

Ranking of beef cattle sires by their breeding value on progeny performance

Húshasznú tenyészbikák rangsora ivadékaik teljesítménye alapján becsült tenyészértékek alapján

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ABSTRACT

The objective of this study was to rank Limousin sires by their different breeding values based on the weaning weight of their progeny. 205-day weaning weight record of altogether 18746 purebred and crossbred calves sired by breeding bulls of the mentioned breed were used for the estimation. Calves were belonging to three different groups by their genotype. Three different BLUP animal models were used for the estimation. According the results the direct heritability (h^2_d) estimates of 205-day weight ranged between 0.49 and 0.59, while that of the maternal heritability (h^2_m) between 0.24 and 0.45. The estimated breeding value of the given sires differed by the genotype (purebred or crossbred) of their progeny calves and the method of estimation. Also, there were differences in the rank of the sires depending on the genotype of their progeny, as well as the estimation methods.

Keywords: Limousin, population genetic parameters, purebred, crossbred, mixed breeding value, rank of the sires

ÖSSZEFOGLALÁS

A munka célja limousin apák rangsorának a meghatározása volt ivadékaik választási súlyadataiból becsült tenyészértékek alapján. A számításokhoz 18746 fajtatiszta és keresztezett borjú 205 napra korrigált választási súlyadatát használták fel. A borjakat genotípusuk alapján három csoportra osztották. A számításokat három különböző BLUP egyedmodellel végezték. Az eredmények alapján a 205 napra korrigált választási súly direkt öröklődhetősége (h^2_d) 0,49 - 0,59 között változott. Az anyai öröklődhetőség (h^2_m) 0,24 - 0,45 közötti volt. Az apák tenyészértéke között számottevő különbséget találtak annak a függvényében, hogy azt milyen adatbázison, melyik módszerrel becsülték. Az eredmények alapján megállapítható, hogy az apák tenyészértékeik alapján felállított rangsora eltért egymástól.

Kulcsszavak: limousin, populációgenetikai paraméterek, fajtatiszta, keresztezett, többfajtás tenyészérték, bikák sorrendje

INTRODUCTION AND LITERATURE REVIEW

Ranking of sires of the given beef cattle breed by their parentage value can help the breeders when selecting sires to produce the next generation both by artificial insemination and natural services. Parentage value i.e. breeding value can be estimated by different methods based on different datasets.

Breeding value estimation is traditionally based on the purebred relatives of a given animal. However, crossbreeding is commonly used in commercial beef production systems which are an important tool to increase the efficiency of beef production. Some sires generally have more crossbred progeny, than purebred ones. Thus, there is a possibility to take the data of crossbred progeny into account for breeding value estimation. While the additive genetic effect in purebreeding systems, on the other hand the heterosis and complementarity in crossbreeding are the advantage that can influence the performance of the progeny. That is the growth of crossbred beef calves is generally better than that of the purebred ones. Calves of the small or middle framed breeds and herds have generally less weaning weight than the calves of large framed breeds (Teixeira et al., 2018). Sires from large framed French origin breeds, such as Limousin, are generally used both for improve purebred population and also as a terminal sire to improve the results of crossbred progeny (Tilsch et al., 1989). Therefore the breeding value of a given sire predicted on the basis of the purebred progeny performances may be different from the breeding value which is predicted on the basis of the crossbred progeny ones. Namely, the traditional general breeding value estimation programs are based on the performance of purebred collateral and offspring relative groups taking into account the additive genetic effects. The specific breeding value estimation, besides the additive genetic effects, takes notice of the heterosis, the dominant and epistatic effects, too (Rodríguez-Almeida et al., 1997; Vallée et al., 2013).

Currently, besides the purebreeding systems, more and more attention is paid to the role of the terminal type

sires of Limousin breed in the crossbreeding systems. Hence, numerous Limousin sires have both purebred and crossbred progeny. This situation provides the possibility of purebred breeding value estimation and the crossbred breeding value estimation, too.

