.866 | 0.257 | 1 | 5 | Little | Large |
| Fleshiness | 2.958 | 0.758 | 0.313 | 1 | 5 | Poor | Excellent |
| Body shape | 2.914 | 0.866 | 0.235 | 1 | 5 | Fine | Heavy |
| Udder | 3.047 | 0.899 | 0.246 | 1 | 5 | Poor | Excellent |
| Linear description | | | | | | | |
| Body size | | | | | | | |
| Stature | 3.127 | 0.975 | 0.230 | 1 | 5 | Short | Tall |
| Body length | 3.177 | 0.913 | 0.246 | 1 | 5 | Short | Long |
| Thorax depth | 3.186 | 0.880 | 0.254 | 1 | 5 | Very thin | Very large |
| Thorax length | 3.007 | 0.793 | 0.296 | 1 | 5 | Short | Long |
| Fleshiness | | | | | | | |
| Shoulder, Fore view | 2.790 | 0.833 | 0.278 | 1 | 5 | Scarce | Developed |
| Back, Loins and Rump | 2.933 | 0.805 | 0.305 | 1 | 5 | Scarce | Developed |
| Thigh, Buttocks side view | 3.008 | 0.796 | 0.298 | 1 | 5 | Hollow | Rounded |
| Thigh, Buttocks rear view | 2.848 | 0.814 | 0.278 | 1 | 5 | Hollow | Rounded |
| Body shape | | | | | | | |
| Thinness | 3.245 | 0.821 | 0.296 | 1 | 5 | Heavy | Fine |
| Rump angle | 2.669 | 0.680 | 0.368 | 1 | 5 | Back-inclined | Counter-inclined |
| Rump width | 3.154 | 0.814 | 0.290 | 1 | 5 | Narrow | Broad |
| Rear legs side view | 3.092 | 0.776 | 0.325 | 1 | 5 | Straight | Sickle |
| Feet | 2.885 | 0.709 | 0.338 | 1 | 5 | Weak | Strong |
| Udder | | | | | | | |
| Fore udder attach | 3.248 | 0.959 | 0.218 | 1 | 5 | Loose | Tight |
| Rear udder attach | 2.970 | 0.901 | 0.250 | 1 | 5 | Short | Tall |
| Udder width | 3.013 | 0.958 | 0.221 | 1 | 5 | Narrow | Broad |
| Udder depth | 3.362 | 0.716 | 0.321 | 1 | 5 | Deep | Shallow |
| Suspensory ligament | 3.216 | 0.828 | 0.319 | 1 | 5 | Weak | Strong |
| Teat placement side view | 2.962 | 0.755 | 0.318 | 1 | 5 | Close | Far |
| Teat length | 3.061 | 0.831 | 0.295 | 1 | 5 | Short | Long |

### 2.2 DATA EDITING

Original data were edited and discarded if the age at first calving was less than 24 months or greater than 60 months, if days in milk was less than 10 days or greater than 350 days, and if herds-year-classifier had less than 2 cows scored. After editing, information regarding 9,776 subjects remained for further analysis. All available pedigree information (16,234 animals) was used to set up the relationship matrix among animals.

### 2.3 MODELS

A preliminary ANOVA (SAS Inst. Inc., Cary, NC) was carried out to establish which non-genetic effects could be taken into account in the final model. A single trait analysis was performed using the REMLf90 program (Misztal, 2008) and applying the EM-REML algorithm.

The final model adopted for the single trait analysis was as follow:

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

where $y_{ijkl}$ is the type score or linear description for cow l, $HYC_i$ is the fixed effect of the herd-year-classifier i (1,380 different levels), $DIM_j$ is the fixed effect of days in milk j (8 classes from 10 to 30 day after calving and from 31 to 210 day after calving using 30-day intervals, or for later evaluation >210 d), $AFC_k$ is the fixed effect of age at first calving k (8 classes: < 26 months, from 27 to 38 using 2-month intervals, and ≥ 39 months for the last class), $u_l$ is the random additive effect of cow l, and $e_{ijkl}$ is the random residual term.

Due to program limitations, the SE for estimated heritabilities were obtained using the following formula (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 intraclass correlation obtained by ($h^2/4$) for paternal half-sib estimates, *k* is the average number of offspring per sire, and *s* is the number of sires.

