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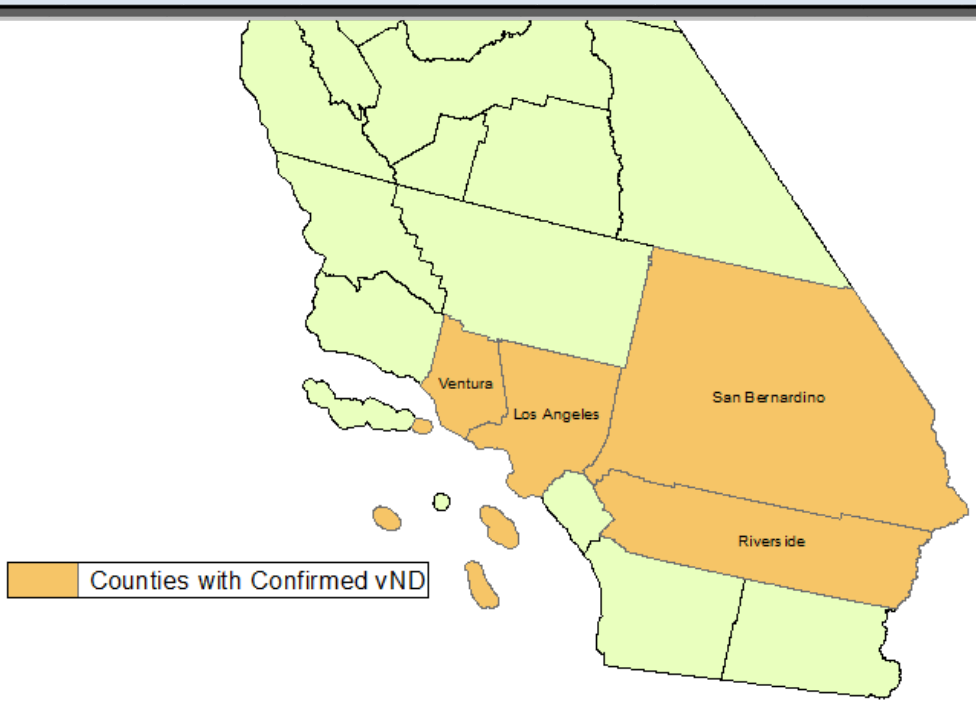
Veterinary Services

Epidemiologic Analyses of Virulent Newcastle Disease in Backyard Birds in California

December 2018



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EXECUTIVE SUMMARY

In May 2018, a backyard-chicken owner brought several ill exhibition chickens to a veterinary clinic in southern California. The birds were displaying signs of virulent Newcastle disease (vND). Biological samples were collected from the chickens and sent the California Animal Health and Food Safety (CAHFS) Laboratory where vND virus was detected. The National Veterinary Services Laboratories (NVSL) confirmed vND in these birds on May 17, 2018. As of November 9, 2018, 175 backyard flocks had been confirmed as infected with the virus.

Once initial response efforts were in place, the U.S. Department of Agriculture's (USDA) Animal and Plant Health Inspections Service's (APHIS) Veterinary Services initiated a series of epidemiologic investigations and studies, which were undertaken collaboratively with bird owners, State agriculture personnel, and the USDA's Agricultural Research Service (ARS). This report provides the most current findings to-date and is intended to provide a better understanding about how the vND virus is introduced and transmitted.

The outbreak predominantly affected backyard chickens in an area crossing four Southern California counties: San Bernardino, Riverside, Ventura, and Los Angeles. Preliminary genetic analysis supports a single introduction followed by secondary spread. Lack of epidemiologic data regarding the index premises, and temporal and geographical gaps in available genetic data, contribute to the uncertainty surrounding the origin of the outbreak.

These affected counties have a high density of backyard flocks, but such flocks are not typically registered and their exact locations are unknown. Using a Bayesian hierarchical model, previously identified socioeconomic and demographic variables found to be associated with urban poultry ownership were used to estimate the probability of backyard flocks in this area. Results suggest that a single 10-km zone could have as many as 4,000 backyard flocks, and that the greater Los Angeles area might have more than 11,000. Modeled backyard ownership maps will help inform ongoing surveillance and response efforts.

Analyses of surveys conducted at case, control, and dangerous contact premises[1] identified flock size, ownership of exhibition birds, high proportions of roosters in flocks, and the use of housing that allows contact with wild birds, all of which were determined to be risk factors for vND in this population. The percentage of premises reporting the use of Newcastle vaccine was low overall. Vaccination of backyard birds is a concern due to the potential for improper administration that may lead to development of reservoirs of vND.

Initial results from disease-spread and control simulations suggested that local disease spread would become increasingly important as the outbreak increased in size. This type of disease spread is distance-dependent and represents mechanisms of spread that are difficult to trace, such as movement of free ranging birds, wildlife, or fence-line contact. Good biosecurity practices and measures are the best way to reduce local spread, but completely preventing this

[1] Dangerous contact premises are defined as premises with backyard birds that are high risk due to either an epidemiologic link or proximity to infected premises.

type of spread is difficult. Overall, the likelihood of disease spillover into commercial flocks is low, but spillover was observed in 7 percent of simulated outbreaks. As the outbreak progressed, modeling scenarios were developed to compare alternative control options and resource levels for response. These scenarios found that minimal response levels (including low surveillance and depopulation capacities) were unlikely to prevent continued disease spread in backyard flocks. Rapid and targeted surveillance, depopulation, and disposal were most effective at minimizing outbreak size and severity. The largest and longest simulated outbreaks frequently involve significant disease spread within Los Angeles County, irrespective of the selected response option.

Using experimental data available from peer-reviewed literature and unpublished data provided by the USDA, ARS, Southeast Poultry Research Laboratory (SEPRL), analysts estimated the mean latent period for this virus to be 0.40 days, and the mean infectious period to be 4.33 days. Using these values, we estimate the time to detect vND in an unvaccinated, 50-bird backyard flock based on observation of increased mortality (two or more dead birds within a 3-day period) to be from 4 to 7 days.

The identification of significant spatial and spatiotemporal clustering patterns of vND in California from May to August 2018 supports control strategies of targeting high risk areas for disease spread with enhanced surveillance and depopulation activities. The results of this analysis identified specific geographic areas, at the census block level, within four vND control areas of significant spatial and spatiotemporal disease clustering, particularly in San Bernardino and Los Angeles Counties. These areas were or have since been identified as targets for enhanced response activities.

INTRODUCTION

California and USDA-APHIS have initiated epidemiologic and genetic investigations in response to the virulent vND outbreak in backyard chickens in Southern California. These investigations will provide a better understanding of factors associated with vND virus transmission among backyard chickens and other susceptible species. These investigations include the following:

- Analysis of the phylogenetic characteristics of the virus
- Estimation of the probability of homes in Southern California owning backyard birds
- A field-based study of backyard case and control premises using data collected through site visits and interviews with backyard-chicken owners
- An epidemiologic disease-spread simulation model of vND spread among bird-owning households in Southern California and comparison of alternative control options
- An examination of within-flock disease transmission and the impact on the time to detection in unvaccinated backyard flocks
- An analysis of spatial and spatiotemporal patterns of disease

This report includes the preliminary results from these investigations, in an effort to provide producers, industry, and other stakeholders with epidemiologic information and to archive the analytical work performed to support outbreak response.

A. Disease Overview

Newcastle disease is the cause of regular, frequent poultry epizootics throughout Africa, Asia, Central America, and parts of South America. The disease is caused by strains of avian paramyxovirus-1, also known as Newcastle disease virus, which can be classified into three pathotypes based on their virulence in chickens. The World Organisation for Animal Health (OIE) defines Newcastle disease as infection caused by highly virulent strains of APMV-1 viruses. This virulent form of New Castle disease (vND) is considered a foreign animal disease in the United States.

Clinical signs of vND vary and can include respiratory, neurological, reproductive, and intestinal signs. During this outbreak, clinical signs seen in chickens include loss of appetite, difficulty breathing, nasal discharge/ocular discharge, swelling around the eyes, diarrhea, blue combs, and death. Morbidity of unvaccinated chickens infected with vND virus strains can reach 100 percent, and mortality ranges from 70 to100 percent. The severity of disease produced varies with the host species and the strain of the virus. Many other avian diseases present with clinical signs similar to vND; therefore, laboratory testing is necessary to distinguish between diseases.

Newcastle disease is transmitted by inhalation or ingestion, and birds shed the virus in both feces and respiratory secretions. The virus can infect many species of domestic and wild birds. Chickens are highly susceptible, and other gallinaceous birds such as turkey, quail, and guinea are also susceptible. There are two species-adapted viruses that are genetically distinguishable

from those found in poultry in the absence of direct transmission: one is maintained in pigeons and doves, and another in double-crested cormorants (Brown and Bevins, 2017). Parrots have been reported to be infected with virulent viruses and have the potential to shed virus for long periods without shoeing clinical signs; however, data supporting virus maintenance in these species is lacking. A detailed summary of susceptible wild bird species is available in Appendix A.

Vaccination of commercial poultry against New Castle disease is common in the Americas, including the United States. The classical vaccine strains are distinguishable from other viruses by genome sequencing. Widespread vaccination of poultry was implemented in Mexico and several Central American countries in the early 2000s, and since this time divergence of subgenotypes circulating in vaccinated poultry has been documented (Susta et al., 2014; Garcia et al., 2013). Outbreaks of vND occurred in California, Nevada, and Arizona in 2002-2003 and in Texas in 2003.

