From the Editor – As I write this note for the summer newsletter, I’m actually “stuck” in Italy! I was provided the opportunity to attend a conference discussing dairy crossbreeding. It has been an interesting experience that led to some broad conversations regarding dairy cow production and resiliency within variable environments and markets. Of course, the trip would not have been complete without opportunities to visit several dairies in the Parma region along with Parmigiano Reggiano cheese plants, a balsamic vinegar facility, and a water buffalo herd. It is always eye opening to see different management styles across the spectrum from calf-rearing to parlor structure. Italian dairies certainly deal with many of the same challenges as we do in terms of managing bedding, nutrition and heat-stress, and overcoming challenges associated with labor availability, drought and regulatory oversight. All-in-all, it has been a great opportunity to challenge my assumptions and broaden my perspective regarding “best practices”. Aside from the inevitable hiccups involved with international travel, I cannot think of a better way to expand one’s viewpoint and make new friends along the way than to reach across international borders if the opportunity arises. And of course, if that opportunity happens to coincide with some amazing Italian cuisine it is all the better!

Given that I have been immersed in conversations regarding crossbreeding and genetics over the past week, I thought I would start this newsletter off with a couple of articles related to those topics and the future of omics technologies such as genomics, proteomics, transcriptomics, metagenomics, and metabolomics. This is definitely a case of “the future is now” considering the rapid developments and applications of what until recently was considered emerging technology.

Aside from that, I would like to thank the other contributors to this newsletter (Drs. Itle, Hoch, Broughton-Neiswanger, and Sischo) who were willing to share their expertise and insights. I hope that everyone had a wonderful 4th of July weekend and look forward to catching up with many of you in the coming weeks and months.
One of the presenters at the conference mentioned above was Dr. Julie Clasen, who is currently a post-doc at the University of Aarhus, Denmark. She delivered a talk regarding herd profit and the genomic prediction of crossbreeding which summarized findings from two of her recent publications (J. Dairy Sci. 103:514–528; J. Dairy Sci. 104:8062–8075). Dr. Clasen pointed out that although dairy crossbreeding is emerging, the economic and genetic consequences of combining it with other breeding tools are somewhat unknown. Her work has explored using numerous scenarios that are modeled using stochastic simulation (SimHerd Crossbred—operational returns; ADAM—genetic returns). Scenarios have included managing pure-breeding or terminal crossbreeding using Swedish Red (SR) or Swedish Holstein (SH) as an initial breed. Although terminal crossbreeding resulted in lower genetic returns across the herd compared with the corresponding pure-breeding scenarios, it was compensated by a higher operational return. The increased profitability was mainly due to improved functional traits, especially fertility. This led to an extended use of beef semen within the crossbreeding strategies that earned more annually per cow from selling live calves for slaughter. Interestingly, milk production was similar between pure-breeding and terminal crossbreeding, and only decreased 1-2% in rotational crossbreeding. Dr. Clasen’s results indicate that crossbreeding between SH and SR can be profitable in both conventional and organic Swedish herds; however, some aspects remain to be investigated such as the economically optimal breeding strategy, genetic improvement, and transition strategies.

Closer to home, Hazel et al. at the University of Minnesota also have investigated the herd life, lifetime production, and profitability of Viking Red-sired (VR) and Montbéliarde-sired (MO) crossbred cows compared with their Holstein (HO) herdmates (J. Dairy Sci. 104:3261–3277). The first 2 generations from a 3-breed rotation of the VR, MO, and HO breeds were compared with their HO herdmates in high-performance commercial herds in Minnesota in a 10-yr designed study. Production of milk, fat, and protein during lifetimes of cows was estimated from test-day observations, and the lifetime profit function included revenue and cost. Revenue was from production, calves, and slaughter of cull cows. Costs were attributed to feed during lactation, lactating overhead, dry cows (including feed cost during dry periods), replacements, health treatments, inseminations, fertility hormones, pregnancy diagnosis, hoof trimming, and carcass disposal. The 2-breed and 3-breed crossbreds had an approximately 150 d longer herd life compared to their respective HO herdmates. In fact, approximately 29% of both the 2-breed and 3-breed crossbreds lived beyond 45 mo after first calving compared with approximately 18% of their respective HO herdmates.

Benefits from heterosis (hybrid vigor) have been reported in previous studies examining crosses of dairy cattle in the US and elsewhere. Advantages have been attributed to improved health, fertility, and income over feed costs. In the Hazel et al. study, this held true in that improved fertility, health, and herd life led to increased daily profit for the 2-breed (+$0.47; +13%) and 3-breed (+$0.34; +9%) crossbreds compared with their respective HO herdmates. The results of their study suggest that 3-breed rotational crossbreeding is a profitable alternative to HO purebreeding for high performance, confinement herds. Specifically, they demonstrated that VR, MO, and HO breeds may be well-suited for 3-breed rotational crossbreeding, because the 3 breeds have been historically selected for traits that complement each other well for use in temperate climates.
Future Considerations-Omics
By CS McConnel, Veterinary Medicine Extension

A primary reason I attended the conference in Italy was because of the research we do within the Field Disease Investigation Unit investigating long-term impacts of disease and livestock resiliency. Crossbreeding has been offered as one mechanism to enhance animal resiliency through hybrid vigor. This plays into the larger picture of novel breeding technologies and molecular technologies such as genomic selection, whole genome sequencing, and gene editing currently contributing tremendously to the selection and breeding of livestock species for sustainable improvement in productivity and profitability. Omics technologies such as genomics, proteomics, transcriptomics, metagenomics, and metabolomics offer powerful analytical and diagnostic tools that can be combined with molecular breeding for the accurate selection of animals for improved productivity. A recent article by Chakraborty et al. published in Frontiers in Genetics offers an excellent primer on the application of omics technology for livestock selection and improvement.

