CHRONIC WASTING DISEASE IN MULE DEER: DISEASE DYNAMICS AND CONTROL

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Abstract: We developed a mechanistic model to simulate dynamics of chronic wasting disease (CWD) in mule deer (*Odocoileus hemionus*) populations. The model projected age-specific disease dynamics, changes in population size, and effects of control strategies. We estimated parameters from observations of infected and uninfected mule deer in Colorado. We used Monte Carlo techniques to evaluate likely responses. Simulations of CWD epidemics were highly unstable. Disease was not sustained in projected populations when transmission rates were low, but CWD eliminated populations when more realistic transmission rates were used. We failed to produce stable coexistence of CWD in simulated mule deer populations. Even low CWD prevalence reduced potential harvest via combined effects of diminished per-capita production and decreased population density. Changes in CWD prevalence within populations were highly sensitive to transmission rate, and small decreases resulted in noticeable damping of prevalence increases. Simulated selective culling programs revealed the importance of initiating control while CWD prevalence was low (<0.01). Low selective culling rates ($<20\%$ of infected populations) effectively eliminated CWD if initiated when prevalence was low, but the likelihood of control diminished rapidly as prevalence increased. Management programs will likely require an effort sustained over many decades if eliminating CWD is the desired goal.

Key words: chronic wasting disease, Colorado, mule deer, *Odocoileus hemionus*, prion, simulation model, transmissible spongiform encephalopathy.

Infectious disease can play an important role in the ecology or management of a wildlife species. Historically, introduced diseases like rinderpest in African ungulates (Scott 1981) and pasteurellosis in bighorn sheep (*Ovis canadensis;* Miller 2001) have had catastrophic effects on host population performance. Although more sparing of infected populations, wildlife reservoirs of diseases such as bovine tuberculosis or bovine brucellosis pose potential threats to domestic livestock that compel economic and political pressure for eradication (Morris and Pfeiffer 1995, Thorne et al. 1997). Similarly, public health threats posed by rabies have driven costly attempts to manage this disease in wild carnivores throughout the Northern Hemisphere (Baer 1991, Rupprecht et al. 1995). Once introduced and established, most infectious diseases are extremely difficult to eliminate from free-ranging populations. It follows that a new or emerging wildlife disease should be carefully evaluated early on to assess both its potential importance and prospects for its effective management.

Chronic wasting disease is a unique transmissible spongiform encephalopathy (TSE) that occurs naturally in deer (*Odocoileus* spp.) and wapiti (*Cervus elaphus nelsoni*) native to North America (Williams and Young 1980, 1982, 1992; Spraker et al. 1997, Miller et al. 2000). As in other TSEs of domestic animals (scrapie, bovine spongiform encephalopathy [BSE], transmissible mink encephalopathy) and humans (kuru, classic Creutzfeldt-Jacob disease [CJD], variant CJD [vCJD]), the agent causing CWD has not been definitively identified. However, microscopic accumulations of protease-resistant prion protein (PrP^{res}) in brain tissue are consistently associated with clinical disease (Spraker et al. 1997, O'Rourke et al. 1998). Chronic wasting disease is the only TSE known to occur in free-ranging wildlife (Miller et al. 2000). At present, the sole epidemic focus of CWD in wild cervids is in north-central Colorado and southeastern Wyoming, United States, where up to 15% of mule deer and 1% of wapiti may be affected in localized management units (Miller et al. 2000). Chronic wasting disease should be regarded as an emerging problem: in addition to evidence of natural spread (Miller et al. 2000), recent detection of CWD in game-farm wapiti (U.S. Animal Health Association 1998) could present avenues for its introduction into wild cervid populations elsewhere.

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The epidemiology of CWD (Miller et al. 1998, 2000) most closely resembles that of scrapie in domestic sheep and goats (Hoinville 1996, Woolhouse et al. 1999). However, because CWD epidemics and studies thereof began relatively recently, many aspects of CWD epidemiology and its implications are uncertain. In particular, long-term epidemic dynamics and effects of CWD on deer and wapiti populations have not been determined. Moreover, a better understanding of CWD epidemiology is needed to develop and evaluate candidate strategies for prevention, control, and management. Quantitative models present useful tools for assembling and synthesizing knowledge about systems where data are few and processes are incompletely understood, and they form a necessary basis for developing adaptive strategies that most effectively combine active

management with research (Holling 1978, Walters and Holling 1990, Starfield 1997). We describe an individual-based epidemic model of CWD in mule deer developed to help evaluate current quantitative knowledge of relevant parameters and identify potential control strategies. This model will also serve as the basis for a fully spatial model that will be applied to evaluate large-scale control measures and design adaptive management strategies for limiting distribution and prevalence of CWD in free-ranging populations.