B. Description of Outbreak

May 16, 2018, to November 9, 2018

On May 16, 2018, the California Department of Food and Agriculture reported vND in sick backyard exhibition chickens presented to a veterinary clinic in Los Angeles County (Figure 1). The National Veterinary Services Laboratories (NVSL) confirmed vND virus on May 17, 2018. This confirmation represented the first case of vND, (formerly referred to as exotic Newcastle disease) in the United States since 2003. Officials were first alerted to the possibility of a new finding of vND when an owner presented sick chickens to a California veterinary clinic. Biological samples were collected from the chickens and sent the California Animal Health and Food Safety (CAHFS) Laboratory where vND virus was detected. The CDFA responded to the incident by creating 3-km control areas around the premises associated with the index case and began targeted surveillance and outreach, including to feed stores and known exhibition bird premises. On May 24, 2018, NVSL confirmed vNDV in a backyard premises in San Bernardino County. On May 26, 2018, a USDA-APHIS incident management team joined the unified incident command in California. By this time, seven premises had been confirmed in San Bernardino County and two in Los Angeles County. On June 30, 2018, a premises in Riverside County was confirmed. On August 14, 2018, vNDV was confirmed in Ventura County. On September 25, 2018, NVSL confirmed vNDV in a live bird market in Los Angeles County. From May 16 to November 9, 2018, 175 confirmed positive premises were identified in four California counties (Figure 2, Table 1).

The owner of the vND-infected live bird market in Los Angeles County reported first observing clinical signs approximately two weeks prior to presumptive diagnosis. Over the four weeks prior to reporting disease, the market received 43 shipments of live birds from four suppliers: 37 shipments of broilers, 4 shipments of spent hens, and 2 shipments of ducks. Bird shipment sizes ranged from 15 to 558 birds (mean=181 birds per shipment). Suppliers used dedicated cages that were washed and sanitized between shipments to transport birds. Suppliers typically made stops at more than one live-bird market on their routes. The market was visited by one

renderer, typically three times per week. The owner of the market reported rarely receiving birds from the community and no community birds were received in the 60 days prior to the onset of clinical signs. Active surveillance of other live bird markets in the area yielded no additional infected markets.

C. References

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Figure 1. Counties with confirmed findings of vND from May 17 to November 9, 2018

Table 1. Number of vND confirmed positive premises, by California counties and dates of earliest confirmation in each county, as of November 9, 2018.

County	Confirmed Premises	Earliest Confirmation Date in County
Los Angeles	38	17 May 2018
Riverside	32	30 June 2018
San Bernardino	104	24 May 2018
Ventura	1	14 August 2018
Total	175	

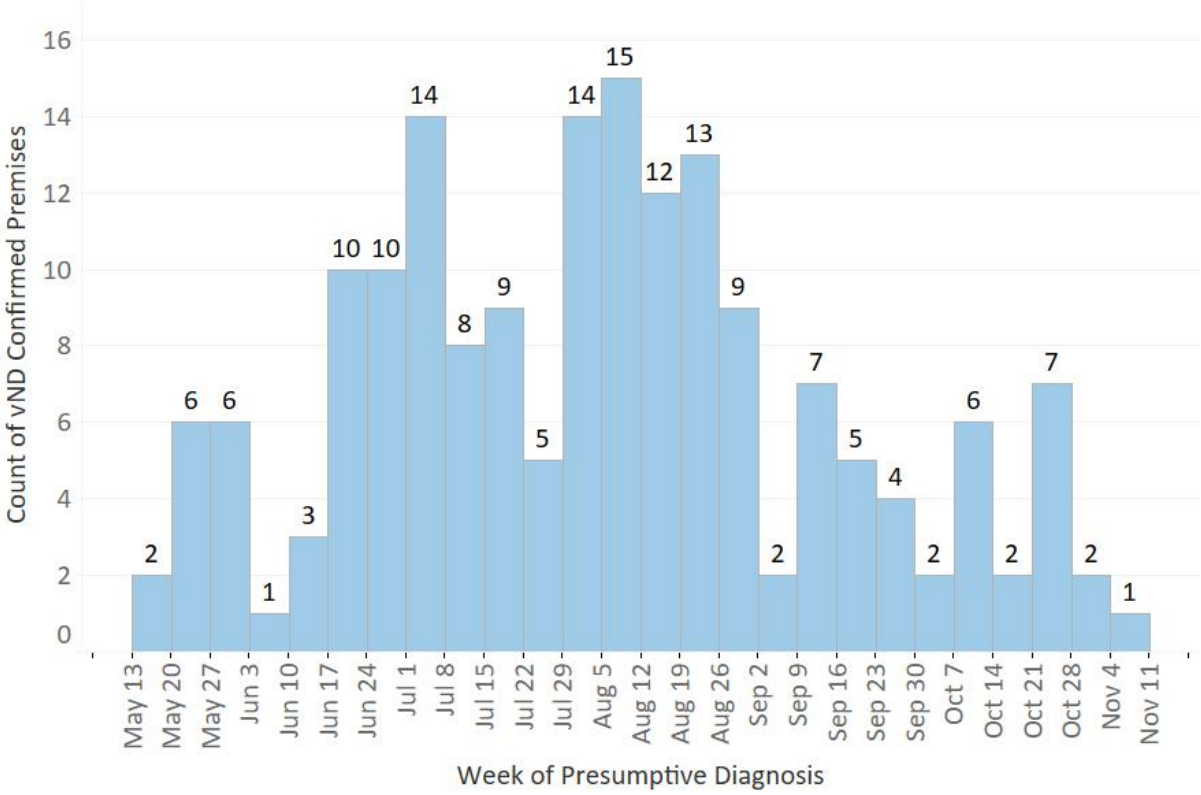

Figure 2. California vND weekly case detection curve based upon the date the case definition[2] was met for a presumptive positive flock, by day from May 17 to November 9, 2018.

[2] Case definitions

- Suspect case: domesticated bird or flock having clinical signs compatible with vND; or detection of APMV-1 by rRT-PCR; or epidemiological information indicating exposure to vNDV
- Presumptive positive case: a suspect case with detection vNDV by the fusion-target rRT-PCR test at a laboratory designated by the Secretary of Agriculture
- Confirmed positive case: domesticated bird or flock from which vNDV has been identified at the NVSL as presumptive positive with confirmation of multiple basic amino acids (either directly via protein or by deduction through sequencing) in the fusion gene at the C-terminus of the F2 protein and phenylalanine at residue 117, which is the N-terminus of the F-1 protein. The term 'multiple basic amino acids' refers to at least three arginine or lysine residues between residues 113 and 116; and/or the vNDV has an intracerebral pathogenicity index (ICPI) in day-old chicks (Gallus gallus) of 0.7 or greater.

II. PHYLOGENETIC ANALYSIS AND DIAGNOSTICS

A. Virulent Newcastle Disease Virus

This section describes viruses characterized from the 2018 vND events in California (CA2018). The index case is chicken/California/18-016505-1/2018, which has an amino acid cleavage site of PGGRRQKR/FVGAII. The intracerebral pathogenicity index (ICPI) conducted on selected isolates in accordance with OIE guidelines confirms virulence and ranges from 1.67-1.75[3]. Chickens have been predominantly affected; other species from which the virus has been recovered include turkey, peafowl (peacock), duck, goose, and pigeon. Preliminary studies with the CA2018 index virus at the Southeast Poultry Research Laboratory suggest that it is highly chicken adapted and very infectious for chickens.

Methods

Genetic sequence data from the virus is used to determine the cleavage site, which serves as disease confirmation. Additionally, full genomic sequence data are generated and analyzed to monitor virus evolution and to inform epidemiologic investigations. Genetic data are also used to confirm that diagnostic assays are fit for purpose.

Results

The CA2018 virus (genotype Vb) is related to older Mexican-lineage viruses from Central American village poultry (Belize 2008, Honduras 2007), and the U.S. (smuggled parrot 1996, CA2002), which represent viruses from birds with low or no vaccine coverage. Preliminary genetic analysis of CA2018 virus isolates supports a single introduction followed by secondary spread based upon the high identity among available sequences from 41 chickens and 1 each from duck, goose, peafowl, pigeon, and turkey, representing 41 premises. Lack of epidemiologic data regarding the index premises and of contemporary sequence data (the most recent available related sequences are from 2008) contribute to the uncertainty surrounding the origin of the outbreak. Evolutionary analysis of available sequences with the CA2018 and CA2002 viruses suggest ongoing circulation of the virus; however, where and in what population remains unclear.

NOTE: The outcomes of phylogenetic analysis should be interpreted in context of all available virus and epidemiologic information and should not be used directly to infer transmission.

[3] The World Organisation for Animal Health (OIE) defines Newcastle disease as an infection with a virulent APMV-1 virus (vNDV) characterized by either an intracerebral pathogenicity index (ICPI) of 0.7 or greater in day-old chickens, or the presence of multiple basic amino acids at positions 113- 116 of the C-terminus of the fusion (F2) protein (either arginine (R) or lysine (K)), plus phenylalanine (F) at residue 117 of the F1 protein.

B. Comparison to Other Viruses/Lineages

The CA2018 virus is not related to classic Newcastle disease vaccine strains, nor to available strains from vaccinated poultry in Mexico (2000-2010). The virus is also unrelated to the species-adapted virus from columbids (pigeons, doves), and is not closely related to virulent viruses endemic to double-crested cormorants.

C. Diagnostics

Testing avian swabs/tissues for APMV-1 involves screening assays (real time reverse transcription polymerase chain reaction [rRT-PCR]), virus isolation, and characterization of the virus (sequencing and in vivo tests). The National Animal Health Laboratory Network (NAHLN) tests swab/tissue first by the APMV-1 matrix-target rRT-PCR test,[4] best suited to detect Class II viruses that contain low and highly virulent pathotypes, including vaccine viruses. Detections by the matrix-target test are subsequently tested by a fusion gene-target rRT-PCR test, which is designed to allow rapid identification of virulent viruses reportable in poultry. This approach does not provide the genetic or geographic lineage of the virus. Sequence analysis of the virus compared to the assay primers and probes confirmed high identity between the CA2018 virus sequences and the fusion gene-target rRT-PCR test. A negative fusion gene-target test in the face of clinical signs requires further testing including virus recovery, sequence, and/or ICPI testing.

Under normal surveillance, all poultry samples with a nonnegative test result by APMV-1 PCR or virus isolation are forwarded to NVSL for confirmatory testing; for the current CA vND event, the NAHLN laboratory is using the highly matched fusion-target assay. The NVSL uses Sanger sequencing protocols to generate partial fusion gene sequence directly from the sample for virulence determination, where sufficient viral RNA is present. Whole genome sequencing is conducted on all isolated viruses, and select viruses are further characterized by ICPI in specific pathogen-free chickens.