The authors point out that conventional animal selection and breeding methods were based on the phenotypic performance of the animals. These methods have limitations, particularly for sex-limited traits and traits expressed later in the life cycle (e.g., carcass traits). The advent of high throughput omics techniques and the availability of multi-omics technologies and sophisticated analytic packages have led to several promising tools and methods to estimate the actual genetic potential of the animals. The article goes on to provide an overview of various omics technologies and their benefits and limitations for animal genetic selection and breeding decisions.

The word ‘omics’ originates from the suffix ‘-ome’, derived from a Greek word that means “whole”, “all” or “complete”. The suffix “-omics” is frequently used to refer to a field of study in life sciences that emphasizes largescale high throughput data/information to understand life summed up in “omes”. The various omics tools that have been developed focus on proteins (proteomics), mRNA transcripts (transcriptomics), gene sequences (genomics), microbial diversity (metagenomics), epigenetic regulation of gene expression (epigenomics), metabolic profile (metabolomics), lipid profile (lipidomics), etc., of a particular cell, tissue, organ or whole organism at a specific time point. More recently, multi-omics has emerged as high-dimensional biology (HBD) for simultaneous study of genetic variations in biological systems at the genes, transcripts, proteins, and metabolites level.

Transcriptomic methods can be used to compare a biological response to different conditions or treatments or to assess physiological responses to external stimuli. To date, extensive research has been carried out in different livestock species using high-throughput RNAseq technology. In RNAseq technology, messenger RNAs are first randomly fragmented into small pieces by shearing and converted to a library of complementary DNA (cDNA) fragments. These cDNA fragments are then amplified and sequenced in parallel and mapped to a given region of the target genome. A count is then determined by the number of reads mapping to each gene which provides a discrete measure of the corresponding gene expression level, and the differentially expressed genes (DGEs) between two samples can be obtained. As an example, functional analysis of DEGs by Moridi et al., 2019, demonstrated that the immune and inflammatory responses were the most impacted pathways between purebred and crossbred cattle populations. RNAseq-based transcriptomic studies on animals of high- and low-genetic merit may be helpful for the selection and breeding of elite animals in the future to enhance health, productivity, and profitability.

On the other hand, proteomics allows analysis of all proteins in a particular cell, tissue, or organ at a specific time. The application of proteomics in livestock research has been limited in the past due to its high cost and lack of optimized protocols for various cell types in different species. Nevertheless, with advancements in new analytical methods and computational tools for the analysis of proteomic data, reports on proteomics studies
in animal science are increasing for understanding animal health status, and production and reproduction efficiency. In fact, as we continue our FDIU research this summer exploring the impacts of calfhood diseases we are incorporating both transcriptomic and proteomic analyses in an attempt to more clearly understand the duration and severity of preweaned calf respiratory disease. This corresponds with one of the major areas of interest in proteomics which is to identify robust protein biomarkers that might prove useful in disease surveillance, monitoring the health and wellbeing of animals, elucidating disease mechanisms, and assessing pharmacologic response to therapeutics. Proteomics can also be applied for different animal products post-harvest such as meat, milk, cheese, etc., to identify genetic variants with desirable traits for selection and breeding.

An emerging area in the application of omics tools is the comprehensive, qualitative, and quantitative study of all the small molecules in an organism (i.e., the metabolome). For example, potential biomarkers of milk yield and quality have been detected by studying the metabolome of different body fluids in dairy cattle. A particular advantage of profiling metabolites has to do with the potential to explore the impact of metabolism on systemic health, by monitoring the production and further metabolism of compounds present in the diet, digest, and plasma. Metabolomic studies on muscle and fat from cattle, pigs, and poultry have shown tissue and species-specific differences in metabolites. Ultimately, metabolomic tools can be combined with molecular breeding tools to increase the accuracy of genetic selection and livestock breeding. Given that genomic prediction to predict breeding values based on phenotypic, pedigree, and genomic data is insufficient to describe the genetic potential of animals, incorporating the whole-metabolomic data in the genomic prediction equation may play a crucial role in increasing the genetic gain by increasing the accuracy of selection.

The power of metabolomics is that it non-invasively detects subtle phenotypic changes, innate phenotypic propensities, and dietary responses in livestock research, breeding, and assessment through new varieties of bio-samples such as semen, amniotic fluid, saliva, urine, and feces. For example, given that the fecal metabolome reflects intestinal microbiota, cellular metabolism, and digestion/absorption of nutrients in the gut, the metabolites present in the feces might reflect everything from feed conversion efficiency to stress responses. Thus, metabolic profiling of fecal matter may be used to identify animals with “metabolic fingerprints” that are known to exist in animals of high feed conversion efficiency or tolerance to stress.

