

AGE (Across Herd Genetic Evaluation)

It's important, and we're doing it wrong.

By Stephen Mulholland, Ph.D.

When the AGE program was launched nearly 8 years ago I was very excited. I am a very big fan of proper quantitative genetics. Done right, a program like AGE can hugely speed the genetic development of a herd- it allows you to make very good and truly informed breeding decisions. We submitted data in one of the first AGE rounds.

Then, as I got to see how the AGE had been designed and implemented, my enthusiasm waned. Of late I have gotten highly critical of the AGE, and since I started expressing that criticism publicly, I was asked to write this article to explain what I think is wrong with the AGE as it now stands, and how we could do it much better.

What is the concept of the AGE?

At its most fundamental level AGE is about distinguishing the genotype (the genetic makeup) of an organism from its phenotype (what it looks like). AGE should allow us to separate and quantify the genetic strengths and weaknesses of a male or female; how likely it is to throw a cria with improved fleece fineness, staple length, or any other measurable and heritable trait.

The AGE analyzes the traits of offspring to determine the genetic contribution of the sire and dam. In theory it should distinguish between the animals that look good but throw mediocre cria from the “gems in the rough” which don't look exceptional and could never win a show ribbon, yet produce cria that are truly outstanding.

This is the so-called “breed value”, the strength and weaknesses of an animal in different traits. This information allows you to then pick the males and females with the best genetics, so that you can make the fastest improvements in your herd.

AGE is objective and quantifiable, and lets you pick the traits that are important to your own breeding program, while showing is subjective, and only provides limited information about an animal's phenotype.

What is the problem with AGE?

There is a very old adage of computer science: Garbage In = Garbage Out. What this means is that no matter how complex your mathematics, and no matter how powerful your computer, if you input meaningless numbers (garbage) you will get meaningless numbers back out. The results might look superficially good, with lots of apparent precision and attached to all sorts of fancy graphs, but if the input was flawed the output will never be good.

And sadly that's what we've done with the AGE system.

Let me explain some of the most fundamental problems.

1: The cria fleece is a terrible measure of alpaca quality

The AGE system is designed to take one sample from each animal entered, and that sample is usually the cria fleece. The problem is that the cria fleece is probably one of the worst possible choices for evaluating the genetic qualities that have been passed on to a cria. Why?

(a) The “fluff” the cria is born with is often very different than the fleece that grows in after they are born. Depending on the age of the cria at time of sampling this neonatal fleece can

play a large biasing role in the measured quality of the fleece. And the AGE has no provision to account for people who trim away this neonatal fleece. Furthermore cria fleece often coarsens considerably after birth. A sample submitted from a 6-month old might appear much finer than a sample submitted from the same animal when 12 months old.

(b) The amount of neonatal fleece can vary a great deal between cria, and this complicates annualizing the fleece traits. Measured staple length and fleece weight can be off by 30% in cria fleeces due to this contribution. The AGE can't account for this, so all the reports it produces of fleece weight and staple length heritability and variability are rendered meaningless.

(c) Cria fleece traits can have no relation to the adult fleece traits (particularly mean micron, SD/CV, and crimp structure). We should be breeding animals that give high quality, commercially valuable fleeces for 10 or more years. Yet the AGE fails to provide valid information for such traits.

Let me provide an example from our own herd- two of our female progeny, “M” and “C”. They both came from very similar dams (this is important, we'll get to more on this later). They were both black, and had very similar life conditions (health, body score, time of first mating, etc. All these are important, and AGE should do a better job at requiring such data to get more meaningful results). The first (cria) fleece for both these girls was taken at 12 months, and was 20 micron. AGE would consider them to be genetic equals, and rate their sires and dams accordingly. But if we wait 2 more years we find that by the third fleece “M” is still 20 microns, while “C” is now 32 microns. These are very different animals, with very different underlying genetics, yet AGE cannot detect such differences.

Based on AGE data you cannot determine the difference between animals that produce offspring with fine, high-quality fleeces and those that make carpet-grade fleece.

As a single data point AGE cannot tell you how animals perform over time. In our experience some animals produce quality fleece only in their first year, while other animals can go anywhere from 2 to 12 years before the fleece quality degrades significantly. This sort of information is absolutely vital for breeding commercially viable fleece production animals, and yet is totally ignored by AGE.

2: Without knowing about the dams the results are meaningless.

To the best of my knowledge, most users of the AGE are mainly interested in studs (sires). Using the progeny to find out what strengths their studs have, and making breeding decisions accordingly. Or they use the AGE rankings of a stud to advertise it, hoping for outside matings and financial gain. The problem is that the stud is only half the picture and by not taking the dam into account we can get a very incorrect assessment of the sire.

The dam provides half the genes, and dams are much more variable than sires (since sires are much more carefully selected).

