Breeding Tactics For A Smaller North American Alpaca Gene Pool

Why do livestock breeders care about genetic diversity?

Genetic diversity allows for selective breeding to continue to improve the breed and to respond to environmental change

Insufficient genetic diversity increases the risks associated with inbreeding depression

The maintenance of genetic diversity comes at a price

“They’re All The Same Chicken”

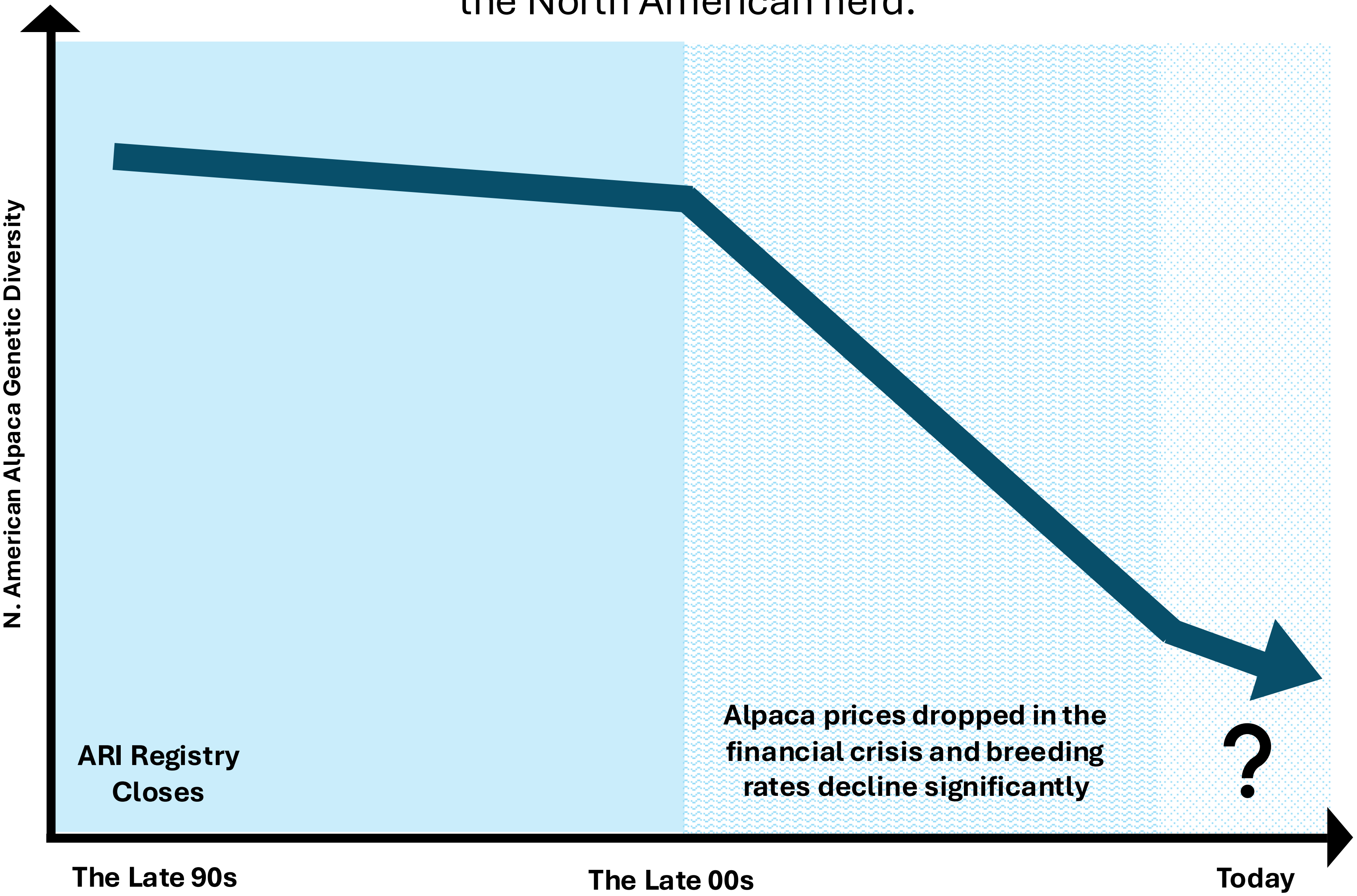
- This was one geneticist’s response to the idea of letting chickens die of bird flu to reveal those with immune mutations that helped provide resistance

- He was referring to the fact that selective breeding has optimized the production qualities of chickens in current industrial agriculture facilities but has resulted in much less available genetic variation

- This means less capacity for incremental adaptation

All the same alpaca?

