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Short communication

POTENTIAL OF GENOMIC SELECTION IN SAHIWAL CATTLE

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A selection program to enhance the genetic potential for milk production of Sahiwal cattle using progeny testing program is going on however, it faces severe implementation issues. Simulated studies have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement. The current study intended to explore the application of genomic selection in a typical developing country situation using Sahiwal cattle in Pakistan as an example. The assumed size of the training population for genomic selection was 10550 cows with lactation records of 28146 present in Research Centre for Conservation of Sahiwal Cattle (RCCSC), Jhang. The results indicated that genomic selection can reduce the generation intervals in the male to male selection pathway from 10.5 years down to 2.75 years. Response to selection increased by 2.15 times compared to that in a progeny testing program. Furthermore, it reduced the costs of proving bulls by approximately 88%. The results from the present study suggest the initiation of genomic selection program for Sahiwal cattle in Pakistan and support the idea of establishing a reference population for Sahiwal cattle as a first step. It may also encourage the researchers and policy makers to use the genomic selection for improving productivity of dairy cattle of other developing countries.

Keywords: Genomic selection, Sahiwal cattle, reference population, cow breeds, cattle conservation

INTRODUCTION

Pakistan is among the top five milk-producing countries in the world. It has an annual gross milk production of about 46440 thousand tons. According to GoP (2011), cattle contribute approximately 35% of the total milk production and Pakistan possesses 35.5 million head of cattle. In this context, there are three established indigenous breeds of dairy cattle i.e. Sahiwal, Red Sindhi and Cholistani. These breeds are very well adapted to the harsh climatic condition of the region and have beneficial disease resistance characteristics. As far as economic importance of Sahiwal cattle is concerned; it is the best milk producing breed in tropics and sub-tropics under harsh climatic conditions (Khan *et al*., 2008). The breed has been used for up gradation of genetic potential of other breeds i.e. East African Zebu, Dinka, Boran to improve their milk potential (Ilatsia *et al*., 2012; Leroy and Marchot, 1987; Rehman and Khan, 2012; Baharizadeh, 2012; Du *et al*., 2013). Furthermore, some cross breeding experiments have also been conducted with temperate region breeds of the world i.e. Holstein and Jersey (Murugaiyah *et al*., 2001), Ayrshire and Brown Swiss (Thorpe *et al*., 1994).

Currently, progeny testing program is underway under the umbrella of the Research Centre for Conservation of Sahiwal Cattle (RCCSC), Jhang (Fig. 1). The salient objectives of the program are; maintenance of nucleus herds of superior germplasm of Sahiwal cattle through registration and documentation of institutional and private herds; performance recording for genetic evaluation and identification of superior germplasm. Currently, the main breeding objective is to improve milk yield (defined as 305-day lactation milk yield). The strategy adopted is open nucleus herd. In the nucleus herd, 7 institutional (government) and 33 private farms are included under bull mother scheme. There are 1196 testing herds with 10550 registered cows. At present there are 400 registered bulls including 128 bulls under progeny testing.

However, the application of traditional progeny testing program under Pakistani conditions seems challenging due to small herd size and less awareness among farmer community and breed organizations regarding pedigree and performance recording of their animals. Moreover, typical progeny testing program, as being practiced in the developed countries, requires more time and expense which appears to be less optimistic enterprise under Pakistani conditions.

Schaeffer (2006) presented a compelling argument of why dairy cattle breeding organizations should consider replacing conventional progeny-testing schemes with breeding schemes that use genomic selection. Therefore, the current study investigated the application of genomic selection using Sahiwal cattle currently being recorded under RCCSC, Jhang as an example that farming community of Pakistan later.

