

Development and utilization of the United States gene bank collection. **H.D. Blackburn^{1*}, C. S. Wilson¹, C. D. Dechow²**

¹ National Animal Germplasm Program United States Department of Agriculture, 1111 South Mason St., CO 80521 Fort Collins, USA

² Penn State University, Department of Animal Science, University Park, PA, USA

Abstract

A large and substantial collection genetic resources, exceeding 59,000 animals and over 1.15 million samples, has been acquired by the national gene bank. Approximately 11,000 animals from the collection have been used for reconstituting genetic diversity and genomic studies. As an example, previous research showed in-situ U.S. Holstein had only two different ancestral Y chromosome lineages. It was determined two additional Y Chromosome lineages were present in the gene bank and they were reintroduced to the in-situ population. Reintroducing these two lost Y chromosomes from collection animals representing 1950's genetics illustrated how the collection can be used to address contracting genetic diversity, like limited Y chromosomes. The relatively high PTA measures for net merit and daughter lactation performance suggest gene bank collections may have broader uses than originally thought. Challenges still exist to increase gene bank collection use and to better quantify the diversity captured.

Introduction

For the last 23 years the national genebank has been charged with conserving livestock, aquatic and insect genetic resources important to agriculture (Blackburn, 2018; Blackburn et al 2019). As a result, we have acquired 1.15 million samples from 59,640 animals, representing 191 breeds, 369 subpopulations within those breeds and 44 species. Approximately 50% of the breeds collected have exceeded 50% of the minimum collection targets recommended by FAO (2016). The collection is still being developed with new and existing breeds in the collection or their subpopulations. At this time, it is beneficial to explore how the collection has been used, by whom and some of the results obtained when using the collection.

Materials & Methods

The collection has been developed by government, universities and private sector interactions. Program funding facilitates collection development, but the private sector has been highly engaged in donating germplasm samples from various populations. Universities have also contributed to collection development, including the donation of orphan collections developed by retired scientists. From its initiation the collection was designed to encompass all breeds and to serve multiple functions (e.g., research, corrective mating, reconstituting breeds). Therefore, the number of germplasm samples acquired for specific animals can exceed the quantity necessary to reconstitute a population in a worst-case scenario. The Animal-GRIN database contains information on collected samples, e.g., animal identification, phenotypes, genotypes, number and types of samples, geographic locations (https://agrin.ars.usda.gov/main_webpage_dev/ars?language=EN&record_source=US). Sample requests and releases are managed on-line through Animal-GRIN. Upon receipt, requests are reviewed to determine alignment with the program's mission.

For the data presented, Animal-GRIN was queried to determine animal birth year, species, and how the requested animals were to be used. Four sample use categories included: reintroduction (to reintroduce genetic variability or corrective mating), reproductive evaluation (samples used to evaluate sperm quality with live animal matings), genomic evaluation (samples genotyped and used to study genetic diversity or lethal alleles), and regeneration for live animals for research. An example of reintroduction and regeneration for live animal research is given for reintroducing lost Y chromosomes (LYC) into the Holstein breed (Dechow et al. 2020). In this example two of the collection's 1950's era bulls were mated to oocytes from current generation cows (ranking in the upper 70th percentile for net merit), resulting in calves from both sexes. The bull calves were raised and placed in a commercial stud and eight daughters remained in the Pennsylvania State University's herd for further study.

Results

To date samples for over 11,000 animals have exited the repository (Figure 1). Most species (cattle, sheep, goats, chickens, pigs, trout, oysters and catfish) in the collection have been used to varying degrees. From 2004 to 2020 a broad range of samples, based upon animal birth year, have been requested and used by stakeholders. There were 10 separate years where samples requested encompassed most birth years, including animals born before 1960. Most of the samples requested were used for molecular genetic studies (92%) by researchers or industry, with 5% being used for reintroduction of genetic variability (480 animals) into *in-situ* populations; the remaining two categories accounted for 3% of animals exiting the collection.