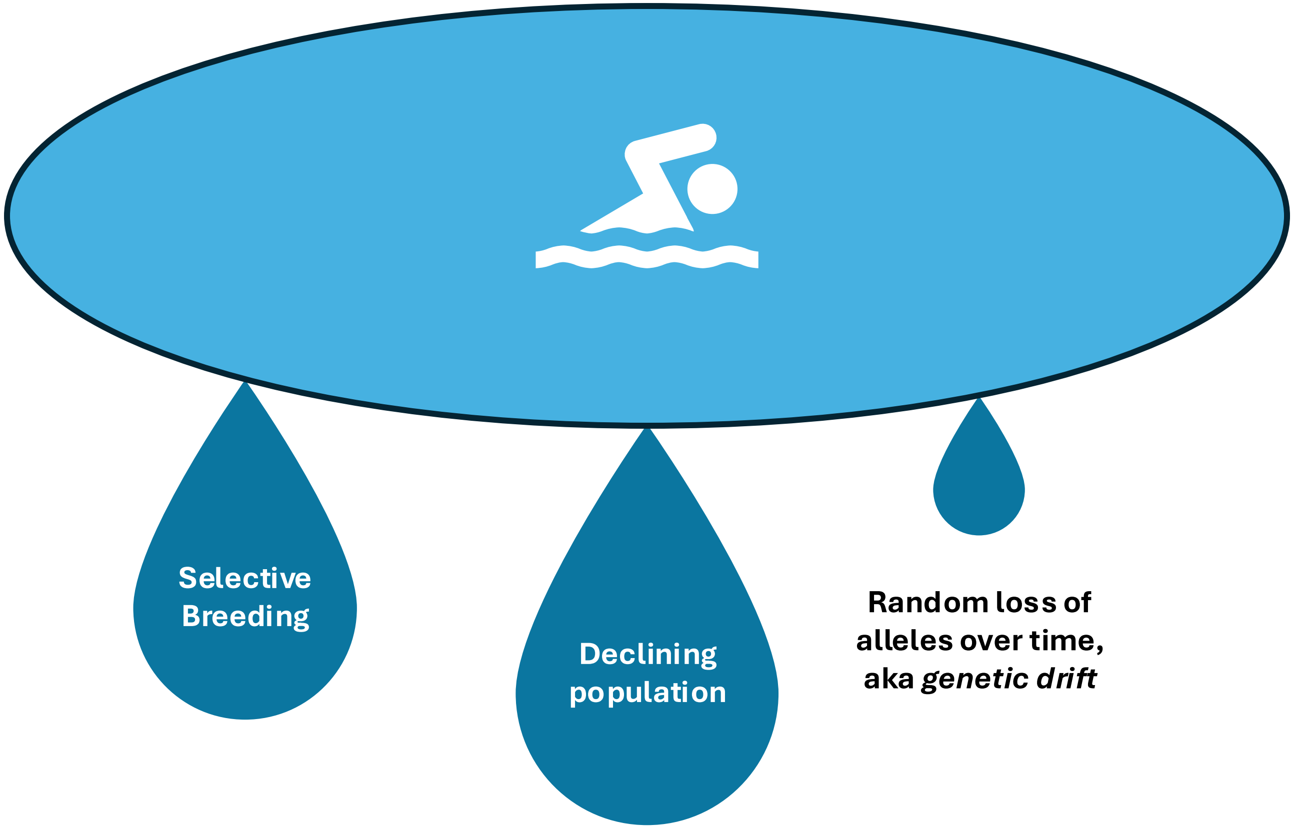
Not yet! But genetic diversity has significantly declined in the North American herd.



ARI Registry Closes

Alpaca prices dropped in the financial crisis and breeding rates decline significantly

Why is the North American alpaca gene pool shrinking?



