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Assessment of genetic gain and its simulation for performance traits in Sahiwal cattle

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Abstract: The study was conducted to estimate the expected genetic gain (ΔG) for first lactation performance traits in Sahiwal cattle as a result of direct selection of animals maintained at the ICAR-National Dairy Research Institute in India. Data pertaining to 305-day milk yield (305DMY), wet average (WA), and calving to first insemination interval (CFI) of the animals considering 13 counts of progenies/sire were initially analyzed. The ΔG through direct selection was 43.68 kg/year, 0.13 kg/year, and 1.68 days/year for 305DMY, WA, and CFI, which was 1.97%, 1.65%, and 2.02% of herd average, respectively. In addition, ΔG was estimated by simulating the number of progenies/sire by 50%, i.e. by 6 and 18. Upon simulation of the number of progenies/sire, the ΔG in 305DMY decreased by 14% and increased by 8%, respectively. A similar trend in ΔG was found when simulating the number of progenies/sire by 50% in WA and CFI. Expected ΔG was also assessed by increasing the number of progenies per sire gradually from 6 to 18. Initially, there was a noticeable increase in ΔG upon increasing the number of progenies/sire gradually from 6 to 11, but with a further increase in the number of progenies/sire, ΔG increased only gradually and the magnitude was found to be low.

Key words: Expected genetic gain, direct selection, simulation, Sahiwal

1. Introduction

The formulation of a dairy breed improvement program through genetic appraisal of animals over generations is a major goal of animal breeders. The evaluation of any genetic improvement program is imperative in order to assess genetic progress and optimize the genetic gain (ΔG) so as to enhance farm profitability. The change in mean performance over a generation brought about by selection in a particular trait is known as direct response to selection. The genetic change in the selected trait, which can be measured only after the selection of animals, is known as realized genetic response. However, biometrical procedures are useful in predicting the direct response in advance if parameters like heritability, variability in the population, and the fraction of selected individual or selection intensity are known; however, in practice, factors such as accuracy of selection and selection intensity differ among male and female animals in small herds. Therefore, there is a need to account for the unequal contribution of male and female parents to ΔG . Rendel and Robertson [1] provided the breakdown of opportunity for improvement by selection in organized herds and suggested the percentage of genetic improvement that can be expected from 4 paths, viz. bulls to breed bulls (BB), bulls to breed cows (BC), cows to breed bulls (CB), and cows to breed

cows (CC) at 43%, 18%, 33%, and 6%, respectively. Since the genetic improvement per unit of time is more important than progress per generation, ΔG per unit of time is always the better parameter as the generation interval is associated with the sex of the animal and will be different for the 4 paths.

The Sahiwal is an important indigenous dairy breed of cattle in many countries around the world. The animal is well known for its higher milk yield, sustainability under the hot climate of the subtropics, and comparative resilience to diseases. Over the years, the Sahiwal breed has been imported by many countries from India and Pakistan for the genetic improvement of their native breeds [2]. The synthetic strains of cattle like the Australian-Friesian-Sahiwal, Australian Milking Zebu, Frieswal, Jamaica Hope, Karan Swiss, and Taurindicus have also been developed using the Sahiwal breed for rearing in tropical conditions. In India, the Karan Swiss and Frieswal strains have been developed by crossing the Sahiwal with exotic breeds like the Brown Swiss and Holstein-Friesian. In general, genetic improvement of Sahiwal cattle has been judged based on the estimated ΔG of a single trait, i.e. milk production [3,4], and attempts have not been made to optimize the number of progenies/sire required in small herds. It has been observed and reported worldwide that increasing milk

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production is antagonistically related to the reproductive performance of the animal [5–7]. It is therefore required to assess ΔG under genetic improvement programs of the Sahiwal breed based on multiple factors like production and reproduction traits. An attempt was therefore made for the first time in India to assess the ΔG for important reproduction traits like calving to first insemination interval (CFI) along with other production traits, i.e. 305-day milk yield (305DMY) and wet average (WA), by simulating the number of progenies/sire in Sahiwal cattle. The findings of this study will facilitate the development of the breeding strategy in small herds in many developing countries with sustainable ΔG for performance traits.

2. Materials and methods

2.1. Data

Data spanning 29 years (1988–2016) pertaining to Sahiwal cattle kept at a structured herd at the ICAR-National Dairy Research Institute in Haryana, India were utilized. In the Indo-Gangetic alluvial plains, the farm is located at an altitude of 250 m above mean sea level. Data editing was carried out and abnormal records were not considered in the present study. The average productivity of indigenous cattle in India is about 3 kg/day; hence, animals with a daily milk yield of less than 3 kg and a lactation length of less than 100 days were excluded from the study. Data were standardized for each trait using mean and standard deviation. The adjustment of the data was done for significant nongenetic factors like season of calving, period of calving, and age group at calving using least squares analysis [8].