METHODS

Model Structure and Parameters

We developed an individual-based model for simulating the dynamics of CWD in mule deer in Colorado. Our model explicitly tracked the sex, age, disease state, transition from latent to infectious state, and death of each member of the population. The model included annual processes of recruitment, harvest, natural mortality, population census, and aging (Fig. 1A). In addition, we included 2 discrete periods during the year in which disease dynamics occurred. These periods are times when disease-caused mortality, infection, or conversion of latent to infectious individuals take place; they roughly corresponded to summer–fall (May–Oct) and winter–spring (Nov–Apr) periods. The model operated on a yearly time step.

Rates for all processes were determined by comparing, for each individual, a random number from a uniform distribution (0–1) to the rate of the process. For example, if the probability of death was 0.50 per year, an individual would die if the random number was ≤0.50. This process accounted for stochasticity inherent to binomial outcomes of events with a small number of trials.

Reference model parameters for stage-specific vital rates were derived from mule deer studies conducted in northeastern Colorado and elsewhere (Table 1). We did not incorporate density-dependent changes in recruitment or survival rates into the model because deer populations in endemic areas are currently at relatively low densities (Colorado Division of Wildlife, unpublished data). Instead, we used harvest to regulate the size of deer populations. We set population objectives for each deer population that corresponded to low, normal, or high population densities. Each year a population "census" was conducted and post-harvest population size recorded (Fig. 1A). Harvest level in the following year was determined
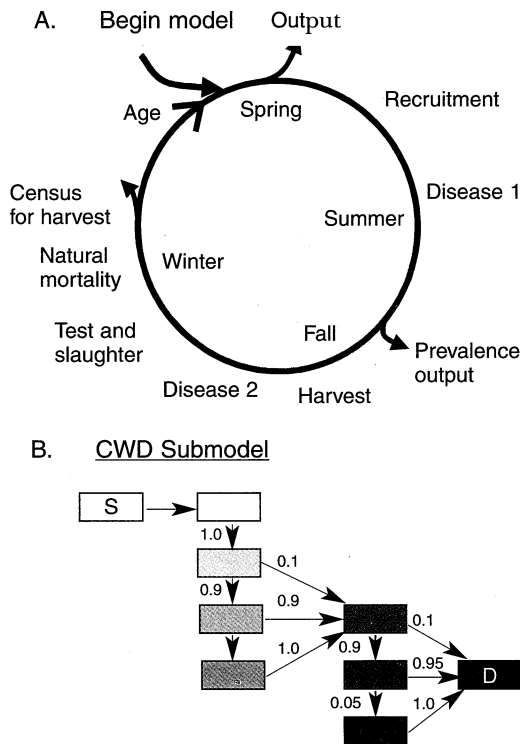

Fig. 1. (A) Flow chart with scheduling for simulated processes in the population model and (B) the CWD submodel. In (B), each box represents 1 disease period of approximately 6 months, and numbers are transition probabilities for disease period 2 (winter). Boxes represent susceptible (S), latent (Lat), infectious (Infx), and dead (D) individuals. Transition probabilities for disease period 1 (summer) are the same as winter, except the likelihood of infectious animals dying after 2 or 3 periods was 0.47 and 0.5, respectively, reflecting CWD-related mortality patterns in captive and free-ranging deer (Miller et al. 2000).

Table 1. Parameter estimates used in the individual-based epidemic model of chronic wasting disease dynamics.

Parameter	Value	Range	References
Survival			
Female: 1–10 yrs	0.85		White et al. 1987; Bartmann
11–16 yrs	Linear decline from 0.85–0		et al. 1992; Freddy et al. 1993;
Male: 1–9 yrs	0.85		Unsworth et al. 1999; Colorado
10–12 yrs	Linear decline from 0.85–0		Division of Wildlife (CDOW),
			unpublished data
Recruitment rate	0.57		White et al. 1987; Bartmann et al.
			1992; Freddy et al. 1993; Unsworth
			et al. 1999; CDOW, unpublished
			data
Fawn sex ratio	0.5		Freddy et al. 1993; CDOW,
(probability female)			unpublished data
Disease:			Williams et al. 2001; Miller et
Incubation period	(variable)	12–24 months	al. 2000; Williams and Miller,
Clinical course (infectious)	(variable)	6–24 months	unpublished data
Infectious contacts/6-month	0.725		Fitted to data
period			
Probability of vertical	0.05		Miller et al. 2000
transmission			

by evaluating whether the population corresponded to a low, normal, or high density and adjusting the harvest level appropriately (Table 2). Harvest levels were initially adjusted to maintain an uninfected population size of about 1,000 deer.