This leads us to metagenomics which involves the collection and analysis of genetic material (genomes) from a mixed community of organisms. This is an area of considerable interest in ruminants particularly regarding microbial communities in milk and the GI tract/rumen. Important applications of metagenomics range from feed efficiency and the inflammatory state in the digestive tract to generating information for genotype and environmental interactions for better control over management. To date, metagenomic studies in cattle and pigs have been used extensively to investigate the importance of the gut and mammary microbiome on feeding efficiency, immunity, and mastitis. Metagenomics has demonstrated that gut microbiota can affect feed intake, feed conversion ratios, production traits such as daily weight gain, immune stress, and the maintenance of intestinal homeostasis. Metagenomic studies have also revealed that the milk microbiome varies with health status (e.g., mastitis, endometritis, bacteremia, etc.), age, parity, lactation duration, and feed composition. Consequently, characterization of milk microbiomes may help identify novel “microbial fingerprints” for healthy mammary glands and genetic selection of healthy dairy animals.

One of the major challenges to integrating omics technology into practical farm management is the lack of phenomics data. In other words, although most farms maintain performance records such as production and reproduction traits, data is often limited regarding different growth phases, various physiological or production stages, dietary changes, or selective breeding. Accurate phenomics data as basic as well-defined disease classifications and as complex as precision technology using remote sensors to capture physiological and
behavioral data, can help generate a more holistic understanding of the biological factors affecting the performance of animals. Ultimately all of us (breeders, biological scientists, veterinarians, statisticians, and computer scientists) require training in order to be conversant in proper data recording, processing, quality control, normalization, and genetic prediction if we are to collaborate to interpret and adequately utilize omics data, including phenomics data for animal improvement.

**Public Policy: FDA and Efforts to Understand Antimicrobial Use in Veterinary Medicine**

By WM Sischo, Professor Emeritus

If you are game-on for a data dump describing the state of veterinary-related antimicrobial use and an immersion in the alphabet soup of FDA (U.S. Food and Drug Administration) speak then head to these two web sites:

- https://www.fda.gov/media/159544/download?utm_medium=email&utm_source=govdelivery
- https://www.fda.gov/media/159519/download?utm_medium=email&utm_source=govdelivery

The first document is the first FDA:CVM (Center for Veterinary Medicine) comprehensive report on veterinary antimicrobial use and brings together sales data, use data, and resistance data into a single 244-page document. The second document provides a progress report on phase 1 of a 5-year plan for supporting antimicrobial stewardship in veterinary settings.

As a refresher, FDA:CVM began a 5-year effort in 2018 with 3 goals:

1. Align antimicrobial drug product use with the principles of antimicrobial stewardship
2. Foster stewardship of antimicrobials in veterinary settings; and
3. Enhance monitoring of antimicrobial resistance and antimicrobial drug use in animals.

Within these goals they defined 32 activities and split implantation across two phases with phase 1 beginning in 2019 and ending in 2021, and phase 2 beginning in 2022 and completing in 2023. This progress report summarizes accomplishments from phase 1. Given the length the reports I am going to highlight a few of the “activities” and progress that grabbed my attention.

- Issue a GFI (guidance for industry) to ensure that all medically important antimicrobial drugs used in feed or drinking water of food-producing animals have an appropriately targeted duration of use. This is an ongoing activity that began in January 2021 with the publication of a concept paper to obtain feedback and ideas on how animal drug sponsors could voluntarily establish defined duration of use. The gap that FDA was addressing was existing labels that essentially said “as needed”. The concept paper drew more than 30,000 comments and FDA is revising the concepts.

- Obtain public input regarding antimicrobial use practices in companion animals and their impact on the development of resistance. While FDA did not make any progress on this activity during this period they recently issued a “Request for Information” (https://www.federalregister.gov/documents/2022/02/16/2022-03245/antimicrobial-drug-use-in-companion-animals-request-for-comments) that closed June 2022. There were 19 comments and several requests to extend the comment period from industry groups. Still a work in progress.

- Expand the comprehensive VFD (veterinary feed directive) compliance strategy to integrate a VFD component into inspections associated with the Drug Residue Inspection Program. Workplans for fiscal years 2019 and 2020 included up to 50 VFD inspections in conjunction with the residue inspection program. It appears that compliance inspections continued in 2021.
Complete pilot projects initiated in 2016 to characterize antimicrobial use practices in the four major food animal species. CVM funded two projects focused on developing methods to support long-term use data. Both projects are ongoing and expected to be completed this year.

The goal for the remainder of the 5-year plan is to focus on existing guidance documents, finalize duration of use, and develop approaches for collecting antimicrobial use information from food-producing animals by exploring public private partnerships.

