Single gene effect and use in genetic evaluations

Genetic evaluation for birth traits in dual-purpose Belgian Blue using a mixed inheritance model[1]

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ABSTRACT: In this study a genetic evaluation, based on a mixed inheritance model, was developed for birth traits (calving ease, gestation length and birth weight) in dual-purpose Belgian Blue (dpBB), a separated type inside Belgian Blue Herd-book. About 80% of dpBB animals have a single or a double copy of the muscular hypertrophy gene. This heterogeneity is the reason of a great variability in birth performance traits like calving ease or birth weight. The muscular hypertrophy gene substitution and dominance effects for calf genotype had a significant impact both on birth weight and calving ease, in accordance with partially recessive expression of the muscular hypertrophy gene. Observed high heritability estimates of direct calving ease (0.334) and birth weight (0.260) suggested that a large genetic variability for birth traits was present in dpBB, and that genetic improvement was possible through selection. This variability has allowed dpBB breeders to apply mass selection successfully in the past. However analysis of breeding values showed that a sire selection for calving ease within genotype was progressively applied by breeders, the selection intensity being more important for calving ease in double muscled lines. This study illustrated the possible confusion that can appear by the use of a major gene in selection, and the importance to use appropriated models combining polygenic and monogenic information, like mixed inheritance models.

Key words: calving ease, double muscling, genetic evaluation, mixed inheritance model

INTRODUCTION

The segregation of the muscular hypertrophy (*mh)* gene in the dual-purpose Belgian Blue (dpBB) population results in higher calving difficulties than in traditional dual-purpose breeds like Normande or Montbeliarde. As dystocia can reduce subsequent productive and reproductive performances of the cow, leading to higher replacement rate, dpBB breeders put an important emphasis on calving ease on a phenotypic level. Establishing adapted genetic evaluations would allow even more efficient selection for this trait.

As birth traits (e.g. calving ease and birth weight) are the result of a direct and a maternal genetic component (Philipsson et al., 1979), traditional genetic evaluations of birth traits take into account both of these components (e.g., Varona et al., 1999).

Moreover, the heterogeneity of the dpBB population at the *mh* locus implies complex modeling to separate effects of the gene at the *m*h locus, and polygenic effects. The use of mixed inheritance models (e.g., Van Arendonk et al., 1999) is an interesting option as it assumes simultaneously both a polygenic and a major gene influence avoiding bias in estimation of breeding values.

The objectives of this study were to develop a genetic evaluation for birth traits (calving ease, gestation length and birth weight) adapted to the dpBB population, based on a mixed inheritance model, to estimate required (co)variance components and to study the selection potential for calving ease.

MATERIALS AND METHODS

Dual-purpose and Beef Belgian Blue

Originally the Belgian Blue Breed was a dual-purpose breed called “Mid and Upper Belgium Breed”. From the fifties to the eighties, selection by breeders for beef lead to the unintentional fixation of the *mh* gene in the major part of the population. This gene was later discovered to be responsible for the muscular hypertrophy in cattle (Grobet et al., 1997). Afterwards, the selection continued using the existing additional polygenic variation to give the current meaty type. Meanwhile, to mark this profound change in the morphology of the animals, the breeders decided in 1973 to change the name of the breed into “Belgian Blue”. However a part of the population did not adopted this breeding objective and today it remains a small population of animals of the original dual-purpose type with a milk production of about 3,500 kg to 5,000 kg and 3.5% fat.

Today, the Belgian Blue breed is composed of two strains; the most important is the beef type (bBB) in a suckler herd system and a small population of the dual-purpose type (dpBB) in milking herds. Today if the bBB animals can be considered homozygous at the *mh* locus, in the dpBB population 3 genotypes *(+/+, +/mh, mh/mh*) segregate because dpBB breeders have kept a significant consideration for beef conformation. Moreover to allow the distinction between the 2 types of *mh/mh* animals, the Herd-Book registers separately the two strains. Animals of the dpBB type as attributed by the Herd-Book need to have both parents registered as dpBB. These latter have to fulfil additional requirements : on the performances for milk production and calving ease of its dam for a sire and a dam have to be officially milk recorded.

