

Alpine Cluster Analysis Summary September, 2014

Data was obtained from the ADGA for 8 dairy breeds. All results were limited to those animals reported as Purebred (PB) or American (AM); however, all animals were included in the pedigree analysis to establish ties between animals, including cases where the ancestors are from another breed. Cluster analysis is a procedure that groups related animals based on pedigree relationship. This is a technique used by NAGP to assess where repository animals are grouping with the currently available genetic pool for each breed. It also establishes a practical approach for obtaining animals for the repository in a way that maximizes genetic diversity. Animals that were included in the cluster analysis included sires of PB and AM offspring born 2010 to present that are also PB or AM themselves. Repository bucks are also included in the clusters.

Table 1 shows the summary statistics based on the pedigree and cluster analyses.

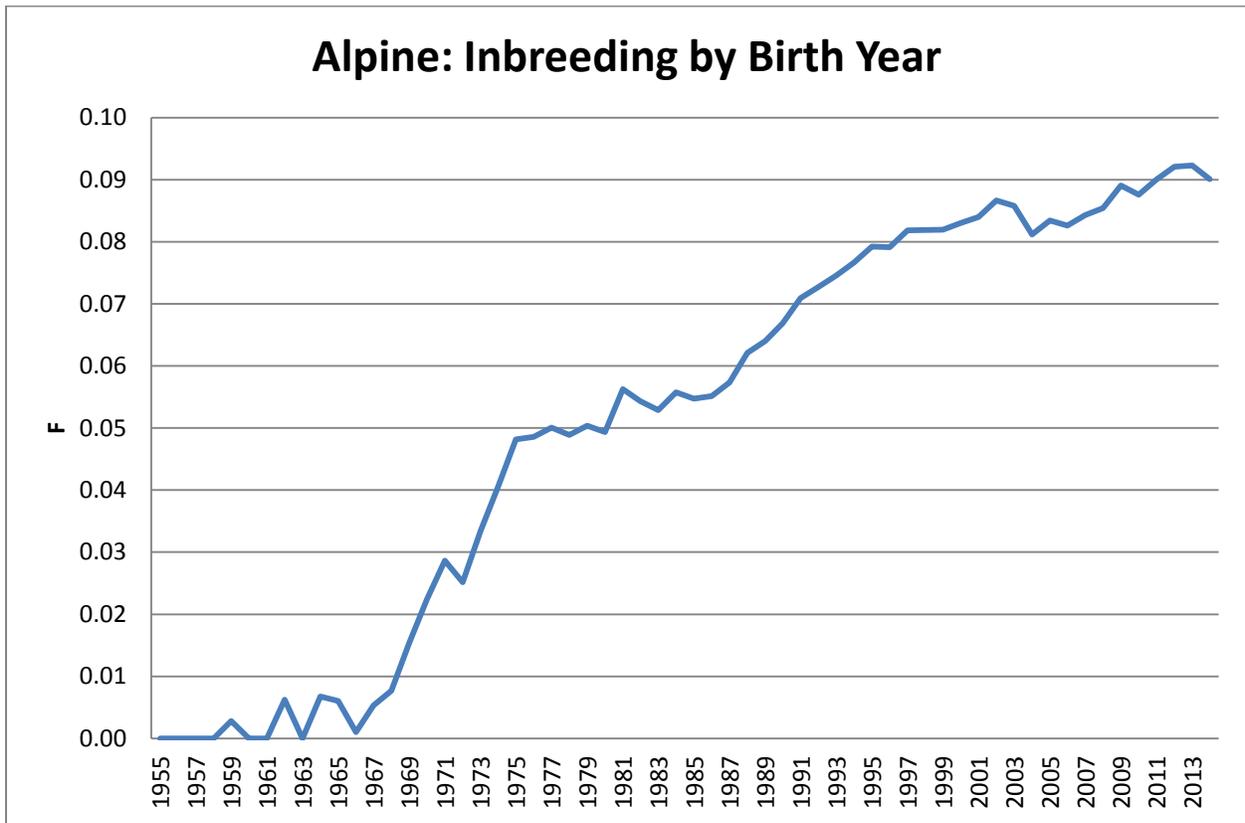
Table 1. Summary statistics for Alpine

	Alpine
Animals that are PB or AM	285,785
Full pedigree file (until all ancestors are unknown)	315,437
Unique sires	30,563
Unique dams	111,736
Mean inbreeding (F)	0.070
F range	0 – 0.65
Repository bucks	2
Clustered bucks	3,706

Pedigree & Inbreeding Analysis

Figure 1 shows the inbreeding trend over time for Alpines. The trend has increased at a fairly linear rate since the 1970's.