There is a pile of collected data in the comprehensive report so a few gems from each of the main focus data collection endeavors (drug sales, antimicrobial use in animal agriculture, and resistance monitoring) are as follows:

- Overall species 2019 sales and distribution of medically important antimicrobials approved for use in food animals had year-over-2018 increase of 3% and between 2015 (the record peak in sales) and 2019 decreased by 36%. Tetracyclines accounted for 67% of sales followed by penicillins at 12%. Cephalosporins and fluoroquinolones accounted for less than 2% of all sales.
- FDA is slowly moving towards collecting on-farm use data. Data from USDA:NAHMS studies exist but these studies are periodic and FDA is pursuing a more consistent approach and has funded cooperative agreements to create data collection systems. It is not clear how this will play out but expect that we might see farm-based systems feeding into a U.S. database.
- There is a cornucopia of data showing resistance trends in bacterial isolates coming from NARMS. These data are parsed out by species, retail, animal, and pathogen associated. A few slices from the cattle dataset. The resistance profile for *Mannheimia haemolytica* between 2018 and 2019 stayed relatively stable with resistance to the 12 tested antimicrobials ranged between 10-20%. The exception was for Tildipirosin which jumped from 1% to 14%. Three percent of the 612 tested isolates were resistant to 11 of the 12 antimicrobials. Nearly 40% of ground beef samples yielded an *E. coli* isolate while 83% of dairy cecal content samples yielded an *E. coli* isolate. Salmonella was found in fewer than 1% of ground beef samples though 22% of dairy cattle cecal content samples were Salmonella positive (this was about double the percent of Salmonella positive beef cecal content samples). As noted in other studies and consistent with historical NARMS data, approximately 10% of dairy cattle *E. coli* are resistant to streptomycin and sulfasoxasole and more than 15% are tetracycline resistant. The resistance profiles for *E. coli* recovered from ground meat are similar.

The overall take-away from the resistance data is that for the bacterial organisms being tested the trend data are stable with neither a dramatic increase nor decrease in resistance. Since the implementation of VFD, sales of antimicrobials have held steady after the initial decrease in sales associated with VFD. While the data for on-farm use is slim it seems likely that there will be an effort to collect this type of data.

**WADDL: Synopsis on Detection of Avian Influenza in Wild Mammals**

*By Liam Broughton-Neiswanger, Washington Animal Disease Diagnostic Laboratory*

Data from the current 2022 highly pathogenic avian influenza (HPAI) outbreak spreading across North America has shown that in addition to avian species the virus has been detected in multiple wild terrestrial mammalian species. Specifically, at the Washington Animal Disease Diagnostic laboratory (WADDL), the H5N1 variant of HPAI has been detected in tissues from racoons (n=2), striped skunks (n=2) and red foxes (n=2). It is believed that a possible route of transmission to these mammalian species is through normal scavenging of carcasses of deceased wild birds infected with influenza. However, other routes of transmission have not been ruled out.
HPAI is a lineage of influenza defined by the presence of H5 or H7 hemagglutinins viral protein and originates from wild birds. During previous outbreaks, HPAI infection has been reported in multiple mammalian species including pigs, felids, mice, and mustelids such as ferrets and martens. Affected animals present with neurologic signs. Additionally, HPAI can infect humans and human infections have significant public health implications. Due to the zoonotic potential for HPAI infection, avoid contact with sick wild birds and mammals.

The bottom line is that avian influenza should be considered a differential in cases of wild animals with rapidly progressive and often fatal neurologic disease, and the zoonotic potential of influenza infection should not be overlooked.

WSDA Tailgate Talks: TB or Not TB? . . . That is the Question
By Dr. Amber Itle, WA State Veterinarian

I think it’s safe to say that the most important things I’ve learned in life have occurred on the tailgate of a pickup truck or at the tail end of a cow. This is the second of a multi-part series, where I will talk to veterinarians about interesting topics. This month, I sat down with Dr. Clair Hibbs, born in rural Missouri in 1923. Clair grew up on his family’s diversified farm, rode a pony named “Cricket” bareback with his brothers 2 miles to school every day, and helped his dad ship cattle on the Chicago rail. After leaving home, Dr. Hibbs worked as a tradesman at Alcoa, served with the Seebees in the Navy during World War II, earned a BS and a DVM at the University of Missouri, and then was a livestock veterinarian for 7 years before furthering his education. He earned a Master’s degree and a PhD at Kansas State University paving the way for a career as a veterinary pathologist in Nebraska, New Mexico, and Kansas. Dr. Hibbs always says he has been unusually fortunate throughout his life and has amazing stories accounting his almost 100 year journey.

Dr. Hibbs and I became fast friends after he invited me to present on the Malignant Catarrhal Fever cases I diagnosed that were connected to the Puyallup Fair in 2006. Recently, Clair celebrated his 98th birthday and moved into a retirement home after his wife, Ann, of 76 years passed away. He only clung to a few important possessions including his scientific publications that he graciously passed on to me. One entitled, “Tuberculosis in New Mexico Dairy Cattle” published in 1986 caught my eye. Interestingly, what he wrote in the discussion 36 years ago, complemented a publication by Washington State Department of Health stating “Tuberculosis cases on the rise globally and in Washington State” in May 2022.

Tuberculosis (TB) is a contagious disease of both animals and humans and has zoonotic potential. TB is caused by one of three specific types of Mycobacterium bacteria: M. bovis, M. avium, and M. tuberculosis. Bovine TB, caused by M. bovis, can be transmitted from livestock to humans and vice versa. When Dr. Hibbs was growing up, bovine tuberculosis was the most prevalent infectious disease of cattle and swine in the United States and
caused more losses among US farm animals in the early part of the 20th century than all other infectious diseases combined.