We based the model's representation of CWD in mule deer (Fig. 1B) on observations of cervids infected with CWD in research facilities and in the wild (Williams and Young 1980, 1982, 1992; Spraker et al. 1997; Miller et al. 1998, 2000; Williams et al. 2001; M. W. Miller, Colorado Division of Wildlife, unpublished data). Susceptibility to CWD appears relatively uniform across sex and age classes in mule deer (Williams and Young 1992, Miller et al. 2000). Although the route(s) of CWD transmission have not been elucidated, some form of lateral transmission appears most likely (Miller et al. 1998, 2000); the CWD agent is presumed to be shed in some combination of saliva, feces, urine, and/or placental tissues and fluids (Miller et al. 2000). Maternal (dam to fawn) transmission may occur, but is not particularly common (Miller et al. 2000).

Once deer are infected, it appears that CWD is progressive and invariably fatal; there is no evidence of either immunity to or recovery from CWD (Williams and Young 1992). The course of infection probably includes both latent and infectious periods that typically span 18–36 months (Miller et al. 2000). Initial infection most likely occurs through the alimentary canal (Sigurdson et al. 1999, Williams et al. 2001), with the earliest detectable accumulation of PrP[res] in attendant

Table 2. Simulated harvest levels for populations at low, normal, or high density.

Density	Females			Males		
	Fawns	Yearlings	Adults	Fawns	Yearlings	Adults
Low (< 500)	0.00	0.00	0.00	0.00	0.00	0.00
Normal (501–1,000)	0.01	0.02	0.07	0.02	0.06	0.20
High (>1,000)	0.03	0.05	0.10	0.03	0.09	0.27

lymphoid tissues. Deer experimentally infected with CWD developed signs of clinical disease ≥15 months later (Williams et al. 2001; E. S. Williams and M. W. Miller, unpublished data), lending plausibility to our selection of 18 months as a lower bound for incubation in natural infections. We believe infected deer become progressively "infectious" as disease progresses (Miller et al. 2000); for simplicity, we equate the transition from a latent to infectious state with the appearance of spongiform encephalopathy and onset of clinical signs (i.e., the latent period is equivalent to the incubation period), although such relationships have not been firmly established. Infectious deer remain capable of transmitting CWD until they die. Once clinical signs appear, however, deer rarely survive >12 months (M. W. Miller, unpublished data). Whether residual excreta or decaying carcasses can serve as additional environmental sources of CWD infection has not been determined (Williams and Young 1992; Miller et al. 1998, 2000; M. W. Miller, unpublished data), and consequently is not considered in our model.

To represent these disease processes in our model, we assigned each individual a disease state of susceptible, latent, or infectious. Susceptible individuals were those deer that had never harbored the infective agent. Latent individuals were deer that had received an infective dose of the infective agent but were not yet transmitting CWD. Infectious animals had contracted the disease, passed through latency, and were shedding the infective agent at a constant rate. Latent or infectious animals never recovered and were removed from the population only by death or dispersal. Transition of individuals from the latent to infectious state occurred as a probability based on the length of time the animal had been infected: deer in latency for ≤2 periods (≤12 months) could not progress to the infectious state, but all latent deer became infectious in ≤4 periods (≤24 months) after being infected (Fig. 1B). Once a deer became infectious, disease-caused mortality (the transition from infectious to dead) was handled similarly and the probability of death increased in each succeeding infectious period; almost all infectious deer (>97%) survived ≤3 periods (≤18 months). Using these parameters, the total potential duration of infection ranged from 18–42 months.

Determining probability of transition of individuals from susceptible to latent state (disease transmission) required a more complicated function. Our representation of CWD transmission was based on several assumptions (McCarty and Miller 1998, Miller et al. 2000). We assumed that each infectious animal produced an estimable number of infectious contacts per unit time, and that all individuals in the host population had an equal probability of contacting an infectious dose. Given these assumptions, McCarty and Miller (1998) showed that the probability of infection of a susceptible individual ($P_{(S \to I)}$) could be estimated as:

$$P_{(S \to I)} = 1 - \left(\frac{1}{N}\right)^{n\beta}$$

where N is total population size, n is the number of infectious individuals, and β is the number of infectious contacts per infectious individual per time step. We chose this mathematical representation over others (Anderson and May 1991) because the transmission parameter could be more easily estimated and all model parameters had intuitive biological interpretations. This formulation resulted in rates of disease transmission that were largely independent of overall population density, which is appropriate for species that tend to aggregate or use habitats in relation to quality. These characteristics are typical of most cervids, including mule deer. We assumed transmission was uniform across all sex-age classes.