Figure 1. Alpine inbreeding trend by birth year



The number of animals registered per year are shown in Figure 2 and the percent of animals with an inbreeding coefficient greater than zero over time is shown in Figure 3. Registrations peaked in the early 1980's and have declined since the mid-1990's. Almost every animal registered since 1990 has at least some inbreeding. This is also demonstrated in Figure 4 showing the inbreeding category for animals born since 2009; there are almost no non-inbred animals in the population.

Figure 2. Alpine goats registered by birth year

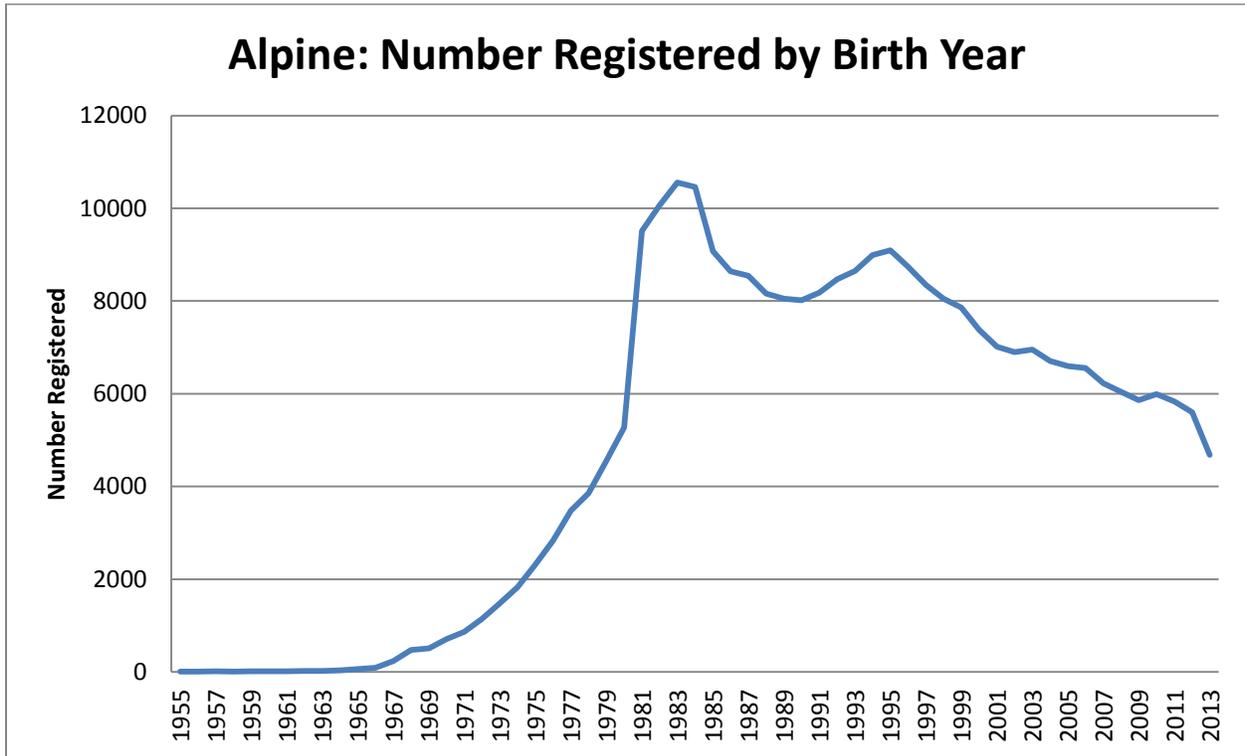


Figure 3. Percent of Alpines with an inbreeding coefficient greater than zero by birth year