While breeding value estimation there are two possibilities in handling the progeny data: 1) Estimation based on purebred and crossbred relatives (progeny) separately; 2) Estimation by the mixed dataset consisting of purebred and crossbred relative performances evaluated simultaneously; 2a) ABBVE (across breed breeding value estimation), 2b) MBVE (multibreed breeding value estimation) (Notter and Cundiff, 1991; Ahunu et al., 1997).

As the population genetic parameters, such as heritability, of a given traits play an important role in the genetic evaluation, it is important to evaluate them, using breeding value estimation. According to some authors there are differences in heritability values between purebred and crossbred population (Sullivan et al., 1999; Newman et al., 2002).

Since, there is no information in the relevant literature about the change of the rank of beef cattle sires obtained by purebred and crossbred progeny with separate and simultaneous evaluation the objective of this study was use different progeny datasets and different methods of breeding value estimation in order to see the rank and the change of the rank of Limousin sires. Based on our previous results it was assumed, as a hypothesis, that the rank of sires should be different depending on the datasets and methods of estimation.

MATERIAL AND METHODS

The databases

Weaning weigh data records of the Hungarian Limousin and Blonde d'Aquitaine Breeder's Association were used for the evaluation (Table 1). Data were divided into four different datasets: DB1 (purebred) purebred Limousin calves (n=7931), DB2 (crossbred) crossbred calves sired by Limousin sires (n=4103), DB3 (mixed) purebred Limousin calves together with crossbred calves sired by Limousin

sires (n=12034). DB4 (multibred) dataset (n=18746) contained data of DB3 (n=12034) furthermore data of purebred Limousin calves that had no crossbred halvesibs (n=1579). Also, this dataset contained data of purebred Blonde d'Aquitaine calves (n=3310) and crossbred calves sired by Blonde d'Aquitaine bulls (n=1823).

So, each dataset contained 205-day weaning weight for individuals of paternal halvesib groups of Limousin or Blonde d'Aquitaine sires. Altogether, there were progeny of 148 sires, 110 Limousin and 38 Blonde d'Aquitaine evaluated. Sires were involved in the study that had at least data of 15 progeny.

Analysis the data with BLUP animal models

The general formula of the BLUP animal models can be written as follows (Henderson, 1975; Szóke and Komlósi, 2000):

$$y = Xb + Zu + Wm + Spe + e$$

(Where: y = the observation vector (trait); b = vector of fix effect(s); u = vector of random effect (animal); m = vector of maternal genetic effect; pe = vector of maternal permanent environmental effect; e = error vector; X = incidence matrix of fixed effects; Z = incidence matrix of random effects; W = incidence matrix of maternal genetic effect; S = incidence matrix of maternal permanent environmental effect.)

Estimation with BLUP animal model the following population genetic parameters, covariance and variance components were determined: additive direct genetic variance (σ_d^2), maternal genetic variance (σ_m^2), direct-maternal genetic covariance (σ_{dm}), maternal permanent environmental effect (σ_{pe}^2), residual variance (σ_e^2), phenotypic variance (σ_p^2), direct heritability (h^2_d), maternal heritability (h^2_m), direct-maternal genetic correlation (rdm), the ratio of the permanent environmental variance to the phenotypic variance (c^2) and the ratio of the residual variance to the phenotypic variance (e^2). The total heritability (h^2_T) was calculated using the following formula (Willham, 1972):

$$h^2_T = (\sigma_d^2 + 0,5 \sigma_m^2 + 1,5 \sigma_{dm}) / \sigma_p^2$$

Three different BLUP Animal Models were used for breeding value estimation (Table 2). Model number 1 (M1) was used for the evaluation the purebred dataset (DB1) only according to Keeton et al. (1996) and Dodenhoff et al. (1999). Herd, parity of the cows, year and season at birth, and sex of the calves were considered as fixed effects (Gregory et al., 1995; Lee et al. 1997). Model number 2 (M2) was used for evaluation of the data of crossbred progeny (DB2) according to the method of across breeds breeding value estimation as suggested by Van Vleck et al. (1992), Lo et al. (1997), Roso et al. (2005) and Brandt et al. (2010). Model number 3 (M3) was used for estimation based on data of calves of mixed genotype (DB3) according to the method of multibreed breeding value estimation (Elzo and Famula, 1985; Arnold et al., 1992; Núñez-Dominguez et al., 1993; Splan et al., 1998; Elzo et al., 2015).