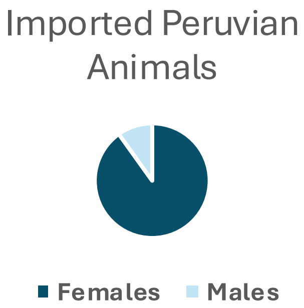
Selective Breeding

Declining population

Random loss of alleles over time, aka ***genetic drift***

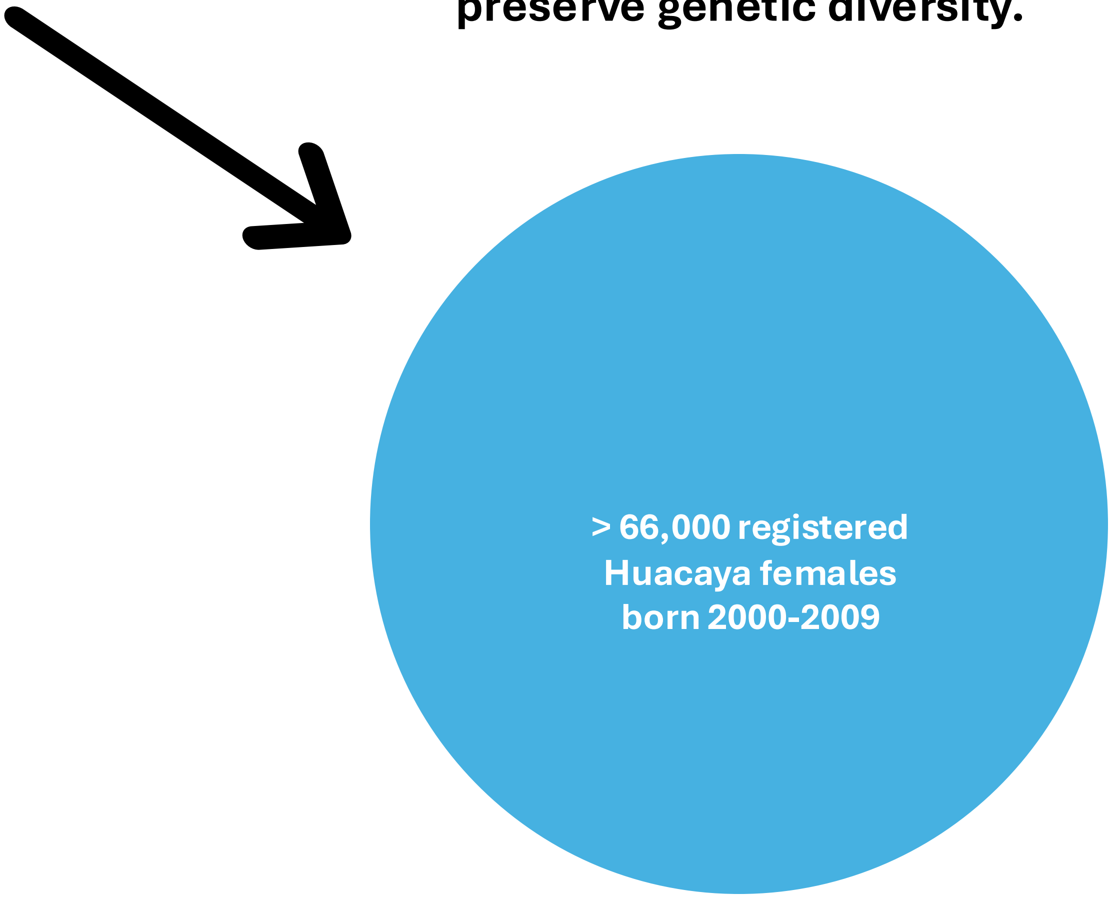
Plus, of course, we have kept the registry closed and not allowed in any outside genetics that could help refill it.

In the growth years of the North American alpaca industry, high population growth and limited selection pressure, especially on females, helped preserve genetic diversity.



Just under 2200 Huacayas were imported to North America from Peru in the 1990s. Ninety percent of them produced at least one registered offspring, and the most successful males had hundreds of registered offspring.

During the decade after the registry closed, alpaca values stayed at very high level and as a result little breeder selection pressure was placed on females. **The average female likely had more than four crias during her lifetime** and the breeding population grew substantially. Almost 40% of males born between 1995-2005 were also used for breeding.



> 66,000 registered Huacaya females born 2000-2009

Of the > 66,000 registered Huacaya females born 2000-2009, 62% produced registered offspring

But the decline in alpaca prices that occurred during the financial crisis and was sustained thereafter led to greater breeder selection pressure, including on females.

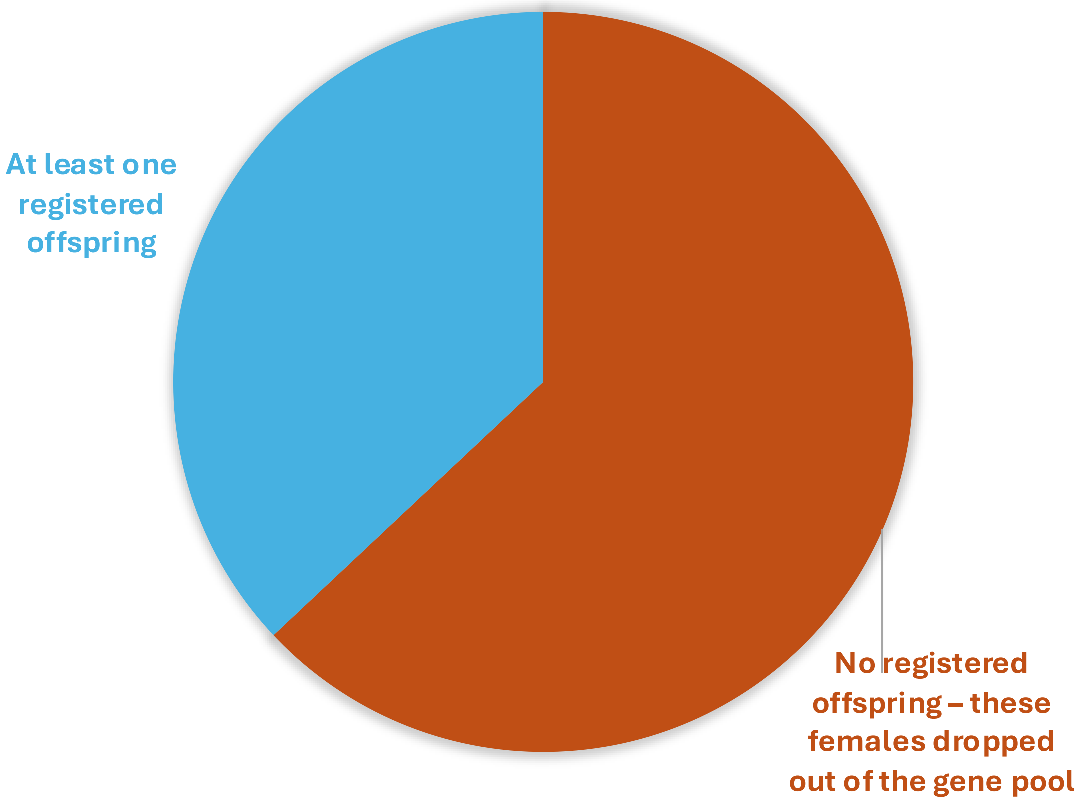
<42,000 registered Huacaya females were born in 2010-2019, and just 37% have produced at least one registered cria

