



A Case for Genotyping

When one thinks about January 2010, it seems like a lifetime ago. In some ways, it was. At this point in time, genotyping was introduced to Jersey breeders and our methods of evaluating Jersey genetics was forever changed.

Fast forward to July 2011, our knowledge base about genetics had greatly expanded. It was then the Board of Directors amended the association's abnormality policy to provide for the designation of undesirable genetic factors determined by analysis of DNA, and developed procedures for determining, labeling and publicizing carrier animals. This came in light of the strength of genomic evidence, genetic inheritance principles, and knowing other discoveries would follow based on the technology of the genomics era.

And how true that has been. In the years since, more than 500,000 Jerseys have been genotyped. This has allowed the discovery of many things, most recently a defective haplotype— Jersey Neuropathy with Splayed Forelimbs (JNS).

In November 2020, the AJCA Board of Directors was made aware of a new undesirable genetic factor. The precedent set previously allowed current leadership to review the facts and move quickly to amend the *AJCA Policy Regarding Undesirable Genetic Factors* to include the Description of Condition and Statement of Designation Procedures for JNS. (see page 25)

Now, what does this mean for Jersey breeders? Simply put, genotyping provides a wealth of information, not the least of which is verifying parentage. The results are more accurate evaluations for use within the herd for management decisions and matings. Genotyping advances the potential rate of genetic gain across the Jersey breed.

Most importantly, genotyping increases our collective ability to provide stewardship for the Jersey breed.

In the instance of JNS, it took several breeders who recognized their responsibility and the importance of reporting unusual conditions to the AJCA. The combined efforts and support of those Jersey breeders, AJCA as your

breed association, veterinarians and pathologists in various states and geneticists at USDA-ARS-AGIL and CDCB to investigate, document, research and identify the new undesirable genetic condition JNS. Together, we have been successful in identifying the condition, its cause and now utilizing tools for minimizing the economic impact of JNS.

About 6% of genotyped Jerseys are carriers of the JNS haplotype. When the JNS haplotype is inherited from both parents, the affected calf cannot stand. The calf is a total loss. The good news is we have tools available to manage the potential losses.

When considering females sired by carriers, genotyping quickly adds value back to the equation. Remember, only half of carrier progeny will inherit the JNS haplotype. A simple genomic test will identify the carrier status of each female and you can proceed with mating those tested free of JNS (JNSF) as you normally would. For designated carriers (JNSC), mindful matings can arrest the impact of JNS in a single generation.

The likely odds of an affected calf from a Carrier to Carrier mating is 25%. The AJCA tool JerseyMate™ eliminates known Carrier to Carrier matings. For untested females JerseyMate™ uses an approach that discounts potential matings by accounting for the probability of inheriting two copies of JNS. Pedigree information is used in lieu of genomic results and is not nearly as effective as a genomic test would be.

The economic impact of a lost calf is estimated to be \$150. For example, if the probability of an affected calf based on pedigree is 20%, a reduction of \$30 would be applied to the value of the potential calf. In most cases, there will be higher-valued matings JerseyMate™ will select and recommend.

BullsEye is another AJCA tool that allows you to sort bulls by carrier status to lower the chance of mating a Carrier to a Carrier. It is as simple as checking a box when sorting the bulls and eliminating JNSC sires from your selection.

The AJCA is here to help add to your bottom line. Put all the tools to work for you in managing your herd. There has never been a clearer case for genotyping.