Data

Data were provided by beef and dual-purpose Belgian Blue performance recording scheme organized by the Walloon Breeding Association (**AWE**). Gestation length was calculated as the difference between calf birth date and service date of its dam. This date was provided by the inseminator or the breeder itself (through declaration of a private IA or a natural service). Estimated birth weight and calving ease were mentioned by breeders at birth registration. Calving ease records consisted in 4 classes: easy (4), easy with help (3), hard with help (2), and cesarean section (1).

Even if bBB cows are usually not milked, some milking Belgian Blue herds have a mixed cow population composed of bBB and dpBB. Also considering that the management of calving ease is more relevant at a herd than at an individual level in Belgian Blue, data were selected according to herd calving performance rather than on an individual basis. Only Belgian Blue herds with less than 80% of cesarean section were considered.

Genotype Probabilities

Because genotype at *mh* locus was not available for each animals, the missing records were replaced with genotype probabilities. They were estimated from the genotypes records of typed relatives by the use of Markov chain Monte Carlo method. The applied program sampled the whole genotype configuration jointly for the entire pedigree within Metropolis-Hastings algorithm. The samples were drawn from the approximate probability calculated by the alternative use of exact simple (Heath, 1998) and iterative peeling algorithms (Van Arendonk et al., 1989). A burn-in period of 1000 rounds was applied, and every 2 of the next 10000 samples were used for estimation. The probabilities were used to calculate the expected content of *mh* allele in genotype of each untyped animal.

Mixed Inheritance Model

The following multiple traits animal mixed inheritance model was used:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{q_o}s_o + \mathbf{h_o}d_o + \mathbf{q_m}s_m + \mathbf{h_m}d_m + \mathbf{Wt} + \mathbf{Z_m p_m} + \mathbf{Z_o u_o} + \mathbf{Z_m u_m} + \mathbf{e}$$

Where $\mathbf{y}$ is a vector of gestation length, birth weight and calving ease records (linear scale from 1 to 4), $\mathbf{b}$ is a vector of fixed effects (herd, season of birth (4 months classes), sex, age (3 months classes) x parity (1, 2, 3 and more) of the dam), $\mathbf{q_o}$ and $\mathbf{q_m}$ are vectors of known or estimated number of *mh* alleles (gene content) of offspring and dam respectively, s_o and s_m are the fixed allele substitution effects related to offspring and dam genotypes respectively, $\mathbf{h_o}$ and $\mathbf{h_m}$ are vectors of known or estimated heterozygosity for the *mh* allele of offspring and dam respectively, d_o and d_m are the fixed dominance effects of *mh*/+ related to direct effect of the offspring and the effect of the dam genotypes respectively, $\mathbf{t}$ is a vector of random herd x year of birth effect, $\mathbf{p_m}$ is a vector of dam random permanent environment effect, $\mathbf{u_d}$ is a vector of random additive genetic effect, $\mathbf{u_m}$ is a vector of maternal genetic random effect and $\mathbf{e}$ is a vector of random residuals. $\mathbf{X}$, $\mathbf{W}$, $\mathbf{Z_m}$ and $\mathbf{Z_o}$ are incidence matrices relating observations to corresponding effects. Herd effects were separated in a global fixed and a yearly random part (**t**) to deal with small herd sizes.

Variance components were estimated with restricted maximum likelihood algorithm using REMLF90 program (Misztal, 2002). Solutions were obtained using BLUPF90 program (Misztal, 2007), which uses direct inversion of the coefficient (**C**) matrix. This program allowed extraction of diagonal elements of $\mathbf{C}^{-1}$ for estimation of standard errors and prediction error variances. Standard errors were then used to assess significance of allele substitution and dominance fixed effects with a Student *t*-test.