Females born since the latter aughts have produced less than one cria on average and many have produced none at all. This has resulted in a substantial loss of genetic diversity. While most of this is due to selection pressure driven by changes in economics, accelerated genetic drift is also playing some role.

We've gone from breeding nearly every female to being very selectiv

<10,000 registered females so far in the 2020s

The genetic loss resulting the low utilization of females born from 2010-2019 has been significant



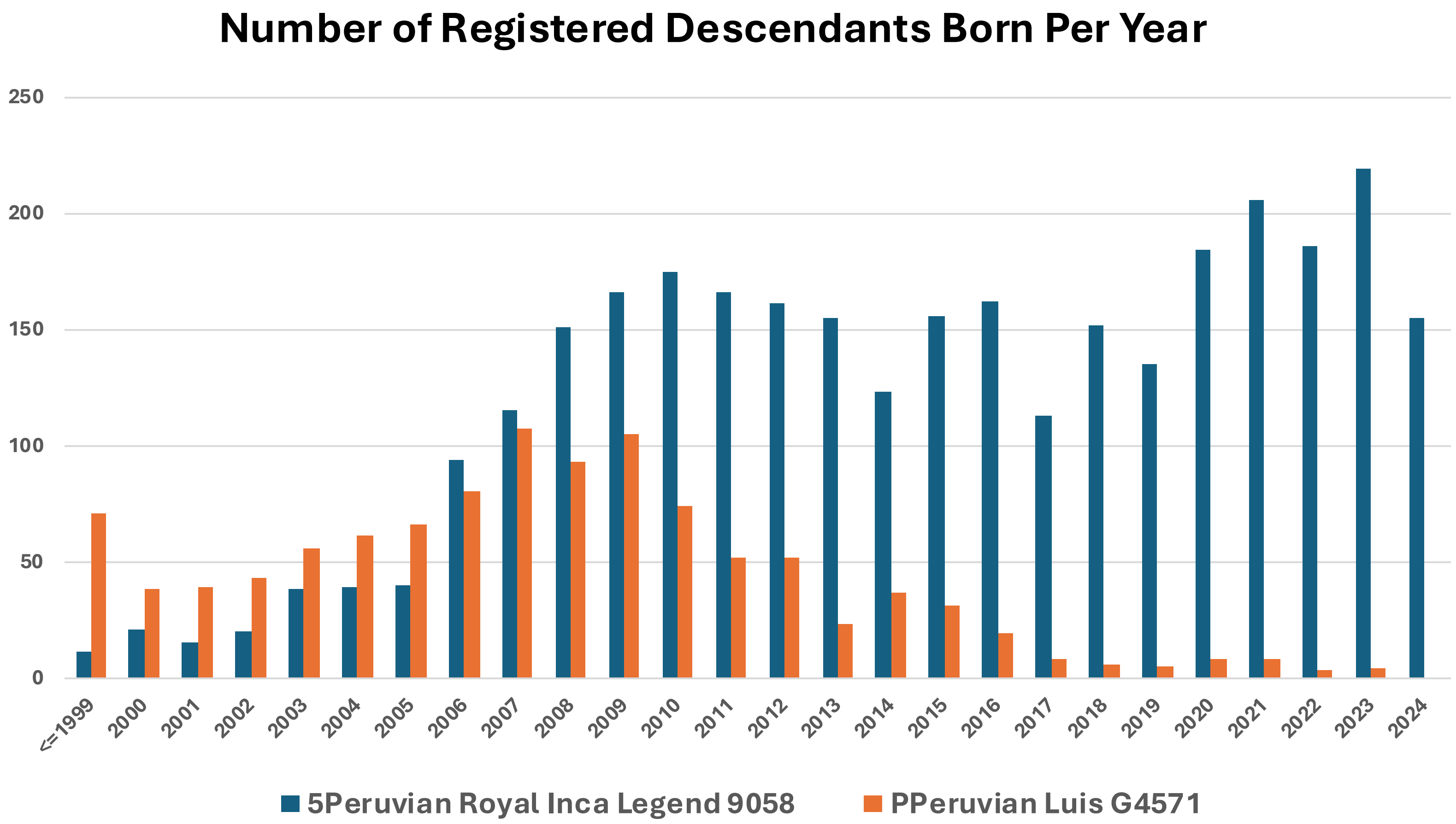
The shrinkage was not random but also the product of high selection intensity that favored some ancestors over others, further reducing available genetic diversity