For the last century, The National Tuberculosis Eradication program has greatly reduced the incidence of tuberculosis in cattle herds across the US; however, sporadic cases continue to be detected, mostly at slaughter. Experts from USDA APHIS believe there are 4 main reasons we continue to find new M. bovis cases in the United States: 1) wildlife reservoirs 2) undetected active US/MX strains 3) Mexican feeders & rodeo imports, and 4) humans.

1) Wildlife reservoir: Last summer, Hawaii reported its first detection of TB since 1997 and believes that wildlife reservoirs including mongoose, feral swine, and axis deer may have played a role in disease transmission. Free ranging white tailed deer serve as a TB reservoir in Michigan making eradication efforts difficult.

2) Undetected active US/MX strains: Outside of Michigan, there have been 58 beef herds and 34 dairy herds determined to be infected with novel strains of TB across the Western States in the last 20 years, most without an epidemiological link. Because many TB infections are latent and do not show clinical signs of disease, it could take years to detect TB in a herd. Slaughter surveillance alone will miss detection in most small herds, resulting in delays in detection for 5-10 years. Delayed detection allows new infections to become established and act as a reservoir of undetected cases and slow but continuous spread at low levels.

3) Mexican feeders & rodeo imports: Last year, approximately 18,500 head of Mexican rodeo cattle were imported into the United States. Routine TB surveillance in the US is built on harvest surveillance at USDA inspected slaughter facilities. USDA APHIS data suggests that from 2001-2011, of the 346 fed cattle infected with Bovine Tuberculosis, 273 originated in Mexico and the origin of 57 of the infected fed cattle was classified as unknown. This was primarily because the animals were sourced from mixed lots consisting of domestic and Mexican-origin cattle, making identification of their origin impossible (Zoonotic Tuberculosis, Mycobacterium Bovis and other pathogenic Mycobacteria; Chapter 22). Similarly, USDA APHIS estimated 68 percent of all tuberculosis cases detected by slaughter inspection of feedlot cattle between 1982 and 1991 were traced back to Mexico (Cooperative State-Federal Bovine Tuberculosis Eradication Program report).

4) Humans: According to the Washington Department of Health, cases rose notably beginning in 2021, when 199 cases of TB were reported, a 22% increase from 2020. Thus far in 2022, 70 cases have been reported and officials continue to monitor the situation closely. An estimated 200,000 people in Washington have inactive form of TB (also called latent TB infection), which does not have any symptoms and is not contagious. However, if people with inactive TB do not receive timely diagnosis and treatment, the infection could develop into active TB disease which can then cause symptoms and be spread to other humans and animals too.

In 2019, some staff members who worked extensively with elephants at the Point Defiance Zoo tested positive for latent tuberculosis. Upon routine annual testing, the healthy appearing elephants also were determined to be TB positive. Some of the workers did report recent international travel to countries where TB is more prevalent, and transmission very well could have been human-to-elephant in this case.
Last month, State Veterinarians in New Mexico and Texas reported that in recent large dairy outbreaks they are isolating multiple strains of tuberculosis (through whole genomic sequencing). Although there is no firm evidence, since there are no TB testing requirements of farm workers, State Animal Health Officials speculate that the workers could be one way that multiple novel strains of TB are being introduced into the herds.

This brings us back to Dr. Hibbs publication from 3 decades ago suggesting that infection may be associated with latent human infection.

In 1986, Dr. Hibbs recommended:
1. Routine periodic tuberculin testing in (dairy) cattle
2. Routine periodic tuberculin testing of (dairy) employees
3. Routine tuberculin testing of all additions to the herd
4. Recertification of practicing veterinarians testing cattle using a training program administered by APHIS

Last month, I said that you should listen to your Dad, and probably mine too. This month, I’m thinking we should have listened to Dr. Hibbs many years ago as a starting point to help us solve the mystery of why haven’t we been able to eradicate TB in the US? We know that our current TB surveillance system in the US cannot detect TB faster than new cases arise and novel strains enter the US every year. With 100 million susceptible cattle and less than 50% detection ability within 5 years, TB infections will continue to spread.

In his lifetime, Dr. Hibbs has survived drought, war, a depression and a global pandemic, but bovine tuberculosis remains 100 years after the inception of the US eradication program.

Is eradication of TB in the US TB or not TB? . . . that remains the question.

WSDA: Highly Pathogenic Avian Influenza is “For the Birds”
By Dr. Amber Itle, WA State Veterinarian

Highly Pathogenic Avian Influenza (HPAI) is certainly “for the birds” in the most undesirable way you can imagine. Since February, the United States Department of Agriculture (USDA) confirmed the detection of HPAI in 377 premises in 36 states. Although detections across the country are trending downward, Washington continues to see cases. The Washington State Department of Agriculture (WSDA) has responded to confirmed cases in 27 backyard, non-commercial premises in 11 counties.

