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A Quantitative Risk Assessment for the Likelihood of Introduction of Highly Pathogenic Avian Influenza Virus Strain H5N1 into U.S. Hunter Retriever Dogs

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SUMMARY

Highly pathogenic avian influenza (HPAI) strain H5N1 has received great attention with regard to its potential spread to North America. This quantitative risk assessment, which is primarily based on wild bird carriage of HPAI from East Asia to Alaska, was conducted to assess the likelihood of a hunter retriever dog becoming infected after harvesting an infected waterfowl during the Alaskan hunting season. Using Monte Carlo Simulation with @Risk software, the expected probability of a hunter retriever dog becoming infected is 2.3×10^{-8} . This model can serve as a tool for decision makers in assessing the risk of HPAI strain H5N1 introduction into Alaska's hunter retriever dogs.

Keywords

Alaska; avian influenza; dogs; quantitative risk assessment; waterfowl

Since late 2003, highly pathogenic avian influenza (HPAI) strain H5N1 has led to the slaughter and death of millions of poultry and wild aquatic birds. In Southeast Asia, where the disease is endemic, migratory waterfowl (ducks, geese, and swans) have proved to be the natural reservoir for all avian influenza A virus (27). This zoonotic and contagious disease, which infects foxes, felines, dogs, pigs, horses, and other aquatic animals (2,25), has infected 442 and killed 262 people, yielding an overall fatality rate of 59% in regions of Asia, Europe, and Africa as of September 27, 2009 (35).

There are many possible routes for the introduction of HPAI into the United States, either intentionally/unintentionally or naturally (26,34). Studies (6,20) indicate that migratory birds contributed to the introduction of H5N1 in Europe. Many believe Alaska, a unique crossroads at which migratory flyways from Asia and North America overlap and in which species of birds that winter in southern Asia return and breed each summer, is the most likely location in which H5N1 would first occur in North America if it was to be introduced by migratory birds (10). For the purpose of this assessment, only the natural route of entry involving wild migratory birds carrying (asymptotically) HPAI strain H5N1 from Asia to Alaska was considered. With reports of H5N1 virus transmission and H5N1 virus adaptation to new species, there is a need to focus on hunter retriever dogs and migratory bird movement from Asia to Alaska during Alaska's waterfowl hunting season.

Hunting dogs, whose job it is to retrieve migratory waterfowl that have been shot by hunters, warrant special attention (15). Dogs may also have a role in the adaptation of HPAI strain

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H5N1 to mammals and its subsequent transmission to humans (7). This quantitative risk assessment gives estimates of the likelihood of introduction of HPAI strain H5N1 into U.S. hunter retriever dogs during Alaska's hunting season.

MATERIALS AND METHODS

The premise in any problem-solving process in any discipline consists of problem identification/characterization and identification of solutions to manage the problem. Consistent with this premise, we used what we call the Epidemiologic Problem-Oriented Approach (EPOA) methodology (9), a two-step process that allows for the systematic collection, organization, and analysis of epidemiologic information, as represented in Fig. 1. The information gathered to create the structured knowledge base was used in the development of this quantitative risk assessment. The EPOA is based on epidemiologic principles that are fundamental in the development of structured knowledge bases about diseases and the underlying framework that decomposes and re-synthesizes the epidemiology of the risk agent, in this case, the HPAI virus strain. The EPOA is composed of two intertwined triads: the Problem Identification/Characterization triad and the Problem Management/Solution/Mitigation triad. Each triad is composed of three pillars: Agent, Host, and Environment pillars and Therapeutics/Treatment, Prevention/Control, and Health Maintenance/Promotion pillars for the two triads, respectively. The two triads are linked together by diagnostic procedures and surveillance systems.

Based on the knowledge base developed using the EPOA, a scenario tree (Fig. 2) was developed to determine a pathway of events that would lead to the introduction of HPAI into the United States and that would ultimately lead to the infection of hunter retriever dogs. The scenario tree also provides visual representation of sequences of possible events (16,18,19,33).