MATERIALS AND METHODS

Key assumptions**:** Approximately, 10,000 cows are hypothesized to be improved over the period of 15 years employing all four paths of genetic selection given in Table 1. For this purpose 1442 bulls are to be tested taken from elite herd of 5170 cows considering 7% mortality, sex ratio of 0.50 and 0.6 calving rate. This many bulls are needed to be evaluated to get high accuracy. The effective population for Sahiwal cattle was reported as 30 animals (Dahlin, 1995). However, the effective population size calculated based on currently registered animals under RCCSC is 1558 animals.

The calculated cost calculation for genomic selection include cost for approximately 2000 US$/bull for purchase of bulls, 4120 US$/bull for their feeding and mangement, 11000 US$/bull for semen storage and insemination costs while 250 US$ for genotyping per animal. Finally the generation interval was calculated based on age of puberty in Sahiwal cows (3.25 Years) and age for start of semen collection from Sahiwal bulls (2 Years) in Pakistan. The expected accuracy for reference population is calculated based on two different effective population sizes cited in literature (30 & 1558) with heritability estimates of 0.30 using method referred by Goddard (2009).

Development of reference population**:** There are 10550 registered cows under RCCSC program. The cows will be evaluated for estimated breeding values (EBVs) based on lactation records and all cows will also be investigated for genomic breeding value using Illumina Bovine 7K SNP chip. Based on estimated breeding value and genomic breeding value, top 70% (7385) of cows will be selected as genomic selection (GS) herd and will then be investigated for genomic breeding value using Illumina Bovine50K SNP chip. Top 70% of the GS herd will be selected as an elite herd. The main genetic parameters are heritability and repeatability of 305-day lactation milk yield.

Bull calves (n=1442) of elite cows will be genotyped using Illumina Bovine 50K SNP chip to validate the chip results against phenotypic records of their dams. Top 5% bull calves (n=72) of the elite cows will be included in breeding program. The bulls included in breeding program will be tested against at least 30 daughter records and best one will retain in the herd (sire of cows). The male bull calves will be investigated for genomic breeding value using Illumina Bovine50K SNP chip and will be included in breeding program (sire of bulls). The daughters of elite cows (n=1442) will be sent back to test herd (Fig. 3).

Testing of existing bulls**:** There are 178 standing bulls with RCCSC. These bulls will be tested with Bovine 50K SNP Chip for further breeding decision. These bulls will be selected or discarded based on all available information including GBVs.

RESULTS AND DISCUSSION

Since the advent of genome wide association studies, SNP markers have been used to improve the production traits of domestic species. SNP chip of 60 K has been developed for chicken (Groenen *et al*., 2011), 7 K SNP chip for Atlantic salmon (Karlsson *et al*., 2011). Finally SNP 50K and 7K Beadchip is available for genomic selection of cattle developed by Illumina.

Table 1. Rates of genetic gain from four selection paths from traditional progeny testing and genomic selection program with two different *Ne*