In the models number M2 and M3 the genotype of calves was considered as fixed effects according to the study of Splan et al. (2002). Each model contained pedigree information for sire, dam, grandparents, maternal genetic effect and maternal permanent environmental effect as random effects.

Used softwares

Variance, co-variance, correlation, heritability and breeding values according to the above mentioned three models were estimated as it can be seen in the studies of Willham (1972), Henderson (1975), Trus and Wilton (1988), Meyer et al. (1993), Lee et al. (1997) and Vanderick et al. (2017). DFREML (Meyer, 1998) and MTDFREML (Boldman et al., 1993) softwares were used for the estimation. There were four kind of breeding values for each sire estimated, namely purebred, crossbreed, across breed and mixed breeding values. The rank of the sires according to their different breeding values was compared moreover rang correlation analysis was done according to Núñez-Dominguez et al. (1995).

Table 1. The structure of the evaluated database

Used database	DB1 (Purebred)	DB2 (Crossbred)	DB3 (Mixed)	DB4 (Multibred)
Time period of examination, the birth date of calves	1992-2009	1992-2008	1992-2009	1992-2009
Number of herds	28	24	31	37
Parity of dam	1-11	1-10	1-11	1-12
Breed or genotype of dams (cows)	LIM	HUS, HUS x LIM	LIM, HUS, HUS x LIM	LIM, BDA, HUS, HUS x LIM, HUS x BDA
Breed of sire	LIM	LIM	LIM	LIM, BDA
Number of sires	70	70	70	148
Breed or genotype of calves	LIM	HUS x LIM (F ₁ ; R ₁)	LIM, HUS x LIM (F ₁ ; R ₁)	LIM, BDA, HUS x LIM, (F ₁ ; R ₁) HUS x BDA (F ₁ ; R ₁)
Number of calves in database	7931	4103	12034	18746
The average number of progeny per sire	113.3	58.6	171.9	126.7
Age at weaning (day)				
- mean±SD	217.1±46.3	214.8±53.2	216.3±48.8	212.2±46.0
- range	120-365	120-365	120-365	120-365
205-day weight (kg)				
- mean±SD	205.1±35.3	208.7±36.7	206.3±35.8	215.8±39.9
- range	100-350	100-350	100-350	100-350

DB1 = database 1

DB2 = database 2

DB3 = database 3

DB4 = database 4

LIM = Limousin

BDA = Blonde d'Aquitaine

HUS = Hungarian Simmental

Table 2. The used models

Type of models	BLUP animal model			
	M1	M2	M3	M3
Used database	Purebred (DB1)	Crossbred (DB2)	Mixed (DB3)	Multibred (DB4)
Method	Breeding value estimation (BVE)	Across breed breeding value estimation (ABBVE)		Multibreed breeding value estimation (MBBVE)
Breed or genotype of calves in database	LIM	HUS x LIM, (F ₁ ; R ₁)	LIM, HUS x LIM, (F ₁ ; R ₁)	LIM, BDA, HUS x LIM, (F ₁ ; R ₁), HUS x BDA (F ₁ ; R ₁)
Random effects				
- sire	+	+	+	+
- animal	+	+	+	+
- dam (cow)	+	+	+	+
Fixed effects				
- genotype of calf	-	+	+	+
- herd	+	+	+	+
- parity of dam	+	+	+	+
- birth year of calf	+	+	+	+
- birth season of calf	+	+	+	+
- sex of calf	+	+	+	+
Other effects				
- maternal genetic effect	+	+	+	+
- maternal permanent environment effect	+	+	+	+
Trait				
- 205-day weight	+	+	+	+

LIM = Limousin

BDA = Blonde d'Aquitaine

HUS = Hungarian Simmental

"+" = the model include this effect

"- " = the model doesn't include this effect

RESULTS

The population-genetic parameters such as variance, covariance, and correlation and heritability values can be seen in Table 3.