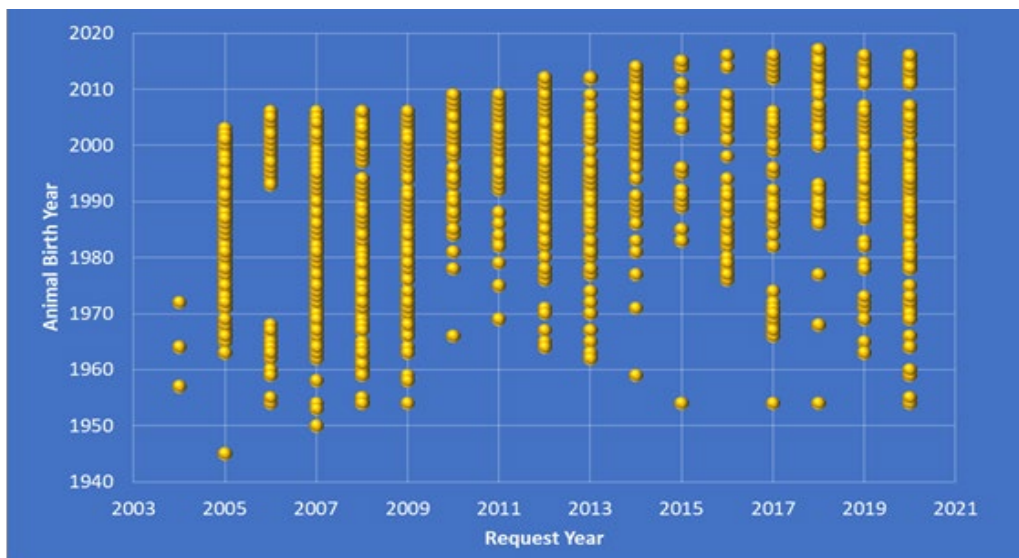


Figure 1. Samples from all species (n = 11,000 animals) exiting the gene bank by year requested and animal birth year.

Table 1 provides a snapshot of collection use and the results/impacts of those efforts. Industry, universities, and government have used the collection for various purposes. Table 1 also shows that some collection uses have made significant economic contributions to livestock sector. For example, animals from the collection were used in the initial development of genomic breeding values. Breed associations have also used the genotyped

animals from the collection to determine if key ancestors were carriers of lethal mutations. Determining the carrier status of these ancestors has led to significant savings in genotyping offspring from sires shown not to carry the mutation.

Genomic predicted transmitting ability (PTA) for founder LYC bulls and their progeny were compared to the national average for net merit and it was determined that progeny from LYC bulls were near breed average (Figure 2) which is contrary to previously thought expectations. Genomic EBV for the LYC daughters averaged 908 kg less than contemporary herd mates; however, the LYC daughters produced 670 and 1702 kg more milk in first and second parity, respectively (Jewell, 2021).

Table 1. Examples and impact of collection use.

Purpose	Breed	User	Results/Impact
Develop genomic BV	Holstein Jersey	Research	\$400 million/yr revenue increase
Identify carriers of lethal genes	Angus, Brangus	Breed Assoc.	Saved breeders >\$3 million in genotyping
Reintroduce lost Y chromosomes from 1950 era bulls	Holstein	University & industry	Increased genetic variability, Y chromosome research, progeny semen sold (Dechow et al., 2020)
Reconstituted halothane/napole pig line	Crossbred	University	New research grants, increased university use
Adding genetic variability to rare breeds	Multiple [#]	Industry	Increased genetic variability for stakeholders
Change in allelic frequencies of imported genetics	Meishan	Gov't	Nagoya Protocol - Informed negotiation & policy positions (Blackburn et al., 2014)

Milking Shorthorn, Dexter, Large Black

Discussion and conclusions

Results indicate that the collection has been widely used and the impact of use has been substantial economically and scientifically. Private breeders of major and minor breeds have used the collection to perform corrective mating for a variety of reasons, including redirecting breeding strategies and adding genetic variation into the *in-situ* population.

