UNITED STATES ANIMAL HEALTH ASSOCIATION

2026 Resolution
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RESOLUTION NUMBER: 21 APPROVED AS AMENDED

SOURCE: COMMITTEE ON WILDLIFE

SUBJECT MATTER: Access to Technology Used to Generate Genomically Estimated Breeding Values for Chronic Wasting Disease

RESOLUTION:

The United States Animal Health Association requests that the United States Department of Agriculture (USDA), Animal and Plant Health Inspection Service (APHIS), Veterinary Services (VS) work directly with USDA-APHIS Wildlife Services' National Wildlife Research Center and the USDA Agricultural Research Service to develop in-house laboratory and analytical capacity to independently perform genetic analyses related to chronic wasting disease (CWD) susceptibility, including genomically estimated breeding values (GEBVs) and prion protein gene genotyping.

BACKGROUND INFORMATION:

It is well known that genetic variation in the prion protein gene (*PRNP*) of cervids influences chronic wasting disease (CWD) pathobiology. For example, findings from multiple research groups have demonstrated that genetic variation in *PRNP* (e.g., at codon 96) in white-tailed deer influences CWD infection and disease progression. Specifically, white-tailed deer homozygous for serine at codon 96 (i.e., 96SS) have reduced susceptibility to CWD, an extended incubation period, and delayed disease progression relative to wild-type deer (i.e., those homozygous for glycine at codon 96; 96GG). Similar relationships between the host prion protein, encoded by *PRNP*, and prion infection exist across multiple prion diseases, and these relationships have been leveraged in disease control programs in conjunction with strong surveillance and culling strategies, such as the scrapie eradication program. However, no *PRNP* genotype provides complete resistance to CWD.

The lack of a fully resistant *PRNP* genotype has led to the exploration of other genes and the development of genomically estimated breeding values (GEBVs), which have been widely promoted for their potential to predict CWD status and aid in CWD control and prevention. Currently, CWD-specific GEBV scores can be obtained only through the North American Deer Registry from a single researcher funded by United States Department of Agriculture (USDA), Animal and Plant Health Inspection Services (APHIS), Veterinary Services (VS). This researcher has indicated that USDA will not be permitted to access his data or the genetic array used in the development of the GEBV (see Tabor et al. 2024). This

limited access has prevented the broader scientific community from adequately and independently replicating or further investigating this research. As such, the lack of access limits progress toward addressing a prior United States Animal Health Association (USAHA) resolution passed in 2024 (USAHA Resolution 21, *Controlled Study to Evaluate Genetic Influence on CWD in White-tailed Deer*), which called for additional scientific investigation of GEBVs before their use in a management framework. Despite the lack of transparency and the need for additional research, programs using GEBVs to inform breeding decisions for the management of farmed white-tailed deer operations are being pursued by state and federal agricultural agencies, universities, and producers. Despite significant federal financial support for this work through USDA-APHIS-VS *Farmed Cervid CWD Management and Response Activities Cooperative Agreements* (approximately $10.7 million from 2021 through 2025, representing 48 percent of such funding), prion scientists and federal and state agency personnel do not have independent access to the technology.

While the original goal of investigating GEBVs was to reduce CWD risk in farmed white-tailed deer, the effectiveness of applying GEBVs within a national CWD management and regulatory framework has not been thoroughly investigated. Furthermore, despite the lack of evidence supporting the application of GEBVs in free-ranging white-tailed deer, legislation has been passed in Oklahoma allowing the release of farmed deer with specific genetic profiles (i.e., 96SS and GEBV < -0.056) into the wild. Additional lobbying and legislative efforts have occurred in other jurisdictions seeking to incorporate GEBVs into CWD management frameworks for farmed cervids. The momentum behind predictive genetics as a CWD management and prevention tool in white-tailed deer is based on two proof-of-concept studies partially funded by USDA-APHIS-VS; however, the lack of transparency and the inability of independent researchers to access the underlying GEBV methodology have limited independent scientific evaluation. Independent researchers have not been able to replicate the work or use GEBV scores in study designs to further investigate the potential utility of GEBVs. For this tool to be properly evaluated for potential use in a national regulatory and management framework, it must be more broadly accessible for independent scientific investigation.

Greater access to the analytical tools, including the specific single-nucleotide polymorphism (SNP) array, and the algorithmic tools used to generate GEBVs would facilitate diverse research approaches to investigating the utility of GEBVs and would increase scientific transparency and trust.