The North American Gene Pool: Male Edition

Out of 314 males imported from Peru:

- 267 (85%) produced at least one registered offspring
- 116 (37%) produced at least 50 offspring
- 51 (16%) produced at least 100 offspring
- 12 (4%) produced at least 250 offspring, and together these 12 males produced over 3800 offspring.
- 3 males (1%) produced over 400 offspring: Royal Fawn (457), Legacy (419), and Hemingway (410).

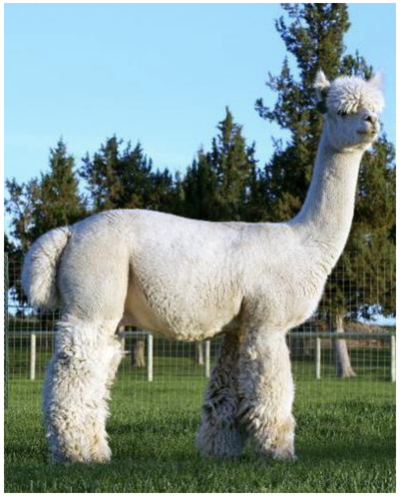
Goodbye Luis



Both males saw higher than average use as imported sires: Royal Inca Legend had 79 offspring and Luis had 64. And the descendants of both were used at similar rates until the late aughts. After that, the descendants of Royal Inca Legend were favored over those of Luis, and now Luis has been effectively eliminated from the North American gene pool.

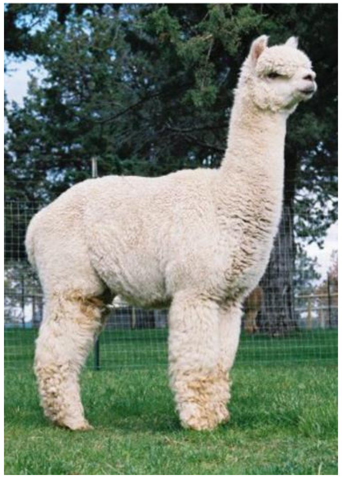
These four imported founders are especially well represented in today's gene pool

**6Peruvian Accoyo
Elite 5057 IMPR98**



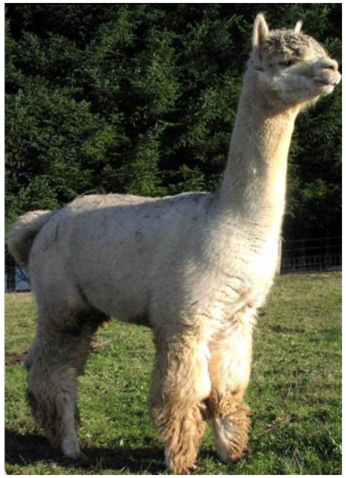
Contributed 8.8% of *the* ***most influential current sires'*** * collective genome, and 42% of his alleles are conserved just within that group. (89.0% are conserved in the Snowmass herd, and a greater percentage within the national herd as a whole.)

**4Peruvian Legacy
6016**



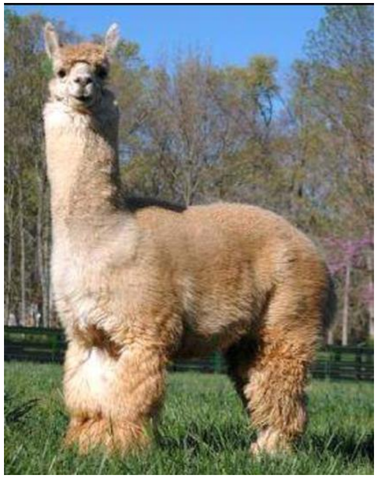
Contributed 7.3% of the most influential sires' genome, and 44% of his alleles are conserved in that group (99.7% conserved in the Snowmass herd.)