The NVSL confirms the virus lineage and virulence through molecular sequencing. Where no virus can be recovered nor sequence obtained directly from sample(s), the virulence is determined by the clinical presentation of the flock compared to the USDA vNDV case definition.

[4] PCR results from the NVSL are reported as “detected” or “not detected” and include the cycle threshold (Ct) value. The lower the Ct value, the more viral nucleic acid was detected.

III. POPULATION AT RISK

A. Predicting Areas of Backyard Bird Ownership

The distribution of backyard bird flocks in the United States is currently unknown. Statistical modeling, however, can be used to estimate the likely locations and densities of backyard flocks in a given geographic area using socioeconomic and demographic variables that historically have been shown to be related to bird ownership. This approach was used to develop neighborhood-level spatial data to facilitate the creation of risk maps to identify and prioritize areas for surveillance during the 2002-2003 outbreak of vND in the United States (Freier et al., 2004, Freier et al., 2007). Building on that historical work, we aimed to identify areas with increased probability of backyard poultry ownership to inform surveillance response efforts for the current outbreak.

Methods

A Bayesian hierarchical model for spatial areal unit data was used to analyze socioeconomic and demographic variables that have previously been found to be associated with urban poultry ownership. Census block groups were used as the unit of analysis. The number of backyard flocks identified during the previous vND outbreak in 2002-2003 were tallied for each census block group. During the 2002-2003 outbreak, all homes within 1 mile of an affected premises were queried about backyard poultry ownership, resulting in a near census of backyard poultry ownership for some census block groups. Census block groups within 1 mile of affected premises were then assumed to have all flocks identified, and the total number of households reported in the census data was used as the total sample size. These census block groups were then used as data to fit the Bayesian model.

The Bayesian model used a binomial likelihood conditional on historical sociodemographic and economic risk factors (Figure 3). The model included a spatial random effect using a convolution model that allows for both weak and strong spatial autocorrelation with neighboring census block groups. Prior to model fitting, 5 percent of the data was randomly withheld for out-of-sample model validation. The withheld data was identified using conditional Latin hypercube sampling. Models were fit using JAGS in R.

Results

Human population size, home value, education level, housing density, household income, and household size were all significant predictors. Figure 3 presents the predicted coefficients for the sociodemographic and economic predictors used in the model. Based on the model's predictions, a single surveillance zone (10km) could have almost 4,000 premises with backyard poultry, while the greater Los Angeles area is predicted to have over 11,000 backyard poultry premises. Figure 4 presents the predicted distribution of backyard flocks by census block group within the current surveillance zone and control areas.

Generally, the model performs well, explaining 79.9 percent of the deviance in the spatial distribution of backyard poultry ownership during the 2002-2003 outbreak. Comparison of the predicted number of households with backyard poultry with the out-of-sample data found a Pearson's correlation of 0.67, indicating that the model has good predictive capacity.

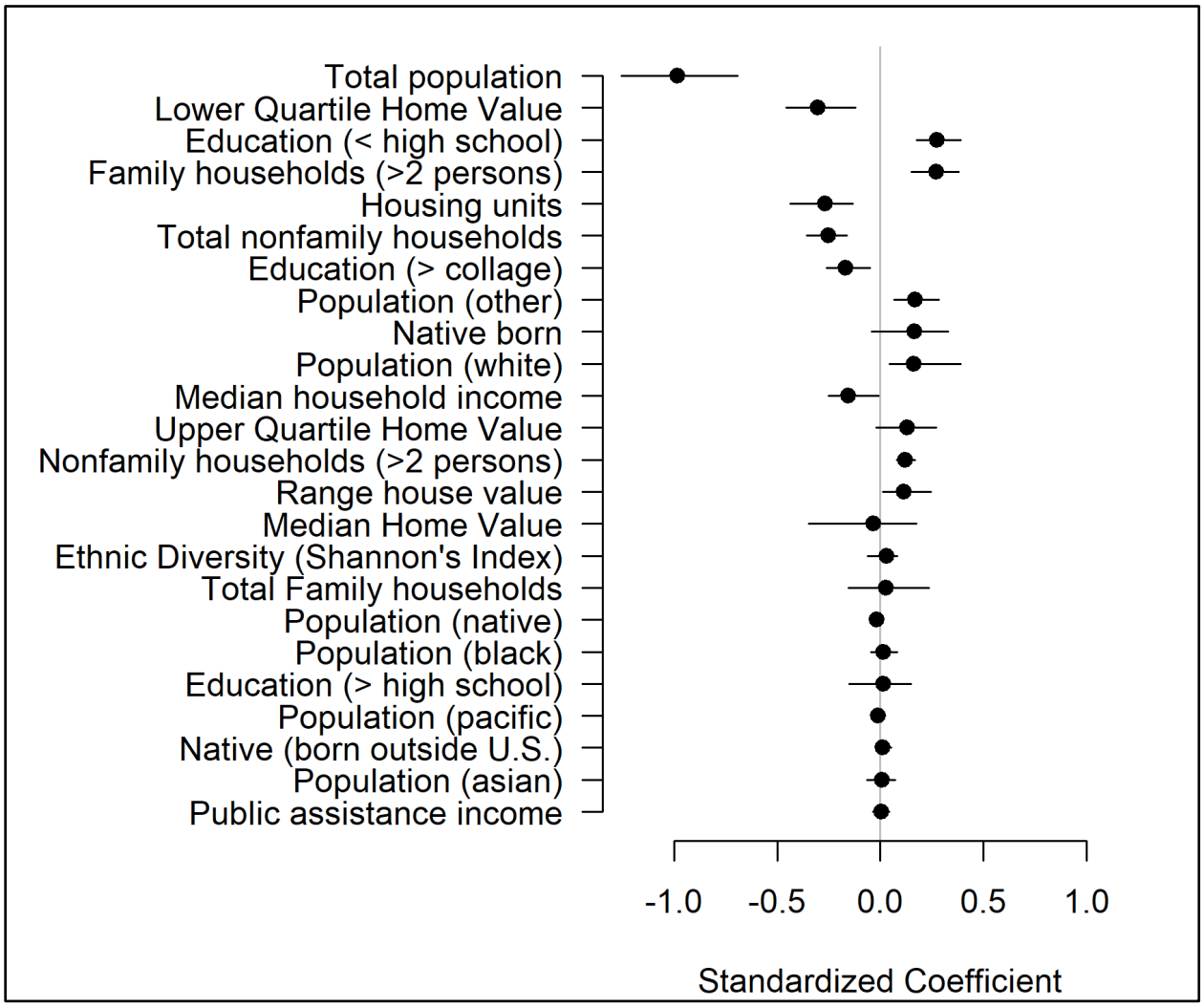

Figure 3. Preliminary sociodemographic variables used in the model to predict the presence of backyard poultry in a census block in Southern California.

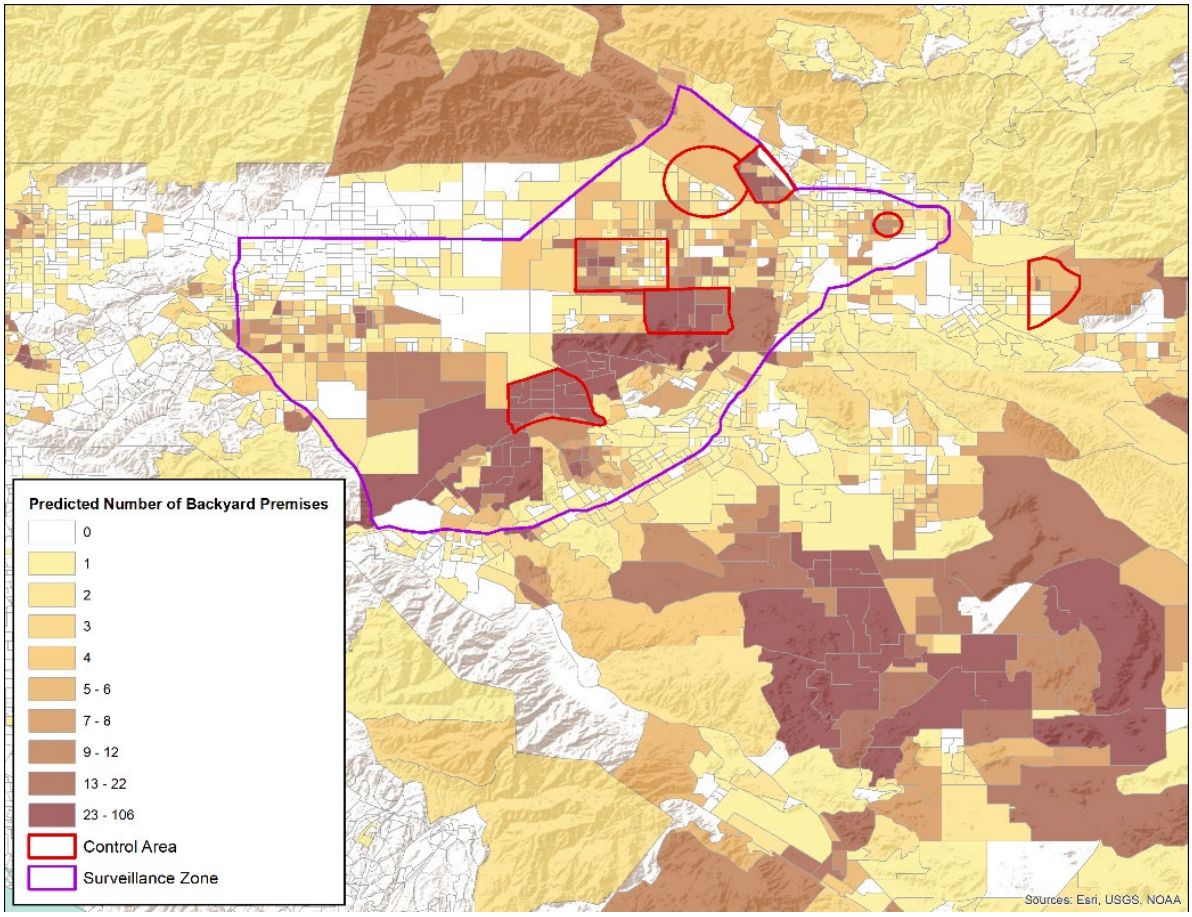

Figure 4. Predicted number of backyard flocks, by census block group in Southern California.