While the risk of avian influenza is always present from interactions with wild waterfowl, unseasonably cold, wet conditions are changing migration patterns and the virus continues to persist in the environment. As birds
moved northward from the Atlantic, Central and Mississippi flyways, infection prevalence of wild birds migrating together increased. Northern States seemed to get hit hardest, especially Minnesota, South Dakota, and most recently Idaho and Washington. For months, WSDA thought that the virus would completely bypass the Pacific Flyway, but there is some evidence that wild birds from the Central flyway have spilled over into our state. Oregon and California, both part of the Pacific flyway, saw very few or no detections at all.

The most common risk factor we have seen in Washington is proximity to water sources or ponds where wild waterfowl congregate, increasing the amount of virus in the environment and risk of transmission. In Washington flocks, we have seen a wide variety of domestic birds impacted including chickens, guinea fowl, turkeys, peacocks, emus, geese, ducks, and peacocks. Small, backyard flocks act as “sentinels,” detecting virus from wild birds as they migrated northwest this spring.

The Washington Department of Fish and Wildlife continues to report increasing numbers of cases in wild birds, including Canada geese, bald eagles, snow geese, sand hill cranes, red tailed hawks, peregrine falcons, ravens, gulls, great horned owls, and mallard ducks in 14 counties. Along with 7 other states in the US, Washington also reported a case of H5N1 in a wild, carnivorous mammal (specifically, raccoon kits that presented with neurologic signs). Other states have reported detections in foxes and skunks.

Dr. Julianna Lenoch, National Coordinator APHIS Wildlife Services, gave a recent update at one of our National State Animal Health Official calls and reported that there have been a total of 1,611 wild bird HPAI detections as of 6/21/2022. Birds of prey have been impacted with 164 detections in bald eagles across 25 states with another 210 detections in other birds of prey (hawks/falcons/owls) across 23 states, 4 detections in Sandhill cranes in 4 states, and 149 detections in vultures (turkey and black) across 19 states. Most detections in wild birds have been detected in mass mortality events or sick/neurologic birds. USGS HPAI Maps

HPAI in 2015 vs 2022

Each year, as birds migrate and settle into their wintering grounds, they share and reassort influenza viruses. There are 16 different H antigens (H1 to H16) and nine different N antigens (N1 to N9) for influenza A affecting birds. Some H5 and H7 influenza A subtypes can cause either Low Pathogenic Avian Influenza (LPAI) or HPAI strains. Highly pathogenic refers to the fact that HPAI kills over 80% of susceptible chickens and domestic poultry. LPAI viruses typically result in few clinical signs in domestic poultry but have potential to reassort to become HPAI.
In 2015, the virus was thought to have moved through the Bering Strait between Russia and Alaska, with Washington detecting the first case in a Gyrfalcon in Whatcom County as birds migrated south. This year’s Eurasian viruses likely came through Greenland/Iceland rather than the Bering Strait. In the fall of 2021, we started to see increasing reports of HPAI in Asia and Europe. The sister virus to the 2015 clade, Eurasian HPAI H5 2.3.4.4b was detected in Labrador, Canada in December 2021. The concerning thing is that Europe continues to battle the virus 18 months into the initial detections, and we are certainly concerned about seeing the same trends here in Washington and across the US.

Although the viruses from 2015 and 2022 seem to be related, they are also very different in their presentation. The biggest difference we have seen in Washington with this strain is that wild waterfowl have become clinically ill, especially domestic, and wild geese and ducks. Other major differences are as follows:

<table>
<thead>
<tr>
<th>2015</th>
<th>2022</th>
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<tbody>
<tr>
<td>232 confirmed flocks</td>
<td>377 confirmed flocks</td>
</tr>
<tr>
<td>211 commercial</td>
<td>186 commercial</td>
</tr>
<tr>
<td>12 backyard</td>
<td>191 backyard</td>
</tr>
<tr>
<td>14 states</td>
<td>36 states</td>
</tr>
<tr>
<td>50 M birds</td>
<td>40 M birds</td>
</tr>
<tr>
<td>99 wild bird detections</td>
<td>950 wild bird detections</td>
</tr>
<tr>
<td>wild bird mortality inconsequential</td>
<td>Wild bird mortality events substantial</td>
</tr>
<tr>
<td>lateral transmission more common</td>
<td>86% independent introductions</td>
</tr>
<tr>
<td>Neurologic Signs in turkeys</td>
<td>Limited neuro signs in turkeys, but neuro signs in geese.</td>
</tr>
<tr>
<td>limited wild bird and backyard involvement</td>
<td>Extensive wild bird and backyard involvement</td>
</tr>
<tr>
<td>Chicken susceptibility smaller</td>
<td>Chicken susceptibility greater</td>
</tr>
<tr>
<td>Waterfowl subclinical</td>
<td>Waterfowl morbidity/mortality events</td>
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<tr>
<td>Mostly dabbling ducks infected</td>
<td>60 different wild bird species infected</td>
</tr>
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**HPAI Response**

