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Comparison of daughter's performance of progeny tested sires with pedigree selected sires in Holstein Friesian crossbred cattle

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ABSTRACT

The present study was conducted to compare the estimated breeding values of progeny tested sires and pedigree selected sires for test day milk yield of crossbred Holstein Friesian cattle. First lactation milk yield records (1,20,198) of 12,971 daughters sired by 267 sires were collected from INAPH database maintained by NDDB. Variance and covariance components for test-day milk yield (TDMY) were estimated by different random regression test day models (RRTDM), viz. Cubic B- Spline function, Quadratic B-Spline function, Legendre polynomial (LP) function and Wilmink function using Average Information Restricted Maximum Likelihood (AIREML). Considering various criteria for comparison of different orders of TDMs, LP of 6th order for TDMY was the best fitted model for further estimation of breeding values. The heritability estimates ranged from 0.15 to 0.39 for TDMY using Leg_2 model. The additive genetic correlations were higher than the phenotypic correlations among different TDs. The additive genetic correlations between test day yields varied from 0.73 to 0.99. The expected progeny difference (EPD) for TDMYcalculated based on dam's yield for the top ten and bottom ten PS bulls was 2,662.5 kg; whereas, the actual progeny difference (APD) for these bulls was -28.47 kg. While, EPD for top 10 and bottom 10 PT bulls selected based on EBVs was 2,820.52 kg whereas the APD for PT bulls was 890.48 kg. The difference in expected and actual MY of progeny was higher in PS bulls as compared to PT bulls indicating that the pedigree information for EPDs had a poor association with APDs and sire superiority is not reflected in progeny's actual performance. The rank correlation between ranks of all PS and PT bulls were very poor and non-significant. The bulls selected based on estimated breeding values will give faster genetic progress and decision to select replacement bulls based on breeding values instead of dam's yield will have positive effect on genetic progress.

Keywords: Breeding value, Crossbred, Holstein Friesian, Pedigree selection, Progeny testing

India's livestock sector is one of the largest in the world, which employs more than 8% of the countries' labour force and has emerged as an important growth leverage of Indian economy with nearly 4.50% of total GDP and 25.8% of agriculture sector's GDP during 2016–17 (Anonymous 2018). Among livestock, dairy cattle and buffalo play a major role in India's total milk production. According to 19th Livestock Census (2012), Govt. of India, cattle and buffaloes contribute about 37.28% and 21.23% of total livestock population of India, respectively. Of the total cattle population, indigenous cattle contribute 79.57% and 20.43% crossbred cattle resulted through crossing exotic dairy breeds primarily Holstein Friesian and Jersey with mostly indigenous descript / non-descript cattle. India is the largest milk producing country of the world, producing 176.3 million tonnes milk during 2017–18 which contributed nearly 21% of world's total milk production (Anonymous 2018). Among the estimates of total milk production of the country, Gujarat contributes about 7.70% and ranks fourth in the country (Anonymous 2018).

For genetic improvement of livestock populations, selection of the best individuals of the current generation and their use as parents of the next generation can be the major goal of an animal breeding scheme. There are several criteria for selection of breeding bulls, viz. pedigree selection (PS), full sib family selection (FSFS) or half sib family selection (HSFS), progeny testing (PT) etc. More commonly criterion used for selection of bulls at younger stage is pedigree selection (PS). An effective PS depends on the accuracy of the genetic evaluation of parents.

In the early days, breeding values of dairy sires and cows for production traits were predicted from 305-day full lactation yields, which usually compiled from the individual milk samples taken at every 30 days in milk. Now-a-days, genetic evaluation of dairy animals for milk production is done based on test-day yields (TDY) instead of 305-days lactation yield. 305-days milk yields (305-DMY) can also be predicted from test days milk yields using various regression methods but they do not account for an individual test-day effect on the test-day yield of a cow and persistency (Schaeffer and Dekkers 1994), while test-day model (TDM) accounts for both the effects along with prediction of

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Estimated Breeding Values (EBVs) for 305-days yields. Among the various test day models, Splines, Wilminks and Legendre polynomial functions of random regression models (RRM) are the models of choice for genetic evaluations of Holstein cattle (Bignardi *et al.* 2009).