2.2. Management practices at the farm

A loose housing system was followed for rearing the Sahiwal specimens at the farm, and separate sheds were provided for each category of animal. Covered calf pens were in place to keep calves up to 6 months of age and, subsequently, the animals were moved to a loose housing system. A standardized, balanced ration of green, dry fodder and concentrates was used to meet the nutritional requirements of the Sahiwal cows. Weaning was done at birth. The calves were fed with colostrum from their own dams for 4–5 days, followed by whole milk up to 30 days. Subsequently, feeding was done according to age groups considering the requirements of the animals for maintenance, growth, reproduction, and production. The milk recording of the cows started from the 6th day after parturition until the date of drying. Milking was done 2 times daily using both systems of milking, i.e. machine and hand milking, according to the milk production of animals and adaptation of the Sahiwal cows to machine milking. Selective breeding under the progeny testing program was done for genetic improvement of the Sahiwal cattle at the farm.

2.3. Traits

Three different first lactation traits, viz. 305DMY, WA, and CFI, were considered in the present study for estimation of ΔG . Initially, 703, 703, and 539 first lactation observations were recorded for 305DMY, WA, and CFI. However, after editing and standardization of data of observations, the numbers were 386, 386 and 280, respectively, for the 3 considered traits. In dairy animals, first lactation 305DMY is very important as it is the earliest production record in the herd and plays a significant role in making future selection decisions regarding retention of the animals. WA is the average per day milk yield up to 305 days or less during lactation. It is one of the most familiar traits for a dairy farmer. Any selection strategy to be applied in field conditions should be understandable to the farmers. Because of this concern, WA may serve as an important trait for the selection of dairy animals in the Indian context. CFI measures the cow's ability to resume estrus cyclicity after calving and is an economically important trait. It is also correlated with the animal's ability to conceive soon after insemination and become pregnant [9].

2.4. Statistical analysis

ΔG was calculated for first lactation production as well as reproduction traits (305DMY, WA, and CFI) using the direct selection method. The ΔG due to selection per generation depends on the intensity of selection, accuracy of selection, and additive genetic standard deviation. Selection intensity and accuracy of selection varied along the 4 paths of inheritance, i.e. sire to bulls, sire to cows, dam to bulls, and dam to cows. The ΔG per generation for 4 paths of inheritance was computed as: $\Delta G = i \cdot r_{IA} \cdot \sigma_A$

where i = selection intensity; r_{IA} = accuracy of selection and σ_A = additive genetic standard deviation (same for all 4 paths).

For SB (sire to bulls) and SC (sire to cows) paths:

$$r_{IA} = 0.5 \sqrt{\frac{nh^2}{1 + (n-1)0.25h^2}}$$

For the DB (dam to bulls) path:

$$r_{IA} = \sqrt{\frac{nh^2}{1 + (n-1)r}}$$

For the DC (dam to cows) path:

$$r_{IA} = h$$

where n = the number of progenies per sire in SB and SC paths and the number of lactations of dams in DB path; h^2 = heritability of trait; r = repeatability of trait; h = square root of heritability.

The annual ΔG was estimated by using the formula suggested by Rendel and Robertson [1]:

$$\Delta G \text{ per year} = \frac{G_{SB} + G_{SC} + G_{DB} + G_{DC}}{L_{SB} + G_{SC} + G_{DB} + G_{DC}}$$

where G_{SB} , G_{SC} , G_{DB} , G_{DC} = ΔG per generation along the sire to bull path, sire to cow path, dam to bull path, and dam to cow path, respectively.

L_{SB} = average age of sires when their male offspring (bulls) were born and used as breeding bulls.

L_{SC} = average age of sires when their female offspring were born and entered the herd.

L_{DB} = average age of dams when their male offspring (bulls) were born and used as breeding bulls.

L_{DC} = average age of dams when their female offspring were born and entered the herd.

Genetic parameters, viz. heritability, repeatability, and additive genetic standard deviation of traits, were estimated using mixed model least squares analysis [8].

2.5. Simulation study

Expected ΔG was estimated by simulating the number of progenies per sire and dam. The number of progenies per sire was increased and decreased by 50%, and the number of progenies/dam was increased gradually. Additionally, expected ΔG was also analyzed by gradually increasing the number of progenies per sire one by one from 6 to 18.