The risk scenario pathway was divided into four phases (nodes) for analysis. The first phase (P_1), which depends on disease condition in Asia and long-distance migration of infected birds, dealt with the potential for the infected waterfowl to reach Alaska. The second phase (P_2), which depends on the number of infected waterfowl arriving and susceptible bird populations in Alaska, dealt with the contact between infected waterfowl and susceptible bird populations. The third phase (P_3), which depends on the prevalence of the disease and the number of hunters in Alaska, dealt with the probability of hunting-infected waterfowl. Finally (P_4), phase 4, which depends on the number of dogs used for hunting, dealt with estimation of the likelihood of a hunter retriever dog harvesting an infected waterfowl.

For each of these risk-associated events (Nodes 1–4), there is a probability (P_1 – P_4) of conditions that cause the persistence of the disease agent in the chain of events. The product of the probabilities, P_1 , P_2 , P_3 , and P_4 , is the probability that HPAI is introduced into Alaskan a hunted waterfowl population harvested by retriever dogs (Table 1).

ASSUMPTIONS MADE

In this study the following assumptions were made:

1. Only waterfowl of the Anatidae family were assumed to be capable of introducing HPAI virus into Alaska.
2. HPAI virus has no physiologic impact on the ability of waterfowl to migrate long distances.
3. Asian waterfowl have the same psychological flying behavior as North American waterfowl with respect to the number of resting days (Asian and North American

waterfowl rest for the same number of stopover days while undergoing spring migration to Alaska).

4. The estimates of HPAI prevalence in Alaskan waterfowl are based on low pathogenicity avian influenza (LPAI) prevalence, which is already circulating in Alaskan waterfowl.
5. Alaska prevalence represents birds engaged in long- and short-distance migration during the Alaska migration season.
6. If a dog harvests an infected waterfowl, the dog is infected.

EVIDENCE GATHERING AND PARAMETER ESTIMATION

All the distributions used in this manuscript are the @RISK-specific designations of distribution functions. In @RISK, probability distributions are functions, each of which represents a type of probability distribution: for example, *Pert* and *Uniform*, which in @RISK are represented as *Risk Pert* and *Risk Uniform*, respectively.

Node 1. Do Asian infected waterfowls carry HPAI strain H5N1 to Alaska?

The number of migratory birds that moves between Asia and Alaska, (*AMB*), is estimated to range from a minimum of 1.5 million (MM), to a most-likely value of 2.3 MM (11), to a maximum of 6.612 MM birds (29).

$$AMB = \text{RiskPert}(1.5\text{MM}, 2.3\text{MM}, 6.612\text{MM})$$

The same study also reported that of the *AMB* population, 561,000 are waterfowl (*W*). The proportion of Asian migrating waterfowl (modeled by beta distribution; *BD*) is given by

$$BD = \text{RiskBeta}(W+1, AMB - W+1).$$

Thus, the number of Asian waterfowl, *NAW*, that migrate from Asia to Alaska is given by

$$NAW = AMB \times BD.$$

Parameter *WD* represents the total number of days that Asian migratory birds winter in Asia. This is the nesting period that Asian migratory birds spend in Asia before departure for spring migration. The *WD* parameter is used to estimate the time interval in days for continuous exposure of migratory birds to HPAI while they are nesting in Asia.

Avian influenza virus circulates continuously from November to March in wintering areas where Asian migratory birds nest before departing for spring migration (8,12). The total number of days that Asian migratory birds winter in Asia (*WD*) ranges from a minimum of 105 days (*D*) to a maximum of 113 *D* (5,8). Thus,

$$WD = \text{RiskUniform}(105D, 113D).$$

The prevalence (*P*) of avian influenza in Asia ranges from 0 to 0.03 (4,12,14). Among the winter sites, both, LPAI and HPAI viruses were isolated from migratory birds of the family