NDDB initiated a robust online and offline data capturing and analysis system for improving dairy cattle-buffalo productivity through the establishment of a national database - Information Network for Animal Productivity and Health (INAPH) in 2008. The INAPH supports the monthly test days milk recording (milk yield, fat%, protein%, lactose%) along with other reproduction and health traits (Anonymous 2012) under progeny testing (PT) programme. The availability of data of performance of progenies of crossbred bulls over large period provides an excellent opportunity to study the changes in breeding values and ranking of bulls based on PT and pedigree. However, to the best of our knowledge, no comparative study has been reported in Crossbred Holstein Friesian (CBHF) cattle because of few PT programmes implemented. The present study was undertaken to compare sire evaluation methods (selection based on dam yield and selection based on progeny testing) for TDMY in CBHF.

MATERIALS AND METHODS

Data were retrieved from INAPH database maintained by NDDB. Data comprised 1,23,135 first lactation test day milk yield records of 15,255 daughters recorded during 2008–2018 of 303 sires born after 2003. The pedigree details of sires were collected from SAG, Bidaj. The animals without sire information were eliminated from the study. After elimination of 2% of data as outliers, 1,20,599 first lactation records of 13,015 daughters sired by 267 sires were retained in data file. Variance and covariance components for test-day milk yield (TDMY) were estimated by various random regression test days models (RRTDM), viz. Cubic B-Spline function at 4, 5, 6 orders, Quadratic B-Spline function at 3, 4, 5, 6 orders, RRM Legendre polynomial (LP) function at 0, 1, 2, 3, 4, 5 orders and Wilmink function were fitted on TDMY for sire evaluation using Average Information Restricted Maximum Likelihood (AIREML). All the models were fitted with herd (village) effect, AFC (age at first calving) classes and YSC (year of calving * season of calving) taken as fixed effects, whereas HYMR (herd * year of milk recording * month of milk recording), OWN (owner effect) as random effects. Permanent environment (PE) and animal effects were taken as random regressions (Table 2).

Spline function: Quadratic spline function at nth orders (n = 3, 4, 5, 6) and cubic function at nth orders (n = 4, 5, 6)

$$Y_{tghijk} = \mu + Herd_h + YSC_j + AFCCL_j + HYMR_g + OWN_k + DIM_t + a_i + b_i \times DIM + e_{tghijk}$$

Wilmink function: (Wilmink 1988)

$$Y_{tghijk} = \mu + Herd_h + YSC_j + AFCCL_j + HYMR_g + OWN_k + DIM_t + a_i + b_i \times DIM + c_i \times \exp(-0.05 \times DIM) + e_{tghijk}$$

Legendre Polynomial (LP) @ 0, 1, 2, 3, 4, 5, 6th orders (Mrode and Thompson 2005)

Table 1. Number of records, mean and its standard error (SE) for test day milk yield for effect of year of recording, month of recording, year of calving, season of calving and AFC classes

Year of recording	N	Mean	SE	Month of recording	N	Mean	SE	Year of calving	N	Mean	SE
2008	598	9.11	0.11	January	9,277	8.88	0.04	2008	891	8.87	0.10
2009	1,050	9.19	0.11	February	9,242	9.18	0.04	2009	1,115	9.04	0.11
2010	1,076	9.66	0.12	March	9,324	9.58	0.04	2010	1,171	9.88	0.11
2011	1,661	9.97	0.08	April	10,181	9.78	0.04	2011	1,919	9.89	0.08
2012	2,599	10.14	0.07	May	11,041	9.83	0.04	2012	3,652	9.76	0.06
2013	6,491	9.76	0.05	June	11,582	9.72	0.03	2013	8,328	9.36	0.04
2014	10,768	9.50	0.03	July	11,510	9.63	0.03	2014	11,810	9.43	0.03
2015	15,864	9.59	0.03	August	11,211	9.28	0.03	2015	19,201	9.21	0.03
2016	27,583	9.06	0.02	September	9,185	8.95	0.03	2016	32,124	8.79	0.02
2017	32,313	8.80	0.02	October	9,257	8.68	0.03	2017	30,699	9.08	0.02
2018 (till July)	20,195	9.51	0.03	November	9,198	8.55	0.03	2018 (till July)	9,288	10.90	0.04
				December	9,190	8.62	0.04				
Overall	120,198 P<0.01	9.26	0.010		120,198 P<0.01	9.26	0.01		120,198 P<0.01	9.26	0.01