RESULTS AND DISCUSSION

Data

The 80% cesarean section threshold was largely superior to the mean cesarean section incidence in dual-purpose Belgian Blue. This threshold was used in order to take into account the more extreme dual-purpose herds that give much more emphasis on beef traits. The calving criteria avoided to select pure bBB herds that are only using cesarean section to avoid any risk during calving. All of the 78 herds selected had at least 10 % dual-purpose cows. Fifty-five were composed of more than 80% of dpBB cows. Twenty-nine of these were single type dpBB herds. All calving records in these herds were kept, even if one parent was defined as bBB. This was done to keep large enough herd classes, and to allow an average estimation of calving ease for bBB sires used by these breeders, that may be considered somewhat different from the ones used by pure beef breeders. This strategy is also more in line with the current practices of these breeders, as some crosses between the two herd-book types occur. Among the 10059 calving records retained for the study, as shown in Table 1, out of the 72 % of dams registered as dpBB, about 10% were mated with bBB sires.

Tables 2 and 3 add information about the influence of herd-book types on phenotypic means of studied traits. While gestation length (data not shown) remained quite stable, birth weight and calving ease were more influenced. Actually, a very small subset of pure bBB population was found in the dual-purpose milking herds and these animals showed a less extreme double muscling phenotype due to the particular breeding goals of the dual-purpose breeders. Therefore the presented results for bBB can not be considered representative of the global bBB population. Mean birth weight and calving ease was similar between *mh/*+ and *mh/mh* calves (Tables 2 and Table 3). Mean birth weight increased for *mh* homozygous animals while calving ease decreased. Similar tendencies were observed for dams, except for *mh/*+ dpBB dams that were in between +/+ and *mh/mh* ones for calving ease. These results were expected since dpBB dams can have calves of the three genotypes. Another consequence of this heterogeneity is the larger observed standard deviation for birth weight (8.2kg) for *mh/*+ dpBB dams. While the mean birth weight of *mh/mh* dpBB (44.3 kg) was similar to the one of bBB (44.7 kg), calving ease was more different (35 percent of cesarean section for *mh/mh* dpBB and 84 percent for bBB).

Genotype Probabilities

The complete pedigree after extraction consisted in 22375 animals, 1866 being genotyped for double-muscling. The genotype frequencies of these 1866 animals were 15, 24 and 61 percent for +/+, *mh/*+ and *mh/mh* respectively. Inclusion of bBB in this study was responsible for the difference with the actual frequency of *mh* gene in dpBB population (20, 37 and 43 percent; P. Mayeres, unpublished data).

Estimated *mh/mh* frequency in the pedigree increased from 51 percent for animals born in 1981 to reach 67 percent for those born in 1991 (Figure 1). Then this frequency decreased to reach 49 percent for animals born in 2006, +/+ and *mh/*+ genotypes becoming more frequent. The new adhesion to the herd-book of dpBB breeders starting in 1998, stimulated by Walloon Region Ministry of Agriculture, was responsible for this phenomenon because many of these breeders had preferentially +/+ or *mh/*+ animals.

mh Gene Effects

While the *mh* gene has a known major impact on muscularity (Grobet et al, 1997), it may also influence birth weight or calving ease, because of the existing correlation between muscularity and these traits. The effect of the major *mh* gene on muscularity is considered partially recessive, the heterozygote being closer to the wild genotype (Hanset and Michaux, 1985a,b). According to these results, we should expect that *mh/mh* calves are born with more difficulty than +/+ calves, *mh*/+ being in between, however closer to +/+ animals. Results confirmed that gene substitution and dominance effects for calf genotype had a significant impact both on birth weight and calving ease (Table 4). For gestation length, substitution effect for calf genotype only was significant, with a smaller significance level. For birth weight and calving ease, substitution and dominance effects were opposite, meaning that *mh*/+ genotype were closer to +/+ genotype as expected.

The maternal substitution effect was only significant for gestation length and no dominance effect was found (Table 4).