PT							GS						
Modified from Schefer Scheme													
Selection pathway	**Selection (%)**	**Intensity (i)**	**Accuracy (rTI)**	**Generation Interval (L)**	**Genetic S.D. (i · rTI)**	**ΔG/Y**	**Selection pathway**	**Selection (%)**	**Intensity (i)**	**Accuracy (rTI)**	**Generation Interval (L)**	**Genetic S.D. (i · rTI)**	**ΔG/Y**
Sire of bulls	5	2.06	0.99	10.5	2.04	34.9	Sire of bulls	5	2.06	0.75	2.75	1.54	101.1
Sire of cows	20	1.4	0.75	7.5	1.05	25.2	Sire of cows	20	1.4	0.75	2.75	1.05	68.7
Dams of bulls	30	1.159	0.6	7.3	1.45	17.1	Dams of bulls	2	2.42	0.75	4	1.82	81.6
Dams of cows	70	0.5	0.5	4.75	0.14	9.4	Dams of cows	85	0.27	0.5	4.9	0.14	4.9
Total				30.05	4.68	86.7	Total				14.4	4.55	256.4
Modified from Schefer Scheme with accuracy calculated from Guddard (2009) Method using Ne = 1558													
Sire of bulls	5	2.06	0.99	10.5	2.04	34.9	Sire of bulls	5	2.06	0.623	2.75	1.54	84.0
Sire of cows	20	1.4	0.75	7.5	1.05	25.2	Sire of cows	20	1.4	0.623	2.75	1.05	57.08
Dams of bulls	30	1.159	0.6	7.3	1.45	17.1	Dams of bulls	2	1.159	0.623	4	1.82	32.4
Dams of cows	70	0.497	0.5	4.75	0.14	9.4	Dams of cows	70	0.497	0.623	4.75	0.14	11.7
Total				30.05	4.68	86.7	Total				14.25	4.55	185.3
Modified from Schefer Scheme with accuracy calculated from Guddard (2009) Method using Ne = 30													
Sire of bulls	5	2.06	0.99	10.5	2.04	34.9	Sire of bulls	5	2.06	0.81	2.75	1.54	109.2
Sire of cows	20	1.4	0.75	7.5	1.05	25.2	Sire of cows	20	1.4	0.81	2.75	1.05	74.2
Dams of bulls	30	1.159	0.6	7.3	1.45	17.1	Dams of bulls	2	1.159	0.81	4	1.82	42.2
Dams of cows	70	0.497	0.5	4.75	0.14	9.4	Dams of cows	70	0.497	0.81	4.75	0.14	15.2
Total				30.05	4.68	86.7	Total				14.25	4.55	240.9

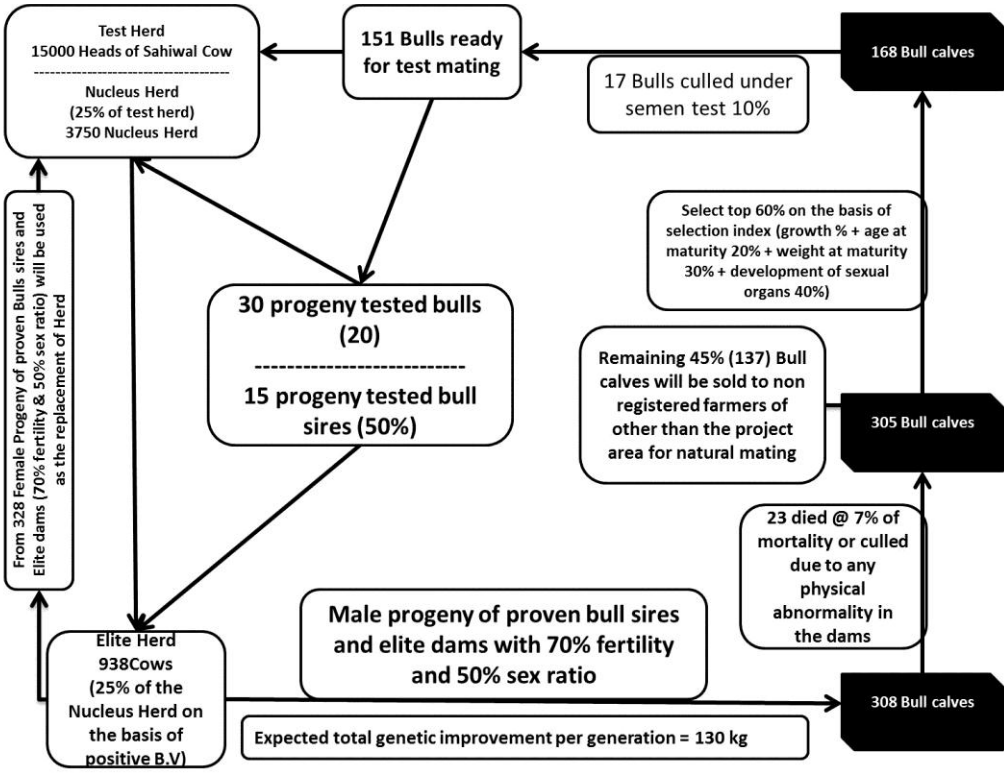

Figure 1. Sketch of undergoing progeny testing program for Sahiwal cattle in Pakistan

