LaMancha 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.

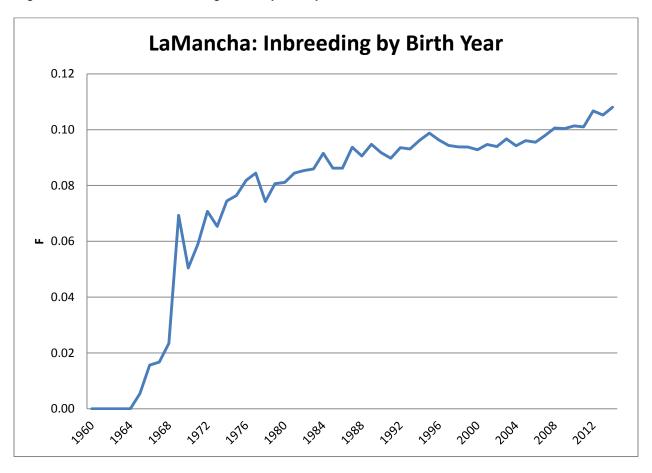
Table 1. Summary statistics for LaMancha

	LaMancha
Animals that are PB or AM	139,122
Full pedigree file (until all	178,144
ancestors are unknown)	
Unique sires	15,705
Unique dams	54,561
Mean inbreeding (F)	0.094
F range	0 - 0.64
Repository bucks	9
Clustered bucks	3,010

Pedigree & Inbreeding Analysis

Figure 1 shows average inbreeding by birth year for LaManchas. After a rapid increase in inbreeding early on, the rate of increase has been much slower over the past 4 decades.

Figure 1. LaMancha inbreeding trend by birth year



Numbers of registrations over time have steadily increased until 2013, as shown in Figure 2.

Figure 2. LaMancha goats registered by birth year

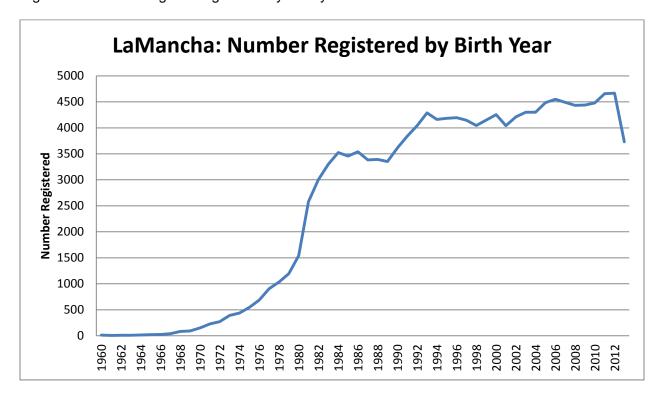
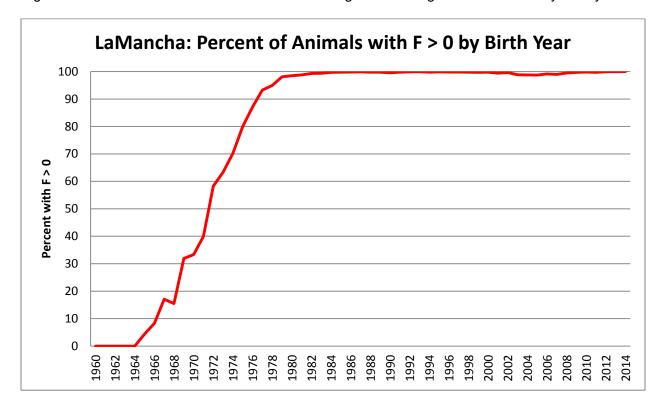


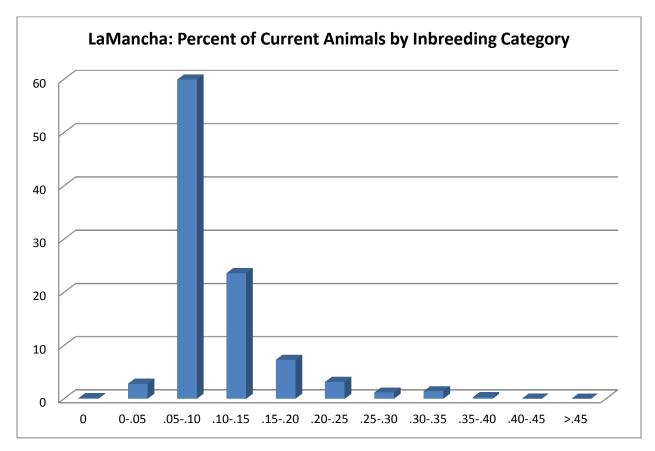
Figure 3 shows the percent of animals with an inbreeding coefficient greater than zero. More than 98 percent of animals have an inbreeding coefficient greater than zero since 1979.

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



The current population broken down by inbreeding category is shown in Figure 4. The majority of animals have a low to moderate inbreeding with few animals that are highly inbred.

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



For the LaMancha cluster analysis, 17 clusters were determined to represent the families within the breed. The clusters are represented in the tree diagram in Figure 5.