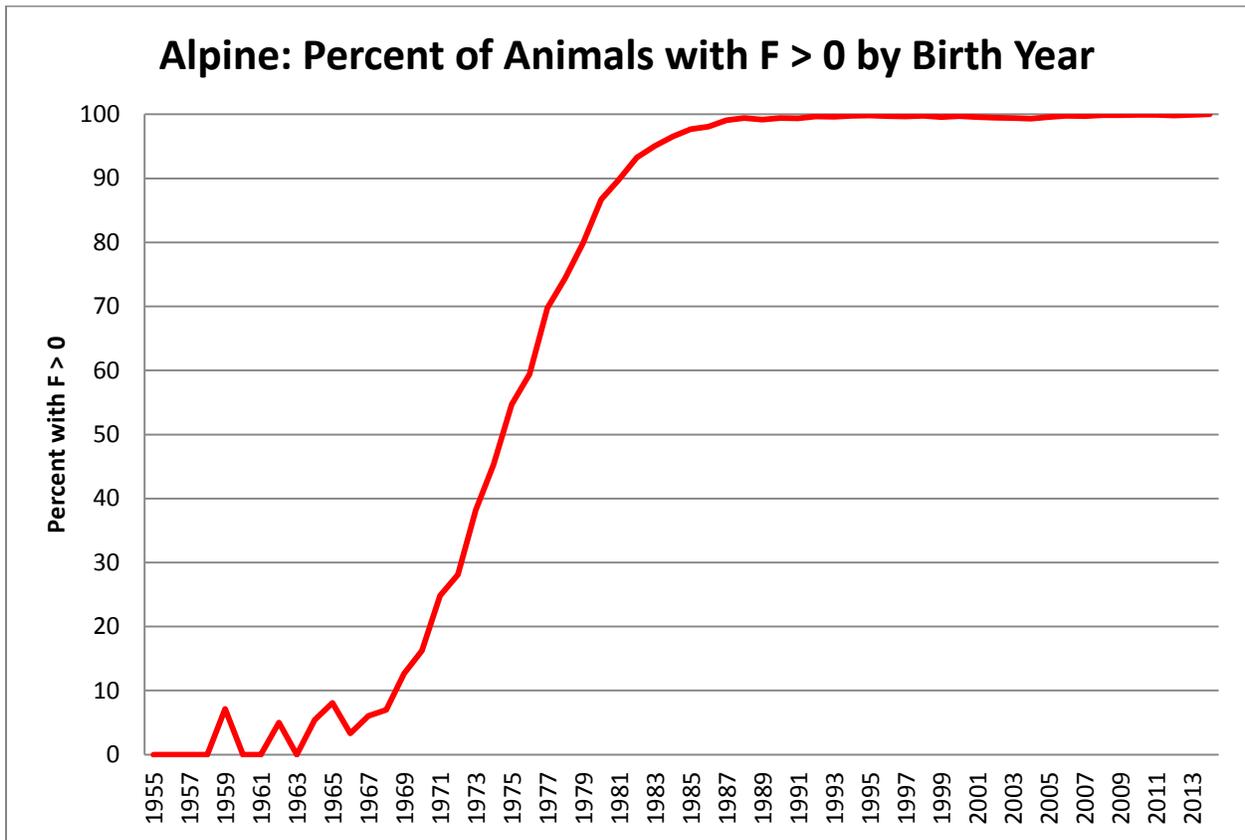