Summary

The outbreak area is likely to have a very dense population of backyard poultry. In addition, there was a strong spatial pattern to the distribution of backyard poultry ownership, indicating that a spatially targeted approach might improve surveillance efficiency. Work continues on improving the model and incorporating data and predictors related to the probability that vND is present in the census block groups. Formal model selection has not been implemented yet but might improve the predictive abilities of the model. The data used to fit the model was restricted to block groups in Southern California to facilitate model fitting (i.e. limit cpu time). However, data are available throughout California, Nevada, and Arizona for the 2002-2003 vND outbreak. Including these data in the model might improve prediction and applicability to other regions of the United States.

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IV. EPIDEMIOLOGIC RISK

A. Case Control Study

A case-control epidemiological analysis was performed on confirmed and presumptive positive virulent Newcastle disease (vND) backyard premises, dangerous contact premises, and noninfected premises. Data were obtained from in-person interviews using the CDFA Non-Commercial Premises Virulent Newcastle disease Epidemology Questionnaire; questionnaire data were entered into the USDA's Emergency Management Response System (EMRS).

Methods

Data were analyzed for 912 premises: 137 confirmed or presumptive positive premises, 68 dangerous contact premises, and 712 noninfected premises. The analysis included data from questionnaires that were completed from May 16 to November 9, 2018, and includes all confirmed and presumptive premises for which questionnaire data were entered into the EMRS as of November 9, 2018. The questionnaire form was updated in July 2018 with additional questions; 69 respondents completed the original questionnaire and 848 completed the updated questionnaire. Questionnaires were not complete for all premises, such as in cases in which the owners refused to provide answers to certain questions. The number (n) of responding premises is noted in Table 1. Odds ratios, p-values and 95-percent confidence intervals for flock characteristics and other risk factors were estimated by univariate logistic regression, using confirmed/presumptive premises as cases and noninfected premises as controls. Dangerous contacts were excluded from the regression analysis. To identify significant risk factors, while controlling for possible confounding variables, two multivariable logistic regression analyses were performed. The first included questions found in both versions of the questionnaire, while the second included questions found only in the newer version of the questionnaire. All variables that had a significant (p-values < 0.1) predictive effect on being a case were included in the analysis, and backward stepwise elimination was used to obtain final models.

Results

Premises characteristics

The reported flock sizes ranged from 1 to 853 birds (mean=51, median=18 birds). Thirty-three percent of all backyard flock owners had multiple bird species on their premises. These premises primarily had backyard chickens (82.9 percent). Fewer premises had exhibition birds/game fowl (8.5 percent), and ducks/geese (11.5 percent). Other types of birds were reported on 30 percent of premises; the most commonly reported species were pigeons, turkeys, peafowl, parrots, and cockatiels. Besides birds, 35 percent of owners had other livestock species on their backyard premises, 76 percent had dogs/cats, and 8.5 percent reported other non-bird species.

Housing types

The majority of respondents (59.6 percent) reported housing birds outdoors in cages or coops, with 28 percent housing birds outdoors in open top pens or enclosures, and only 7 percent housing birds indoors. Only 5 percent of respondents reported keeping birds individually tethered, and 35 percent reported having free-range birds.

Illness and mortality

Sixty-four percent of case premises reported bird illness, and 65.7 percent reported mortality. The mean time reported between onset of illness and presumptive detection was 9.6 days (median=6.0, range 1-90 days). The mean time between onset of mortality and presumptive detection was 10.1 days (median=4.7 days, range 1 to 90 days). As an indicator of background morbidity and mortality, the percentage of control premises reporting illness was 10.5 percent and mortality was 17.6 percent.

Risk factors – Univariate analysis

- Flock size

  Case premises reported larger flock sizes than control premises. The odds of being a case were significantly greater for flock sizes greater than 100 birds (OR = 11.6, 95% CI: 6.4-21.0) or from 20 to 99 birds (OR = 5.0, 95% CI: 3.0 – 8.5) when compared with flock sizes of fewer than 20 birds.

- Bird types

  Case premises were more likely to report having flocks that included exhibition birds or other non-chicken bird species than control premises (OR = 7.7, 95% CI: 4.6-12.8).

  The odds of becoming a case premises were also higher when roosters comprised more than 50% of the adult birds in the flock (OR=4.3, 95% CI: 2.7-6.7).

- Contact with other domestic and wild birds

  Although only 8.8 percent of case premises reported keeping birds at other premises, the odds of being a case were higher (OR = 3.9, 95% CI: 1.8-8.2) when birds were kept at multiple locations.

  A high percentage of both case and control premises reported having neighbors with birds (75.9 percent and 55.0 percent, respectively); however, premises that reported that their birds visit neighboring properties or that their neighbors' birds visit their property did not have increased odds of becoming a case. Contact with wild birds (OR = 3.5, 95% CI 2.0-6.2) was associated with greater odds of becoming a case premises.

- The use of Newcastle vaccine

  The percentage of premises reporting the use of Newcastle vaccine was low overall (6.9 percent). The percentage of case premises that reported using Newcastle vaccine was much higher than the percentage of controls that reported using Newcastle

vaccine (18.9 percent vs 5.6 percent, respectively), and the risk of disease was greater among flocks that reported use of Newcastle vaccine (OR = 4.2, 95% CI: 2.4-7.5).

Risk factors – Multivariate analysis

Many of the risk factors described previously are related. A multivariate analysis was performed in order to provide adjusted odds ratios for risk factors, while taking into account the interrelationships among these flock management characteristics and behaviors. For the multivariate analysis including both versions of the questionnaire, 103 cases and 579 controls were examined. Larger flock sizes (OR = 3.9, 95% CI: 2.2-7.1 for 20-99 birds; and OR = 5.7 95% CI: 2.8-11.7 for flocks with more than 99 birds), the presence of game fowl on the premises (OR = 4.6, 95% CI 2.5-8.6), and having greater than 50 percent of adult birds as roosters (OR = 2.4, 95% CI 1.4-4.1) significantly increased the odds of becoming infected. A nested analysis looking only at questions found in the newer version of the survey (84 cases and 622 controls) identified these same factors, as well as wild bird contact with domestic birds (OR = 3.1, 95% CI: 1.7-5.9), and having neighbors with birds (OR = 2.2, 95% CI: 1.2-3.9) as significant risk factors.

Summary

These results suggest that flock size, ownership of exhibition birds, a high proportion of roosters in the flock, and housing that facilitates contact with nearby domestic and wild birds are risk factors for vND infection in this population. Some of these practices have been shown to be risk factors in other studies or previous vND outbreaks in the United States, as summarized below. However, not all epidemiology questionnaires were complete, and it is likely there is misclassification bias for some of these results, such as the type and number of birds on premises, the number of owners, and use of Newcastle vaccine; therefore, results should be interpreted with caution.

Summary of Historical Epidemiologic Risk Factors

An epidemiological study of backyard premises during the 2002-2003 California vND outbreak identified the following risk factors for vND infection on premises: presence of game fowl, presence of feral chickens, flock sizes larger than 40 birds, and multiple owners of a flock. Epidemiological descriptions of infected backyard premises in the 1971-1974 outbreak identified contact with infected commercial layer farms as the primary source of infection, followed by active trading of birds among backyard flocks and purchases of infected exotic birds from dealers. The severity of infection among commercial premises during the 1971-1974 outbreak was attributed to the high density of egg-laying premises and extensive contact among those premises. In both the 1971-1974 and 2002-2003 California vND outbreaks, a suspected risk factor for vND infection in commercial premises was movement of contaminated equipment, such as egg carts.

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Table 2. Characteristics of backyard case premises (confirmed/presumptive positive for vND), dangerous contact (DC) premises, control premises (C), and odds ratios (OR) and p-values calculated by univariate logistic regression (dangerous contacts excluded).

Characteristic	Level	n			OR	p-value
		Case	DC	Control		
Number of birds	1-19	20/125	8/43	385/698	Ref	
	20-99	64/125	9/43	245/698	5.0	**<0.001**
	100+	41/125	8/43	68/698	11.6	**<0.001**
Bird species on premises	Backyard chickens	98/125	23/25	635/695	0.34	0.207
	Exhibition birds	37/125	5/25	36/695	7.7	**0.005**
	Ducks/geese	18/125	5/25	82/695	1.3	0.329
	Other species	45/125	8/25	217/695	1.2	**0.019**
Adult birds >50% roosters		43/103	3/23	84/583	4.3	**0.001**
Owners keep birds on other premises		12/119	1/23	19/676	3.9	**<0.001**
Nonbird species or wildlife on premises		17/67	3/9	38/193	1.4	0.328
Housing	Inside home	3/93	0/19	52/671	0.4	0.126
	Outdoor open top	34/93	10/19	217/671	1.2	0.417
	Outdoor cage/coop	76/93	13/19	458/671	2.1	**0.009**
	Individual tether	6/93	0/19	43/671	1.0	NA
	Free range	46/93	10/19	266/671	1.5	0.072
Movement of new birds onto the premises within 30 days prior to the interview		12/121	2/24	44/674	1.7	0.123
Movement of birds off the premises within 30 days prior to the interview		8/119	0/23	30/651	1.5	0.33
Give/sell eggs		11/92	2/19	79/662	1.0	NA
Neighbors have birds		66/87	13/19	357/649	2.6	**<0.001**
Birds visit neighbors		16/88	2/18	392/624	1.8	0.063
Wild birds have contact with domestic birds		77/92	16/20	392/660	3.5	**<0.001**
Newcastle disease vaccine	No	84/122	22/25	589/683	Ref	
	Yes	23/122	2/25	38/683	4.2	**<0.001**
	Unsure	15/122	1/25	56/683	1.9	0.776

Table 3. Adjusted odds ratios (OR) for significant risk factors identified in multivariate regression analyses.