Reintroduction of two LYC (Table 1) into the Holstein breed is an instructive example of collection use. Figure 2 compares founding sires, their progeny, and the national average PTA for net merit from 1953 to 2019. By mating the bulls to elite cows, the gap between current average bull breeding values and Y-chromosome progeny was substantially narrowed. Bull progeny (born in 2017) PTA were approximately equivalent to breed averages from 2012 to 2014. The lactation performance of LYC daughters was based on a relatively small sample, but substantially exceeded expectations. The LYC project underscores the need to further evaluate collection progeny to determine the extent that current genomic prediction methodology under-estimate phenotypic performance.

In the LYC project it was noted the two 1950 era sires PTA exceeded breed average for milk production by two standard deviations. Blackburn (2019) reported many breeds with animals in the collection exceed the mean BV when compared to other animals of their birth year by

an equally large deviation. This finding suggests that while a particular animal may be chronologically older its genetics may be more useful than expected and when mated to above average females the gap between old and new genetics can be narrowed considerably. Generally, we have observed across species that animals in the collection that are outliers for BV may be above breed average for 4 to 6 future generations (8 to 30 years), depending upon selection pressure and generation interval within the breed. This observation has ramifications for how such individual animals might be utilized.

In summary, the collection has been widely used and made substantial contributions supporting its continued growth and development. Future challenges will be to better understand the genetic aspects of the collection, to use the collection effectively in corrective mating programs, and to encourage scientists and industry to increase their use of the collection for any variety of purposes.

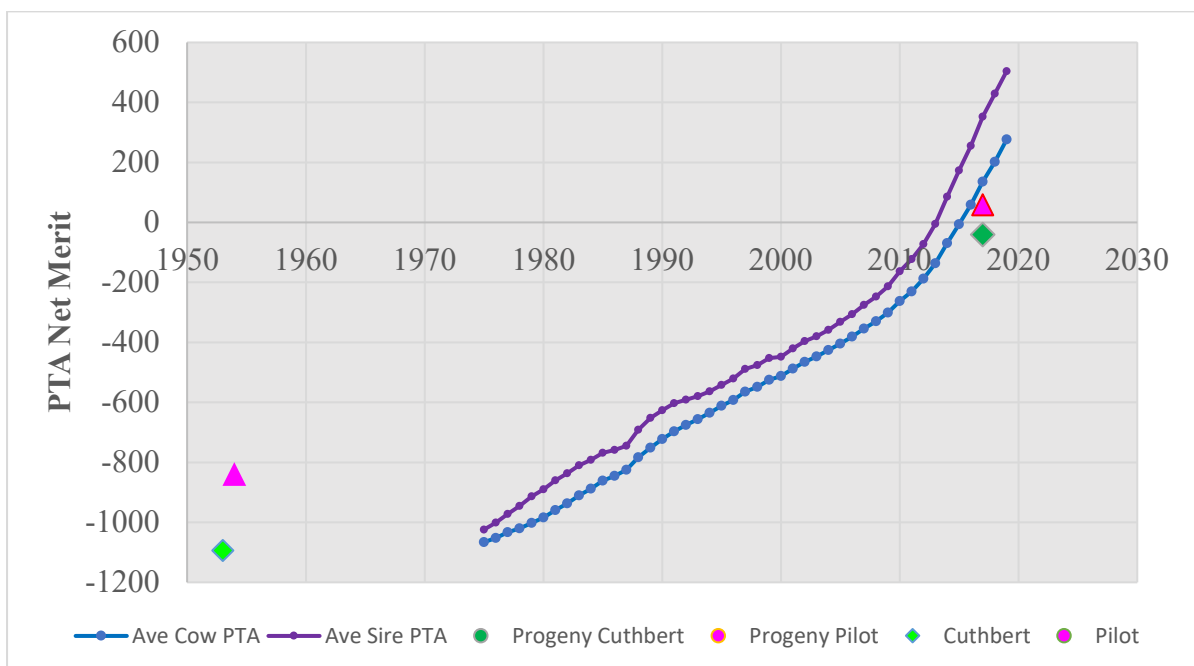


Figure 2. Comparison of 1950 era bulls (Cuthbert and Pilot), progeny of 1950 era bulls to the national average breeding value for net merit (Council of Dairy Cattle Breeding computed PTAs).

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