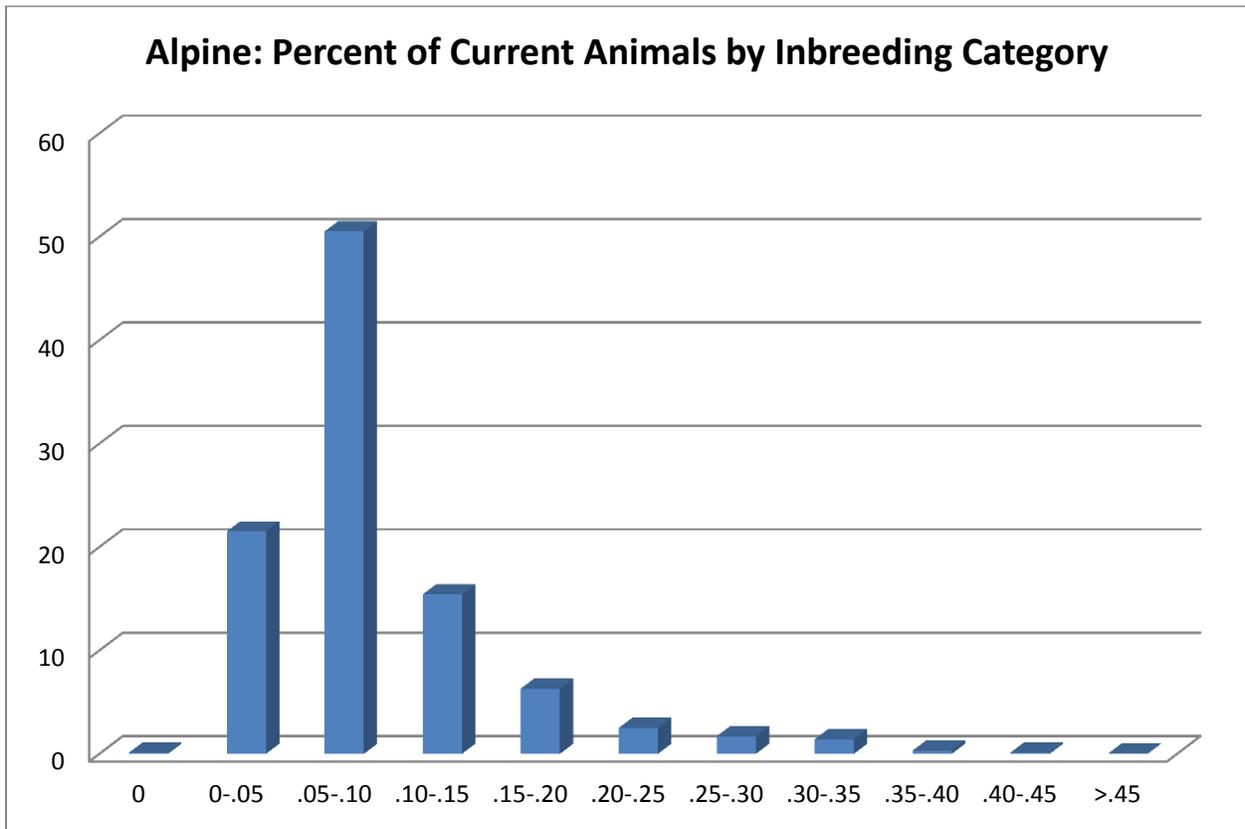