Anatidae. Observations of monthly prevalence in virus isolation were fit to a distribution that would produce a goodness-of-fit statistic value as low as that calculated for the observed data. A chi-square goodness-of-fit statistic indicates that inverse Gaussian distribution with $0.011199(\mu)$ and $0.0023(\lambda)$ was found to be the best fit given; there are fewer than 30 data points:

$$P = \text{RiskInvgauss}(\mu, \lambda).$$

To determine the total number of Asian infected migratory birds (NIB), a Poisson distribution was used to characterize a constant and continuous probability that birds can be infected while nesting in Asia. The Poisson process models the number of events, *NIB* (Asian infected migratory birds), that occur in an interval, *WD* (wintering days), given *P* (prevalence) per wintering period:

$$NIB = \text{RiskPoisson}\left(\frac{WD}{P}\right).$$

According to the assumption made, in which only migratory birds of the family Anatidae (ducks, geese, and swans) are able to carry the HPAI strain H5N1 (8) over long distances, the number of infected waterfowl (*NWI*) is given by

$$NWI = \left(\frac{NAW}{AMB}\right) \times NIB.$$

Kalthoff *et al.* (13) experimentally inoculated five mute swans (*n*) with HPAI, which resulted in the survival of only one mute swan (*s*) for 21 days. Survival ability of infected waterfowls (*SIW*) after exposure from H5N1 was modeled using a discrete composite distribution nested in a beta distribution. Values of 1 and 0 were used to indicate survival and death, respectively, and were weighted by probability distributions *RiskBeta* and $1 - \text{RiskBeta}$, with shape parameters $s + 1 = 2$ and $n - s + 1 = 5$, respectively:

$$SIW = \text{RiskDiscrete}(\{1, 0\}, \{\text{RiskBeta}(2, 5), 1 - \text{RiskBeta}(2, 5)\}).$$

Assuming that infected and noninfected waterfowls can both attain a duck's flying speed (*DFS*) of a minimum of 40 miles per hour (*mph*), a most-likely speed of 50 *mph*, and a maximum speed of 60 *mph* (3,28), the flight speed of Asian infected migratory birds is given by

$$DFS = \text{RiskPert}(40\text{mph}, 50\text{mph}, 60\text{mph}).$$

Waterfowl's flight hours per day (*FHD*) could range from a minimum of 8 hr (*H*), to a most-likely value of 10 *H*, to a maximum of 12 *H* (3,28).

$$FHD = \text{RiskPert}(8H, 10H, 12H).$$

The distance from Asia to Alaska (DAA), as calculated from Japan (3776 miles [M]), Thailand (6017 M), and Indonesia (7032 M), was used to obtain the migration distance (ArcGIS 9.3.1, ESRI Inc, Redlands, CA).

$$DAA = RiskPert(3776M, 6017M, 7032M)$$

Assuming that Asian migratory birds exhibit the same psychological flying behavior as North American waterfowl, cumulative stopover days (SOD) ranged from a minimum of 7 days (D), a most-likely value of $10D$, to a maximum of $40D$ (17):

$$SOD = RiskPert(7D, 10D, 40D).$$

Therefore, the number of days it takes infected waterfowls to reach Alaska (NRA) is given by

$$NRA = \left\lceil \frac{DAA}{(DFS \times FHD)} \right\rceil + SOD.$$

If logic statement was used to determine if spring migration is less than or equal to 21 days (S), the survival period for waterfowls carrying HPAI (13) would be determined by

$$S = \begin{cases} 1 & \text{if } NRA \leq 21D \\ 0 & \text{if } NRA > 21D \end{cases}.$$

A function, based on the logic if an infected bird migrates in ≤ 21 days and survives and is still infected, was used to model the total number of infected waterfowls (NWI) that arrive in Alaska:

$$IF_2 = IF(S \times SIW, NWI, 0) = \begin{cases} NWI & \text{if } S \times SIW = 1 \\ 0 & \text{if } S \times SIW = 0 \end{cases}.$$

The probability P_1 , which is the probability that Asian infected waterfowls carry HPAI strain H5N1 to Alaska, is given by

$$P_1 = \frac{IF_2}{AMB - (NIB - IF_2)}.$$

Node 2. Do Asian infected waterfowl transmit HPAI virus to other migratory birds?

