

Genetic parameters for calving ease, gestation length and stillbirth in three endangered Austrian blond cattle breeds

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Abstract

Genetic parameters were estimated for stillbirth, calving ease and gestation length in three endangered Austrian blond cattle breeds, Carinthian Blond, Murboden and Waldviertel Blond. REML analysis based on an animal model including direct and maternal genetic effects was applied. Direct heritability estimates for calving ease, stillbirth and gestation length varied from 0.003 to 0.111, 0.006 to 0.044 and 0.235 to 0.512, respectively, while maternal heritabilities ranged from 0.001 to 0.007 for calving ease, 0.005 to 0.014 for stillbirth, and 0.002 to 0.063 for gestation length. All pairwise genetic correlations for direct traits were generally moderate to high except for stillbirth-calving ease (-0.077 , Carinthian Blond). The genetic correlations of all pairs of the 3 direct traits were positive for Murboden (0.520 to 0.700) and Waldviertel Blond (0.253 to 0.707) while negative genetic correlations were detected for Carinthian Blond (-0.077 to -0.943). Close positive genetic correlations were found between direct stillbirth and calving ease of Murboden (0.700) and between direct calving ease and gestation length of Waldviertel Blond (0.707), while a close negative genetic correlation was found between direct calving ease and gestation length of Carinthian Blond (-0.943).

Keywords: cattle, calving ease, stillbirth, gestation length, direct genetic effect, maternal genetic effect, heritability, Austrian blond cattle breeds

Zusammenfassung

Genetische Parameter für Kalbeverlauf, Trächtigkeitsdauer und Totgeburtenrate bei drei gefährdeten österreichischen Blondviehrassen

Für drei gefährdete österreichische Blondviehrassen (Kärntner Blondvieh, Murbodner und Waldviertler Blondvieh) wurden genetische Parameter für die Merkmale Totgeburtenrate, Trächtigkeitsdauer und Kalbeverlauf geschätzt. Es kam eine REML Analyse basierend auf dem Tiermodell zur Anwendung, wobei direkte und maternale genetische Effekte berücksichtigt wurden. Die Schätzwerte der direkten Heritabilität variierten von 0,003 bis 0,111 für den Kalbeverlauf, von 0,006 bis 0,044 für die Totgeburtenrate und von 0,235 bis 0,512 für die Trächtigkeitsdauer, während hingegen die maternalen Heritabilitäten von 0,001 bis 0,007, 0,005 bis 0,014 und 0,002 bis 0,063 schwankten. Die paarweisen genetischen Korrelationen zwischen direkten Merkmalen waren generell moderat bis

hoch mit Ausnahme Totgeburtenrate-Kalbeverlauf beim Kärntner Blondvieh. Die genetischen Korrelationen zwischen direkten Merkmalen waren beim Murbodner (0,520 bis 0,700) und Waldviertler Blondvieh (0,253 bis 0,707) generell positive, während negative Beziehungen beim Kärntner Blondvieh ($-0,077$ bis $-0,943$) geschätzt wurden. Eine enge positive genetische Korrelation wurde sowohl zwischen direktem Effekt der Totgeburtenrate und dem Kalbeverlauf beim Murbodner (0,700) als auch zwischen direktem Effekt des Kalbeverlaufs und der Trächtigkeitsdauer beim Kärntner Blondvieh (0,707) gefunden. Eine sehr enge negative genetische Beziehung ($-0,943$) wurde zwischen direktem Kalbeverlauf und Trächtigkeitsdauer beim Kärntner Blondvieh geschätzt.

Schlüsselwörter: Rinder, Kalbeverlauf, Totgeburtenrate, Trächtigkeitsdauer, direkter genetischer Effekt, maternaler genetischer Effekt, Heritabilität, österreichische Blondviehrassen