Figure 4. Percent of Alpines born 2009 and later by inbreeding category



The results of the cluster analysis are shown in the tree diagram. Defining the number of clusters for a population is a combination of statistics and also selecting a practical number to work with to meet the objectives of the analysis. For the Alpine clusters, 6 clusters were selected as representing the groups within the breed.

Figure 5. Tree diagram for Alpine cluster analysis of sires of PB and AM offspring born 2010 and later that are PB or AM themselves (gold line depicts cluster level)

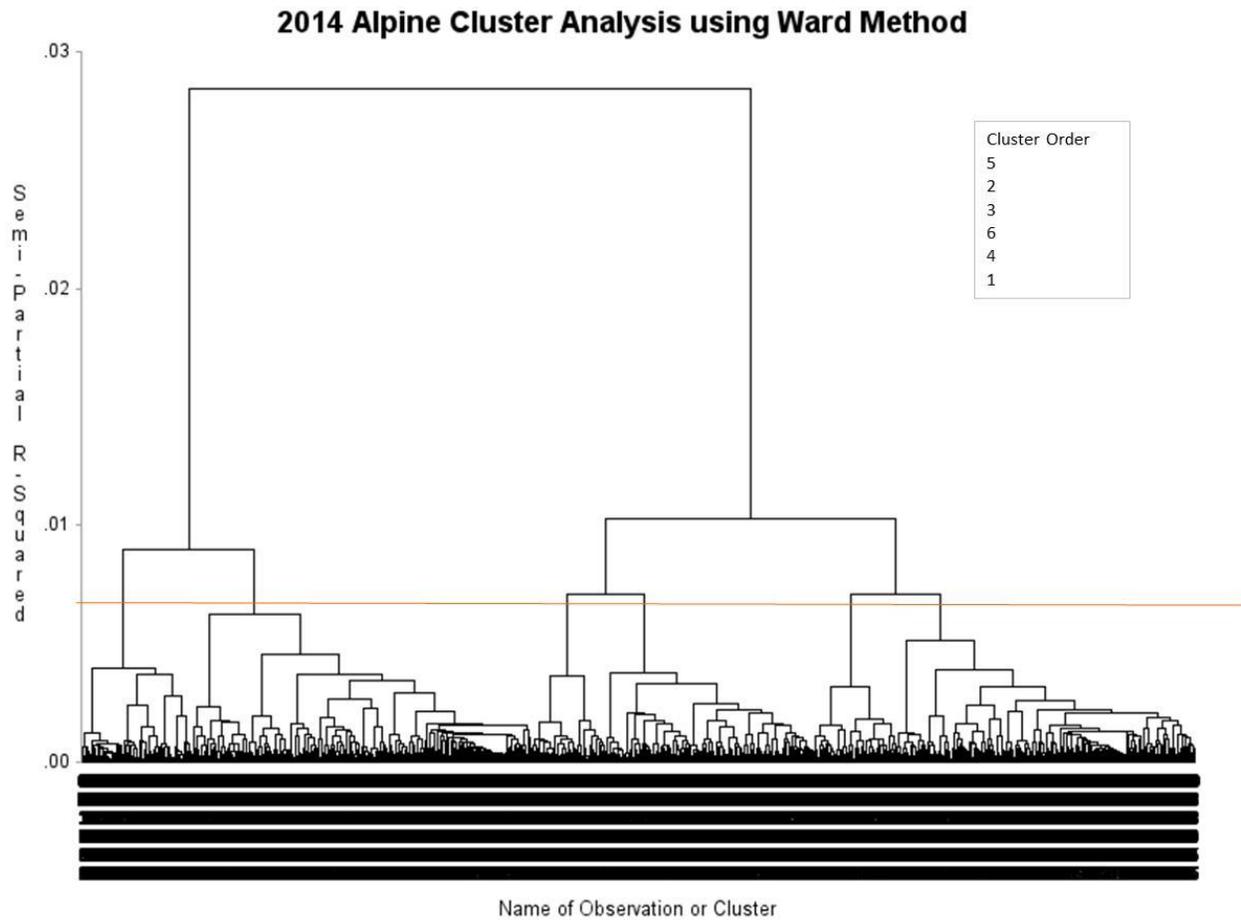


Table 2 shows the overall relationship between the 3,706 clustered animals as 0.101. The number of animals within each cluster, the cluster mean and variance, and where the bucks within the repository fit are also shown. A good cluster analysis would be expected to have most clusters with a higher average relationship than the overall relationship, although 1 'miscellaneous' cluster is usually present that contains animals that were not a good fit for any other cluster.

Table 2. Alpine cluster results showing the number, mean, and variance for between and within cluster relationships in addition to repository bucks

Between Clusters				
	n	Mean	Variance	
	3706	0.101	0.001	
Within Cluster				
	n	Mean	Variance	Bucks in Repository
Cluster 1	992	0.109	0.002	1
Cluster 2	1132	0.103	0.002	
Cluster 3	243	0.184	0.006	
Cluster 4	274	0.161	0.005	
Cluster 5	369	0.166	0.005	
Cluster 6	696	0.154	0.003	1

The within and between cluster relationship matrix is shown in Figure 6. The heat map shows low relationships as blue and higher relationships as red. The within cluster relationships would be expected to be higher in general than the between cluster relationships.

Figure 6. Within and between cluster relationship matrix for Alpine

	1	2	3	4	5	6
1	0.109	0.080	0.111	0.106	0.092	0.114
2		0.103	0.082	0.079	0.106	0.088
3			0.184	0.115	0.097	0.133
4				0.161	0.087	0.108
5					0.166	0.104
6						0.154

In addition to selecting animals for the repository that represent the lowest relationships within the breed, it is also important to make sure these animals represent the full range of production across the breed. Repository animals were plotted against the genetic trends for Milk, Fat, and Protein PTA. This data was obtained from the Council of Dairy Cattle Breeding website (<https://www.cdcb.us/eval/summary/goats.cfm>). Although there is only one Alpine repository buck with PTA data, it provides a starting point for NAGP to see the range of production that should be represented in the repository.