Direct heritability (h^2_d) of 205-day weaning weight varied between 0.49 and 0.61, the maternal heritability (h^2_m) between 0.24 and 0.45, while the total heritability (h^2_T) between 0.10 and 0.33.

The results for breeding value estimation conducted by different methods are summarized in the Table 4.

As it is seen, there are differences in breeding values depending on whether the progeny were purebred or crossbred, or sired by different breed sires, ones. In case of some sires such as No. 18853, however they were above

or below the average, there were significant differences between purebred and crossbred breeding values. There were some sires, as a No. 14284, who had breeding value below the average obtained by they purebred progeny 205-day weaning weigh, while had above the average estimated on the basis of they crossbred or mixed genotype progeny performances.

The rank correlation estimated for evaluating the rank of different sires by their different breeding values is summarized in Table 5. The rank of the sires according to their different breeding values obtained by the 205-day weaning weight of their different progeny groups show meaningful differences (Figure1).

There were a moderate correlation ($r_{\text{rank}}=0.52$; $p<0.01$) between the ranks of sires by their purebred breeding

Table 3. The estimated population genetics parameters of 205-day weight

Genotype Method Database Model	Purebred BVE DB1 M1	Crossbred ABBVE DB2 M2	Mixed ABBVE DB3 M2	Multibred MBBVE DB4 M3
σ^2_d	496.24	677.33	675.71	652.98
σ^2_m	265.98	517.02	284.15	276.00
σ_{dm}	-285.54	-547.49	-352.88	-325.96
σ^2_{pe}	76.11	0.00	74.60	83.15
σ^2_e	452.40	509.01	427.77	480.25
σ^2_p	1005.18	1155.88	1109.35	1166.42
h^2_d	0.49±0.09	0.59±0.11	0.61±0.10	0.56±0.06
h^2_m	0.26±0.05	0.45±0.12	0.26±0.05	0.24±0.03
r_{dm}	-0.79±0.06	-0.93±0.07	-0.81±0.04	-0.77±0.04
c^2	0.08±0.02	0.00±0.06	0.07±0.02	0.07±0.01
e^2	0.45±0.07	0.44±0.08	0.39±0.07	0.41±0.04
$h^2_m+c^2$	0.34	0.45	0.33	0.31
h^2_T	0.33	0.10	0.26	0.26

σ^2_d = additive direct genetic variance; σ^2_m = maternal genetic variance; σ_{dm} = direct maternal genetic covariance; σ^2_{pe} = maternal permanent environmental effect; σ^2_e = residual variance; σ^2_p = phenotypic variance; h^2_d = direct heritability; h^2_m = maternal heritability; r_{dm} = direct-maternal genetic correlation; c^2 = the ratio of the permanent environmental variance to the phenotypic variance; e^2 = the ratio of the residual variance to the phenotypic variance; h^2_T = total heritability

value and the rank by crossbred breeding value. More close ($r_{\text{rank}}=0.72$; $p<0.01$) correlation was observed between the mixed breeding value rank and purebred breeding value rank, and ($r_{\text{rank}}=0.74$; $p<0.01$) between the mixed breeding value rank and crossbred breeding value rank. Stronger correlation was found between the

purebred and mixed ($r_{\text{rank}}=0.89$; $p<0.01$), and mixed and multibreed mixed ($r_{\text{rank}}=0.82$; $p<0.01$). So, the rank of the different sires according to their breeding value is different depending on if the estimation was based on purebred or crossbred progeny records.