Introduction

Carinthian Blond (CB), Murboden (MU) and Waldviertel Blond (WB) are considered as highly endangered autochthonous cattle breeds in Austria (DUCHEV *et al.* 2006, ÖNGENE 2008). CB are white to maize-yellow cattle. CB has been developed in the federal state Carinthia and Styria since the late 18th century by crossing with Hungarian gray and alpine cattle. In the early 20th century, CB was particularly crossed with Franconian, Simmental and Red and White cattle breeds. WB are cream to rust-coloured cattle raised in the federal state Lower Austria. In the 19th century WB was crossed with MU, Franconian cattle and Glan-Donnerberger breeds. In early 20th century, WB was gradually replaced by Simmental cattle for better milk production (MANATRINON *et al.* 2008). However, WB was still kept in the Waldviertel region. Typically, MU has a light-coloured triangle on the slate-blue muzzle. Cows are flaxen with a reddish and even light-grey touch with white spots. MU was raised in Styria, parts of Carinthia, Lower Austria and Slovenia. MU cattle were very popular before the Second World War; afterwards they were replaced by other breeds, or were crossed with Franconian cattle.

Therefore, in the early 1980's, The Austrian Association for Rare Endangered Breeds (ÖNGENE) was established for conservation of such breeds. Since then, the numbers of calves born per year increased constantly from around 200 calves in 2000 to around 500 calves for CB and WB, and around 1 800 calves for MU in 2007 (Figure 1). The number of animals per farm is quite low (Table 1).

Table 1
Number of cattle and farms in the year 2007 (based on own data)
Anzahl Rinder pro Betrieb im Jahr 2007 (basierend auf eigenen Daten)

	Carinthian Blond	Murboden Blond	Waldviertel Blond
Number of animals	697	1 839	559
Number of farms	97	356	98
Mean \pm SD ¹	7 \pm 8	5 \pm 5	6 \pm 5
Median ¹	4	3	4
Min ¹	1	1	1
Max ¹	59	31	30

¹ mean \pm SD (standard deviation), median, min and max for number of animals per farm

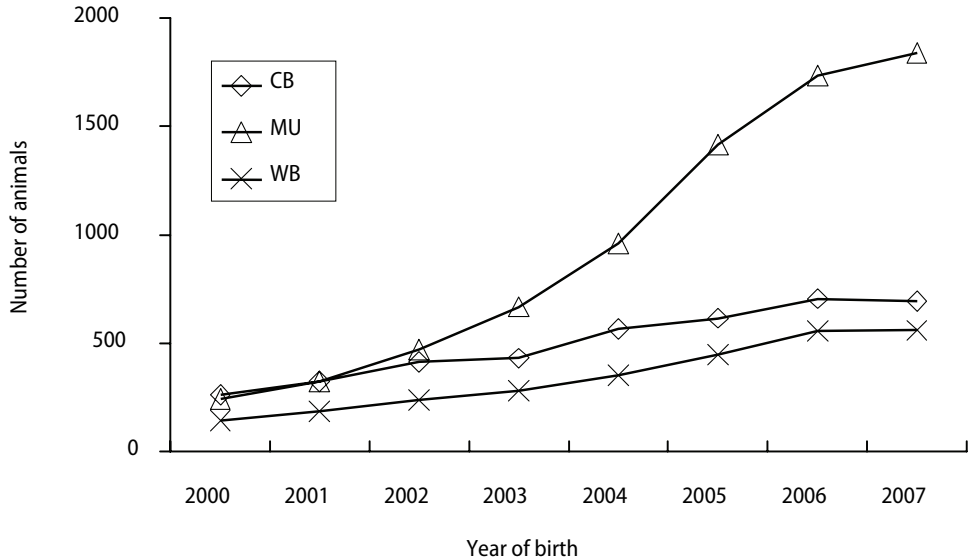


Figure 1
 Number of animals per year (based on own data)
 Anzahl Tiere pro Jahr (basierend auf eigenen Daten)

MANATRINON *et al.* (2008) estimated the genetic diversity of CB and WB based on 25 microsatellites loci. They found that the genetic diversity of these two breeds was rather high (0.675 and 0.655, respectively). However, the measurement was only from a small number of loci (25 loci) but variation in quantitative traits is usually polygenic or controlled by many loci. So estimation of variation of quantitative genetic characters would be another option to provide valuable information for making conservation decisions (STORFER 1996). It is generally more likely to be correlated with overall genetic variation than variation measured by DNA at single loci (FALCONER and MACKAY 1996, LANDE 1982). PFRENDER *et al.* (2000) reported that there is a lack of concordance between genetic diversity estimates at the molecular and quantitative-trait level.