Eradicating foreign animal disease is a mission-critical activity for WSDA because of the economic devastation, animal welfare concerns, and trade implications imposed by the World Organization of Animal Health (OIE). WSDA and USDA have been working in joint command to detect, contain, and eradicate Highly Pathogenic Avian influenza. You may be wondering how this all works. First of all, we follow our state and federal HPAI response plans. The federal plan is often referred to as “the Red Book,” and is used by State Animal Health officials across the country for consistency in our response efforts. Although response is similar for both commercial and backyard flocks, all of our detections thus far have been in backyard, non-commercial flocks. There are 10 basic steps we take during a response for backyard flocks:

1) **Detect** - Detections usually start with calls from private veterinarians or flock owners who report sick or dead birds to our sick bird hotline. One of our field veterinarians call the owner and complete an epidemiological investigation to determine if the birds require sampling. So far this year we have had over 170 calls and about 35 of them have met the sampling criteria. Samples are sent to WSU WADDL for preliminary results and if non-negative, are sent to the National Veterinary Services Laboratory for confirmation.
2) **Quarantine**- A stop movement, or quarantine order, is issued at the time of sampling to ensure no poultry, poultry products or equipment is moved on or off the premises. This is the first step for disease containment. If the sample is confirmed positive, the quarantine will stay in place for a 150-day fallow period.

3) **Notify Department of Health**- As soon as the HPAI is detected, WSDA notifies the Department of Health so that they can follow up with owners and start symptom monitoring and discuss public health concerns. Although there has only been one human case in the US, we know that there is potential for H5 and H7 strains to quickly mutate and become zoonotic.

4) **Appraise/Compensate**- Upon arrival to the farm, a flock plan and inventory is performed for indemnity purposes. The number, species, type, and age of all birds is recorded, and market value is paid for all birds remaining on the premises.

5) **Euthanasia**- Infected flocks are euthanized by small container CO2 (an AVMA-approved method) whenever possible within 24 hours of detection. Sometimes, US Wildlife Services assists with euthanasia of at-large or feral domestic birds that cannot be caught or handled.

6) **Manage Disposal**- WSDA works with Department of Ecology to dispose of all carcasses from the site. Methods outlined in this new guidance are determined based on local resources and include incineration, landfill, composting, burial and rendering. To date, only incineration and landfill have been used.

7) **Surveillance**- After euthanasia and disposal is complete, a 10 km (6.2 mile) zone is established around the infected premises and is designated as a surveillance or control area (depending on OIE poultry designation). WSDA/USDA field veterinarians make every effort they can to locate and contact other backyard and commercial flocks in the area to educate them about the virus and ask them to monitor their flocks for signs of illness. If flock owners report sick or dead birds, the investigation process starts over, and sampling occurs. Flock owners can self-identify by placing their address into this map.

8) **Eliminate Virus**- Thorough cleaning and disinfection is required to kill the pathogen. However, most backyard flocks have free-range poultry/domestic waterfowl, so a fallow period of 150 days replaces the virus elimination and environmental testing step.

9) **Restock**- After cleaning and disinfection of coops, and the 150-day fallow period, the quarantine is lifted and owners may restock. We recommend keeping waterfowl and gallinaceous birds (e.g., domestic poultry) separate to reduce infection risk.

10) **Maintain biosecurity**- We encourage all flock owners to have a biosecurity plan or follow basic principles such as keeping poultry away from wild waterfowl, avoiding commingling of birds, restricting visitors to their farm, separating sick birds, isolating new additions, etc.

We never expected that we would still be responding to HPAI in July, but as long as resident waterfowl spend time in Washington, we can anticipate continued detections. We can only hope that the end is near, but current trends suggest that we must stay vigilant and prepared to respond for weeks and months to come. HPAI is “for the birds” but WSDA is here to provide protection FOR the birds.
African Swine Fever (ASF) is a highly contagious viral hemorrhagic disease of domestic and wild swine. While it is not currently present in the US, globally ASF is responsible for severe economic losses and is a serious threat to the swine industry. ASF is not a zoonotic disease thus not a threat to public health; however, human behavior can play an important role in the spread of the disease.

**Geographic Distribution:**
ASF was first described in Kenya in 1921. Since then, it has been endemic in many sub-Saharan countries and Madagascar. In 1960 ASF was confirmed in Spain, Portugal and Sardinia; it was eradicated in Portugal in 1993 and Spain in 1995, it is still endemic in Sardinia. During the 1970s and 1980s there were limited outbreaks of ASF in the Netherlands, Italy, France and Belgium, the Dominican Republic and Brazil. The disease was introduced to the Caucasus region in 2007 via Georgia and has since spread to neighboring countries, affecting wild boar and domestic swine. In 2014, ASF spread to Eastern Europe where it has been present in wild boar ever since. In 2017, the disease was detected in wild boar in the Czech Republic and Romania. In 2018, ASFV was detected in domestic pigs in China and has since spread to other Asian countries including Vietnam, Mongolia, Cambodia, Lao and North Korea. In 2019, ASF was reported in Romania, Bulgaria, Poland, Hungary and Belgium.

Since January of 2020 ASF has been reported in 32 countries within 5 world regions; 6 countries have new reports of ASF and 10 countries reported the spread to new zones. As of 2021 the disease reappeared in the Americas—in the Dominican Republic and Haiti.