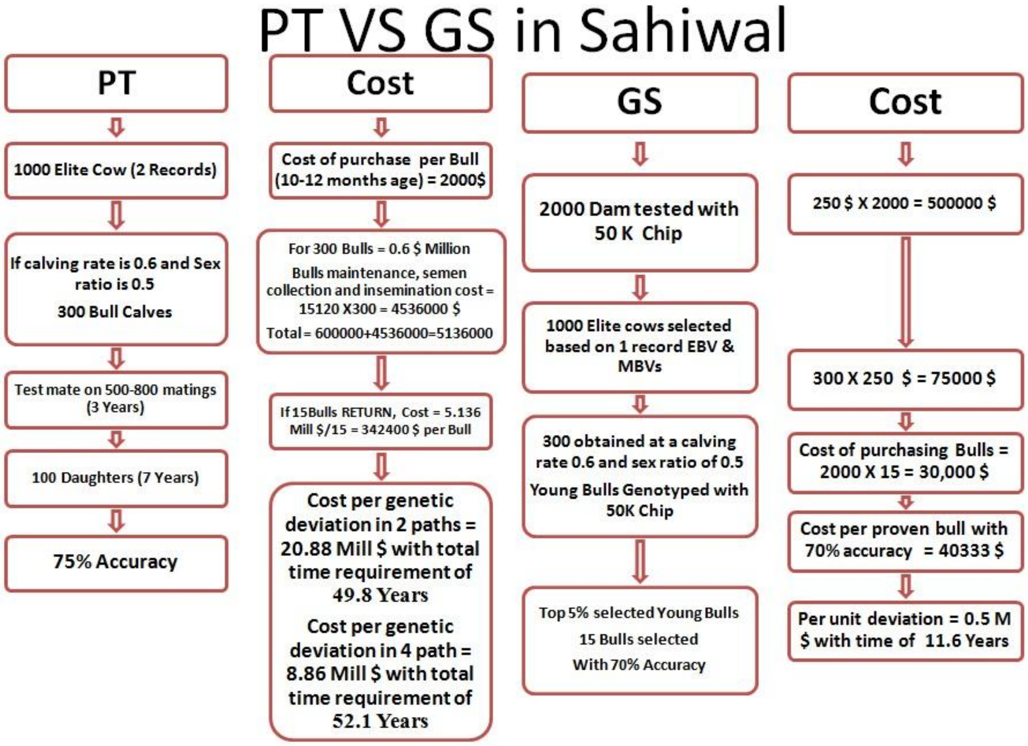

Figure 2. Cost of proving a bull under progeny testing (PT) VS genomic selection (GS) in Sahiwal cattle