Furthermore, in conservation studies, heritability can be used to determine the proportion of genetic variation in a population by choosing traits that are related to fitness or survival (STORFER 1996). Variation in these traits may provide information on how well an animal might persist in a changing environment. Functional traits like stillbirth, calving ease and gestation length are good options because they are not only directly related to survival but also biologically and economically important. Therefore, estimates of heritability are an indicator of the opportunity of response to selection, and thus, the evolutionary potential of populations (ANTONOVICS 1976, LANDE 1982).

The main objectives of this study were to estimate genetic parameters for important functional traits, by evaluating direct and maternal genetic as well as environmental effects for stillbirth, calving ease and gestation length in three endangered blond cattle breeds.

Material and methods

Data

Data of the three endangered cattle breeds CB, MU and WB were provided by ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria. Data were restricted to a minimum number of 10 records/farm; 5 records/sire and 3 records per farm and year. Lactation numbers higher than 25 were discarded while lactation numbers higher than 8 (9-25) were set to lactation 8. After restrictions, the number of records used in this analysis was 3 471 (CB), 3 357 (MU) and 1 929 (WB) for calvings during the period from year 2000 to 2007, whereas the complete pedigree files contained 5 545 records for CB, 9 479 records for MU and 2 447 records for WB, respectively. Twin births were not considered in the analysis. Stillbirth was recorded as binary trait (0 = born alive or 1 dead at birth or within 48 h), whereas calving ease was scored subjectively by the farmer and explained the amount of difficulty a heifer or cow had giving birth. Calving ease scores ranged from 1 to 4 (1 = easy calving without help, 2 = help from 1 person, 3 = with help from more than 1 person or mechanical assistance, 4 = veterinarian needed). The scores were transformed by applying the Snell transformation (SNELL 1964). Gestation length was defined as the number of days between the date of the latest insemination and the date of calving. In this study gestation lengths were restricted from 270 to 300 days.

Model

The (co)variance components were estimated via REML method by using the VCES5 package (KOVAC *et al.* 2002). Data were analyzed with an animal model including direct and maternal genetic effects in accordance to the model used routinely in the joint Austrian-German breeding value estimation:

$$Y_{ijklmno} = \mu + HY_i + YS_j + S_k + LA_l + a_m + m_n + pe_n + e_{ijklmno} \quad (1)$$

where Y is the stillbirth, calving ease or gestation length, HY_i the fixed herd-year effect ($i=482, 554$ and 391 for CB, MU and WB, respectively), YS_j the fixed year-season effect (years: 2000 to 2007; season 1: January to March; season 2: April to June; season 3: July to September and season 4: October to December), S_k the fixed effect of sex of the calf, LA_l the fixed lactation number-age class at calving (age classes for first lactation = 19-22, 23-24, 25, 26, 27, ..., 37, 38, 39 and 40-43 months; age classes for second lactation = 23-33, 34-35, 36, 37, 38, ..., 52, 53, 54 and 55-57; no age classes for higher lactations), a_m the random direct additive genetic effect of the calf m , m_n the random maternal additive genetic effect of dam n , pe_n permanent environmental effect of dam, and $e_{ijklmno}$ the random residual effect. In our analysis, the first and the higher lactations were analyzed as one trait because of the small number of data in endangered cattle breeds. However, this is the first time that genetic parameters of these three breeds were estimated.

Results

Descriptive statistics

The distributions of calving ease scores, stillbirth and gestation length are shown in Table 2. The rates of easy calving were greater than 80% in all breeds. CB showed the highest percentage for calving difficulty (4.0%) while MU showed the lowest (2.8%). CB showed the highest stillbirth rate (0.32%) in this study, but this value can still be considered as very low compared to other breeds where stillbirth ranged between 2 to 13 percent (MEYER *et al.* 2001, FUERST and EGGER-DANNER 2003, FÜRST and FÜRST-WALTL 2006). The mean gestation length was 286 days for CB and 287 days for MU and WB.