Season of calving	N	Mean	SE	AFC classes	N	Mean	SE
Winter (November–February)	38,155	9.59	0.019	547–912	15,530	9.89	0.03
Summer (March–June)	52,579	9.23	0.015	912–1,277	57,240	9.47	0.02
Monsoon (July–October)	29,464	8.87	0.020	1,277–1,642	33,979	8.91	0.02
Overall	120,198	9.26	0.010	1,642–2,007	10,894	8.48	0.03
P<0.01				2,007–2,372	2,555	8.42	0.07
				Overall	120,198	9.26	0.01
				P<0.01			

Table 2. Summary of effect-wise levels, mean, standard deviation, minimum and maximum values for TDMY

No. of record	Mean (kg)	SD (kg)	Min. (kg)	Max. (kg)	Levels of fixed effects			Levels of random effects		Random Regressions	
					Herd	AFCCL	YSC	HYMR	Owner	Animal	PE
120,198	9.26	3.56	1.00	33.0	462	5	32	15,334	8,349	14,541	12,971

$$Y_{tghijkl} = \mathrm{Herd}_h + \mathrm{YSC}_j + \mathrm{AFCCL}_j + \mathrm{HYMR}_g + \mathrm{OWN}_k + \sum_{k=0}^{nf}\phi_{ktl}\ \beta_l + \sum_{k=0}^{nf}\phi_{ktl}\ u_{kl} + \sum_{k=0}^{nf}\phi_{ktl}\ pe_{kl} + e_{tghijkl}$$

where $Y_{tghijkl}$, jth test-day milk yield of tth test day; μ, intercept; HYMR, herd × year of milk recording × month of milk recording as random effect with subclass *g*; Herd, herd effect as fixed effect with subclass *h;* AFCCL, age at first calving classes as fixed effect with subclass *j*; OWN, owner effect as random effect with subclass *k*; YSC, year and season of calving as fixed effect with subclass *l;* DIM, number of days in milk on test-day, DIM$\geq$5, if DIM< 5 then DIM = 5; a_i, random effect of ith animal (genetic plus within lactation permanent environment effect), b_i, random regression coefficient on Spline factors for tth DIM; c_i, random regression coefficient on the Wilmink (1987) factor for tth DIM; β_l, fixed regression coefficients; u_{kl} and pe_{kl} the lth random regression for animal additive genetic and permanent environmental effects, respectively, for animal *k*; $\O_{ktl}$, lth Legendre polynomial for the test-day record of cow k made on tth day in milk; nf, order of polynomials fitted as fixed regressions (Legendre polynomial of nth order used as fixed effects); nr, order of polynomials for u and pe effects (Legendre polynomial of nth order used as random effects); e_{thijkl}, random residual effect; u_{kl} and pe_{kl}, lth random regression for animal additive genetic and permanent environmental effects, respectively, for animal k; $\O_{ktl}$, lth Legendre polynomial for the test-day record of cow k made on tth day in milk.

All test day models at various orders were evaluated using various criteria, viz. Log likelihood function (LogL) (Mrode and Thompson 2005), Akaike's information criterion (AIC) (Akaike 1973), Corrected Akaike's information criterion (AICc) (Akaike 1987), Bayesian information criterion (BIC) (Schwarz 1978), Root Mean Square Error (RMSE), Mean Absolute Error (MAE) and Mean Square Error (MSE) (Barnston 1992) and selected best order of test day model for estimation and comparison of breeding values of sires using Univariate Best Linear Unbiased Prediction (BLUP) model.