## 3 RESULTS AND DISCUSSION

With only few exceptions, all analyzed non genetic fixed factors reported a significant amount of the total variance when analyzed with ANOVA (Table 2). The HYC effect was significant for all the traits considered ($P < 0.001$). Moreover, DIM and AFC were significant for almost all traits ($P < 0.001$), except for the rump angle, feet and teat placement side view for the first factor, and body shape, rump angle and rear legs side view for the second factor (Table 2). The lower significant values were found for udder ($P < 0.01$), and rear legs side view ($P < 0.05$) for DIM, and udder depth ($P < 0.05$) for AFC. The coefficient of determination ($R^2$) ranged between 0.19 (e.g., thinness) and 0.36 (e.g., shoulder – fore view). Moreover, for all fleshiness traits (e.g, shoulder, back, loins and rump, thigh and buttocks), determination coefficients are greater than 0.30 (Table 2).

### 3.1 HERITABILITIES

Estimated variance and heritability values are shown in Table 3. Analyzing the results for all morphological traits, the most heritable trait was the stature (0.53), whereas the lowest value of heritability was found for feet (0.13). Moreover the heritability for overall score was quite high (0.26), and also the other four type traits exhibited appreciable values, with the exception of body shape that showed the smaller value (0.17). Regarding linear descriptions, thorax length also showed a low value (0.16). On the other, hand all fleshiness traits had a rather high heritability, from 0.29 for shoulder – fore view, to 0.33 for thigh – buttocks side view. Significantly lower heritability values for body size, fleshiness and thinness were reported for Piemontese hypertrophic cows by Mantovani *et al.,* 2010 (i.e., 0.26, 0.15 and 0.12 respectively).

Among the seven udder traits only the suspensory ligament exhibited a low heritability value (0.17), while the others ranged from 0.30 to 0.43. Similar value of heritability was reported by Wall *et al.* (2005) for suspensory ligament in a study conducted on Holstein-Friesian cows (i.e., 0.16). Slightly greater heritability values for udder depth and for teat placement side view were reported for Holstein-Friesian primiparous cows by Berry *et al.*, 2004 (i.e., 0.33 and 0.38).

Standard errors of heritabilities resulted generally low, ranging from 0.022 to 0.038. This may be attributed to the larger data set used, derived from measurements obtained over 18 years.

## 4 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 heritabilities

***Table 2:*** *Results of ANOVA on nongenetic fixed factors used in the final model using type traits, and linear description of 9,776 Rendena primiparous cows*

| | Mean squares | | | | |
|---|---|---|---|---|---|
| Trait | HYC[1] | DIM[2] | AFC[3] | Residual | $R^2$ |
| Type trait | | | | | |
| Overall score | 1.95*** | 3.50*** | 8.82*** | 0.79 | 0.25 |
| Body size | 2.13*** | 7.21*** | 27.29*** | 0.79 | 0.28 |
| Fleshiness | 2.84*** | 16.93*** | 19.81*** | 0.67 | 0.33 |
| Body shape | 1.75*** | 1.60 | 6.14*** | 0.82 | 0.23 |
| Udder | 1.72*** | 14.36*** | 2.70** | 0.85 | 0.23 |
| Linear description | | | | | |
| Body size | | | | | |
| Stature | 2.00*** | 5.68*** | 8.72*** | 0.91 | 0.26 |
| Body length | 2.08*** | 6.46*** | 36.65*** | 0.84 | 0.28 |
| Thorax depth | 2.07*** | 4.17*** | 45.50*** | 0.81 | 0.28 |
| Thorax length | 2.63*** | 16.28*** | 34.51*** | 0.71 | 0.32 |
| Fleshiness | | | | | |
| Shoulder, Fore view | 3.37*** | 12.98*** | 13.43*** | 0.72 | 0.36 |
| Back, Loins and Rump | 2.99*** | 22.31*** | 14.32*** | 0.71 | 0.34 |
| Thigh, Buttocks side view | 2.67*** | 16.05*** | 18.37*** | 0.71 | 0.32 |
| Thigh, Buttocks rear view | 2.77*** | 15.87*** | 26.44*** | 0.72 | 0.33 |
| Body shape | | | | | |
| Thinness | 1.38*** | 3.42*** | 4.03*** | 0.80 | 0.19 |
| Rump angle | 1.76*** | 1.95 | 1.01 | 0.65 | 0.23 |
| Rump width | 2.40*** | 12.33*** | 83.17*** | 0.73 | 0.32 |
| Rear legs side view | 1.74*** | 0.89 | 2.26* | 0.74 | 0.23 |
| Feet | 1.76*** | 4.37*** | 2.00 | 0.67 | 0.23 |
| Udder | | | | | |
| Fore udder attach | 2.22*** | 17.34*** | 9.08*** | 0.87 | 0.29 |
| Rear udder attach | 1.66*** | 12.52*** | 3.64*** | 0.85 | 0.23 |
| Udder width | 1.73*** | 8.06*** | 5.49*** | 0.91 | 0.23 |
| Udder depth | 1.91*** | 2.16* | 18.45*** | 0.67 | 0.24 |
| Suspensory ligament | 1.62*** | 16.58*** | 18.60*** | 0.78 | 0.23 |
| Teat placement side view | 1.81*** | 4.14*** | 1.28 | 0.71 | 0.24 |
| Teat length | 1.54*** | 5.82*** | 5.42*** | 0.80 | 0.22 |