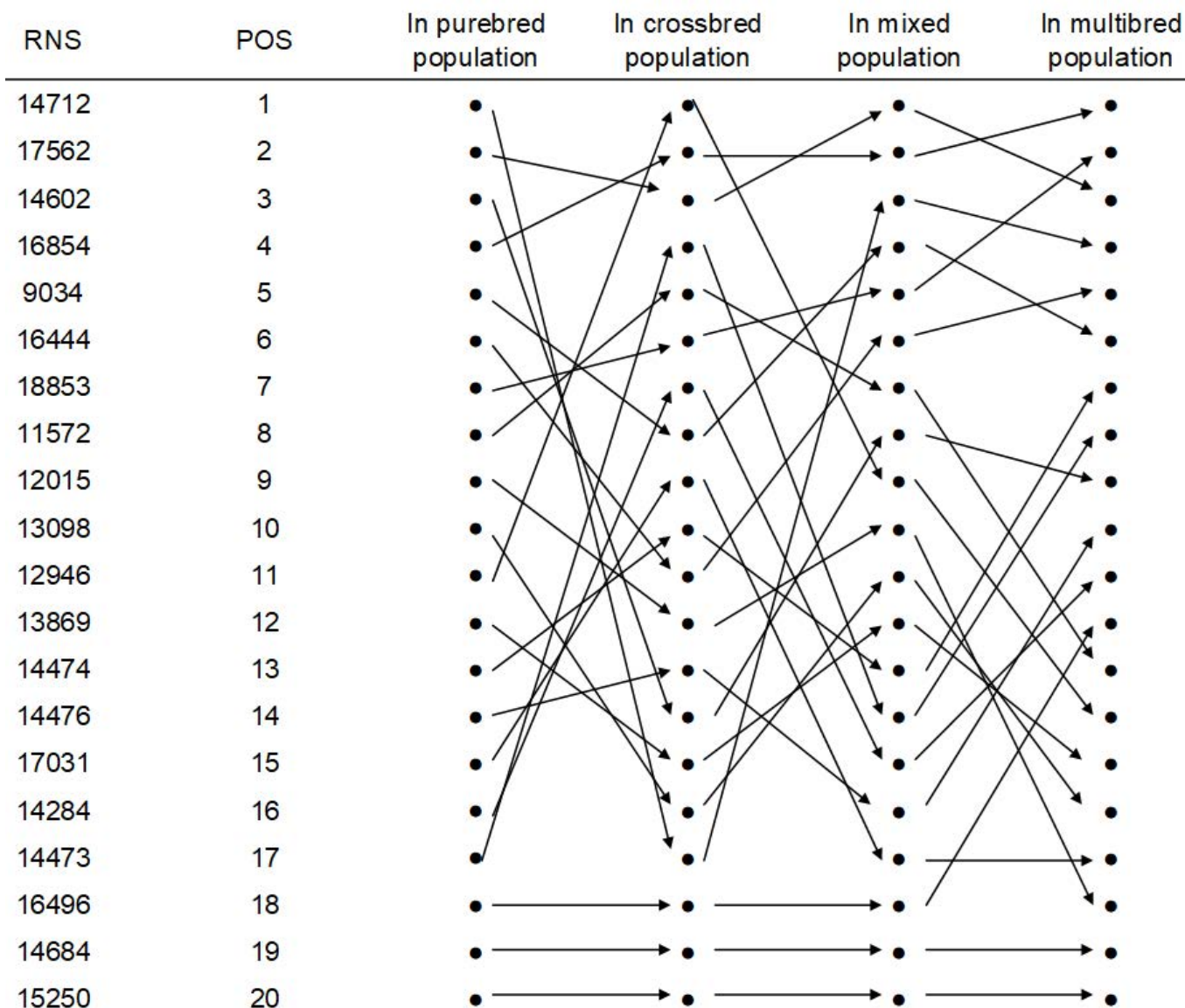
Table 4. Breeding value and rank of Limousin sires in different populations based on 205-day weight of their calves