The genetic parameters, heritability and genetic correlations at various test days for TDMY were estimated. Comparison of breeding values of bull selected based on Dam's performance (Pedigree based selection (PS bulls)) and bull selected based on progeny's performance (PT bulls) was carried out by comparing expected progeny difference (EPD) with Actual progeny difference (APD) for both criteria. The Expected progeny difference (EPD) for TDMYwas calculated based on dam's yield for the top 10 and bottom 10 PS bulls ((avg. Dam's MY of top ten bulls – avg. Dam's MY of bottom ten bulls) / 2), while for PT bulls, EBVs is not comparable directly to daughter's yield, so, the EPD for PT bulls was calculated as ((avg. EBVs for MY of top ten bulls – average EBVs for MY of bottom ten bulls) / 2×h^2 of trait).

RESULTS AND DISCUSSION

Three different lactation curve parameters of Random Regression (RR) test day models, viz. Spline function, Wilmink function and Legendre polynomials were found significant for non-genetic effects included in RR models (P<0.01), viz. year of recording, month of recording, calving year, calving season and age at first calving classes. The number of records, mean values and standard errors for various effects, viz. year of recording, month of recording, year of calving, season of calving and age at first calving for test day milk yield are presented in Table 1. The highest TDMY was observed in winter followed by summer and monsoon, however the highest TDMY was observed during May month of summer season.

Assessment of different test day models of various orders namely B-Spline Cubic function of 4, 5, 6 orders and B-Spline Quadratic function of 3, 4, 5, 6 orders, Legendre polynomials of 0, 1, 2, 3, 4, 5, 6 orders and Wilmink function were successfully converged of the iterative process. Only Bignardi *et al.* (2012) have reported problems of convergence of the iterative process, viz. B-spline quadratic and cubic models of 8th order for milk yield trait. While, Legendre polynomial functions were successfully converged for iterative process of 3rd and 4th orders (Padilha *et al.* 2017), of 3rd to 6th orders for MY, FY and PY (Biassus *et al.* 2010), of 4th order for MY (Naserkheil *et al.* 2016) and of 3rd to 5th orders for MY (Dornelles *et al.* 2016).

Comparison of efficiencies and selection of best fitted test day models of different orders: The goodness of fit of all TDM models was investigated using various criteria, viz. Log *L*, AIC, AICc, BIC, RMSE, MAE, MSE and are presented in Table 3. Based on the lowest values of each criteria best test day model at best order was selected for estimation and comparison of breeding values of sires. Based on all criteria, LP function of 6th order was the best fitted model. While, LP function of 5th order and B-spline cubic function of 6th order were found as second and third best fitted models, respectively. Peixoto *et al.* (2014) earlier reported that the LP model of 6th order attained the best values of *Log* L and AIC, while of 3rd order for BIC criteria. Biassus *et al.* (2010) also reported the models with the highest orders of LPs showed the best quality of adjustments of records. Mostly higher orders of LP are suggested as best for various yield traits based on *Log* L and AIC e.g. 4th

Table 3. Comparison of efficiencies and selection of best fitted TDM

Model	No. of parameters	–2 Log L	AIC	AICC	BIC	MSE	MAE	RMSE
Leg_0	5	282,932.38	282,942.38	282,942.38	282,990.84	1.98	0.96	1.41
Leg_1	9	261,426.10	261,444.10	261,444.10	261,531.32	1.25	0.76	1.12
Leg_2	15	248,751.96	248,781.96	248,781.96	248,927.34	0.89	0.64	0.94
Leg_3	23	241,934.42	241,980.42	241,980.42	242,203.36	0.70	0.57	0.84
Leg_4	33	238,767.02	238,833.02	238,833.04	239,152.88	0.60	0.52	0.77
Leg_5	45	237,321.46(2)	237,411.46(2)	237,411.50(2)	237,847.64(2)	0.53(2)	0.49(2)	0.73(2)
Leg_6	59	236,643.48(1)	236,761.48(1)	236,761.54(1)	237,333.34(1)	0.48(1)	0.47(1)	0.69(1)
Qua_3	15	249,378.42	249,408.42	249,408.42	249,553.80	0.89	0.64	0.94
Qua_4	23	242,986.46	243,032.46	243,032.46	243,255.40	0.72	0.57	0.85
Qua_5	33	239,646.74	239,712.74	239,712.76	240,032.60	0.62	0.53	0.78
Qua_6	45	237,898.10	237,988.10	237,988.14	238,424.28	0.54	0.49(2)	0.74
Cub_4	23	242,209.36	242,255.36	242,255.38	242,478.30	0.71	0.57	0.84
Cub_5	33	239,010.64	239,076.64	239,076.66	239,396.50	0.61	0.52	0.78
Cub_6	45	237,417.12	237,507.12	237,507.14	237,943.28	0.53(2)	0.49(2)	0.73(2)
W_1	5	363,426.94	363,436.94	363,436.94	363,485.40	4.02	1.41	2.00