Table 2

Frequencies of calving ease and stillbirth, as well as mean of gestation length (\pm SD)*Frequenzen für Kalbeverlaufsklassen, Totgeburtenrate und mittlere Trächtigkeitsdauer (\pm SD)*

Breeds	Calving ease score, %				Stillbirth, %	Gestation length (means \pm SD)
	1	2	3	4		
CB	86.7	7.0	0.9	4.0	0.32	286 \pm 5
MU	86.9	8.7	0.6	2.8	0.16	287 \pm 5
WB	84.1	11.2	0.4	3.3	0.04	287 \pm 6

SD standard deviation

Genetic parameters

Table 3 shows the resulting heritability estimates of the direct effect (h^2), maternal effect (m^2) and the estimated genetic correlation between the direct and the maternal effect (r_{am}) and their standard errors (SE). The direct heritabilities of stillbirth (0.006 to 0.044) and calving ease (0.003 to 0.111) were very low while the direct heritabilities of gestation length were quite high (0.235 to 0.512). However, the maternal heritabilities were close to zero in all breeds and all traits (0.001 to 0.063). The genetic correlations between the genetic component of the calf and the maternal component were relatively high for stillbirth (negative correlation) and gestation length (positive correlation) while weak to moderate negative correlations were found in calving ease. However, most of standard errors of h^2 , m^2 and r_{am} were very high, most likely due to the small number of records.

Table 3

Genetic parameters for stillbirth, calving ease and gestation length

Genetische Parameter für Totgeburtenrate, Kalbeverlauf und Trächtigkeitsdauer

Trait	Breed	$h^2 \pm$ SE	$m^2 \pm$ SE	$r_{am} \pm$ SE
Stillbirth	CB	0.044 \pm 0.030	0.014 \pm 0.009	-0.512 \pm 0.439
	MU	0.007 \pm 0.008	0.005 \pm 0.004	-0.869 \pm 0.297
	WB	0.006 \pm 0.100	0.007 \pm 0.007	-0.847 \pm 0.226
Calving ease	CB	0.003 \pm 0.004	0.007 \pm 0.006	-0.039 \pm 0.787
	MU	0.111 \pm 0.031	0.001 \pm 0.009	-0.154 \pm 0.398
	WB	0.019 \pm 0.022	0.006 \pm 0.006	-0.480 \pm 0.944
Gestation length	CB	0.235 \pm 0.039	0.004 \pm 0.005	0.369 \pm 0.257
	MU	0.512 \pm 0.076	0.002 \pm 0.005	0.891 \pm 0.501
	WB	0.491 \pm 0.067	0.063 \pm 0.029	0.838 \pm 0.239

h^2 direct heritability, m^2 maternal heritability, r_{am} genetic correlation between direct effect and maternal effect, SE standard error

The genetic correlations between direct-direct and maternal-maternal traits are shown in Table 4. Positive genetic correlations among direct-direct traits were found in MU and WB while for CB negative genetic correlations were observed. The strongest positive genetic correlation between direct effects were found in MU (stillbirth-calving ease; 0.700) and WB (calving ease-gestation length; 0.707) while a strong negative genetic correlation was found in CB between calving ease and gestation length (-0.943). High genetic correlations between maternal-maternal components were only found in WB for stillbirth-calving ease (0.997) and stillbirth-gestation length (-0.732), respectively.

Table 4

Genetic correlations (direct-direct, maternal-maternal) among traits

Genetische Korrelationen (direct-direkt, maternal-maternal) zwischen den Merkmalen

Genetic correlation	Stillbirth-calving ease	Stillbirth-gestation length	Calving ease-gestation length
Direct-direct			
CB	-0.077 ± 0.019	-0.120 ± 0.251	-0.943 ± 0.249
MU	0.700 ± 0.438	0.584 ± 0.421	0.520 ± 0.131
WB	0.465 ± 0.849	0.253 ± 0.286	0.707 ± 0.531
Maternal-maternal			
CB	0.060 ± 0.603	-0.349 ± 0.773	0.425 ± 0.474
MU	-0.172 ± 0.626	-0.546 ± 0.974	0.590 ± 0.616
WB	0.997 ± 0.068	-0.732 ± 0.256	-0.490 ± 0.441