Genotype Method Database Model N	In purebred population			In crossbred population			In mixed population			In multibreed population			
	BVE DB1 M1 7931	BVE DB2 M2 4103	ABBVE DB3 M2 12034	ABBVE DB4 M3 18746	NS	BV	RK	NS	BV	RK	NS	BV	RK
RNS	NS	BV	RK	NS	BV	RK	NS	BV	RK	NS	BV	RK	
9034	41	14.4	5	257	9.3	8	298	13.6	4	298	0.1	6	
11572	298	7.3	8	27	13.5	5	325	2.4	7	325	-11.9	13	
12015	612	3.1	9	295	-4.6	12	907	-0.8	10	907	-17.8	18	
12946	232	-2.1	11	27	38.4	1	259	-0.5	9	259	-12.5	14	
13098	917	2.0	10	566	-7.6	16	1483	-1.6	11	1483	-13.2	16	
13869	244	-2.6	12	33	-7.6	15	277	-3.5	12	277	-13.2	15	
14284	157	-8.9	16	41	9.4	7	198	-7.8	15	198	-10.7	11	
14473	148	-13.1	17	53	25.4	4	201	-6.2	14	201	-7.0	8	
14474	184	-5.7	13	66	3.0	10	250	-5.7	13	250	-6.6	7	
14476	188	-7.2	14	48	-6.8	13	236	-8.9	16	236	-8.0	10	
14602	37	22.3	3	150	-7.5	14	187	1.3	8	187	-7.5	9	
14684	721	-25.1	19	211	-15.3	19	932	-23.7	19	932	-25.5	19	
14712	55	37.7	1	133	-9.6	17	188	22.4	3	188	14.4	4	
15250	531	-34.2	20	155	-44.7	20	686	-36.9	20	686	-38.1	20	
16444	445	12.5	6	77	-1.9	11	522	9.9	6	522	6.1	5	
16496	222	-17.3	18	20	-11.0	18	242	-17.4	18	242	-10.9	12	
16854	173	19.4	4	66	28.4	2	239	26.0	2	239	25.3	1	
17031	150	-7.4	15	35	5.0	9	185	-9.8	17	185	-13.3	17	
17562	121	23.7	2	68	25.5	3	189	27.5	1	189	21.9	3	
18853	199	9.7	7	4	11.5	6	203	10.0	5	203	22.4	2	
OM	205.1±35.3			208.7±36.7			206.3±35.8			215.8±39.9			

N = number of calves in database; RNS = registration number of sire; NS = number of progeny of sire; BV = breeding value (kg); RK = the position of sires in the rank based on their breeding value; OM = overall mean of population (\pm SD; kg)

Table 5. Spearman rank correlation between the ranks of Limousin sires in different populations

r_{rank}	Rank of sires in crossbred population	Rank of sires in mixed population	Rank of sires in multibred population
Rank of sires in purebred population	0.52 ($p < 0.01$)	0.89 ($p < 0.01$)	0.70 ($p < 0.01$)
Rank of sires in crossbred population		0.75 ($p < 0.01$)	0.59 ($p < 0.01$)
Rank of sires in mixed population			0.82 ($p < 0.01$)



RNS = registration number of sire

POS = the position of sires in the rank based on their breeding value

Figure 1. The rank of Limousin sires in different populations

DISCUSSION

The heritability values for purebred population are similar or a little bit lower than that of obtained by Keeton et al. (1996) and Dodenhoff et al. (1999). There are differences between this study and literature results in heritability values obtained for crossbred population. Crews and Kemp (1999), Splan et al. (1998) and Lukaszewicz et al. (2015) published lower heritability values for crossbred Limousin population than it was observed in this study. Similarly, Ahunu et al. (1997) and Roso et al. (2005) published lower heritability for the mixed crossbred population.

The maternal heritability values estimated both in purebred, crossbred, mixed and multibreed population were higher in the studied Limousin population, than published in the literature, consideration of maternal genetic effect can be suggested in case of this breed when estimating breeding value or selecting for improving weaning performance.

The differences between the breeding values obtained by purebred and crossbred progeny dataset for the same sires may due to the heterosis effects in crossbreds. This finding corresponds to the results of Pribyl et al. (2003), who reported that heterosis effects are applied mainly to the adjustment of breeding values.

CONCLUSIONS

According to the results of the breeding value estimation trials there were differences obtained in the rank of sires depending on the record data of their progeny and on the estimation method. This outcome offers the possibility of different breeding value estimation in different breeding strategy. It can be recommended to choose different methods, depending on the purpose is the purebred improvement or to produce crossbred end-product progeny for fattening and slaughter. Also, attention have to pay for choosing estimation method depending on the structure of the weaned calf progeny dataset.

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