Characteristic	Level	OR	p-value
Number of birds[1]	1-19	Ref	
	20-99	5.4	**0.04**
	100+	9.0	**0.001**
Game fowl on premises[1]		4.8	**0.001**
Adult birds >50% roosters[1]		2.4	**<0.001**
Neighbors have birds[2]		2.2	**0.007**
Wild birds have contact with domestic birds[2]		2.6	**0.003**

[1]Results from analysis that included questions found on both versions of the survey (102 cases and 538 controls)

[2]Results from analysis that included questions found only on the newer version of the survey (84 cases and 604 controls)

V. ESTIMATING DISEASE SPREAD

A. Flock Disease Spread Model–Early Outbreak

Methods

An epidemiologic scenario was developed in InterSpread Plus® v. 6.01.44 (Stevenson et al., 2013) to model the introduction and spread of vND from confirmed premises in San Bernardino county, California following the first case detection. Commercial and backyard farm units from the Western United States (17 states) were incorporated into the model. The Farm Location and Animal Population Simulator was used to generate likely farm locations based on geospatial characteristics, with backyard farm locations adapted from current and historic outbreak-related data. Model parameters were developed to reflect the impact of sustained outreach activities, incorporate preliminary experimental data on viral pathogenesis in chickens, include current strategies for active surveillance of commercial operations, and describe the potential geographic extent of disease spread during the silent-spread period. The model was updated regularly in order to provide timely results to the response during the early phase of the outbreak.

Results

Summary outcomes for a 300-iteration scenario were generated from ten seeded-sites. The seeded sites were based on the latitude/longitude of initial confirmed cases of vND in San Bernardino County. Simulations include control activities implemented in the vND response, including outreach, quarantine, euthanasia/depopulation of detected premises, movement controls, tracing, and active and passive surveillance. Note: These outcomes are based on a completely naïve poultry population. The variable levels of vaccination applied within backyard farms is not explicitly modeled in this scenario.

The summary of results and their potential implications for the current vND outbreak are as follows:

- Initial disease spread commonly involves direct movements of infectious birds, but local spread becomes more prevalent as outbreaks become greater than 50 infected premises.

  Direct contacts associated with live animal movements accounted for 36 percent of spread for simulated outbreaks that resulted in less than 50 infected premises, and 27 percent of spread for simulated outbreaks that resulted in 50 or more infected premises.

  Local area spread became more prevalent as simulated outbreaks became larger, being responsible for 56 percent of disease spread for simulated outbreaks that resulted in 50 or more infected premises.

  Implications: As the number of detected premises continues to increase, outcomes from simulated outbreaks suggest that local spread of vND among premises

might be responsible for additional infections. Local spread is associated with distance between infectious and susceptible premises and represents mechanisms of spread that are difficult to trace, such as movement of free ranging birds, wildlife, or fence-line contact. Good biosecurity practices and measures are the best way to prevent local spread (e.g., keeping outside birds in cages, moving cages away from neighboring fence lines, repairing damaged/missing fences, rodent control, covering/tarping cages to decrease wildlife/rodent/loose-chicken exposures, and the spread of vND viral particles into the environment).

- Small backyard operations[5] are the primary premises involved in outbreaks; large backyard operations or commercial poultry farms have a lower likelihood of becoming infected.

  Across all simulated outbreaks, large backyard operations represented slightly less than 1 percent of all infected premises, and commercial poultry farms represented 0.14 percent of all infected premises.

  vND-infected small backyard operations in 100 percent of all simulated outbreaks, large backyard operations in 22 percent of all simulated outbreaks, and commercial poultry farms in 7 percent of simulated outbreaks.

  All spread to commercial operations resulted from indirect contact (e.g., people or vehicles moving from operation to operation) with infected, primarily small backyard operations.

  Implications: Unless generated by indirect contacts with infected backyard operations, outcomes from simulated outbreaks suggest a low probability of spreading vND to commercial farms.

- The extent of spread for simulated outbreaks is primarily in San Bernardino, Los Angeles, and Riverside counties.

  When considering disease spread within the silent period of the outbreak (three days prior to the first observation of clinical signs to the day of first detection), spread from infected premises in San Bernardino County to backyard chicken premises in Riverside County occurred in 66 percent of simulated outbreaks and to backyard chicken premises in Los Angeles County in 65 percent of simulated outbreaks.

[5] In the model operations are defined as follows:

1) Commercial poultry farms: more than 75,000 table egg laying chickens, or more than 100,000 meat-type chickens, or more than 30,000 meat-type turkeys
2) Large backyard operations: more than 1,000 birds but fewer than the number of birds described for commercial operations
3) Small backyard operations: fewer than 1,000 birds

In the current modeling scenario, 42 percent of simulated outbreaks involved 50 or more infected premises, and 19 percent of outbreaks involved 100 or more infected premises.

Implications: Simulated outbreaks suggest future detections in other Southern California counties, most commonly Riverside and Los Angeles. In addition, some infected premises might not be detected due to natural viral elimination from these premises (i.e., birds die and go unreported) and/or no new, naïve birds being brought onto previously infected premises.

B. Comparing Alternative Control Strategies–Mid-Outbreak

Methods

As the outbreak progressed, selected parameters were revised from preliminary scenarios described previously to compare the impact of alternative control strategies on the severity and duration of simulated vND outbreaks. This analysis was performed and supplied to the Incident Coordination Group approximately 3 months into the outbreak.

Summary outcomes for a series of four 250-iteration scenarios were generated from 57 selected sites. The initially infected sites in the model were based on the latitude/longitude of initial confirmed cases of vND in San Bernardino and Riverside counties and from premises frequently infected during the silent spread period identified in previous modeling analyses. Each simulated outbreak was allowed to run for a maximum of 365 days from detection of the first infected premises. All disease spread was considered lateral spread between infected and susceptible farms. Simulations varied in the availability of resources for conducting disease control activities, including outreach, quarantine, euthanasia/depopulation of detected premises, movement controls, tracing, and active surveillance. We assumed a completely naïve population, and the variable levels of vaccination possibly applied within backyard farms was not modeled explicitly.

Four levels of response were evaluated. A specific combination of integrated control strategies was associated with each response option, with a general increase in response intensity from response 1 to 4 (see Appendix B for detailed information on specific activities modeled in each response option). Disease control activities are identical for the first 161 days of each scenario to reflect the actual outbreak response up to that point in time. Alternative disease control activities, based on resource level, were applied at day 162 of each iteration (75 days post first detection). The model was run for 250-iterations for each of the four response options.

A summary comparison of response options and associated control activities are described in Table 4. The 'X's are provided to estimate a qualitative comparison between control strategies. They are not intended to approximate a quantitative comparison between response options.

Table 4. Qualitative summary comparison of the four alternative response options examined.

Response Option	Surveillance Capacity	Surveillance Zones	Movement Restrictions	Depopulation Capacity	Depopulation Zones
1	X	X	X	X	X
2	XX	X	XX	XX	X
3	XX	XX	XX	XX	XX
4	XXX	XX	XXX	XXX	XXX

Results

The best response option was dependent on the desired outcome. If limiting disease spread, as expressed by the mean number of infected backyard premises, was the only goal, response option 4 achieved the greatest reduction in the number of infected backyard premises. Reducing the total number of infected commercial premises was best achieved with response options 3 or 4.

Both response options 3 and 4 reduced the likelihood of extremely large outbreaks. However, any increase over response option 1 reduced the mean number of infected backyard premises, suggesting that minimal response is unlikely to achieve an adequate reduction in disease spread among backyard premises.

Outbreak duration, as expressed by the percentage of simulated outbreaks continuing into the months following the application of the response option was shortest, on average, for response options 3 or 4. Pronounced differences were observed when comparing response options 1 or 2 with response options 3 or 4, with little difference observed between response options 3 and 4.

Surveillance effectiveness, as expressed by the percentage of infected premises that were detected through passive and active surveillance activities, was significantly improved under response option 4, in comparison with any of the other response options. Little difference was observed in detection rates between response options 1 and 2, with some improvement observed with response option 3.

With all response options, the predominant site of disease spread shifts from San Bernardino County to Los Angeles County shortly after applying the alternative response. This shift was most pronounced with response options 3 or 4. Surveillance surges within the first 30 days post-implementation of the response option generally increased the rates of detection in San Bernardino County and reduced further spread within the county, to the extent that the majority of future infections occurred in Los Angeles County.

The largest and longest simulated outbreaks frequently involve significant disease spread within Los Angeles County, irrespective of the selected response option. A relatively small number of simulated outbreaks became extremely large (greater than 1,000 infections) and persistent (remaining active for at least 3 months following the selection of a response strategy), irrespective of the selected response option.

C. Within-Flock Transmission Model

Within-flock models and their results are used to evaluate surveillance options, support risk assessments, and assess different control measures. Statistical distributions for bird-level disease state durations are key inputs for within-flock disease transmission models.

We estimated bird-level disease state durations and a lower bound on the rate of transmission (β) using experimental data available from the peer-reviewed literature and unpublished data provided by the USDA, ARS, Southeast Poultry Research Laboratory (SEPRL). The estimated parameters were then used to predict the time to detect vND in an unvaccinated, 50-bird, backyard flock, based on observation of increased mortality (2 or more dead birds within a 3-day period).

Methods

Estimating the latent and infectious periods and time to death at the bird level

For this analysis, we defined the latent period as the interval between when an individual bird is exposed to the virus and when it begins shedding virus in detectable concentrations. We estimated the distribution of the latent period from viral shedding data collected on various days post inoculation (DPI), as reported in experimental studies in the literature and from unpublished SEPRL data[6]. Data were available from 122 unvaccinated chickens. Oropharyngeal swabs were collected at specific sampling times post inoculation and starting on 1 or 2 DPI. These data points represented the CA 2018 vND strain, CA 2002-2003 vND strain, and a mesogenic vND strain. An additional 73 data points (birds) were available for the time to death post inoculation (observed at daily intervals). These data included unvaccinated chickens inoculated with vND-CA 2002-2003, vND-CA 2018,vND-Peru 2008 or vND-India 2012. Contact bird data from unvaccinated birds were not included for estimating the infectious period, as data was only available for five birds, and the first sampling time was 2 days post contact. The non-inoculated birds in this experiment all died by day 6 post contact, indicating that the range of time to death is comparable to that for inoculated birds.