Discussion

The results of direct and maternal heritabilities for stillbirth and calving ease in this study were lower than the results from other studies ranging from 0.07 to 0.10 for direct stillbirth, 0.05 to 0.13 for direct calving ease, 0.06 to 0.13 for maternal stillbirth and 0.05 to 0.06 for maternal calving ease (LUO *et al.* 1999, AMIN *et al.* 2000, HANSEN *et al.* 2004, HERINGSTAD *et al.* 2007). Lower heritabilities for calving ease in cows (0.017 direct, 0.014 maternal) were however found by CUE *et al.* (1990). In the Austrian-German breeding value estimation, assumed values for calving ease and stillbirth are also low for cows (0.03 and 0.02 for calving ease direct and maternal; 0.01 for stillbirth direct and maternal, FÜRST and FÜRST-WALTL 2006). Low estimates of heritabilities for stillbirth and calving ease suggest that improving such traits through direct selection will be a slow process. The low heritability estimated here could be explained by the data structure available. Another reason might be that a linear model was applied while other studies used threshold models. In general, linear model estimates of heritability are lower than those obtained from threshold models (HERINGSTAD *et al.* 2007). However, in this study we followed the linear model applied in the Austrian-German routine breeding value estimation.

The genetic correlation between direct and maternal effects of stillbirth and calving ease were found to be negative like in other studies (LUO *et al.* 1999, FÜRST and FÜRST-WALTL 2006, HERINGSTAD *et al.* 2007, LÓPEZ DE MATORANA *et al.* 2007). Genetic correlations between direct and maternal effect of gestation length (0.002-0.063) were lower than results found in earlier studies (PHILIPSSON 1976, NADARAJAH *et al.* 1989, HANSEN *et al.* 2004). Negative genetic correlations were observed between direct and maternal genetic components for calving ease and stillbirth. This negative relationship

between direct and maternal genetic component makes selection for these two traits even more difficult in practice (LUO *et al.* 1999).

The genetic correlations between direct stillbirth and direct calving ease in MU and WB were in agreement with results from HERINGSTAD *et al.* (2007) while CB showed a negative genetic correlation similar to LUO *et al.* (1999). For the genetic correlation between maternal stillbirth and maternal calving ease, the results of this study were similar to the results of HERINGSTAD *et al.* (2007) for CB only while MU showed lower and WB showed higher correlations.

The genetic correlations between direct stillbirth and direct calving ease were close to zero in CB (-0.077 for direct effect and 0.060 for maternal effect). This might be interpreted that an increase in calving difficulty is not associated with an increased probability of stillbirth. Therefore, improving calving ease genetically would not affect the rate of stillbirth in CB while this conclusion can not be drawn for MU and WB based on our results. However, correlations for these breeds were not significantly different from zero.

In general, strong genetic correlations were found in MU and WB for stillbirth and gestation length both between direct-direct effects and between direct-maternal effects. These positive correlations are favorable in the sense that selection for one of the traits would result in a favorable selection response for the second trait (HINRICHS *et al.* 2006a, HERINGSTAD *et al.* 2007). On the other hand, a weak association between direct and maternal effect was found in calving ease. Therefore, selection on any of the direct traits will have limited effect on any of the maternal traits (HANSEN *et al.* 2004, HARDER *et al.* 2004). However, the negative genetic correlations between direct and maternal effects detected for stillbirth and calving ease might limit the genetic improvement of those two traits. Therefore, both direct and maternal effects of these two traits should be included in the selection index (DISTL 2001, HINRICHS *et al.* 2006b).

This study showed that the direct heritability of gestation length was moderate to high and the direct heritabilities of stillbirth and calving ease were low while the maternal genetic heritabilities of all 3 traits were very low. CB showed the lowest direct heritability for gestation length (0.235) not only compared to MU and WB but lower than in other studies indicating that CB has a low level of genetic diversity than other breeds. This result indicates that measuring genetic diversity based on single loci only (microsatellite data) is not sufficient in a conservation breeding program of endangered breeds. Functional traits are especially important, as they are determined by many genes. They can be evaluated by estimating genetic parameters. Furthermore, all the estimates calculated show high standard errors, most likely due to the small size of the data set. Therefore, the results should be confirmed by further analyses as soon as larger data sets can be provided.