3. Results

The herd averages for 305DMY, WA, and CFI were found to be 2209.86 kg, 7.87 kg/day, and 83.04 days, respectively, in the Sahiwal cattle. Heritability estimates for 1st lactation

305DMY, WA, and CFI were 0.28, 0.36, and 0.18, respectively [10,11]. Expected ΔG by direct selection for 305DMY, WA, and CFI as observed in existing conditions is presented in Tables 1, 2, and 3, respectively. The number of progenies for the 4 different paths, i.e. sire to bull, sire to cow, dam to bull, and dam to cow, were found to be 13, 12, 3, and 3, respectively. Expected ΔG by direct selection was found to be 43.68 kg/year, 0.13 kg/year, and 1.68 days/year for traits 305DMY, WA, and CFI in the Sahiwal cattle. ΔG for milk yield was found to be 1.97% of the herd average in this study. Genetic change per generation from paths sire to bull, sire to cow, dam to bull, and dam to cow for milk yield was found to be 352.33 kg, 347.30 kg, 306.04 kg, and 42.01 kg, respectively, which was 15.94%, 15.71%, 13.84%, and 1.9% of the herd average. Genetic change per year from paths sire to bull, sire to cow, dam to bull, and dam to cow for milk yield was found to be 48.20 kg, 45.63 kg, 50.58 kg, and 13.95 kg, respectively, which was 2.18%, 2.06%, 2.28%, and 0.63% of the herd average.

It is evident from Table 2 that ΔG for WA was found to be 1.65% of the herd average in this study. Genetic change per generation for WA through paths sire to bull, sire to cow, dam to bull, and dam to cow for milk yield was found to be 1.04 kg, 1.01 kg, 0.92 kg, and 0.13 kg, respectively, which was 13.21%, 12.83%, 11.68% and 1.65% of the herd average. ΔG for calving to CFI was observed as 40.44 days

Table 1. Expected genetic gain in 305-day milk yield by direct selection method upon changing the number of progenies in Sahiwal cattle.

Path	i	n	r	σ_A	ΔG (kg)	L	ΔG / generation	ΔG / year	% of H.A.
Decrease in number of progenies/sire									
Sire to bull: G_{SB}	1.27	6	0.56	396.32	281.86	7.31	905.55	37.76	1.71
Sire to cow: G_{SC}	1.27	5	0.52	396.32	261.73	7.61			
Dam to bull: G_{DB}	1.17	4	0.69	396.32	319.95	6.05			
Dam to cow: G_{DC}	0.20	4	0.53	396.32	42.01	3.01			
Existing condition									
Sire to bull: G_{SB}	1.27	13	0.70	396.32	352.33	7.31	1047.68	43.68	1.97
Sire to cow: G_{SC}	1.27	12	0.69	396.32	347.30	7.61			
Dam to bull: G_{DB}	1.17	3	0.66	396.32	306.04	6.05			
Dam to cow: G_{DC}	0.20	3	0.53	396.32	42.01	3.01			
Increase in number of progenies/sire									
Sire to bull: G_{SB}	1.27	18	0.76	396.32	382.53	7.31	1131.25	47.17	2.13
Sire to cow: G_{SC}	1.27	17	0.75	396.32	377.49	7.61			
Dam to bull: G_{DB}	1.17	5	0.71	396.32	329.22	6.05			
Dam to cow: G_{DC}	0.20	5	0.53	396.32	42.01	3.01			

i = Selection intensity, n = Number of progenies, r = Accuracy of selection, σ_A = Additive genetic standard deviation, ΔG = Genetic gain, L = Generation interval, H.A. = Herd average.

Table 2. Expected genetic gain in wet average by direct selection method upon changing the number of progenies in Sahiwal cattle.

Path	i	n	r	σ_A	ΔG (kg)	L	ΔG / generation	ΔG / year	% of H.A.
Decrease in number of progenies/sire									
Sire to bull: G_{SB}	1.27	6	0.61	1.09	0.84	7.31	2.73	0.11	1.40
Sire to cow: G_{SC}	1.27	5	0.57	1.09	0.79	7.61			
Dam to bull: G_{DB}	1.17	4	0.76	1.09	0.97	6.05			
Dam to cow: G_{DC}	0.20	4	0.60	1.09	0.13	3.01			
Existing condition									
Sire to bull: G_{SB}	1.27	13	0.75	1.09	1.04	7.31	3.10	0.13	1.65
Sire to cow: G_{SC}	1.27	12	0.73	1.09	1.01	7.61			
Dam to bull: G_{DB}	1.17	3	0.72	1.09	0.92	6.05			
Dam to cow: G_{DC}	0.20	3	0.60	1.09	0.13	3.01			
Increase in number of progenies/sire									
Sire to bull: G_{SB}	1.27	18	0.80	1.09	1.11	7.31	3.31	0.14	1.78
Sire to cow: G_{SC}	1.27	17	0.79	1.09	1.09	7.61			
Dam to bull: G_{DB}	1.17	5	0.77	1.09	0.98	6.05			
Dam to cow: G_{DC}	0.20	5	0.60	1.09	0.13	3.01			