order by Padilha *et al.* (2017), 6th order for MY, FY and PY by Biassus *et al.* (2010), 6th order of LP by Bignardi *et al.* (2011), 4th order for MY by Naserkheil *et al.* (2016) and 5th order of LP for MY by Dornelles *et al.* (2016), 5th and 6th order of LP for AG effect and PE effect by Behzadi and Mehrpoor (2018) for TDMY. As the orders of Legendre polynomial, B-spline function or B-spline quadratic function increased, relative efficiency in models was also improved. However, the relative contribution of each eigenvalue of the additive genetic (co) variance to total explainable variation (Table 4) suggested that as orders of lactation curve parameters for TDMs increased, the relative contribution of eigenvalues got decreased. The contribution of third eigenvalue were observed as only 1.10%, 0.94%, 0.90%, 0.90%, 0.89% for LP of 2nd, 3rd, 4th, 5th and 6th orders, respectively. While, for B-spline cubic and Quadratic functions, contribution of fourth eigenvalue was negligible to total explainable variation. Hence, for present study and routine genetic evaluations of MY, Legendre polynomial function of 2nd order was suggested because the contribution to explainable variability for animal effects at higher orders (> 2nd order) was found negligible.

Estimation of genetic parameters from test day models of different orders: The genetic parameters, heritability and genetic correlations at various test days, viz. 30, 60, 90, 120, 150, 180, 210, 240, 270, 300 and 330 days were estimated using variance, covariance values of different test day models. The heritability estimates ranged from 0.15 to 0.39 using Leg_2. Heritability estimates have been reported in the range of 0.13 to 0.66 in Holstein cattle by Behzadi and Mehrpoor (2018) and 0.18 to 0.50 in Sahiwal cattle by Monalisa *et al.* (2014), 0.39 in Holstein Frisian by Swalve (1995), 0.32 in Hostein by Jamrozik and Schaeffer (1997), 0.40 in Holstein by Mostert *et al.* (2004). Whereas, lower to moderate heritabilities have been reported as 0.17 to 0.32 in Guzerat cattle by Peixoto *et al.* (2014), 0.16 to 0.24 in Gyr breed by Ledic *et al.* (2002), 0.07 to 0.19 in Holstein by Bignardi *et al.* (2009), 0.14 to 0.34 in Girby Herrera *et*

Table 4. Eigenvalues and relative contributions (%) of nth eigenvalue (in bracket) of the additive genetic (co)variance matrix to total explainable variation for different TDMs

Model	% contribution of nth eigenvalue						
	First	Second	Third	Fourth	Fifth	Sixth	Seventh
				MY			
Leg_1	5.56 (96.92)	0.18 (3.08)	–	–	–	–	
Leg_2	5.87 (95.53)	0.21 (3.36)	0.07 (1.10)	–	–	–	–
Leg_3	5.51 (96.05)	0.17 (2.96)	0.05 (0.94)	0.00 (0.04)	–	–	–
Leg_4	5.57 (96.11)	0.17 (2.91)	0.05 (0.90)	0.00 (0.06)	0.00 (0.02)	–	–
Leg_5	5.48 (96.04)	0.17 (2.91)	0.05 (0.90)	0.01 (0.11)	0.00 (0.05)	0.00 (0.00)	–
Leg_6	5.44 (95.81)	0.17 (3.04)	0.05 (0.89)	0.01 (0.20)	0.00 (0.04)	0.00 (0.01)	0.00 (0.01)
Cub_4	281.23 (95.48)	9.79 (3.32)	2.35 (0.80)	1.18 (0.40)	–	–	–
Cub_5	93.55 (87.34)	9.45 (8.83)	3.44 (3.22)	0.62 (0.58)	0.04 (0.04)	–	–
Cub_6	52.59 (82.70)	9.77 (15.36)	0.97 (1.52)	0.24 (0.37)	0.03 (0.05)	0.00 (0.00)	–
Qua_3	27.09 (74.67)	7.30 (20.13)	1.89 (5.20)	–	–	–	–
Qua_4	15.21 (64.77)	7.80 (30.17)	1.04 (4.41)	0.15 (0.65)	–	–	–
Qua_5	12.13 (71.49)	3.76 (22.14)	1.03 (6.10)	0.03 (0.19)	0.01 (0.09)	–	–
Qua_6	14.11 (78.11)	3.09 (17.09)	0.78 (4.30)	0.08 (0.42)	0.02 (0.09)	0.00 (0.00)	–