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

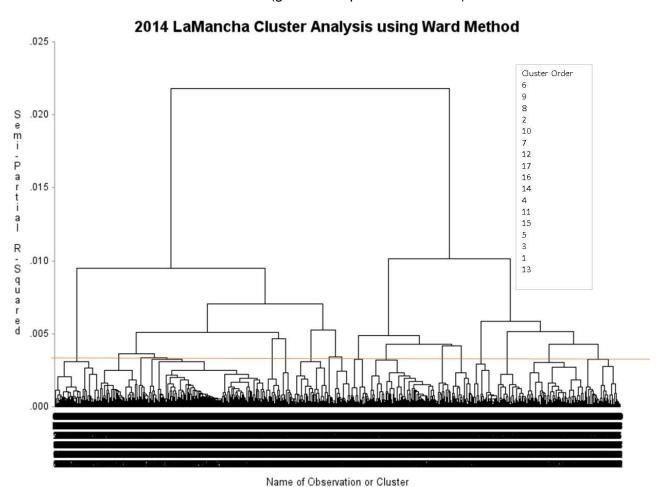


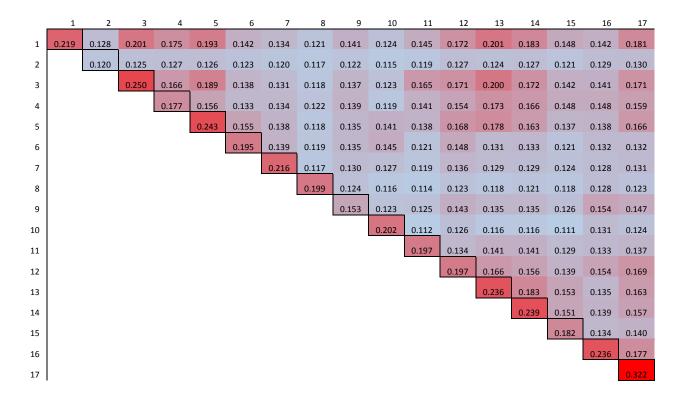
Table 2 summarizes the results of the within and between cluster relationships. Many of the clusters are as closely related as half-sibs (0.25). Repository bucks are represented in 5 of the 17 clusters.

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

Between Clusters						
	n	Mean	Variance			
	3010	0.143	0.002			
Within Cluster						
				Bucks in		
	n	Mean	Variance	Repository		
Cluster 1	305	0.219	0.004			
Cluster 2	625	0.120	0.001		4	
Cluster 3	159	0.250	0.007			
Cluster 4	361	0.177	0.003		1	
Cluster 5	126	0.243	0.008		1	
Cluster 6	240	0.195	0.005		1	
Cluster 7	71	0.216	0.009			
Cluster 8	54	0.199	0.008			
Cluster 9	205	0.153	0.003		2	
Cluster 10	80	0.202	0.008			
Cluster 11	76	0.197	0.009			
Cluster 12	181	0.197	0.005			
Cluster 13	190	0.236	0.006			
Cluster 14	100	0.239	0.009			
Cluster 15	116	0.182	0.007			
Cluster 16	88	0.236	0.008			
Cluster 17	33	0.322	0.010			

Figure 6 shows the within and between cluster relationships; the off-diagonal showing the between cluster relationships is mostly blue, indicating low relationships while the diagonal is mostly red, indicating higher relationships. This indicates the cluster analysis has done a good job of partitioning animals into clusters.

Figure 6. Within and between cluster relationship matrix for LaMancha



The genetic trends for Milk, Fat, and Protein PTA are plotted against the repository bucks in Figures 7, 8, and 9, respectively. Although PTA are only available for 2 repository bucks, they represent opposite extremes for these traits, suggesting good genetic diversity within this small sample size.

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

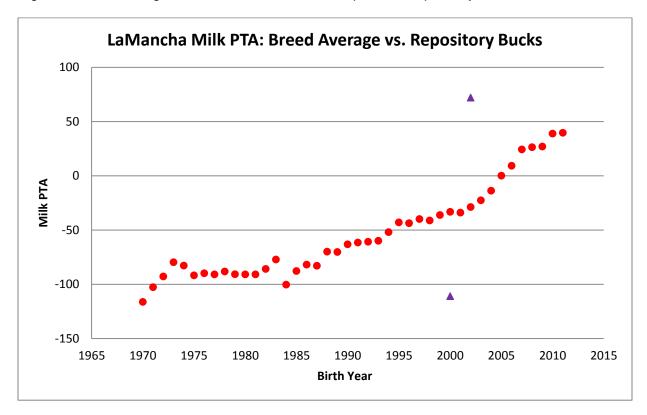


Figure 8. LaMancha genetic trend for Fat PTA compared to repository bucks

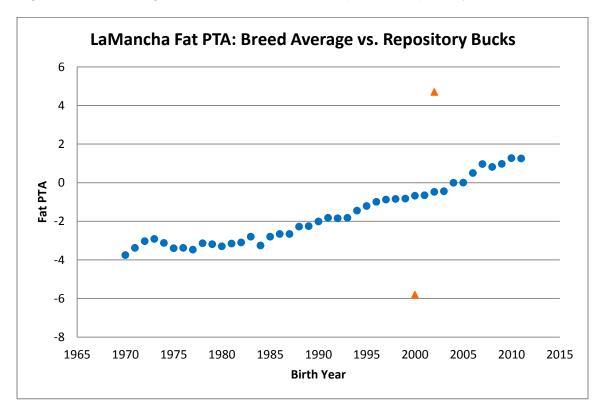


Figure 9. LaMancha genetic trend for Protein PTA compared to repository bucks