i = Selection intensity, n = Number of progenies, r = Accuracy of selection, σ_A = Additive genetic standard deviation, ΔG = Genetic gain, L = Generation interval, H.A. = Herd average.

Table 3. Expected genetic gain in calving to first insemination interval (CFI) by direct selection method upon changing the number of progenies in Sahiwal cattle.

Path	i	n	r	σ_A	ΔG (days)	L	ΔG / generation	ΔG / year	% of H.A.
Decrease in number of progenies/sire									
Sire to bull: G_{SB}	1.27	6	0.47	17.41	10.39	7.31	34.41	1.43	1.72
Sire to cow: G_{SC}	1.27	5	0.44	17.41	9.73	7.61			
Dam to bull: G_{DB}	1.17	4	0.63	17.41	12.83	6.05			
Dam to cow: G_{DC}	0.20	4	0.42	17.41	1.46	3.01			
Existing condition									
Sire to bull: G_{SB}	1.27	13	0.62	17.41	13.71	7.31	40.44	1.68	2.02
Sire to cow: G_{SC}	1.27	12	0.60	17.41	13.26	7.61			
Dam to bull: G_{DB}	1.17	3	0.59	17.41	12.01	6.05			
Dam to cow: G_{DC}	0.20	3	0.42	17.41	1.46	3.01			
Increase in number of progenies/sire									
Sire to bull: G_{SB}	1.27	18	0.68	17.41	15.03	7.31	44.52	1.86	2.24
Sire to cow: G_{SC}	1.27	17	0.66	17.41	14.59	7.61			
Dam to bull: G_{DB}	1.17	5	0.66	17.41	13.44	6.05			
Dam to cow: G_{DC}	0.20	5	0.42	17.41	1.46	3.01			

i = Selection intensity, n = Number of progenies, r = Accuracy of selection, σ_A = Additive genetic standard deviation, ΔG = Genetic gain, L = Generation interval, H.A. = Herd average.

per generation and 1.68 days per year in this study (Table 3). Genetic change per generation for CFI from paths sire to bull, sire to cow, dam to bull, and dam to cow was

found to be 13.71 days, 13.26 days, 12.01 days, and 1.46 days, respectively, which was 16.51%, 15.96%, 14.46%, and 1.75% of the herd average.

3.1. Expected ΔG on simulation

Expected ΔG and accuracy was assessed by increasing as well as decreasing, the number of progenies/sire. The number of progenies per sire and per dam had a direct effect on the accuracy of selection in all paths except in the dam to cow path. The expected ΔG estimated for 305DMY, WA, and CFI on simulating 'n' is presented in Tables 1, 2, and 3, respectively. On increasing and decreasing the number of progenies/sire by 50% from the existing number of progenies/sire, i.e. 13, the expected ΔG in 305DMY increased by 8% and decreased by 14%, respectively. An almost similar trend in expected ΔG was found while increasing and decreasing the number of progenies/sire by 50% in WA and CFI. If Table 1 is observed, it is evident that in 305DMY there was a 20% and 24.63% decrease in the genetic contribution from sire to bull and sire to cow when decreasing the number of progenies/sire to 50%; however, 8.57% and 8.69% increases were observed in genetic contribution through these paths when increasing the number of progenies by 50%. Genetic contribution through the dam to bull path increased gradually with a gradual increase in the number of progenies per dam, although there was no effect of progenies on the genetic contribution through the dam to cow path.

Furthermore, the effect of the number of progenies per sire on expected ΔG was observed and is depicted in the Figure. Initially, there was a noticeable increase in the expected ΔG (5.04 kg/year) upon increasing the number of progenies/sire from 6 to 11. However, with a further increase in the number of progenies/sire, the expected ΔG was found to have increased, yet the increase was gradual and the magnitude was found to be low.