The infectious period was defined as the interval from when an individual bird begins shedding virus in detectable quantities to when it either recovers or dies. In several experimental studies, only the time to death was observed, and oropharyngeal swabs were not collected. We jointly fit the parameters of the latent and infectious periods given all of the observed data, including instances in which only the time to death was observed.

We used the Metropolis MCMC algorithm implemented in R for parameter estimation. The three chains were run for 10,000 iterations with burn-in of 2,000 iterations. There was no significant autocorrelation beyond 60 lags. Uniform priors with wide limits that included the MLE estimate were used in the current analysis.

[6] Courtesy of Kiril M. Dimitrov, Helena L. Ferreira, Mary Pantin-Jackwood, Tonya L. Taylor, Iryna V. Goraichuk, Claudio L. Afonso, David L. Suarez

Estimating the rate of transmission (β)

The adequate contact rate is a key parameter that determines the rate of within-flock spread. In the SEIR model, the adequate contact rate or the transmission parameter (β) is the average number of contacts that a bird has with other birds per unit time, such that the contact can transmit infection. We estimated the adequate contact rate using data provided in Miller et al., 2003, in which the transmission to contact birds was studied. We used direct forward simulation to obtain the posterior distribution for the adequate contact rate, given the observed experimental data on viral shedding and the timing of death for the contact birds.

Estimating Time to Detection in Unvaccinated Flocks

We estimated the time to detection in backyard flocks of 50 unvaccinated birds using a stochastic within-flock simulation model (SEIR), applying the maximum likelihood estimates of the parameters (as described above) and a trigger criteria of observing 2 or more dead birds within a 3-day period.

Results

Latent and infectious periods and time to death at the bird level

- Latent Period Parameters

  The mean latent period was 0.40 days (95% CI: 0.30 – 0.51 days).

- Infectious Period

  The mean infectious period was 4.33 days (95% CI: 4.03-4.98 days). The maximum likelihood estimate for the infectious period was shape parameter of 13.07 (95% CI: 3.6-18.6) and a scale of 0.33196 (95 % CI: 0.23-1.33).

- Time to Death

  The maximum likelihood estimate for the bird-level mean time to death was 4.73 days (95% CI: 4.45-5.4 days).

Rate of transmission (β)

There was considerable uncertainty for this parameter, given the limited amount of data available. However, based on the estimated posterior, a value of 1.7 contacts per day (95% CI: 1.69-9.79 adequate contacts per day) may be used as a conservative estimate.

Time to detection in unvaccinated flocks

Under the baseline scenario, the time to detection was 5.5 days (95% PI: 4-7 days) based on 20,000 iterations of the model.

D. Spatial and Spatiotemporal Patterns of the Outbreak

Knowledge of disease patterns in space and time can identify areas at higher risk for disease spread and allow disease control, prevention, and surveillance strategies to be implemented effectively (Ward, 2007). We performed a spatiotemporal analysis on confirmed and presumptive positive vND in backyard premises in California. We obtained data on confirmed

and presumptive positive premises from in-person interviews using the CDFA Non-Commercial Premises Virulent Newcastle Disease Epidemiology questionnaire, which were entered into the USDA's Emergency Management Response System (EMRS). For population data, we used the results of a spatial analysis predicting the geographic area and density of backyard bird ownership in California at the census block level (see Section III, Part A: Predicting Areas of Backyard Bird Ownership).

Methods

We used spatial and spatiotemporal scan statistics to detect significant high-risk clustering of vND cases (Kulldorff, 1997). For the analysis, we defined cases as confirmed or presumptive positive premises. Data from 137 cases detected from May 16 to August 25, 2018, in Los Angeles, Riverside, San Bernardino, and Ventura counties, were included in the analysis. Case information consisted of the location and reported date of onset of clinical disease. Cases were aggregated at the census block level within each county. Population information consisted of the estimated number of premises of predicted backyard bird ownership in each census block for the outbreak area. We used the centroid (latitude, longitude) of each census block as location information for the analysis.

A Poisson model was used to estimate the number of cases that might be expected to occur in the absence of any clustering. For both the spatial and spatiotemporal cluster analyses, data were scanned with a 5-km radius spatial window. For the spatiotemporal cluster analysis, a temporal window of 15 days was used, which is the higher range of the flock-level incubation period of vND. We determined statistical significance (p-value < 0.05) of clusters using the likelihood ratio test and Monte Carlo simulation implemented in SaTScan (version 9.6).

Results

The 137 detected cases from May 16 to August 25, 2018, were located within 14 control areas. The cases were located within 31 census blocks, with the number of cases ranging from 1 to 26 premises within an individual block. San Bernardino County had the highest number of reported cases, with 91 of the 137 detected cases occurring in this area (Figure 5).

The primary (or, most likely) spatial and spatiotemporal statistically significant clusters (log likelihood ratio = 264.92 and 114.01, respectively; p-value <0.001 for both) of detected vND cases occurred in the same control area in San Bernardino County (Figure 6). In the spatial cluster, 75 cases were reported out of an estimated at-risk population of 222 premises with predicted backyard bird ownership (or, 34 cases per 100 premises at risk). Based on the Poisson model, 1.15 cases would be expected to be detected from this population size; therefore, 65.2 times as many cases were observed as would be expected to be reported in this area. In the primary spatiotemporal cluster, 26 cases occurred out of an estimated population at risk of 174 premises from June 26 to July 10, 2018 (Figure 7). In this cluster, the relative risk of cases occurring in this area and time period was 242.20 times more likely, relative to outside this area (Table 5).

An additional three secondary statistically significant spatial and spatiotemporal clusters (p-value < 0.01) were identified within three control areas in Los Angeles, Riverside, and San Bernardino counties (Figure 6). The number of cases within the spatial clusters ranged from 10 to 17 cases within an estimated population of 250 premises with backyard birds (or, 4 to 7 cases per 100 premises at risk). The number of cases within the spatiotemporal clusters ranged from 5 to 10 cases within an estimated population of 237 premises with backyard birds, which occurred from May 23 to August 15, 2018 (Table 5 and Figure 7). The relative risk of cases occurring within these areas was highest in Los Angeles County, followed by Riverside and San Bernardino counties.

Twenty-four of the 137 cases detected during the time period for this analysis did not occur in any spatial or spatiotemporal cluster. In addition, there was no clustering identified in 10 of the 14 control areas. Only one case was detected in Ventura County; no areas of spatial or spatiotemporal clustering were identified in this county.

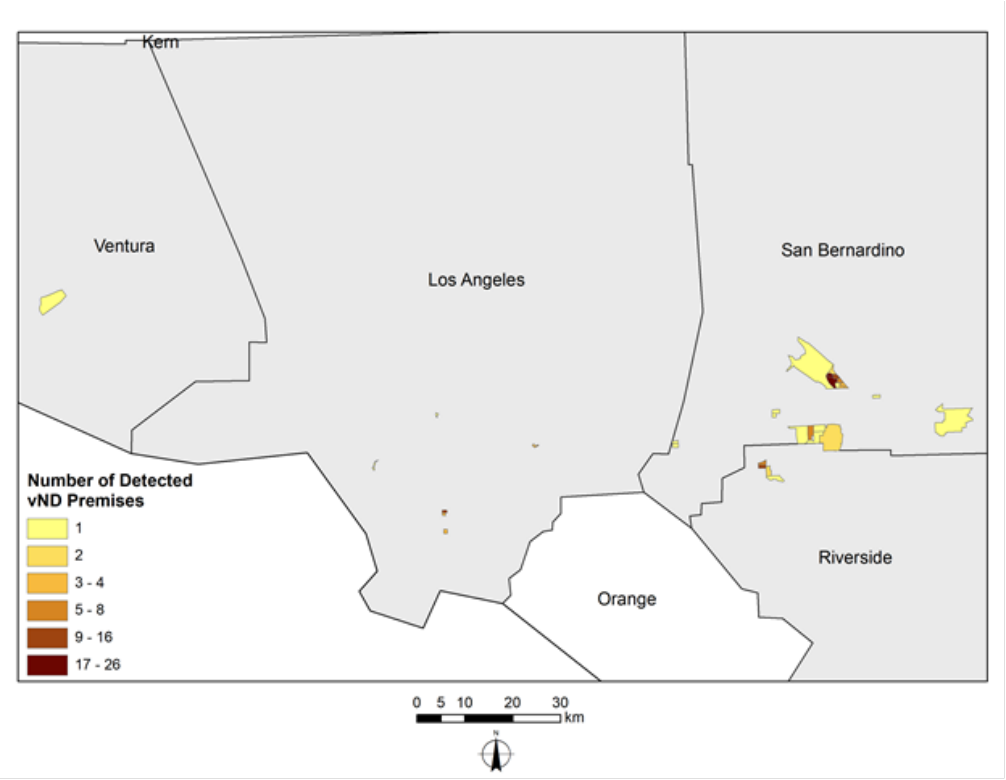

Figure 5. Cumulative number of confirmed and presumptive positive vND premises detected in California from May 16 to August 25, 2018; data are aggregated at the census block level.

