Canadian Charolais Genetic Evaluation Summary Fall 2008

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2008 Canadian Charolais Genetic Evaluation Summary

1.1. Introduction

In recent years, the Canadian Charolais Association (CCA) combined basic growth data with the American International Charolais Association (AICA) to compute North American Charolais EPD for birth, weaning and yearling weights, milk and total maternal value, which were computed at the University of Georgia. In 2008, CCA moved to receive all of their national cattle evaluation (NCE) programs from the Center for Genetic Evaluation of Livestock (CGEL) at Colorado State University, led by Dr. Denny Crews. In addition to the basic growth run, CGEL will also be conducting the TGE (carcass), fertility, calving ease, and feed efficiency NCE for CCA.

1.2. Model Development

As indicated, Dr. Denny Crews from the Center for genetic evaluation of livestock at Colorado State University (CGEL) is leading the development and production of the new Canadian Charolais genetic evaluation programs. Dr. Crews has vast experience with the Canadian Charolais data as he in collaboration with Dr. Bob Kemp and the Canadian Charolais breed improvement committee developed and has producing the TGE, Calving Ease and Scrotal Circumference EPDs since their inception.

This evaluation differs from those recently published in that only Canadian data were used rather than data from Charolais across North America. Extensive research and development was conducted to ensure the integrity of the new CCA growth NCE. Compared to the final 2008 North American Charolais growth evaluation, Canadian animals in this current run were compared on the basis of ranking between the two evaluations, as well as the EPD ranges and accuracy values. Canadian animals in the current run had rank correlations above 0.94 compared to the last North American run.

1.2.1. Genetic parameters

Genetic parameters (heritabilities and genetic correlations) were computed exclusively using Canadian growth data for this run. The results of this analysis were published in 2004 in the Canadian Journal of Animal Science, and are summarized in the table 1:

Table 1: Heritability and genetic correlation estimates for Canadian Charolais growth traits

Trait	BWT	WWT	YWT	MLK
BWT	**0.53**			
WWT	0.33	**0.22**		
YWT	0.29	0.39	**0.21**	
MLK	-0.16	-0.35	0.00	**0.10**

BWT = birth weight, WWT = weaning weight, YWT = yearling weight, MLK = milk

1.2.2. Inclusion criteria

The 2008 CCA growth run contains 854,246 animals. To be included in this NCE, an animal had to satisfy one or more of the following criteria: 1) have a valid record for either birth, weaning, or yearling weight, 2) be born since 1978, and(or) 3) be related to an animal with at least one data point within five generations.

1.2.3. Contemporary Group Definition

Contemporary groups were formed for each of the three traits (birth weight, weaning weight, post-weaning gain). The definition of contemporary group for each of the traits is:

Birth Weight:
year of birth × herd of origin × sex × birth management group

Weaning Weight:
year of birth × herd of origin × sex × birth management group × weaning management code

Post-weaning Gain:
year of birth × herd of origin × sex × birth management group × weaning management code × yearling management

For these group definitions, birth management group was created in order to limit the age range in birth contemporary groups to a maximum of 30 d. This also limits the range in age when calves were weighed near yearling (for computation of yearling weight and post-weaning gain) to a maximum of approximately 7 days.

1.2.4. Adjustment Factors

Contemporary groups were formed in order to better approximate adjustments for sex, but pre-adjustments were applied for age of dam to birth and weaning weight according to the standards developed by CCA and reported in the Beef Improvement Federation guidelines. This is the same approach used in previous years with the North American run. Also according to Beef Improvement Federation guidelines, both weaning weight and yearling weight (prior to computing post-weaning gain) are adjusted linearly to 205 d and 365 d, respectively. Because post-weaning gain is computed as the non-negative difference between adjusted 365-d and 205-d weights, post-weaning gain is automatically adjusted to a constant growth period of 160 d.

1.2.5. Traits in the Evaluation

The actual evaluation model includes birth weight, weaning weight, and post-weaning gain, so that information from each trait is used to improve the predictions and accuracy values for the other traits simultaneously. Post-weaning gain is used instead of 365-d yearling weight because the system solves much quicker when avoiding the part-whole relationship between 205-d and 365-d weights. The total maternal EPD is defined as one-half of WWT EPD plus MLK EPD, and as such is computed after the evaluation system is solved. Accuracy values are computed using the same three-trait model as the EPD, so that pedigree ties and phenotypic records contribute to accuracy for all traits.