**Causative Agent?**
African swine fever is caused by African Swine Fever Virus (ASFV), a dsDNA virus. ASFV is highly resistant in the environment and can remain infectious for several months at room temperature. It can survive freeze/thaw events, differing pH, and processing.

**Transmission?**
Transmission can occur by:
- Direct contact with infected pigs: aerosolized respiratory secretions, urine, feces, saliva, blood, soft tissue, etc.
- Indirect contact via fomites such as clothes, boots/shoes, equipment, trucks, etc.
- Pigs eating infected pig meat/pig containing products: such as swill, ham, sausages and bacon.
- Biological vectors (*Ornithodoros* ticks).

**Clinical Signs:**
The disease can range from acute, sub-acute, or chronic in nature. Clinical signs range from mild to severe. Incubation period is reported to be 5-19 days in naturally acquired cases.
Clinical Signs:
- Sudden death
- Abortions
- High fever
- Reddening of the skin (tips of ears, tail, distal extremities, ventral aspects of chest and abdomen)
- Inappetence, listlessness, decreased mobility
- Incoordination
- Vomiting, Diarrhea, ocular discharge

Mortality can range up to 100% but those that survive are persistent shedders and in general unthrifty.

Photo credit: USDA APHIS

Control Measures:
Biosecurity is key in prevention. Some basic prevention includes:
- Only allow essential visitors to enter the farm, ensure they wear clean (specific to farm) clothing or disposable clothing and footwear. Shower-in/Shower-out is ideal.
- Insist staff and visitors have a pig-free period prior to entry.
- Only allow vehicles and equipment on to the farm if they have been cleaned and disinfected.
- DO NOT feed swill to pigs.
- Do not allow staff or visitors to bring pork products to the farm.
- Keep feral swine away from domestic swine.
- Only source pigs and semen from places of known health status.

Human behavior while travelling is also important to ensure ASFV is not accidentally introduced. Important things to remember when travelling are as follows: do not import illegal pork products, do not interact with wild or domestic swine populations if possible, if exposure to swine is unavoidable ensure pig-free time is observed and follow strict biosecurity protocols.

Treatment:
There is no effective treatment but attempts at developing a vaccine are ongoing, with one recently demonstrating promise.

In September of 2020, USDA vaccine candidate ASFV-G-DI177L, a live attenuated vaccine with a gene deletion, was selected by NAVETCO for commercial development. Multiple experiments were conducted, and results demonstrated 100% of vaccinated pigs were protected when exposed to toxicity in the lab, 80% of vaccinated pigs in production demonstrated protection, and immunity lasted 6 months post-vaccination. In April of 2022, USDA announced that ASFV-G-DI177L had passed an important test that was required for regulatory approval. In June of 2022, Vietnams Ministry of Agriculture and Rural Development announced the successful production of a commercial vaccine, NAVET-ASFVAC.
Summary:
African Swine Fever is a highly contagious viral hemorrhagic disease, that causes increased mortalities in domestic and wild swine and results in severe economic losses. Although ASF is not currently in the US, it is important to continue to be vigilant in ensuring it is not introduced in our domestic or wild swine population. USDA estimates that if ASFV were detected in the US that $50+billion dollars would be lost over a 10-year period.

ASF is a notifiable disease—if it is suspected report immediately to the local district veterinary office or the USDA. For more information visit:

- USDA APHIS: https://www.aphis.usda.gov/aphis/resources/pests-diseases/asf?gclid=EAIaIQobChMIjnlmoLWhvT-AIVV8LCBB1wgmOEAAAYASAAEgLKfVd_BwE

References:
5. WORLD ORGANIZATION FOR ANIMAL HEALTH, 2022. African Swine Fever (ASF), Situation report, March/12/2022

WSU CVM Senior Paper Highlights

The case for cluckers: adding backyard poultry to your species repertoire
By Jack Schmitz (Advisor: Dr. George Barrington)

Summary: This paper discusses the current state of veterinary care for backyard poultry, including a discussion on the differences between commercial and backyard poultry, the needs of backyard poultry owners, and the demographics of backyard poultry owners. It provides a baseline of knowledge to any veterinarians who may wish to pursue integration of backyard poultry medicine and surgery into their own practice. An enterprising veterinarian is one who is always looking for ways to make themselves a better practitioner, their practice more efficient and profitable, and their community better served. Opening themselves to backyard poultry service is an excellent opportunity to complete all those goals. Not only is there a demonstrated need for service, as evidenced by the growing number of poultry in the U.S., but with some business acumen they can become an important and profitable part of practice. The current lack of engagement with backyard poultry owners coupled with those owners’ desire for engagement provides a large, willing clientele base that has been searching for service. Serving these clients is not an end in and of itself either, as an expansion of species seen may be the sort of option that brings in more traditional small animal clients by opening the door to patients that would not have been seen otherwise by courting the other animals these owners have. Finally, providing backyard poultry services provides a valuable health and biosecurity role. With the prevalence of avian diseases in wildlife, poultry services allow veterinarians to survey the local avian population for diseases of economic importance such as Marek’s, HPAI, and Newcastle Disease, fulfilling the veterinary public health role and protecting commercial poultry producers in the community.
Continuing Education
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1. Pacific NW Veterinary Conference. Tacoma WA. September 30 – October 2.

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