

STR to SNP: What's Coming in Genetics for the ABBA

Beginning in 2023, the 5-year DNA plan for the American Brahman Breeders Association outlines some changes to the parent verification process. In 2025, the plan also brings the requirement of having genotype data into the mix for ALL sires and embryo transfer dams of any calf that is to be registered. Having spent a few years in graduate school for breeding and genetics, I will be the first to tell you that the terminology can make your head spin. I hope to break it down to the basics here so that we can all understand the new processes we will be implementing.

Before I break down the differences, it's important to define what we're looking at. A string of DNA is made up of 4 bases: Adenine (A), Cytosine (C), Guanine (G), and Thymine (T). As we read the DNA at sequence level (reading every base of the entire string), it would appear as AGCTGCTAATGTAGTA, or something like that, for about 3 billion bases. When we read portions of that string, we find that individuals pass on changes (mutations) in their DNA string to their offspring in predictable ways. This allows us to compare these mutations and determine the degree of relatedness between two individuals, including parent verification. However, we can do this in a few different ways as new technologies have been developed.

The old way of doing things is to use a Short Tandem Repeat (STR). When we read these in the string of letters that make up our DNA from earlier, this particular form of mutation would look something like **AGCGCGCGCGCGTA**. This STR would get marked as a 6, because it has mutated over many generations to have 6 GC repeats in the string, as opposed to only 1 GC in the earlier string. A bull will pass on this STR, and we can use it to trace lineage. However, the number of repeats found in the offspring can be slightly different from the parent and thus, errors can be introduced. To combat this, we use around a dozen of these for parent verification, which has worked well for a long time. However, today we have tests that allow us to trace lineage much further back in time with greater accuracy than STRs do, and this has led to the phasing out of STR technology for this purpose.

Instead, a SNP, or Single Nucleotide Polymorphism, sometimes referred to as a "point" mutation, is used today. In the original DNA string above, a SNP would be read as AGCTGCTAAT**A**TAGTA. There is now an A where there used to be a G, and the SNP is read simply as "A". The change from a number to a letter is also important because the function of each of the four bases is different, but that's outside the scope of what we're talking about here. These single points also mutate at a much lower rate than STRs do, allowing us to find more mutations in common among distantly related individuals. We use around 100 of these for parent verification, so you can see how this additional information gives us better accuracy. This same technology is used in a genotype, but 50,000 to 150,000 SNPs are used in the panel, allowing us to read a large amount of the DNA string and make associations with animal performance. A genotype panel is then read using a combination of chemistry and math to tell us whether the animal is homozygous or heterozygous for a specific SNP. Again, an oversimplification, but it holds here. It's important to note that a genotype and parent verification test can be completed as part of the same test on the same DNA sample.

The reason that an STR isn't convertible to a SNP should be reasonably apparent when you understand that they aren't comparable in how they are read, even though they're closely related in terms of how we use them to determine parentage. Further, we can't use a parent's STR to determine a relationship to a calf with SNP data, which is why we are encouraging our breeders to upgrade their STR animals to a SNP profile this year. To help facilitate this, for 2023, the ABBA is offering a discounted rate, with a price of \$10 to upgrade an animal's DNA from an STR to a SNP profile and \$30 for a genotype. Please take advantage of this great offer today to avoid any DNA conflicts moving forward.

If I can be of any assistance in explaining this further, please don't hesitate to reach out to me at ajknowles@brahman.org