Prevalence of scrapie resistant genotypes in U.S. goats as part of the NAHMS Goat 2019 Study

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Introduction

Scrapie is a transmissible spongiform encephalopathy that infects sheep and goats. Scrapie disease in the U.S. greatly impacts the sheep and goat industry with annual economic losses of approximately \$10 to \$20 million. Research shows that an S or D allele present at codon 146 or a K allele present at codon 222 have a longer incubation period (4-5 times longer) following oral or intracerebral inoculation in goats with scrapie than the wildtype alleles (N-146 or Q-222), and animals with resistant alleles remained disease-free throughout the study period. The objective of this study was to estimate the prevalence of resistant alleles in U.S. goats to assess the risk of goat scrapie occurrence.

Materials and methods

NAHMS is a nonregulatory program within USDA APHIS VS, that was initiated in 1983 to collect, analyze, and disseminate data on animal health, management, and productivity across the U.S. In 2019, NAHMS conducted its second national cross-sectional study to collect health and production information about the U.S. goat industry.

The NAHMS Goat 2019 study included 24 of the top goat-producing states, representing 76.6% of U.S. goat operations with 5 or more adult goats.

Producers were interviewed by federal or state veterinary personnel from September through March, 2020. Operations that completed questionnaires were invited to participate in scrapie genotype testing. Participating operations had blood collected from up to 15 unrelated goats that were at least 15 months of age. Genotype testing at NVSL was completed using PCR. Weighted descriptive estimation was carried out using SAScallable SUDAAN software which accounted for complex study design.

Results

Scrapie genotype testing was completed on 6,029 clinically normal goats from 654 operations. The primary production type of the sampled operations were 45.8% dairy, 34.0% meat, and 20.2% other. The sampled goats represented 19 different breeds, with the most common being crossbred (17.8%), Boer (16.8%), and Nubian (11.9%). A higher percentage of does were sampled (82.4%) than bucks (17.6%). At codon 146, 33.3% of U.S. goats had a resistant allele (had S or D genotype), with 22.0% being NS (carrying the S resistant allele). Relatively high percentages of Savannah, Spanish, Boer and Nubian goats (65.5%, 42.6%, 47.0%, and 38.6%, respectively) had at least 1 resistant allele at codon 146 (NS or SS). A higher percentage of does (33.3%) carried resistance alleles compared with bucks (23.6%). In this study, 72.2% of all operations had any goats with a resistant allele at codon 146. A higher percentage of meat operations (88.9%) had goats with a resistant allele compared with dairy and other operations (51.0% and 57.6%, respectively).

At codon 222, only 0.6% of sampled goats had a resistant allele. All of these goats had 1 copy of the K allele and 1 copy of the Q allele. Overall, 2.1% of operations had any goats with a resistant allele at codon 222.

If the genotypes at codons 146 and 222 were both considered, 33.8% of goats in the U.S. possessed at least 1 resistant allele to scrapie, with 34.7% of does and 24.4% of bucks having any resistance. These goats were spread across 72.8% of operations. Resistant does were found on 69.5% of operations and resistant bucks were found on 21.3% of operations.

Significance

Resistant alleles are found on most operations across the U.S., but the percentage of goats with resistance represents a relatively low percentage of goats. Therefore, testing for resistant genotypes is important to help eradicate scrapie. Knowing which bucks are resistant to scrapie will allow producers to breed resistance into their herd faster, which ultimately will increase the scrapie resistant genotypes seen in goats throughout the U.S. Implementing a testing and breeding protocol selecting for scrapie resistance will help minimize the risk of goats developing scrapie and help to eradicate scrapie in the U.S.