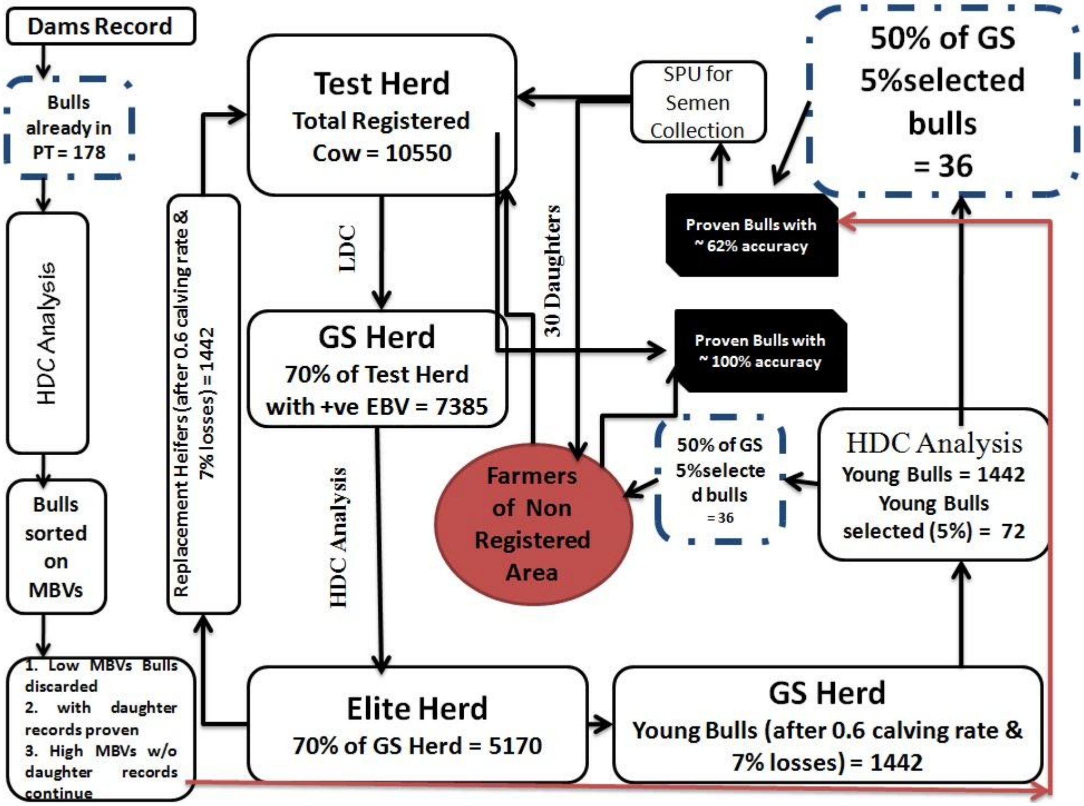

Figure 3. Sketch of genomic selection program for Sahiwal cattle genetic improvement

A prediction equation is estimated based on reference population phenotypic data with genomic data in genomic selection programs that is used to predict breeding values in animals without phenotype data (Borner and Reinsch, 2012). Now it is possible to decide breeding value of very young bull (at birth) with great accuracy based on parent's average. There seems to be, potentially, no need to wait for record on milk production of candidate to achieve required accuracy rather young bulls with no progeny but having genomic information combined with the parent average can be used as potential sires as they have the required accuracy (the confidence level is about 72% without any daughter record) (Schaeffer, 2006). As a results of high throughput genotyping and reduced genotyping cost; genomic selection feasible now.

The accuracy of genomic selection is an important aspect to be considered before actually going for it. The main determinants of accuracy are effective population size (Ne), number of records (N) of reference population, and heritability for the trait (Goddard, 2009). In the current scenario, there are no proven bulls with highly accurate EBVs that can be used as a reference population as opposed to the situation in most of the developed countries (Buch *et al*., 2012). The improvement in the accuracy of genomic predictions with increasing size of the reference population is non-linear as the reference population size increased from 500 to 100,000 animals, the accuracy raised from 0.42 to 0.98 (Goddard 2009). However, it is dependent on how accurately the phenotypic measures reflect heritability (the true breeding value) of the animals (Daetwyler *et al*., 2008; Goddard, 2009). As the heritability estimate for milk production is moderate, therefore, accuracy estimate is likely to be reasonable (Berry *et al*., 2011; Daetwyler *et al*., 2008). However, relatedness is another important factor and, for the same size of reference population, the greater the relatedness of the reference population to the population predicted, the more will be the accuracy of the genomic predictions (Habier *et al*., 2007; Habier *et al*., 2010).