Asian migratory birds will be joined by a large number of North American migratory birds in Alaska as fall migration progresses (21). Assuming (Collins, pers. comm.) that a minimum of 30 million (MM), a most-likely value of 40MM, and a maximum of 50MM migratory birds winter in the Pacific flyway (WPF), the total number of North American migratory birds that nest in the Pacific Flyway can be modeled as

$$WPF = RiskPert(30MM, 40MM, 50MM).$$

From the 4-yr study of Miller *et al.* (17), which indicated that 65(*s*) of 129(*n*) northern pintails migrated to Alaska, the proportion of migratory birds from the Pacific Flyway that migrates to Alaska can be estimated by a beta distribution, thus:

$$BD_2 = (s+1, n - s+1).$$

Thus, the number of migratory birds from the Pacific Flyway that migrate to Alaska (*NMMA*) is given by

$$NMMA = WPF \times BD_2.$$

The total number of nondiseased migratory birds in Alaska (*TND*) is given by

$$TND = NMMA + (AMB - NIB).$$

Rate of contact (*C*) between diseased and nondiseased migratory birds was estimated by

$$C = \frac{TND}{IF_2}.$$

According to our assumption number 4, the estimates of virus transmission rate (*TR*) were based on the Alaskan LPAI. *TR* could range from a minimum of 0.03%, to a most-likely value of 2.5%, to a maximum of 3.1% (11):

$$TR = RiskPert(0.003, 0.025, 0.031).$$

The number of newly infected migratory birds (*NIMB*) was estimated by

$$NIMB = C \times TR \times IF_2.$$

The probability P_2 , which is the probability that infected waterfowl transmit HPAI virus to other migratory birds, is given by

$$P_2 = \frac{NIMB}{TND}.$$

Node 3. Were infected waterfowl hunted?

Different types of waterfowl (duck [*n* = 75,675], goose [*n* = 4673], sea ducks [*n* = 3998], and brants [*n* = 1058]) are harvested during Alaska's hunting season (23,24,30). The sum of each waterfowl harvest composition (*WHC*), modeled by individual mean (μ), SD (σ),

minimum value (min), and maximum value (max), was obtained from a truncated normal distribution:

$$WHC = \sum_{n=1}^4 RiskTNormal(\mu, \sigma, \min, \max).$$

During 2006 and 2007 sampling for highly pathogenic Asian H5N1 avian influenza in migratory birds in Alaska (31,32), 83 (x) infected hunter shot birds were observed over a period of 6 days (t). The mean number of infected hunter shot birds ($IHSB$) per day is given by

$$IHSB = \frac{RiskGamma(x, \frac{1}{t})}{2}.$$

Alaska hunting dates vary throughout the state, but the hunting season is no longer than 3.5 mo (107 days) for any species and region ($TAHD$) (22). The total number of infected hunted shot birds for the entire Alaskan hunting season is represented by

$$TIHB = IHSB \times TAHD.$$

The probability P_3 , which is the probability that infected waterfowls were hunted, is given by

$$P_3 = \frac{TIHB}{WHC}.$$

Node 4. Do retriever dogs harvest an infected waterfowl?

Waterfowl hunters in Alaska are grouped according to types of migratory birds hunted (23,24,30). The sum total of each category of active hunters (H), with individual mean (μ), SD (σ), minimum value (min), and maximum value (max), was modeled by a truncated normal distribution:

$$H = \sum_{n=1}^4 RiskTNormal(\mu, \sigma, \min, \max).$$

A survey from Pheasant forever (1) was used to estimate the probability of owning a dog (OD), owning two or more dogs ($O2D$), and using dogs for hunting (DH), thus:

$$\begin{aligned} OD &= RiskBeta(69, 120+1; 108,000 - 69, 120+1) \\ O2D &= RiskBeta(20, 736+1; 69, 120 - 20, 736+1) \\ DH &= RiskBeta(90, 685+1; 108,000 - (2 \times 20, 736)+1). \end{aligned}$$