al. (2008), 0.14 to 0.24 in Guzerat breed by Santos *et al.* (2013), 0.20 to 0.35 in Holstein cattle by Bignardi *et al.* (2011) and 0.05 to 0.32 in Sahiwal cattle by Dongre and Gandhi (2014).

Heritability estimates for TDMY were lower in last month (0.15) while highest in third and fourth month of lactation (0.39). The heritability trend was found to follow lactation curve, it had increasing trend during the period of peak yield, but declined slightly at the end of lactation. The heritability estimates during different months of lactation were medium and high, indicating that there is scope of individual selection for genetic improvement for crossbred cattle. Low heritability estimates at the end of lactation might have been due to low milk production, stress of cows from calving in initial phase and insufficiency of energy due to early gestation in terminal phase of lactation responsible for high variation in TDMY.

The additive genetic correlations among different TDs were higher than the phenotypic correlations varied from 0.73 to 0.99 and 0.24 to 0.74, respectively (Table 5). The higher values of genetic correlations were observed between adjacent test-day records in the beginning but slightly lower at the end of lactation. Higher estimates of genetic correlations among TDMY are reported in Holstein as 0.47 to 0.98 (Torshizi *et al.* 2013). Rekaya *et al.* (1999), Olori *et al.* (1999) and Cobuci *et al.* (2005) also reported high genetic correlation estimates between test days milk yield records using RRM. The phenotypic correlations between test days were moderate to high. The phenotypic correlations had also higher values in adjacent periods but decreased with increasing interval between TD yields. Phenotypic correlations among different test days for TDMY of similar magnitude were reported, viz. 0.24 to 0.81 in Guzerat cattle (Peixoto *et al.* 2014) and 0.21 to 0.63 (Naserkheil *et al.* 2016) for TDPY in Iranian Holstein, obtained between last adjacent test day records.

Comparison of breeding values of bulls selected based on Dam's yield (*pedigree selection*) *and bulls selected based on their progeny's yield* (*progeny testing*): The breeding values of sires for TDMY and reliability (from lowest to highest) ranged from –951.77 kg to 1,683.70 kg and 28% to 96%. Out of 172 sires, 72 sires with positive EBVs and 152 sires with greater than 60% reliabilities of EBVs. Daughter's performances of first lactation were compared for top ten and bottom ten bulls selected based on Dam's milk yield (pedigree selection) and bulls selected based on their progeny's yield (progeny testing). Here, only sires with the reliabilities of EBVs >60% were considered for comparison. All second lactation dam's yield were corrected to first lactation yield using modified sender correction factors.