**Peruvian
Hemingway G171**



Contributed 5.5% of the most influential sires' genome, and 32% of his alleles are conserved in that group (99.9% conserved in the Snowmass herd)

**Ppperuvian Royal
Fawn 6014**



Contributed 4.7% of the most influential sires' genome, and 39% of his alleles are conserved in that group (58.9% conserved in the Snowmass herd.)

*** We'll get to what we mean by this on the next slides.**

What sire lines are having the biggest impact on the current generation? AOA makes it hard to be sure, but we can look two ways.

Recent Sires That Produced The Most Registered Crias

Sires Born 2010-2020	Number of Offspring
Snowmass Loro Piana	256
Snowmass Mr Sizlin Rose	210
Snowmass Divine Love	193
Snowmass Midnight Diamante	187
Accoyo America Polar Storm	163
Snowmass Oblivion	153
Sunset Hills Zagato	153
Snowmass Everlasting Paramount	145

The sires shown in the table at right have produced more than one-quarter of the younger males aged 4 to 8 who have produced at least 10 registered offspring to date.

Influential Sires That Produced The Highest Number of "Heavier Use" Sons Currently Aged 4 - 8

Influential Sires	No of Heavy Use Sons
Sunset Hills Zagato	7
Snowmass Oblivion	6
Snowmass Midnight Diamante	6
Snowmass Loro Piana	6
Snowmass Defiance *(b. 2009-183 reg. offspring, and sire of Snowmass Oblivion)*	6
CCNF Elixir *(b. 2011-141 reg. offspring)*	5
Avalon's Jacob Black *(b. 2010-132 reg offspring)*	4
CCNF Legionnaire *(b. 2012-92 reg offspring)*	4
Snowmass Enchanted *(b. 2011-114 reg offspring)*	4
Snowmass Mr Sizlin Rose	4

Either way you look at it the genetic story is similar

These founder males contributed a combined 31.7% of the genome of the eight sires born from 2010-2020 with the most offspring (in order of contribution):

- Elite
- Hemingway
- Pperuvian Caligula
- Royal Fawn
- Legacy

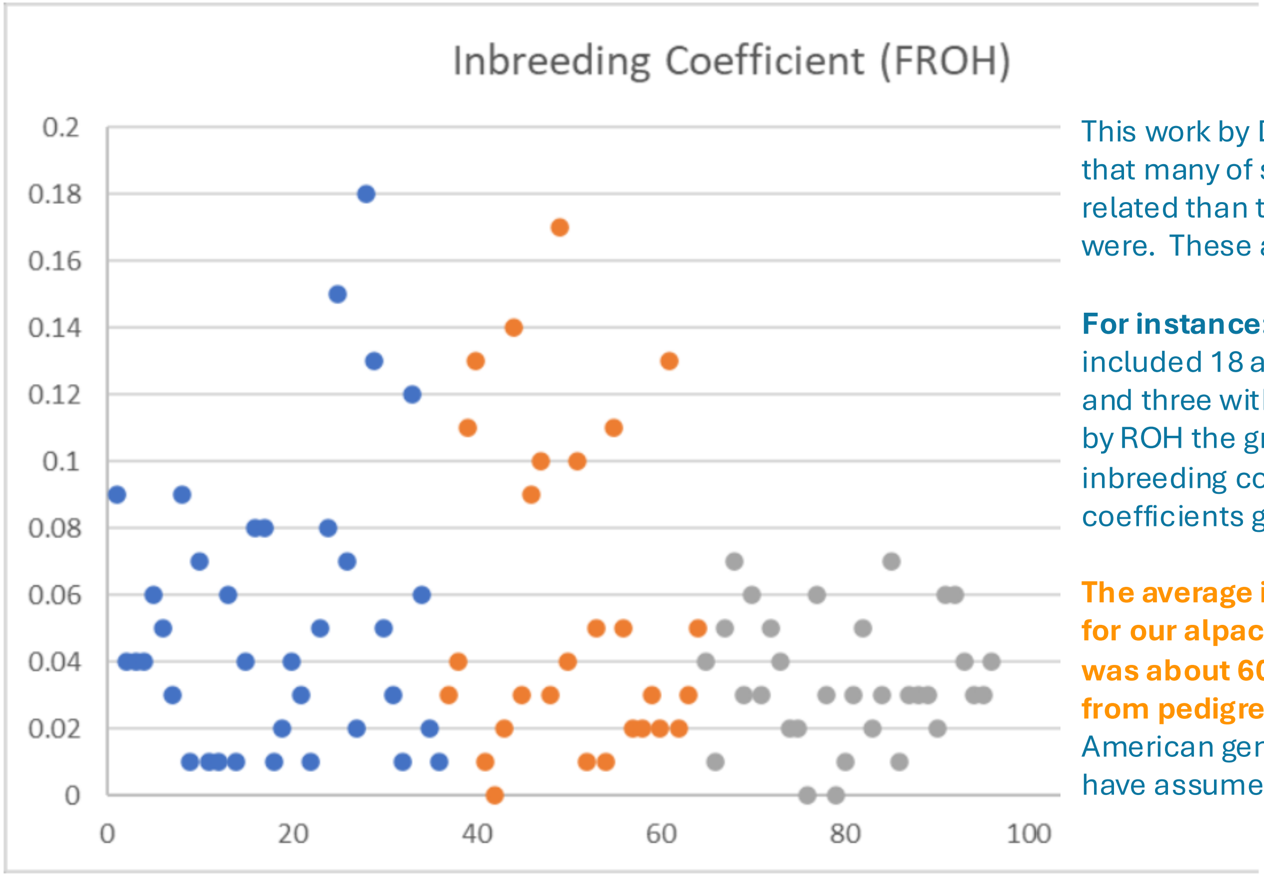
These founder males contributed a combined 30.1% of the genome of the 10 “most influential” sires producing the greatest number of heavier use sire offspring(in order of cont.):