1.2.6. Base adjustment

The CCA Board of Directors indicated that they wanted the EPD to appear and be very similar to the North American Limousin EPD in look and feel. The approach used was to force the average EPD of active sires from the Canadian run to be equal to the average from the North American Limousin run.

All active sires (calf reported since January 1st, 2006) were pulled from the Canadian database. The average EPD for each trait was then calculated. North American Active sire averages were retrieved from the CLA website. The difference between the two averages was used as an adjustment factor.

Table 2: Average EPD from North American and Canadian genetic evaluations and resulting adjustment factors

	N	BW	WW	YW	Milk
LM Active Sires	4387	2.00	39.90	75.30	20.20
Canadian Active Sires	2205	1.50	15.20	28.55	2.77
Adjustment Factor		+0.50	+24.70	+46.75	+17.43

Notes:

LM Active Sire Averages taken from FALL 2008 North American Limousin Genetic Evaluation Quick Stats (October 3, 2008)

1.3. Evaluation Summary

As is tradition three sets of summary statistics are prepared and presented. Summary data on the current non-parent population (defined as all animals born in the past two years), the active sires and active dam populations (defined as all animals with a progeny record in the past two years) are presented. Summary statistics, genetic trend and percentile rank plots for each population can be utilized to assist in selection or mating decisions.

1.3.1. Summary statistics by population

Table 3: Summary statistics for the non-parent population

Trait	N	Avg	SD	Min	Max
BW	34,989	2.0	2.21	-10.8	16.0
WW	34,989	39.8	7.37	3.6	78.3
YW	34,989	75.5	13.59	10.7	134.5
Milk	34,989	20.3	3.84	3.2	35.0
TM	34,989	40.2	4.92	15.2	63.7

Table 4: Summary statistics for the active sire population

Trait	N	Avg	SD	Min	Max
BW	2,205	2.0	2.51	-10.0	12.7
WW	2,205	39.9	9.18	6.5	73.1
YW	2,205	75.3	16.74	20.2	137.7
Milk	2,205	20.2	5.21	-0.1	39.8
TM	2,205	40.2	6.35	13.7	61.0

Table 5: Summary statistics for the active dam population

Trait	N	Avg	SD	Min	Max
BW	26,161	2.2	2.25	-9.7	14.9
WW	26,161	37.9	7.81	-1.1	69.7
YW	26,161	71.3	14.24	1.5	134.4
Milk	26,161	20.2	4.89	-2.7	42.5
TM	26,161	39.2	6.10	10.7	66.7

1.3.2. Percentile ranking (based on summary statics from the non-parent population)

Pctl	BW	WW	YW	Milk	TM
1	-3.7	57.7	108.2	29.3	51.5
2	-2.9	55.5	104.7	28.2	50.0
3	-2.4	54.0	101.9	27.5	49.2
4	-2.0	53.0	100.0	27.0	48.5
5	-1.7	52.2	98.3	26.6	48.0
10	-0.7	49.3	93.0	25.2	46.3
15	-0.1	47.4	89.5	24.2	45.2
20	0.3	45.9	86.6	23.5	44.3
25	0.7	44.6	84.3	22.8	43.5
30	1.0	43.5	82.3	22.2	42.8
35	1.3	42.4	80.4	21.7	42.2
40	1.6	41.5	78.6	21.2	41.6
45	1.9	40.6	76.8	20.8	41.0
50	2.1	39.7	75.2	20.3	40.4
55	2.4	38.8	73.5	19.8	39.7
60	2.6	37.9	71.8	19.4	39.1
65	2.9	37.0	70.1	18.8	38.5
70	3.2	36.0	68.3	18.3	37.8
75	3.5	35.0	66.3	17.7	37.0
80	3.8	33.8	64.2	17.1	36.1
85	4.2	32.4	61.7	16.4	35.1
90	4.7	30.6	58.5	15.4	33.9
95	5.5	28.0	53.7	14.0	32.0
100	16.0	3.6	10.7	3.2	15.2