Therefore, the number of Alaskan hunters who own a dog (NOD) is given by

$$NOD=OD \times H.$$

The number of hunters who own two or more dogs ($NO2D$) is given by

$$NO2D=NOD \times O2D.$$

The total number of dogs used for hunting (NDH) is given by

$$NDH=(NOD+(2 \times NO2D) \times DH).$$

The average number of waterfowl a hunter harvests each season (AWH) is given by

$$AWH=\frac{WHC}{H}.$$

The number of birds harvested by a hunter with a dog ($HBWD$) is given by

$$HBWD=AWH \times NOD \times DH.$$

The number of infected birds harvested by a hunter who used a dog for hunting ($IHBWD$) is given by

$$IHBWD=HBWD \times P_3.$$

The probability P_4 , which is the probability that retriever dogs harvest an infected waterfowl, is given by

$$P_4=\frac{IHBWD}{NDH}.$$

Finally, for a hunter dog to get infected with HPAI, the following sequences of events have to take place: 1) An infected migratory bird from Asia must reach Alaska; 2) Given 1, the infected migratory bird has to mingle with susceptible Alaskan migratory birds; 3) Given 2, a hunter in Alaska must hunt an infected waterfowl; and 4) Given 3, a hunter retriever dog must harvest an infected waterfowl. P_1 through P_4 are conditional independent probabilities, and their product is the probability that HPAI is introduced into Alaskan hunted waterfowl harvested by retriever dogs. Using introduction of HPAI (infected hunting dogs) as the dependent variable and the probabilities of the nodes in the scenario tree as independent variables, @Risk software was used for the sensitivity analysis (at 10,000 iterations) to single out factors that play the most significant role in the likelihood of introduction of HPAI to hunter retriever dogs.

RESULTS

The probability of a hunting dog harvesting an HPAI-infected waterfowl during the Alaska hunting season is less than or equal to 2.3×10^{-08} (range = 1.03×10^{-10} to 2.3×10^{-07} ; Fig. 3). Based on the current prevalence, the expected number of years before a hunter retriever dog harvests a waterfowl infected with HPAI strain H5N1 during the Alaskan hunting season is estimated to be 4.4×10^7 yr (range = 8.0×10^4 to 4.7×10^8). The fifth and 95th percentiles for the years are 2.4×10^6 and 1.3×10^8 yr, respectively (Table 2).

The sensitivity analysis showed that the congregation of Asian infected migratory birds and the prevalence of LPAI in Alaska (used to simulate the transmission of HPAI strain H5N1 to new susceptible migratory birds), respectively, produced the highest effect of 19% and 4.5% on the likelihood of a hunter retriever dog harvesting a waterfowl infected with HPAI strain H5N1 during the Alaskan hunting season (Fig. 4). Asian infected migratory birds and the LPAI prevalence in Alaska, respectively, had a -5.8% and a 2.5% degree of relation with the probability of a hunter retriever dog becoming infected after harvesting a waterfowl infected with HPAI strain H5N1 during the Alaskan hunting season (Table 3).

DISCUSSION

Under the circumstances and assumptions specified in this study, the expected value for a hunter retriever dog to become infected is 2.3×10^{-08} . This low risk estimate is mainly due to low prevalence of HPAI (8). In addition to the successful migration of Asian HPAI-infected migratory birds, the HPAI transmission rate (based on the data related to Alaska's LPAI transmission rate) was found to be the second most critical factor in the risk estimates. This is because of the high intensity of commingling in the Alaskan arctic water among migratory birds originating from different continents (34). It was previously stated that if Asian H5N1 strain is introduced into North America through Alaska, it would move southward with about 150,000 swans, 1 million geese, and 12 million ducks, beginning in August, with greater than 60% of the migrating birds oriented toward the Pacific Flyway (21). Dogs warrant special attention within the United States because of spring migration and the sport of waterfowl hunting, which may result in infection of dogs after harvesting of the infected birds. On the contrary, infected dogs show little to no clinical signs of infection with HPAI strain H5N1; therefore, dogs may have a role in the adaptation of HPAI virus H5N1 to mammals and in its subsequent transmission to humans (7).