4. Discussion

In the present study, the herd average for 305DMY was 2209.86 kg, and similar (as well as) comparatively lower 305DMY was found in Sahiwal cattle as reported in several

other studies [12–14]. The WA observed in the present study was higher than the findings of other researchers in cattle [15,16]. A higher [17,18] as well as a lower [19] CFI was reported by researchers in HF cattle. Banik and Gandhi [20] observed a similar estimate of heritability for 305DMY in Sahiwal cattle, although other researchers observed comparatively lower and higher estimates of heritability for the same trait in Sahiwal cattle [21,22]. The heritability (0.39 ± 0.07) of WA reported in Karan Fries cattle [23] was similar to the present study, while a higher heritability (0.54) of WA in Jersey crossbred cattle was observed by Ratwan et al. [16]. A slightly lower heritability of CFI compared to the present study was observed in Holstein Friesian cattle [24].

In the present study, ΔG per year for 305DMY from paths sire to bull, sire to cow, dam to bull, and dam to cow was 48.20 kg, 45.63 kg, 50.58 kg, and 13.95 kg, respectively, which was 2.18%, 2.06%, 2.28%, and 0.63% of the herd average. High impact through the dam to bull path may be due to high production performance of dams whose male offspring were selected for future breeding. In a closed Harijana herd, maintained in Hisar over a period of 16 years, a genetic change of 2.5% of the herd average was reported by Acharya and Lush [25] using the direct selection method and genetic change from sire to son, sire to daughter, dam to son, and dam to daughter paths and these corresponded to 34.9%, 1.2%, 39.0%, and 2.9% of herd average per generation, respectively. Rendel and Robertson [1] reported a ΔG of 15.45 kg milk per year, which was 0.7% of the herd average (2107 kg), and this was reported in a closed herd of Ayrshire cattle while measuring the genetic superiority and generation interval from the 4 paths of parent to offspring. Bara et al. [3] reported a comparatively lower (20.17 kg/year) expected ΔG per year for milk production in Sahiwal cattle. In Guzerat cattle, the expected ΔG by direct selection of 305DMY was found to be 137.6 kg/year by Santos et al. [26], which is higher than

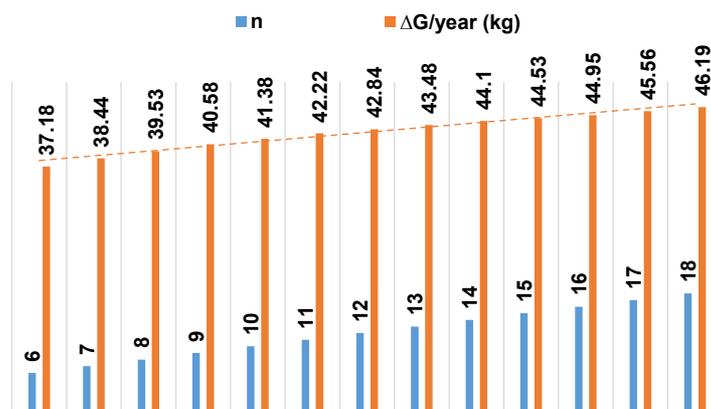


Figure: Effect of change in the number of progenies/sire (n) on expected genetic gain of 305-day milk yield in Sahiwal cattle.

the present estimates in this study. Parveen [4] estimated expected ΔG per generation for 305DMY using the direct selection method in Sahiwal cattle through paths sire to bull, sire to cow, dam to bull, and dam to cow as 239.72 kg, 236.09 kg, 181.61 kg, and 22.30 kg, respectively, which was 12.15%, 11.97%, 9.20%, and 1.13% of the herd average. The author also reported genetic change per year from paths sire to bull, sire to cow, dam to bull, and dam to cow for milk yield as 27.75 kg, 29.52 kg, 24.68 kg, and 4.56 kg, respectively, which was 1.40%, 1.49%, 1.25%, and 0.23% of the herd average. No references were found in the literature pertaining to the estimation of 305DMY for WA and CFIs using the direct selection method in Sahiwal cattle.

This study concludes that in order to continue a breed improvement program in small herds, it is strategically imperative to optimize the number of progenies/sire. This will lead to an estimated ΔG using the production and reproduction traits of Sahiwal cattle in a more sustainable manner. It was envisaged that the expected ΔG could

increase through all paths except in the dam to cow path with an increase in the number of progenies. Moreover, a noticeable increase was observed in the expected ΔG when gradually increasing the number of progenies/sire one by one from 6 to 11. Although increasing the number of progenies/sire to 18 led to an increase in expected ΔG , the increase was gradual and the magnitude was found to be low. The present findings will facilitate the development of breeding strategies in small cattle herds in many developing countries to obtain sustainable ΔG for performance traits.

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Conflict of interest

The authors declare that they have no conflict of interest.

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