Variance Components

Direct heritability estimate of calving ease (0.334, Table 5) was higher than generally found in literature for other breeds. Koots et al. (1994a) reported that genetic parameters of calving ease were affected by the breed, and that heritabilities for calving ease had a tendency to be higher for beef than for dairy breeds. For calving ease (direct) of cows expressed as a percentage of unassisted calvings, these authors reported mean heritability estimates of 0.16 and 0.04 for beef and dairy breeds respectively. For the Braunvieh and Simmental dual-purpose breeds, Hagger and Hofer (1990) reported heritability estimates with a threshold model of 0.172 and 0.268 respectively. Heritability estimates of direct birth weight, maternal calving ease and birth weight (Table 5) were within the range of the weighted mean values reported by Koots et al. (1994a). Estimated gestation length direct heritability was below the range of literature estimates (e.g., 0.59 [Crews, 2006]; and 0.64 [Bennett and Gregory, 2001]). Direct and maternal genetic correlations between birth weight and calving ease (-0.712 and –0.494 respectively, Table 5) compared well with the weighted mean values of –0.74 and –0.60 reported by Koots et al. (1994b). However these authors reported smaller mean values for direct-maternal genetic correlation for calving ease (-0.35 vs. -0.666 [Table 5]) and for birth weight (-0.30 vs -0.646 [Table 5]). Estimated correlations between direct gestation length and direct or maternal traits were generally different than literature estimates for other breeds, particularly the correlation with direct birth weight (0.00 vs . 0.34 [Crews, 2006], and 0.36 [Bennett and Gregory, 2001]). For maternal gestation length, genetic parameters were in the range of literature estimates.

Selection for Calving Ease

Potential impact of selection can be appreciated through estimated polygenic direct and maternal additive effects. High heritability estimates (Table 5) of calving ease suggested that a large genetic variability of birth traits was present in dpBB, and that genetic improvement was possible through selection on polygenic effect. This was strengthened by the magnitude of estimated direct and maternal genetic standard deviations for birth weight (2.89 and 1.69) or calving ease (0.69 and 0.40), that were larger than estimated allele substitution effects, 1.35 for birth weight and –0.30 for calving ease in calves.

An important phenotypic difference in calving ease was observed between dpBB and bBB lines (Table 3), resulting from the different selection between the two herd-book types (Figures 2 and 3). The genetic make-up of the two herd-book types was similar at the time of herd-book separation, but from 1980 the two types evolved with a reduction of birth weight and calving difficulties in dpBB.

Despite the negative correlation between direct and maternal genetic effects (Table 5), dpBB breeders succeeded in selecting on direct effects for decreased birth weight and calving difficulty, and keeping maternal effects quite stable. In bBB selection on direct effects increased birth weight and calving difficulty while maternal ability to calve did not increase as expected through negative genetic correlations (Figures 2 and 3). Results showed that maternal calving potential of bBB and dpBB is quite similar, and that differences in calving ease are more depending on genes transmitted to calves or on direct genetic effects.

Even if dpBB is a single herd-book type, different breeding strategies according to herds and regions exist regarding genotypes at the *mh* locus. The analysis of mean breeding values, weighted by corresponding reliabilities, showed that direct effects were –0.68, -1.09 and –1.46 for birth weight, and 0.31, 0.34 and 0.41 for calving ease, for +/+, *mh*/+ and *mh/mh* animals respectively. So it appeared that the selection intensity for calving ease of *mh/mh* dual-purpose breeders was stronger than the one of other breeders, this in order to reduce the negative impact of *mh*. For maternal genetic effects, mean weighted breeding values were 0.22, 0.21 and 0.37 for birth weight, and -0.09, -0.05 and -0.07 for calving ease, respectively for +/+, *mh*/+ and *mh/mh* animals.