- Elite
- Legacy
- Hemingway
- Royal Fawn
- 6 Peruvian Monarch

Out of over 300 sires imported from Peru, these males have become the most important foundation sires of the North American Huacaya breeding effort.

One wrinkle: Not all founders were unrelated. Some important ones may have been closely related.

Inbreeding coefficients estimated using runs of homozygosity for select Huacayas from three herds



This work by Dr Curt Youngs indirectly revealed that many of sample animals were more closely related than their pedigrees suggested they were. These animals' founders were related.

For instance: The blue/orange sample group included 18 animals with pedigree COIs of 0% and three with COIs above 12%. But estimated by ROH the group has just one animal with an inbreeding coefficient of 0% and seven with coefficients greater than 12%.

The average inbreeding coefficient estimated for our alpacas using runs of homozygosity was about 60% higher than the one estimated from pedigree data. This suggests our North American gene pool has never had the depth we have assumed.

From the report "Evaluation of an Alpaca DNA Microarray (Genomic SNP Chip) for Potential Use by the North American Alpaca Industry" prepared for the Alpaca Research Foundation by Dr. Curt Youngs, Iowa State University.

Why am I looking at cows?

- **Managing a breed's gene pool is an important shared task that livestock breeders undertake together, no matter what species they breed.**

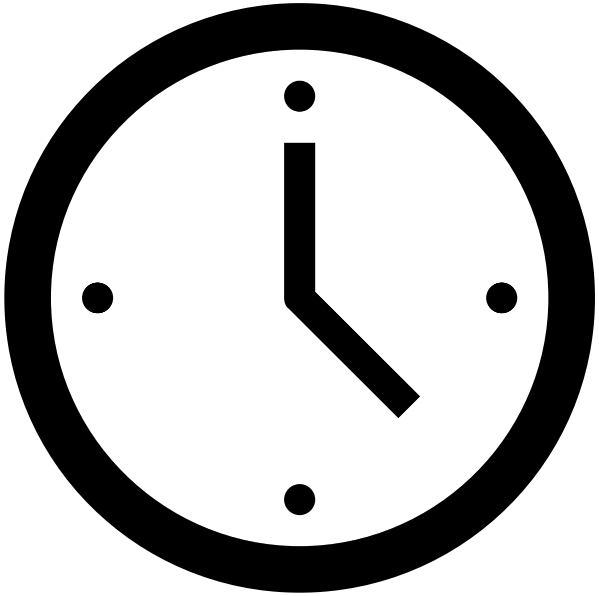
- **Providing good data on a breed's genetic diversity is an important job for breed organizations.**

- **Alpaca breeders will be reliant on pedigree-related measures because genotyping data is limited.**

Parameter	**Brown Swiss Cows Born In The US from 1990-2014***	**Snowmass alpaca herd as of March 2025**
Total unique ancestors		3315
Reference population	922333	1285
% Inbred animals (COI>0%)	91%	93%
Number of founders (f)	96696	502
Effective number of founders (fe)	63.6	35.6
Effective number of founder genomes (fg)	20.3	27.5
Number of of ancestors explaining 30% of the gene pool	4	4
40% of the pool	8	7
50% of the pool	13	10
60% of the pool	20	14
70% of the pool	36	24
80% of the pool	82	42

* Wirth A, Duda J, Distl O. Genetic Diversity and the Impact of the Breed Proportions of US Brown Swiss in German Brown Cattle. Animals (Basel). 2021 Jan 11;11(1):152. doi: 10.3390/ani11010152. PMID: 33440788; PMCID: PMC7828010.

It’s time to start thoughtfully managing genetic diversity in the North America alpaca herd



- Historically, genetic diversity in the North American herd has been supported by
  - the requirement of live cover combined with the geographic distribution of alpaca breeding operations
  - the lack of genomic information to drive more intense selection
- However, we are now in the same boat as livestock breeders working with more intensively bred breeds because
  - Our founding population was small
  - Some key founders were related
  - ***Most importantly, the population of breeding animals has significantly declined in recent years***

How should this influence our individual business decisions?