Table 5. Genetic (above diagonal) and phenotypic (below diagonal) correlations among different test days for TDMY using Leg_2

Test days	5	86	169	252	335
5	1.00	0.96± 0.01	0.92± 0.02	0.89± 0.06	0.73± 0.06
86	0.65± 0.005	1.00	0.99± 0.003	0.95± 0.01	0.86± 0.05
169	0.46± 0.008	0.74± 0.004	1.00	0.98± 0.006	0.77± 0.06
252	0.36± 0.009	0.61± 0.006	0.71± 0.004	1.00	0.88± 0.03
335	0.24± 0.01	0.24± 0.01	0.48± 0.01	0.55± 0.007	1.00

The breeding values for top 10 and bottom 10 progeny tested bulls ranged from 505.23 kg to 1,683.70 kg and –951.77 kg to –509.68 kg for MY (Tables 6 and 7). The differences in daughter's performance of top and bottom progeny tested bulls were compared with pedigree selected bulls. The differences in daughter's performance for top 10 and bottom 10 PS bulls was observed as –17.50 kg while, the differences in daughter's performance for top ten and bottom ten PT bulls was observed as 890.48 kg for MY. The observed differences in daughter's performance between top 10 and bottom 10 were statistically significant for PS bulls and PT bulls. Expected progeny difference (EPD) for MYcalculated based on dam's yield for the top 10 and bottom 10 PS bulls was 2439.56 kg ((Average Dam's MY of top ten bulls – Average Dam's MY of bottom ten bulls) / 2), whereas, the actual progeny difference (APD) for these bulls was –28.47 kg. However, for PT bulls, EBVs is not comparable directly to daughter's yield, so, the EPD for PT bulls was calculated as ((average EBVs forMY of top ten bulls – avg. EBVs for MY of bottom ten bulls) / 2 × h^2 of trait). The EPD for PT bulls based on EBVs for top ten and bottom ten bulls was 2,820.52 kg whereas the APD for these PT bulls was 890.48 kg. The difference in expected and actual MY of progeny was much higher in PS bulls as compared to PT bulls. The daughter's average yield of bottom 10 PS bulls was higher than that of top 10 PS bulls. If EPDs were calculated based on EBVs of the sire, the difference in EPDs closely represented APDs for PT bulls. So, the pedigree information for EPDs had a poor association with APDs. The progenies of bulls with highest lactation yield of dams are expected to have poor association with EBVs. The present finding indicating that the selection based on progeny's performance (daughter's yield) is more reliable than based on pedigree (dam's performance). Consequently, for accurate selection of young bulls, pedigree index based on EBVs of their parents is suggested to use instead of simple based on dam's performance.

Rank correlation of sires' estimated breeding values for MY: Spearman's rank correlation was estimated to know the correlation between ranks of the both PS and PT bulls. Based on overall reliabilities of estimated BVs, the rank correlation between ranks of all PS and PT bulls were very poor and non-significant, 0.122. Rank correlation remained poor and non-significant (0.142) even when only bulls with EBVs with greater than 60% reliability were considered. Thus, ranking of sire based on less than 60% and greater than 60% reliabilities of EBVs is not much affected. The

Table 6. Comparison MY of daughters of top 10 and bottom 10 PS bulls

Bull No	Top ten PS sires					Bottom ten PS sires					
.	Dam's yield	EBVs	Rel. (%)	No. of daughters	Daughters' average milk yield	Bull No.	Dam's yield	EBVs	Rel. (%)	No. of daughters	Daughters' average milk yield
Top_PS_1	8768.26	655.28	78	25	3845.53	Bott_PS_1	3082.11	-77.90	84	39	3158.84
Top_PS_2	7819.11	216.32	80	31	3476.12	Bott_PS_2	2929.76	-351.82	72	19	3066.97
Top_PS_3	7591.45	-270.57	94	104	2627.97	Bott_PS_3	2918.37	139.41	63	12	3164.14
Top_PS_4	7591.45	-142.56	86	47	3292.22	Bott_PS_4	2856.21	525.44	65	12	2949.13
Top_PS_5	7591.45	-10.21	93	92	2854.69	Bott_PS_5	2800.00	-757.36	94	116	2545.83
Top_PS_6	7591.45	106.59	95	147	2902.64	Bott_PS_6	2716.11	343.06	67	14	3742.16
Top_PS_7	7426.84	580.00	71	18	3778.16	Bott_PS_7	2653.07	-23.79	87	46	2780.13
Top_PS_8	7381.31	-155.59	91	69	2937.82	Bott_PS_8	2640.81	89.88	80	30	3500.19
Top_PS_9	7381.31	23.28	94	110	3025.25	Bott_PS_9	2495.46	-82.60	63	12	3443.98
Top_PS_10	7164.16	-468.97	95	125	2622.43	Bott_PS_10	2423.66	108.11	72	17	3186.45
Average	7630.68	53.36	88	76.80	3136.28	Average	2751.56	-8.76	75	31.70	3153.78