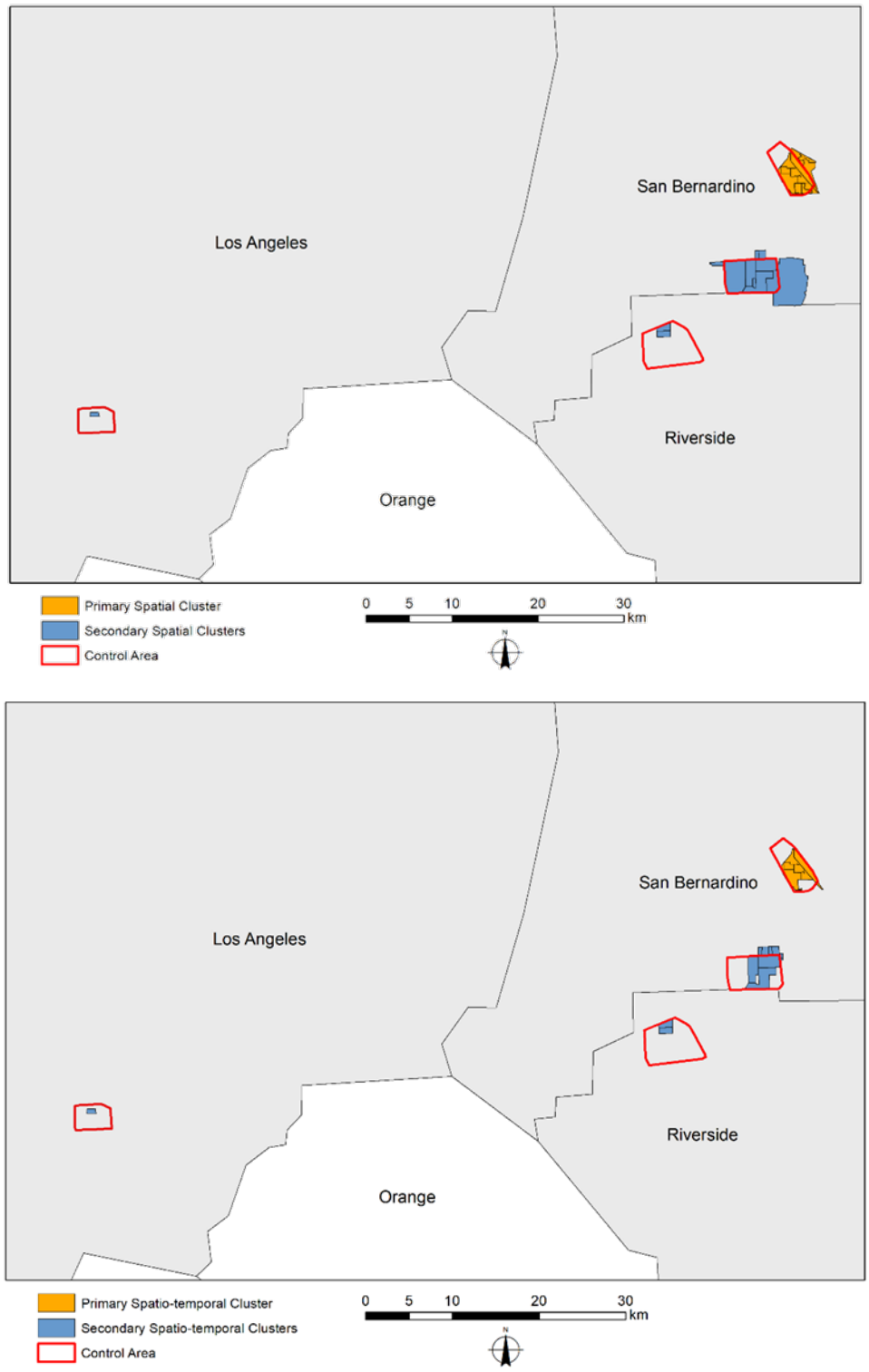

Figure 6. Location of spatial (upper) and spatiotemporal (lower) clusters of vND in California from May 16 to August 25, 2018.

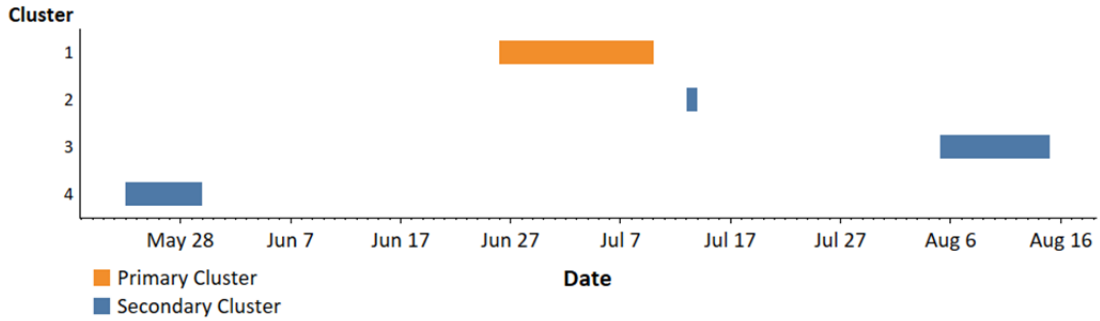

Figure 7. Time period of occurrence of spatiotemporal clusters of vND in California from May 16 to August 25, 2018. Colors shown relate to the lower part of Figure 6.

Table 5. Spatiotemporal clusters of vND cases in California from May 16 to August 25, 2018.[a]

Cluster[b]	Radius (km)	Time Period	Estimated Population[c]	No. Census Blocks	No. Cases	No. Exp.	Log Likelihood Ratio	Relative Risk
San Bernardino County								
1	1.36	June 26 – July 10, 2018	174	6	26	0.13	114.01	242.20
4	2.13	May 23 – 30, 2018	158	7	7	0.06	26.08	114.87
Los Angeles County								
2	0[d]	July 13 – 14, 2018	2	1	5	0.0002	45.65	25,544.73
Riverside County								
3	0.71	August 5 – 15, 2018	77	2	10	0.04	44.90	250.77

No.: number; Exp.: expected
[a]All clusters were statistically significant (p-value < 0.001)
[b]1, primary cluster; 2–4, secondary clusters
[c]Number of premises with predicted backyard bird ownership
[d]Radius is zero as there is only one census block in the cluster

Conclusions

Results identified specific geographic areas at the census block level within four vND control areas of significant spatial and spatiotemporal disease clustering. The primary spatial and spatiotemporal clusters were located within the same control area in San Bernardino County, identifying this area as the location of the highest occurrence of vND cases detected from May 16 to August 25, 2018. This finding is consistent with the subsequent increase in outbreak response activities initiated in this area based on epidemiologic investigations during the end of the time period that this clustering occurred (June 26 – July 10, 2018).

The spatiotemporal cluster identified in Los Angeles County had the highest relative risk of vND occurrence (RR: 25,544.73; Table 5). Although the clustering occurred over a two-day time period (July 13 – 14, 2018) within an area with low numbers of predicted backyard flocks, the results indicated that this area might have a high risk of vND spread. In the weeks following the

period included in this analysis, a sharp increase in the number of detected flocks occurred in this area, and enhanced disease detection and control activities were established.

This approach has some limitations. vND cases may be underreported, which can result in misclassification of cases and non-cases. In addition, actual data of true backyard bird ownership in the outbreak area remains limited. We used an estimated population at risk based on the predicted number of premises of backyard ownership using 2002 census block data. As such, the true number of premises with backyard birds used in this analysis may be under- or overestimated, resulting in the number of detected clusters and estimated risk to be over or underestimated.

Case detections have been ongoing in the California vND outbreak area after the time period of this analysis. The addition of newly detected cases could further enhance and/or change the results presented here. Future analyses will incorporate additional cases and evaluate the spatial distribution of risk factors that might further explain areas at higher risk for vND occurrence.

In conclusion, the identification of significant spatial and spatiotemporal clustering patterns of vND in California from May to August, 2018, support control strategies of targeting high risk areas for disease spread with increased response efforts in order to maximize the effectiveness of disease response strategies and control the outbreak.

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VI. ACKNOWLEDGEMENTS

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This report would not have been possible without a large group of researchers, epidemiologists, laboratory staff, and data scientists who participated in the various analyses, and the drafting and review of this report. We appreciate their dedication and professionalism in providing the best information possible to help bird owners reduce the risk of Newcastle disease spread.

APPENDIX A: QUESTIONNAIRE

California Department of Food and Agriculture
CA VND 2018
Non-Commercial Premises
Virulent Newcastle Disease Epidemiology Questionnaire

Investigator name: _____Date of Investigation: _____/_____/_____

Investigator name: _____

Quarantine # _____ Date Quarantine Issued: _____/_____/_____

1. Name of **Premises Owner**:

_____
(First) (MI) (Last)

2. Premises Address (location of birds):

_____

_____

Latitude: _____ Longitude: _____

3. Premises Owner Telephone #:
   a. Mobile: _____
   b. Home: _____
   c. Other: _____

*If **Premises Owner** is the **Bird Owner** skip to Question 7*

4. Name of **Bird Owner**:

_____
(First) (MI) (Last)

5. Bird Owner Address: _____

_____

6. Bird Owner Telephone #: _____

7. Other than the interviewee, how many **other** owners with birds are on this premises: #_____

8. How many birds do you have on the premises today? # _____

9. What percent of the adult **chickens** are: a) Roosters %_____
b) Hens %_____

10. Which of the following birds are on the premises? *Complete table below.*

Type of Bird	**# Adults**	**# Young birds**	**Total**
Backyard Poultry	a	b	c
Exhibition Birds/gamefowl	d	e	f
Ducks/Geese	g	h	i
Other Specify j	k	l	m
Other Specify n	o	p	q

11. Which of the following animals are on the premises (potential fomites)?

a) Livestock (Horses, Cattle, Swine, Sheep, Goats) ☐1 Yes ☐3 No
b) Dogs/Cats ☐1 Yes ☐3 No
c) Other (specify _____) ☐1 Yes ☐3 No

12. Which of the following housing types are used to house birds?

a) Inside the home ☐1 Yes ☐3 No
b) Outdoor **open** top poultry pen or enclosure ☐1 Yes ☐3 No
c) Outdoor cages or coops - **fully enclosed** ☐1 Yes ☐3 No
d) Individually tethered ☐1 Yes ☐3 No
e) Free range ☐1 Yes ☐3 No
f) Other (Specify_____) ☐1 Yes ☐3 No

13. Has there been an increase in illness in your birds on your premises? ☐1 Yes ☐3 No

a) If yes, how many days ago did the birds first show signs of illness: _____days

Which of the following clinical signs of illness have you observed?