In conclusion, it appeared that the dual-purpose Belgian Blue heterogeneity regarding double muscling was responsible for major variations in birth traits, i.e. calving ease, mainly through the genotype status of the calf. High estimates of heritability for direct and maternal calving ease allowed mass selection to be applied successfully by dpBB breeders during the last 30 years. Unfortunately the presence of the mutation at the *mh* locus introduced some confusion in sire evaluation. Since genotyping is available, a sire selection for calving ease within genotype has been progressively applied by breeders, the selection intensity being more important for calving ease in *mh/mh* sires. For +/+ sires, fewer constraints were applied since no *mh/mh* calves occurred in the first generation and the potentiality to have *mh/mh* animals in the next generations was not taken into account. Given the small size of the population, breeders are now aware of the necessity to give global objectives to selection. To achieve this goal the use of mixed inheritance models appeared to be a good solution since it provided a nearly unbiased estimation of polygenic contribution, independent of sire genotype. Perfect unbiasness would have required the perfect knowledge of all genotypes. Despite this the mixed inheritance models using observed or predicted gene content is a viable option for a correct genetic evaluation system.

In the near future, a global economic index will be available for dpBB breeders, further balancing functionality (including direct and maternal calving ease), milk and beef production. Studies are under way to assess effect of *mh* within the dpBB context on each of these economically important traits, in order to include them correctly in the global economic index.

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Table 1. Distribution of calving records according to sire and dam herd-book type[1]

		Sire type		
		Undefined	dpBB	bBB
Dam type	Undefined	7 (0.1 %)	222 (2.0%)	296 (2.9%)
	dpBB	68 (0.7%)	6472 (64.3%)	699 (6.9%)
	bBB	50 (0.5%)	615 (6.1%)	1630 (16.2%)

[1] dual-purpose Belgian-Blue (dpBB), beef Belgian-Blue (bBB) or undefined.

Table 2. Mean and standard deviation of birth weight for +/+, *mh*/+ and *mh/mh* (true genotypes) dual-purpose Belgian Blue (dpBB), and beef Belgian Blue (bBB) calves and dams (in italic)

	+/+ dpBB	*mh*/+ dpBB	*mh/mh* dpBB	bBB
Mean	39.1	39.3	44.3	44.7
	39.9	*40.2*	*44.2*	*44.5*
STD	5.9	7.4	6.4	6.0
	7.6	*8.2*	*7.0*	*6.4*

Table 3. Percent of birth observed in each calving ease categories for +/+, *mh*/+ and *mh/mh* (true genotypes) dual-purpose Belgian Blue (dpBB), and beef Belgian Blue (bBB) calves and dams (in italic)

	+/+ dpBB	*mh*/+ dpBB	*mh/mh* dpBB	bBB
cesarean section	15	16	35	84
	16	*28*	*42*	*75*
hard with help	4	3	2	1
	7	*3*	*1*	*1*
easy with help	19	23	21	5
	25	*17*	*19*	*6*
easy	62	58	42	10
	52	*51*	*37*	*17*

Table 4. Estimated substitution and dominance fixed effects and related significance levels for gestation length, birth weight and calving ease

	Gestation Length		Birth Weight		Calving Ease	
	Substitution	Dominance	Substitution	dominance	Substitution	Dominance
Calf	0.78 *	0.08 NS	1.35 ***	-0.58 ***	-0.30 ***	0.16 **
Dam	-0.54 *	0.38 NS	0.24 NS	0.36 NS	0.01 NS	-0.08 NS

*$P < 0.05$; **$P < 0.01$; ***$P < 0.001$; NS not significant.

Table 5. Heritabilities, genetic correlations and correlations between direct and maternal genetic effects for gestation length, birth weight and calving ease

	Direct			Maternal		
	Gestation length	Birth Weight	Calving ease	Gestation length	Birth Weight	Calving ease
Gestation length direct	0.191	0.000	0.062	-0.074	0.162	-0.007
Birth weight direct		0.260	-0.712	-0.338	-0.666	0.414
Calving ease direct			0.334	-0.064	0.449	-0.646
Gestation length maternal				0.093	0.547	-0.182
Birth weight maternal					0.089	-0.494
Calving ease maternal						0.113

Figure 1. Calculated mean frequency of +/+ (▲), *mh*/+ (■) and *mh/mh* (♦) genotypes by birth year in pedigree file from 1981 to 2006.