Table 7. Comparison of MY of daughters of top 10 and bottom 10 PT bulls

Bull No	Top ten PT sires					Bottom ten PT sires					
.	Dam's yield	EBVs	Rel. (%)	No. of daughters	Daughters' average milk yield	Bull No.	Dam's yield	EBVs	Rel. (%)	No. of daughters	Daughters' average milk yield
Top_PT_1	4,570.63	1,683.70	81	27	3,711.00	Bott_PT_1	4,300.00	–509.68	92	79	2,691.16
Top_PT_2	6,065.28	1,019.60	82	31	3,552.60	Bott_PT_2	4,582.89	–520.46	93	96	2,605.43
Top_PT_3	6,684.33	764.18	84	37	3,362.26	Bott_PT_3	4,793.91	–541.03	90	67	2,749.74
Top_PT_4	5,820.99	662.53	84	35	3,194.81	Bott_PT_4	4,304.00	–553.56	95	132	2,564.37
Top_PT_5	8,768.26	655.28	78	25	3,845.53	Bott_PT_5	4,464.68	–591.78	90	61	2,784.68
Top_PT_6	7,426.84	580.00	71	18	3,778.16	Bott_PT_6	4,378.00	–722.38	94	122	2,451.77
Top_PT_7	6,831.43	570.73	65	14	4,066.79	Bott_PT_7	5,332.40	–733.70	95	153	2,571.72
Top_PT_8	2,856.21	525.44	65	12	2,949.13	Bott_PT_8	4,728.24	–748.74	93	87	2,484.27
Top_PT_9	5,077.60	505.30	94	111	3,061.51	Bott_PT_9	2,800.00	–757.36	94	116	2,545.83
Top_PT_10	3,441.11	505.23	74	18	3,137.40	Bott_PT_10	4,644.00	–951.77	94	122	2,305.47
Average	5,754.27	747.20	78	32.80	3,465.92	Average	4,432.81	–663.05	93	103	2,575.44

present finding indicated that the huge changes are expected in ranking of top ten sires if selected based on dam's performance in place of selected based on progeny performance. Almost 88% for sires changed from the set of top 10 bulls irrespective of R% for MY. High magnitude of change in the sire ranking may lead to change in the genetic gains for both criteria of selection of bulls under large-scale field-based animal breeding programmes. Thus, for genetic improvement, selection and use of PT sires are more promising than sires selected based on their dam's performance.

Random Regression models with lactation curve parameter as Legendre polynomial function were the optimum model among all test day models compared under the study. Amongst various orders of Legendre polynomials of RRM, as the order of LP increased, the efficiency of model also increased. Model with LP of 6th order was found as best fitted model, however, for routine genetic evaluations of MY model with Legendre polynomial of 2nd order is suggested because the contribution to explainable variability for animal effects at higher orders (> 2nd order) was negligible. The heritability trend for TDMY was found to follow lactation curve, it showed increasing trend up to the period of peak yield during the period of third and fourth (4th) month (0.39), later remained stable in the mid-lactation followed by slight decline (0.15) at the end of lactation (11th month of lactation). The higher values of genetic correlations were observed between adjacent test-day records in the beginning but decreased slightly at the end of lactation. The difference in expected and actual MY of progeny of top and bottom 10 was higher for PS sires as compared to PT sires, indicating that the superiority of dams is not translated in daughters' superiority reliably. Thus, selection of sires based on progeny's performance is more reliable than that based on pedigree (dam's performance) for achieving stable genetic gain. Bull selection based on dam's yield is thus prone to error. The bulls selected based on EBVs will give faster genetic progress, hence all efforts should be made to select replacement bulls based on breeding values instead of dam's yield. It is suggested that standards in India for selection of bulls for frozen semen production may include breeding values of bull as one of its selection criteria for breed improvement programmes.

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