1.3.3. Genetic trend for growth traits

Table 6: Genetic trend for growth traits (tabular)

Year	Num	BW	WW	YW	Milk	TM
2008	323	2.4	42.6	82.1	20.0	41.3
2007	15395	2.0	40.1	76.1	20.4	40.4
2006	19271	2.1	39.6	74.8	20.2	40.1
2005	20964	2.1	39.9	73.3	20.1	39.6
2004	22819	2.0	38.6	72.6	20.0	39.4
2003	27203	2.1	38.0	71.2	19.9	38.9
2002	31264	2.2	37.5	70.6	20.0	38.8
2001	33200	2.2	36.9	69.3	19.8	38.2
2000	33035	2.3	36.4	68.4	19.5	37.7
1999	35076	2.3	35.6	66.9	19.4	37.2
1998	36510	2.3	35.0	65.8	19.1	36.6
1997	31145	2.3	34.5	64.7	19.1	36.4

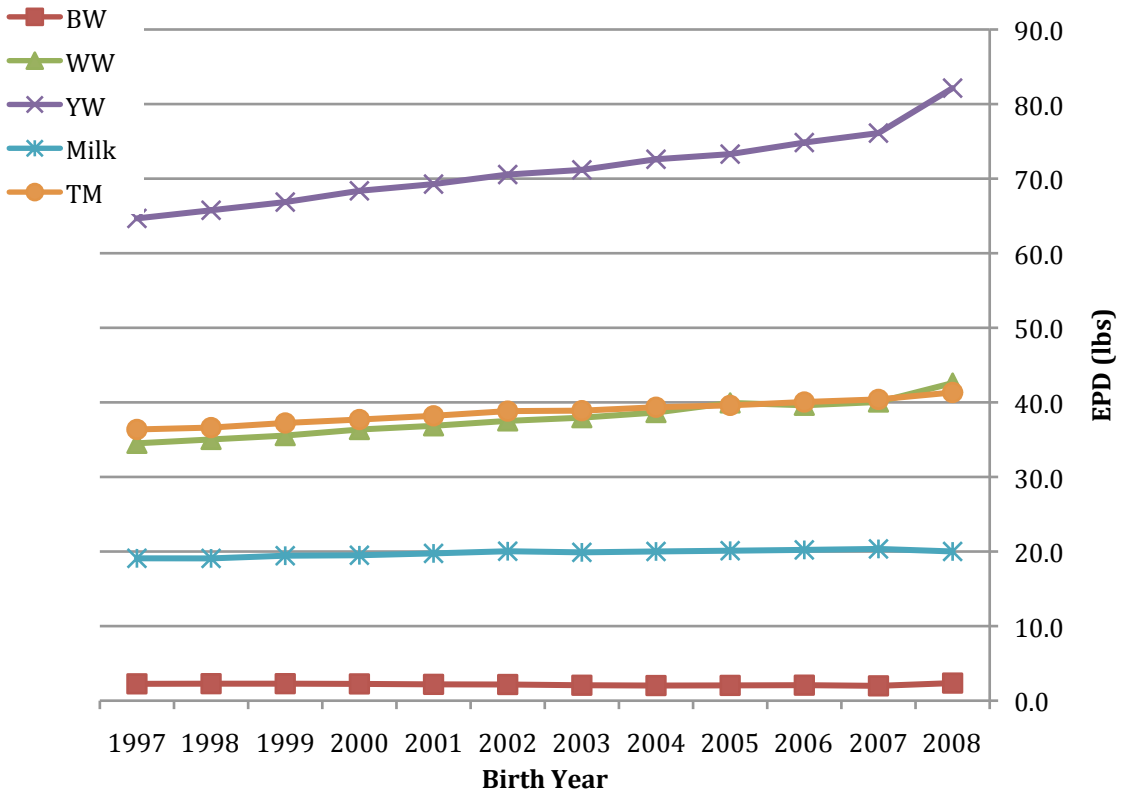

Figure 1: Genetic trend for growth traits (graphical)