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References

- Amin AA, Gere T, Kishk WH (2000) Additive genetic variance and covariance in some reproductive disorders in Hungarian Holstein Friesian using multi-trait animal model. *Arch Tierz* 43, 573-81
- Antonovics J (1976) The nature of limits to natural selection. *Ann MO Bot Gard* 63, 224-47
- Cue RI, Monardes HG and Hayes JF (1990) Relationships of calving ease with type traits. *J Dairy Sci* 73, 3586-90
- Distl O (2001) Implication of health traits in breeding of dairy cattle. *Arch Tierz* 44, 365-80 [in German]
- Duchev Z, Distl O, Groeneveld E (2006) Early warning system for loss of diversity in European livestock breeds. *Arch Tierz* 49, 521-31
- Falconer DS and MacKay TFC (1996) *Introduction to Quantitative Genetics*. Longman, Malaysia
- Fuerst C and Egger-Danner C (2003) Multivariate evaluation for calving ease and stillbirth in Austria and Germany. *Interbull Bull* 31, 47-51
- Fuerst C and Fuerst-Waltl B (2006) Breeding aspects of the calving process rate of stillbirths and longevity in dairy cattle. *Züchtungsk* 78, 365-83 [in German]
- Hansen M, Lund MS, Pedersen J and Christensen LG (2004) Gestation length in Danish Holsteins has weak genetic associations with stillbirth calving difficulty and calf size. *Livest Prod Sci* 91, 23-33
- Harder B, Junge W, Bennewitz J, Kalm E (2004) Investigations on breeding plans for organic dairy cattle. *Arch Tierz* 47, 129-39
- Heringstad B, Chang YM, Svendsen M and Gianola D (2007) Genetic analysis of calving difficulty and stillbirth in Norwegian Red cows. *J Dairy Sci* 90, 3500-7
- Hinrichs D, Stamer E, Junge W, Kalm E (2006a) Genetic analysis of several disease categories using test day threshold models in German Holstein cows. *Arch Tierz* 49, 3-16
- Hinrichs D, Stamer E, Junge W, Kalm E (2006b) Genetic analysis of several economically important disease traits in German Holstein cows. *Arch Tierz* 49, 209-11
- Kovac M, Groeneveld E and Garcia-Cortes LA (2002) VCE-5 package for the estimation of dispersion parameters. Congress paper of 7th WCGALP August 2002, Montpellier, France
- Lande R (1982) A quantitative genetic theory of life history evolution. *Ecology* 63, 607-15
- Luo MF, Boettcher PJ, Dekkers JCM and Schaeffer LR (1999) Bayesian analysis for estimation of genetic parameters of calving ease and stillbirth for Canadian Holsteins. *J Dairy Sci* 82, 1848-58
- López de Maturana E, Legarra A, Varona L and Ugarte E (2007) Analysis of fertility and dystocia in Holsteins using recursive models to handle censored and categorical data. *J Dairy Sci* 90, 2012-24
- Manatrion S, Fischerleitner F and Baumung R (2008) Genetic characterization among some Austrian and Hungarian cattle breeds. *Arch Tierz* 51, 426-37
- Meyer CL, Berger PJ, Koehler KJ, Thompson JR and Sattler CG (2001) Phenotypic trends in incidence of stillbirth for Holsteins in the United States. *J Dairy Sci* 84, 515-23
- Nadarajah K, Burnside EB and Schaeffer LR (1989) Factors affecting gestation length in Ontario Holsteins. *Can J Anim Sci* 69, 1083-6
- ÖNGENE (2008) Austrian association for rare endangered breeds. Available at <http://www.oengene.at>
- Pfrender ME, Spitze K, Hicks J, Morgan K, Latta L and Lynch M (2000) Lack of concordance between genetic diversity estimates at the molecular and quantitative-trait levels. *Conserv Genet* 1, 263-9
- Philipsson J (1976) Studies on calving difficulty stillbirth and associated factors in Swedish cattle breeds. III. Genetic parameters. *Acta Agric Scand* 26, 211-20
- Snell EJ (1964) A scaling procedure for ordered categorical data. *Biometrics* 20, 592-607
- Storfer A (1996) Quantitative genetics a promising approach for the assessment of genetic variation in endangered species. *Trends Ecol Evol* 11, 343-8

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