A major problem encountered in developing this risk assessment model was the availability of the required data for the nodes in the scenario tree. This difficulty stemmed mainly from the limited scientific research in this area. Of greatest significance, there is an urgent need to investigate the effect of HPAI strain H5N1 on migratory birds' ability to migrate long distances. It should be noted that risk assessment is a dynamic process; the results from this study as well as the whole model can be updated to reflect the future status when new information and data become available.

Abbreviations

EPOA	Epidemiologic Problem-Oriented Approach
HPAI	highly pathogenic avian influenza
LPAI	low pathogenicity avian influenza

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Fig. 1.
EPOA, as applied to HPAI virus strain H5N1 (adapted from Habtemariam *et al.* (9)).

Fig. 2.
Scenario tree for HPAI virus introduction into U.S. hunter retriever dogs.

Fig. 3. Cumulative risk distribution for the probability of a hunter retriever dog becoming infected after harvesting an infected waterfowl with HPAI virus strain H5N1.

Fig. 4.

Regression sensitivity analysis for the likelihood of a hunter retriever dog harvesting an infected waterfowl with HPAI strain H5N1.

Table 1

Parameter estimation.^A

Event	Description	Equations and distribution	Reference
Node 1: Do Asian infected waterfowl carry HPAI strain H5N1 to Alaska?			
<i>AMB</i>	Asian migratory birds that move between Asia and Alaska	<i>Risk Pert</i> (1.5, 2.3, 6.612)	(11,29)
<i>BD</i>	Percentage of Asian migrating waterfowl 541,000 (<i>W</i>)	<i>Risk Beta</i> (<i>W</i> + 1, <i>AMB</i> – <i>W</i> + 1)	(29)
<i>NAW</i>	Number of Asian waterfowl	<i>AMB</i> × <i>BD</i>	
<i>WD</i>	Total days Asian migratory birds winter in Asia	<i>Risk Uniform</i> (105, 113)	(5,8,12)
<i>P</i>	Prevalence of HPAI in Asia	<i>Risk Invgauss</i> (0.011199, 0.0023)	(4,12,14)
<i>NIB</i>	Total number of Asian migratory birds infected	<i>Risk Poisson</i> (<i>WD/P</i>)	
<i>NIW</i>	Proportion of infected waterfowl	(<i>NAW/AMB</i>) × <i>NIB</i>	(8)
<i>SIW</i>	Survival of infectious waterfowl	<i>Risk Discrete</i> ({1,0}, {(2,5),1 – (2,5)})	(13)
<i>DFS</i>	Waterfowl flight speed	<i>Risk Pert</i> (40, 50, 60)	(3,28)
<i>FHD</i>	Flight hours per day	<i>Risk Pert</i> (8, 10, 12)	(3,28)
<i>DAA</i>	Distance from Asia to Alaska	<i>Risk Pert</i> (3776, 6017, 7032)	
<i>SOD</i>	Stopover days from Asia to Alaska	<i>Risk Pert</i> (7, 10, 40)	(17)
<i>NRA</i>	Days to reach Alaska from Asia	[<i>DAA</i> /(<i>DSF</i> × <i>FHD</i>)] + <i>SOD</i>	
<i>S</i>	Spring migration less than or equal to 21 days	<i>IF</i> (<i>NRA</i> , <i>NRA</i> ≤ 21 days)	(13)
	Evaluates migration and infected waterfowl survival	<i>S</i> × <i>SIW</i>	
<i>IF₂</i>	Number of Asian infected waterfowls that arrived in Alaska	<i>IF₂</i> = (<i>AND</i> , <i>NWI</i> , 0)	
<i>P₁</i>	Probability Asian infected waterfowl arrived in Alaska	<i>IF₂</i> / <i>AMB</i> – (<i>NIB</i> – <i>IF₂</i>)	
Node 2: Do Asian infected waterfowl transmit virus to other migratory birds?			
<i>WPF</i>	Number of migratory birds in Pacific Flyway	<i>Risk Pert</i> (30, 40, 50)	PC
<i>BD₂</i>	Percentage of migratory birds that flew to Alaska	<i>Risk Beta</i> (66, 65)	(17)
<i>NMMA</i>	Number of migratory birds that flew to Alaska	<i>WPF</i> × <i>BD₂</i>	
<i>TND</i>	Total nondiseased migratory birds in Alaska	<i>NMMA</i> + (<i>AMB</i> – <i>NIB</i>)	
<i>C</i>	Contact between disease and nondiseased migratory birds	<i>TND/IF₂</i>	
<i>TR</i>	Virus transmission rate	<i>Risk Pert</i> (0.003, 0.025, 0.031)	(11)
<i>NIMB</i>	Newly infected migratory bird	<i>C</i> × <i>TR</i> × <i>IF₂</i>	
<i>P₂</i>	Probability Asian infected waterfowls transmitted virus	<i>NIMB/TND</i>	
Node 3: Were infected waterfowls hunted?			
<i>TW</i>	Total Alaskan waterfowl harvest	<i>Risk T normal</i> (m, s, min, max)	(23,24,30)
<i>IHSB</i>	Infected hunted shot birds per day	<i>Risk Gamma</i> (83, 1/6)/2	(31,32)
<i>TAHD</i>	Total Alaskan hunting days	107	(22)
<i>TIHB</i>	Total infected hunted shot birds for season	<i>IHSB</i> × <i>TAHD</i>	
<i>P₃</i>	Probability infected waterfowl was hunted	<i>TIHB/TW</i>	
Node 4: Did retriever dogs harvest an infected waterfowl?			
<i>H</i>	Active waterfowl hunters in Alaska	<i>Risk T normal</i> (μ, σ, min, max)	(23,24,30)
<i>OD</i>	Percentage that own a dog	<i>Risk Beta</i> (69,121, 38,881)	(1)
<i>O2D</i>	Percentage that own two or more dogs	<i>Risk Beta</i> (20,737, 48,385)	(1)
<i>DH</i>	Percentage that use dog for hunting	<i>Risk Beta</i> (90,686, 66,529)	(1)
<i>NOD</i>	Number that own a dog	<i>OD</i> × <i>H</i>	