[1] HYC = effect of herd-year-classifier (i.e., 1,380 different levels);
[2] DIM = effect of days in milk (8 classes: from 10 to 30 day after calving and from 31 to 350 day using 30-day intervals);
[3] AFC = effect of age class at first calving (8 classes: from 24 to 26 month and from 27 to 60 month using 2 mo intervals);
* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

obtained in this research 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. These rather high heritability indicate a good possibility for using linear description or type traits in routinely genetic evaluation of Rendena cattle.

***Table 3:*** *Estimated variance and heritabilities for type traits, and linear description of Rendena primiparous cows*

| | Parameter[1] | | | |
|---|---|---|---|---|
| Trait | $\sigma^2_g$ | $\sigma^2_e$ | $\hat{h}^2$ | SE $_{\hat{h}^2}$ |
| Type trait | | | | |
| Overall score | 0.165 | 0.476 | 0.26 | 0.027 |
| Body size | 0.298 | 0.369 | 0.45 | 0.035 |
| Fleshiness | 0.153 | 0.311 | 0.33 | 0.030 |
| Body shape | 0.118 | 0.564 | 0.17 | 0.023 |
| Udder | 0.262 | 0.491 | 0.35 | 0.031 |
| Linear description | | | | |
| Body size | | | | |
| Stature | 0.468 | 0.412 | 0.53 | 0.038 |
| Body length | 0.298 | 0.439 | 0.40 | 0.033 |
| Thorax depth | 0.195 | 0.478 | 0.29 | 0.028 |
| Thorax length | 0.081 | 0.426 | 0.16 | 0.024 |
| Fleshiness | | | | |
| Shoulder, Fore view | 0.151 | 0.377 | 0.29 | 0.028 |
| Back, Loins and Rump | 0.155 | 0.361 | 0.30 | 0.029 |
| Thigh, Buttocks side view | 0.171 | 0.350 | 0.33 | 0.030 |
| Thigh, Buttocks rear view | 0.174 | 0.362 | 0.32 | 0.030 |
| Body shape | | | | |
| Thinness | 0.236 | 0.425 | 0.36 | 0.031 |
| Rump angle | 0.154 | 0.270 | 0.36 | 0.032 |
| Rump width | 0.133 | 0.411 | 0.24 | 0.027 |
| Rear legs side view | 0.115 | 0.438 | 0.21 | 0.025 |
| Feet | 0.059 | 0.396 | 0.13 | 0.022 |
| Udder | | | | |
| Fore udder attach | 0.238 | 0.552 | 0.30 | 0.029 |
| Rear udder attach | 0.234 | 0.523 | 0.31 | 0.029 |
| Udder width | 0.374 | 0.498 | 0.43 | 0.034 |
| Udder depth | 0.141 | 0.327 | 0.30 | 0.029 |
| Suspensory ligament | 0.105 | 0.518 | 0.17 | 0.023 |
| Teat placement side view | 0.160 | 0.362 | 0.31 | 0.029 |
| Teat length | 0.219 | 0.436 | 0.33 | 0.030 |

[1] $\sigma^2$g is the additive genetic variance, $\sigma^2$e is the random residual variance, $\hat{h}^2$ is the estimated heritability, and $\hat{h}^2$ is the SE of the estimated heritability.

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