

TALKING POINTS

Oppose the proposed Scrapie Rule change.

An accelerated scrapie eradication was initiated in the early 2000's at the request of the sheep industry. The program has accomplished its objectives and has for practical purposes been eradicated from the US. The US has not had a classical case of scrapie for 5 years (case in Pennsylvania in 2019) and the last case of scrapie in Texas occurred in 2016. It was in a Southdown in north Texas that this regulation change would not have prevented.

The last case of scrapie in Texas was in 2016. The revised rule is not necessary and will impose a significant cost on Texas producers. It will severely restrict the availability of superior breeding stock available to Texas producers.

Current Texas import regulations requiring genotype testing on BF sheep are among some of the most restrictive in the Western Sheep states. Wyoming is similar to ours in requiring genotype testing on blackface but not whiteface. However, Wyoming Wool Growers are considering petitioning their animal health division to remove their blackface genotype requirement. Most other states (Montana, Idaho, Utah, Mexico, Colorado, Oregon, California, North Dakota, South Dakota, Minnesota, Ohio, Kansas, Oklahoma, Tennessee, and Indiana do not require genotype testing.

When the program began, a higher prevalence of classical scrapie cases were identified in the blackface breeds. In fact, I believe there has only been a couple of cases of classical scrapie identified in purebred wool whiteface breeds. Initially, these data were used to support additional surveillance and genotype testing requirements for those breeds and their crosses. Because of the higher prevalence of scrapie in blackface breeds of sheep, genotype testing has been a priority for those breeders. The prevalence of classical scrapie has not increased in whiteface wool breeds of sheep but has decreased substantially in blackface breeds and their crosses to the point that the prevalence of scrapie in the US sheep flock is basically too small to measure. These data support the reduction of genotype testing requirements rather than expanding them.