Example: Let's look at two imaginary studs, “Able” and “Baker”, and try to see which one produces offspring with finer fleece. Each has ten offspring. The offspring of Able were all 23 micron, while those of Baker were all 25 micron. Which stud has better genetic fineness? With just this information you (and the AGE) would say Able.

But what if all the dams Able was put across were 18 micron, while all the dams Baker was put across were 40 micron? Able's offspring are five micron coarser than their dams, while

Baker's are 15 microns finer. Which stud would you say has the better genetic fineness now?

Without knowing the contribution of the dam it is impossible to accurately measure the genetic contribution of the sire. AGE does not require the dam's fleece data be entered, and if it were present (because she had been entered into AGE as a cria in a previous pass) then it would most likely be her cria fleece which probably has no relation to her actual adult fleece quality. If you don't take the adult fleece information of the dam into account, you cannot measure the true genetic contribution of any sire.

3: By ignorance or malice the AGE system can be distorted, and thus abused.

While the AGE system is itself badly constructed, the results it produces can be further distorted by the data input by the user. Because many people still trust the AGE, they can be badly misled and make poor breeding decisions.

(a) The AGE requires that all animals input be registered in the IAR (for establishing family relationships). Yet only slightly more than half of all males are now registered. In addition, the guidelines state that “All progeny born in an analysis year need to be submitted to AGE to ensure the AGE analysis is not biased by missing genetic data”, this is correct, yet there is no mechanism I know of to test that this is true. If people aren't registering their pet-boys, then those animals are being excluded from AGE calculations.

(b) Breed values don't take into account the number of progeny. Studs with very few offspring can have very distorted (not statistically valid) results. Furthermore, studs used for different purposes can end up with deceiving results in the AGE analysis. An “improver” stud might be used across very primitive, low-quality females, and thus look much worse than he actually is, while a “refiner” might only be used across the best females, and thus look better than he actually is (see the hypothetical example of Able and Baker above).

(c) The “cherry-picked” result can be very deceiving. This could be done by honest mistake, or as a deliberate attempt to mislead people as to the genetic quality of a stud male. If I enter a stud into the AGE, and carefully pick only a few progeny with the most fantastic fleece results (the product of either exceptional females, or just the occasional wild luck of a great cria that comes from otherwise mediocre parents), then I can have a stud that suddenly rates as one of the best in the country. And he might not be. Honestly, we can't know or tell how good he is, as AGE results are worthless (garbage in = garbage out).

I know people who are “doing it right”, and doing their best. They input all the progeny data, and carefully record many traits with good accuracy and precision. But they are trapped in a flawed system. They might be able to use their results effectively within their own breeding program on their farm to make better decisions, but their animals cannot be fairly and quantitatively compared to others within Australia or NZ due to the poor and inconsistent way in which the AGE data is collected and processed.

I would love to have a proper AGE-type system. On our farm we are trying to run a very good science-based system applying semi-quantitative genetic evaluation (within the limits set by statistical certainty in our relatively small herd size). But we find it nearly impossible to buy males, females, or stud services because almost no breeders keep enough or the right kind of records for us to assess the genetic worth of their animals.

It would be great if we could use an actual, functional, AGE-type system to go out and find the studs that are carrying the traits we want to breed for. It would make stud selection an informed choice, and not a trip to the used-car salesman (see my other article in the issue about selecting

animals and reading advertisements). If we all could make those kind of informed decisions, it would not take long before the quality of the NZ herd soared.

We need an AGE that:

- Accounts for the contribution of the dam
- Looks at more than the cria fleece, giving us information on the adult fleece production
- Can track progeny over time, so that we can breed for fleeces that stay good for longer
- Encourages people to participate, and enter more data for the benefit of all (meaning tracking more than just the traits any one individual is interested in)
- Can better sort the data by time and generation. (Did you know that we have no idea if, or by how much, the average alpaca has improved in NZ over the last 20 years? We can't consider ourselves a forward-looking industry if we're stumbling around blind.)

A new and improved AGE could be integrated with a new and improved registry system. (The current registry is filled with bad data, and has a number of design flaws. If the AGE is going to rely on the registry for relationship and other data, we need to make sure the registry is modern and functional, too.) It would be possible to provide web-based tools which would allow members to input lots of historic fleece information. This could let us test our new AGE to make sure it is working- we could see how the predicted breed values of the studs of the past match the actual outcome of their progeny generation upon generation. Yes, it would take hours of work for each of us to input all that historic data, but if it would allow us to make better breeding decisions, and thus save years of time improving the national herd, I think it would be time well spent.

We (the AANZ) could do an AGE-type system right, and we could do it ourselves. It wouldn't cost too much, and we would have an actual breed development tool under our control that could make us world leaders in alpaca genetics. It just requires the will. We have to fight the inertia of "we already have something, so it must be good enough". It's not. We need a good breed development system, and if we won't make a new one, we need to simply dump the old one. The AGE as it stands now is deceptive, it's not grounded in good science, and it has the disturbing potential to do more harm than good, especially if any bad actors decide to deliberately rort the system.