Check all that apply.

b)	Not eating	☐1 Yes ☐3 No
c)	Coughing/gasping	☐1 Yes ☐3 No
d)	Depressed	☐1 Yes ☐3 No
e)	Twisting of the neck	☐1 Yes ☐3 No
f)	Paralysis	☐1 Yes ☐3 No
g)	Diarrhea	☐1 Yes ☐3 No
h)	Swellings around the eyes and neck	☐1 Yes ☐3 No
i)	Sudden death	☐1 Yes ☐3 No
j)	Other (specify_____)	☐1 Yes ☐3 No

14. Have there been any deaths in your birds on this premises during the past 30 days? ☐1 Yes ☐3 No

a) If yes, when did the first bird die? _____/___/_____

b) If yes, how many birds died in the first 7 days? # _____

c) If yes, how many birds have died in the past 7 days? # _____

15. Do you keep any birds at another premises? ☐1 Yes ☐3 No

a) If yes, where are the birds housed?

_____

_____

16. Have you brought new birds onto this premises during the past 30 days? ☐1 Yes ☐3 No

If Yes, list date and name the source and location of the new birds:

Date	Source/Location
___/___/___a	_____b
___/___/___c	_____d
___/___/___e	_____f

17. Have any of the following had contact with your birds, feed or water sources on your property in the last 30 days?

a) Wild birds (e.g., pigeons, doves, sparrows) ☐1 Yes ☐3 No
b) Neighborhood/community chickens ☐1 Yes ☐3 No
c) Wild animals ☐1 Yes ☐3 No

18. Have any of your **birds** left these premises during the last 30 days? ☐1 Yes ☐3 No

If Yes, for what purposes listed below were the birds moved?

Purpose	**Date**	**Destination (City/State)**	**# of birds**
Sale	a	b	c
Show	d	e	f
Competition	g	h	i
Veterinary care	j	k	l
Gift/trade m	n	o	p
Other Specify q	r	s	t

If Yes, did any birds leave and then return to these premises? ☐1 Yes ☐3 No

19. Do you give away or sell **eggs** from this premises? ☐1 Yes ☐3 No

20. Do your neighbors have birds? ☐1 Yes ☐3 No
*If **No**, skip to Question 23.*

*If **Yes**, please note location(s) on the map at the end of the questionnaire.*

21. When not cooped, do your birds ever visit the neighbor's property? ☐1 Yes ☐3 No

22. Do your neighbor's birds ever come onto your property? ☐1 Yes ☐3 No

a) If Yes, do the neighbors birds have contact with your birds? ☐1 Yes ☐3 No

23. Do you have **family members or close friends** who own/keep birds? ☐1 Yes ☐3 No

If Yes, do any of the following situations occur (evaluating direction of exposure):

a) Your family or friends handle birds when they visit. ☐1 Yes ☐3 No
b) When visiting family/friends do you handle their birds. ☐1 Yes ☐3 No

24. What is the name and location of the store(s) where you get feed and supplies for your birds?

Name	Location (City)
_____a	_____b
_____c	_____d
_____e	_____f

25. Have the birds on your premises **today** been vaccinated with Newcastle vaccine? ☐1 Yes ☐2 Unsure ☐3 No

Vaccine does not protect against disease!

a) If Yes, at what age(s) were your birds vaccinated with Newcastle vaccine?

26. Have you seen any dead wild birds on your premises in the last 30 days? ☐1 Yes ☐3 No

If Yes, what type of wild bird(s)?

_____a _____b

_____c_ _____d

Additional comments, observations and leads:

Insert Google Maps Image of the premises or draw a map and specify bird locations. Please indicate which neighbors, if any, have birds.

I _____certify that I have _____birds on / / @ _____
(owner signature) (number) (date and time)

APPENDIX B: MODELING SCENARIO DESIGN

Control Activities Associated with Respective Response Options

Scenario Design Overview

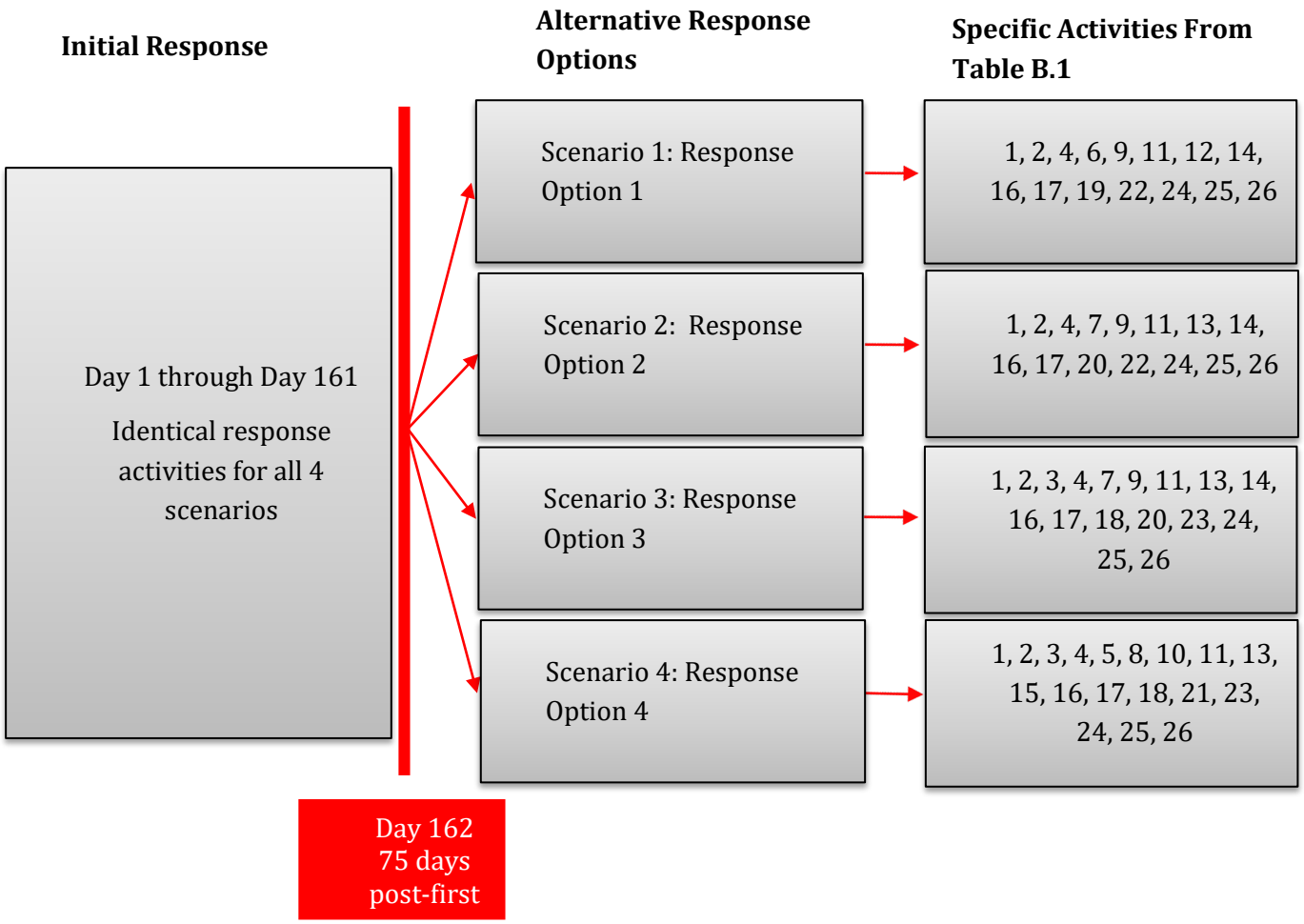

Table B.1 Individual Control Activities Included In Response Options

	Control Activity	Response Options 1	2	3	4
1	Depopulation: detected backyard premises	X	X	X	X
2	Depopulation: backyard premises in proximity to detected backyard premises in Muscoy	X	X	X	X
3	Depopulation: backyard premises in proximity to detected backyard premises in other high-risk zones (e.g.,Bloomington, Fontana, Riverside)			X	X
4	Depopulation: detected commercial premises	X	X	X	X
5	Depopulation: backyard premises in proximity to all detected backyard premises				X
6	Depopulation: capacity (low – maximum of 6 backyard premises per day)	X			
7	Depopulation: capacity (medium – maximum of 10 backyard premises per day)		X	X	
8	Depopulation: capacity (high – maximum of 30 backyard premises per day)				X
9	Movement restrictions for live animal movements originating from zoned backyard premises (low capacity – 30% of high capacity)	X	X	X	
10	Movement restrictions enhanced for live animal movements originating from zoned backyard premises (high capacity)				X
11	Movement restrictions for live animal movements originating from zoned commercial	X	X	X	X
12	Movement restrictions for live animal movements originating from traced premises (low capacity – 50% of high capacity)	X			
13	Movement restrictions for live animal movements originating from traced premises (high		X	X	X
14	Surveillance – Passive: Sick calls – initiates active surveillance visit (low public disease awareness)	X	X	X	
15	Surveillance – Passive: Sick calls – initiates active surveillance visit (high public disease awareness – results in greater number of calls and surveillance visits)				X
16	Surveillance – Active: 1-km radial zone around detected backyard premises	X	X	X	X
17	Surveillance – Active: Irregular zone surge (Muscoy) [enhanced surveillance for backyard premises]	X	X	X	X
18	Surveillance – Active: Irregular zone surge (e.g., Bloomington, Fontana, Riverside) [enhanced surveillance for backyard premises]			X	X
19	Surveillance – Active (post-irregular zone surge): Low capacity – fewest number of backyard premises eligible for surveillance (approx. 30% of high capacity)	X			
20	Surveillance – Active (post-irregular zone surge): Medium capacity (approx. 67% of high capacity)		X	X	
21	Surveillance – Active (post-irregular zone surge): High capacity – greatest number of backyard premises eligible for surveillance				X
22	Surveillance – Active: baseline response time after zone formation (approx. 2X longer response time tnan for enhanced response)	X	X		
23	Surveillance – Active: enhanced response time after zone formation			X	X
24	Surveillance – Active: weekly to bi-weekly sampling of commercial premises	X	X	X	X
25	Tracing live animal movements originating from detected farms (movements occurred prior to detection)	X	X	X	X
26	Tracing indirect contacts originating from detected commercial farms (movements occurred prior to detection)	X	X	X	X

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