Schaeffer (2006) suggested replacing conventional progeny-testing schemes with breeding schemes that use genomic selection. Following the Schaeffer calculations; we modified a simple four-pathway selection model for progeny testing with accuracies predicted by (Goddard, 2009; Meuwissen *et al*., 2001) of 0.623 and reduced the generation intervals in the male pathways from 10.5 years down to 2.75 years. The time required to implement four selection paths is redued from 30.05 in a typical progeny testing program to 14.25 years with genomic selection by virtue of reduced generation interval especially in male pathways (Table 1). The results for similar simulation studies were reported by (Berry and Moorepark, 2007) for Irish dairy cattle in which generation interval was reduced from 23.75 years in progeny testing to 9.53 years for genomic selection. The difference of our values might be because of breed difference. However, as indicated in lower part of Table 1, the accuracy values are 0.623 and 0.810 if the effective population size is considered 1558 and 30 respectively with heritability estimates of 0.30. In the current scenario, the accuracy level of 0.623 seems to be more realistic. We used available literature estimates on Sahiwal cattle to modify the proposed scheme of (Schaeffer, 2006). The additive genetic standard deviation used was 180 Kg milk based on performance data already reported for Sahiwal cattle (Bilal *et al*., 2008) (Rehman *et al*., 2008). The estimated rates of genetic gain and relevant parameters (calculated based on existing setup of Sahiwal genetic improvement program sketched in Fig. 1) are given in Table 1. The proposed genomic selection scheme resulted in an increase in response to selection by a factor of approximately 2.15, compared to that in a progeny testing scheme. Our results are similar to the finding of Schaeffer (Schaeffer, 2006)

We calculated the cost and input efforts required to implement the geneomic selection in Sahiwal cattle within existing progeny testing scheme. Furthermore, progeny testing (PT) was compared with genomic selection (GS) (Fig. 2). The details of these calculations are given in Figure 2. Briefly these include cost for purchase of bulls, their feeding and mangement cost, semen storage and insemination costs. Current calculations indicated that a cost of 40333 US$ are required to prove one bull and cost per unit deviation is 0.630 M US$ using genomic selection. Whereas, the cost of traditional progeny testing using four paths of selection (not present in current selection scheme) is 342400 US$. The cost is much higher (20.88 M US$) if selection is practied for only two pathways as is the case with existing Sahiwal breeding program (Fig. 2). The use of genomic selection may potentially reduce the costs of proving bulls by 88% compared to progeny testing program. This is closer to the value reported by Schaeffer (92%) (Schaeffer, 2006).

Application of genomic selection may enhance the rate of genetic gain and accuracy of selection in Sahiwal breed of Pakistan. Therefore, the idea of genomic selection presented in the current paper may have implications for the direction of research and policies regarding genetic improvement of dairy animals in the country.

***Potential limitations of application of GS*:** As breeding scheme design under genomic selection is a new area of research so, it is especially uphill task in developing countries perspective. In the absence of a well structured reference population for genomic selection and lack of proven bulls and performance recording system, scope of genomic selection appears to be challenging under existing conditions. However, it could be a wise strategy to take advantage of genomic selection tools in a developing country situation because these are potentially expected to be more robust and less demanding as compared to tradition progeny testing program. The results from some recently published literature have shown promising effects of genomic selection on the rates of genetic gain (Bouquet and Juga, 2012; Hayes *et al*., 2009; Humblot *et al*., 2010; Pszczola *et al*., 2011).

As opposed to developed countries, farmers in developing countries are less aware of the basic breeding principals, breeding schemes and technologies. There are no commercial companies involved in breeding schemes. So, it could be a challenging task to implement genomic selection in absence of these factors. However, genomic selection coupled with current progeny testing program under government umbrella could be a better alternative to overcome the problems. It is worth mentioning that despite of the immense potential of genomic selection in improvement of dairy animals, it may not be considered an immediate alternative of traditional progeny testing program under the current circumstances. The performance recording of animals is almost always required, as suggested by the Punjab livestock breeding act 2012, for establishing and subsequent updating of reference population which is a pre-requisite of a genomic selection program.

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