Figure 2. Genetic trends of calving ease for dual-purpose Belgian Blue direct (▲), and maternal (Δ) effects, beef Belgian Blue direct (♦) and maternal (◊) effects.

Figure 3. Genetic trends of birth weight for dual-purpose Belgian Blue direct (▲), and maternal (Δ) effects, beef Belgian Blue direct (♦) and maternal (◊) effects.

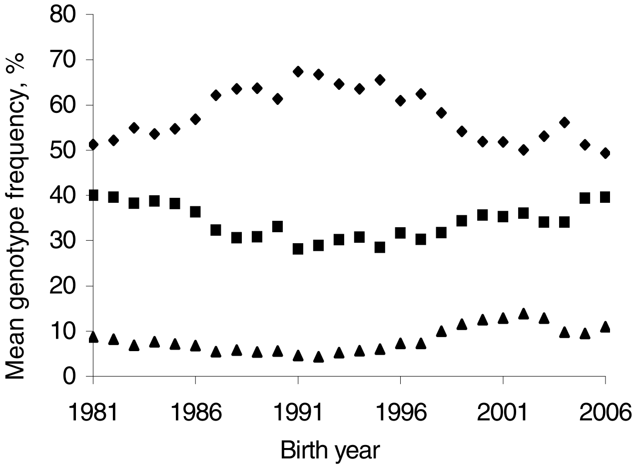
80
70
60
50
40
30
20
10
0
Mean genotype frequency, %
1981
1986
1991
1996
2001
2006
Birth year

Figure 1

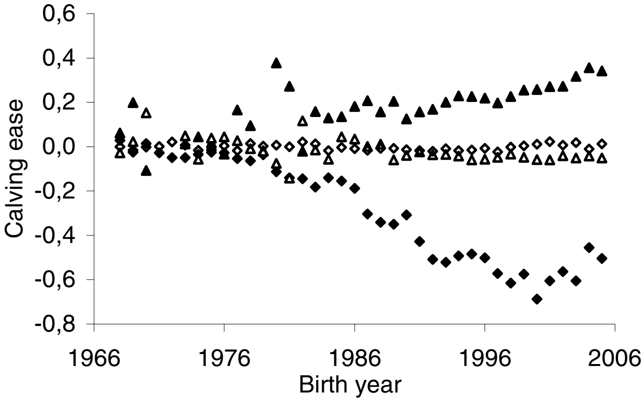
0,6
0,4
0,2
0,0
-0,2
-0,4
-0,6
-0,8
Calving ease
1966
1976
1986
1996
2006
Birth year

Figure 2

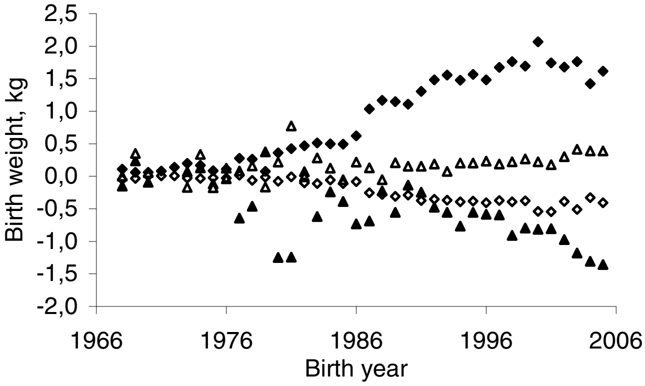
2,5
2,0
1,5
1,0
0,5
0,0
-0,5
-1,0
-1,5
-2,0
Birth weight, kg
1966
1976
1986
1996
2006
Birth year

Figure 3