Event	Description	Equations and distribution	Reference
<i>NO2D</i>	Number that own two or more dogs	$NOD \times O2D$	
<i>NDH</i>	Total number of dogs used to hunt	$NOD \times O2D$	
<i>AWH</i>	Average number of waterfowls harvested by hunter	TW/H	
<i>HBWD</i>	Number of birds harvested by a hunter with a dog	$AWH \times NOD \times DH$	
<i>IHBWD</i>	Number of infected birds harvested by a hunter with a dog	$HBWD \times P_3$	
P_4	Probability dog harvests infected waterfowl	$IHBWD/NDH$	
	Total risk	$P_1 \times P_2 \times P_3 \times P_4$	

^A HPAI = highly pathogenic avian influenza; PC = personal communication.

Summary statistics for the probability of a hunter retriever dog becoming infected with HPAI after harvesting an infected waterfowl with HPAI during the Alaskan hunting season

Table 2

	Minimum	Mean	Maximum	5th Percentile	95th Percentile
Probability of a of hunter dog infection (Fig. 3)	1.03×10^{-10}	2.29×10^{-08}	2.32×10^{-07}	6.80×10^{-10}	8.71×10^{-08}
Number of years before first hunter dog infection (Fig. 4)	7970	4.36×10^{07}	4.66×10^{08}	2,425,437	1.29×10^{08}

Table 3

Regression and correlation coefficients for hunter retriever dogs harvesting an infected waterfowl with HPAI strain H5N1.

Rank	Name	Regression coefficient	Correlation coefficient
1	Asian infected migratory bird	0.194	−0.058
2	LPAI prevalence in Alaska	0.045	0.025
3	Asian migratory birds	−0.044	0.03
4	Infected shot birds	0.03	−0.005