Figure 7. Alpine genetic trend for Milk PTA compared to repository bucks

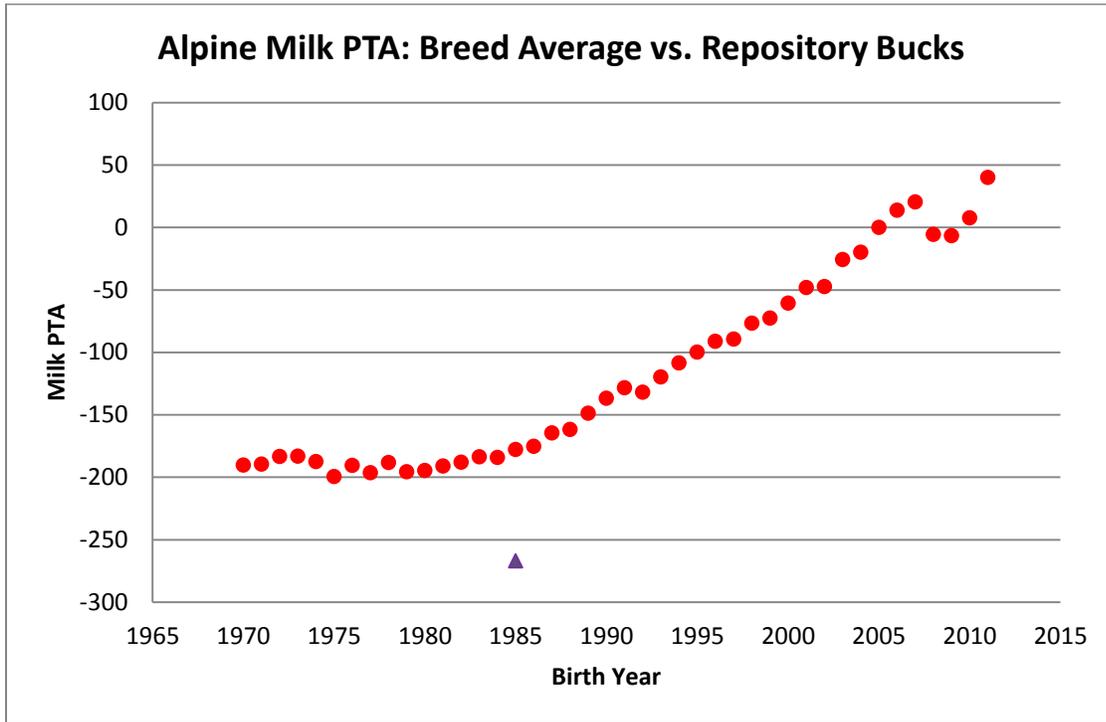


Figure 8. Alpine genetic trend for Fat PTA compared to repository bucks

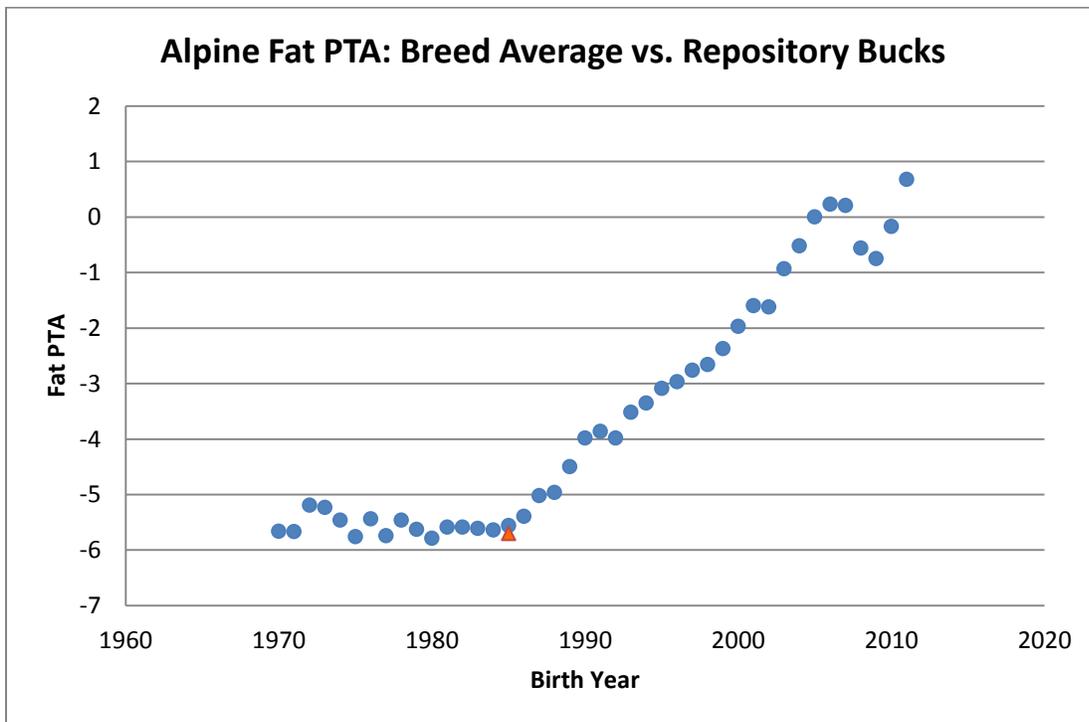


Figure 9. Alpine genetic trend for Protein PTA compared to repository bucks