Three things we should do

Use more males

Manage herd kinship to a target level that is both supports both business health and genetic diversity

Press AOA to produce more information to help breeders exploit population-level data in their business planning

Next: How to make these efforts pay

Use More Males

Using more males helps us retain genetic diversity even when overall birth rates are low

- Maintain selection pressure and turn this into a business win by being a data expert. Selection pressure can be kept high (even increased, given our industry's current inefficient use of information) by using <u>all</u> of the genetic and production data we have available:
    - EPDs and other pedigree- and phenotypically-derived information
    - Color genotyping
    - Comparative farm-based production records

- Love your sire? Fine. Rotate his sons (and their dams' genetics) into production more quickly.

Longer Term Strategies For Using More Males

- **<u>Plan</u>** to rotate through a long-term sire roster, using each male for a couple of years and then moving on to either his sons (if you produce your own sires) or a new male from outside of your program. Think about how this plan should affect your current breeding decisions as well as the price you are willing to pay for outside males.

- Keep an eye out for higher quality, proven older males with good production records. These males are often priced very competitively relative to younger animals and can help you maintain both selection intensity and genetic diversity more affordably.

- Consider supporting opening the AOA registry to imported males
    - Great males makes <u>all</u> females more valuable, so everyone benefits
    - More pedigree diversity in high quality males will mean less tension between trait improvement and maintaining diversity

Help maintain selection accuracy and minimize the cost of maintaining diversity by increasing what you know about your sire prospects' dams

- Is she of very **high quality** herself? Would you use her as a stud if she were male?

- Is she **phenotypically similar** to the sire of your sire prospect? The more similar they are with respect to their phenotypes (age- and environmentally-adjusted) the more likely the sire prospect is to be a consistent producer of those traits. This is helpful context to have.

- Has she **produced other offspring** (especially other sires) with production records you can evaluate?

- If she is closely related to the rest of your herd, is she so superior that you are willing to sacrifice genetic diversity in the herd to have more of her genotype in circulation ?

Managing Herd Relatedness: An Example From Our Herd

- Oblivion is one of our top herdsires. Although he has a COI of 0.0%, his *mean kinship* statistic reveals he is closely related to the rest of the Snowmass herd through his important sire (who produced 98 other offspring for us) as well as because he himself now has offspring in the herd.
- ***Mean Kinship: The average relationship of an animal with the rest of the population.***
- The table reveals that almost all of Oblivion's sons now working in the herd, as well as his three grandsons who have started breeding, are less related to the rest of our herd than is Oblivion. By shifting our production from Oblivion to his descendants, we are helping maintain genetic diversity in the Snowmass herd.

2025 Working Oblivion Sons and *Grandsons*	**Snowmass Herd Mean Kinship**	**Animal's COI**
Seven Solutions	*3.1%*	*1.6%*
Gullfoss	*4.6%*	*0.9%*
Defiant Rendezvous	5.0%	6.6%
Sub-Seven	5.0%	5.1%
Ideal Solution	*5.1%*	*3.6%*
Astrologer	5.1%	4.7%
Best Freedom	5.3%	2.1%
Dire Sraits	5.5%	2.4%
Marvelous Oblivion	5.6%	6.8%
Irresistible Oblivion	5.7%	3.7%
Global Solutions	5.8%	4.1%
Oblivion	5.8%	0.0%
Best Bet	6.1%	2.5%

For context, the average mean kinship of animals currently in the Snowmass herd is 3.9%

In the short run, maintaining a low average coefficient of inbreeding will help maintain genetic diversity in your herd. ***In the long run managing mean kinship levels directly will produce superior results and put less pressure on individual breeding decisions.***

You can ”eyeball” both in small herds, but for medium-sized or larger herds consider the following software options:

- **Zooeasy** – currently available for less than $6 per month for single-user accounts. Provides COIs, mean kinships, relationship matrices, and a host of other herd management options. May also be a substitute for other aspects of your existing herd management software.
- There are free programs that will calculate COIs from pedigree data files, including on prospective pairings. Some provide more detailed herd- or population-level analyses as well. These take a little more technical know-how to set up and use.

Coefficients of inbreeding, mean kinships, or both?

AOA: Help Preserve American Alpacas!

It is the primary responsibility of any breed organization to provide its members with information that helps them maximize the success of the breed.

- Information about about the population of breeding age Huacayas and Suris, including trends in mean kinship and coefficients of inbreeding as well as identification of key ancestors and founders contributing to current populations could help breeders manage diversity and even monetize providing it.

- For example, an annual subscription for AOA to Zooeasy would cost the organization less than $3500 and would not only let AOA generate such a report but would also make Zooeasy available to all of us breeding members for our own herd analyses at no additional cost. Win win win!