Simulation Procedures and Reference Conditions

We used Monte Carlo techniques (Manly 1991) to evaluate the relative likelihood of simulated scenarios. To evaluate each set of parameter values we began each simulation with a population of 1,000 deer that included 4 infectious and 4 latent 2-year-old females. For each set of parameters, we conducted 250 simulations that each lasted 100 years. Each simulation was initialized with multiple infectious individuals because we wanted the initial prevalence of the disease to be very low, but we also wanted to ensure there were a sufficient number of infected animals to prevent CWD from rapidly disappearing from the population simply through stochastic effects (e.g., sampling error). We determined initial sex and age composition of the deer population by conducting simulations without disease and using the sex and age structure of the stable population to initialize subsequent simulations. Because harvest increased mortality rates of males relative to females, the initial population was female-biased and consisted of 408 males and 592 females.

Model response to input parameters was evaluated by determining the change in population growth or disease prevalence (sum of latent and infectious individuals) to a range of likely parameter values. We were most interested in dynamics of CWD prevalence and the impacts of disease-related mortality on population performance as measured by population persistence and productivity, and in the efficacy of potential management options for controlling or eliminating CWD in infected populations. Model results were ultimately evaluated by comparing simulated populations to independent observations on age-specific prevalence of CWD in mule deer from endemic portions of north-central Colorado (Miller et al. 2000).

Management Strategies

Currently, no vaccines or treatments exist for preventing or eliminating CWD infection (Williams et al. 2001). It follows that options for managing CWD are few (Miller et al. 2000), and revolve almost entirely around some form of population management. Because selective culling is likely to be much more effective in disease management than random culling (Barlow 1996), we focused primarily on evaluating treatments that target diseased animals for removal. Although nondestructive methods for detecting CWD in latent animals have not been fully evaluated, ongoing research seeks to identify tests that may permit early detection of infected individuals. Consequently, we compared the forecasted effects of selective culling programs affording early detection of infected animals (≥ 6 months of latency) to those where only clinically affected (= infectious; ≥ 18 months after infection) individuals could be detected; we varied the relative "program efficacy" (the product of sampling effort and "test" sensitivity) from 0.1 to 0.8. To evaluate

Table 3. Sensitivity of growth rate to vital rates in disease-free, unharvested populations.

% of reference	Female survival	Fecundity	Male survival
0.85	0.92 (0.05)	1.03 (0.02)	1.06 (0.02)
0.90	0.97 (0.03)	1.04 (0.02)	1.06 (0.02)
0.95	1.01 (0.02)	1.05 (0.02)	1.06 (0.01)
1.00	1.06 (0.01)	1.06 (0.02)	1.06 (0.02)
1.05	1.10 (0.01)	1.07 (0.01)	1.07 (0.02)
1.10	1.14 (0.01)	1.08 (0.01)	1.07 (0.02)
1.15	1.18 (0.01)	1.09 (0.01)	1.07 (0.03)

the utility of prospective management programs across a range of prevalence rates, we also projected the consequences of initiating management programs when CWD prevalence was low (0.01), moderate (0.05), or high (0.10).

Alternatively, management strategies for epidemic containment might rely on population manipulation, such as controlling population size, density, sex and age structure, or creating buffer zones without animals around infected populations. Buffer zones could be used to reduce the likelihood of dispersal of infected animals to uninfected populations. To evaluate the potential effects of reducing population density, and thereby dispersal and movement rates, we examined the likelihood of disease transmission into an uninfected population by starting runs with 1–7 infected, 2-year-old females and evaluating the persistence of CWD in the population.

RESULTS

Reference Conditions and Sensitivity Analysis

Populations without simulated disease or harvest grew at an average rate of 6.4% per year. For harvested populations, a mean harvest level of 12.8% of the population per year resulted in a stable population size. Harvested populations were more productive because harvest increased mortality rates of males, and these populations therefore contained a higher proportion of reproductively active females than unharvested populations. Productivity was relatively insensitive to changes in fecundity, survival rate of fawns of either sex, or survival of males (Table 3). In contrast, population growth rates were highly sensitive to changes in survival of adult females.

Mean population size and productivity of simulated populations infected with CWD contrasted sharply with uninfected populations. Uninfected populations exhibited relatively constant population sizes that were completely controlled by harvest. After a few years of infection, the average size of infected populations was smaller and much more variable than that of uninfected populations (Fig. 2). High variance in size of infected populations was caused in part by highly variable rates of increase in CWD prevalence and the resulting impact of disease on population productivity (Fig. 3). In some simulations, CWD rapidly increased in prevalence and population size immediately declined. In other simulations, initial rates of transmission were relatively low
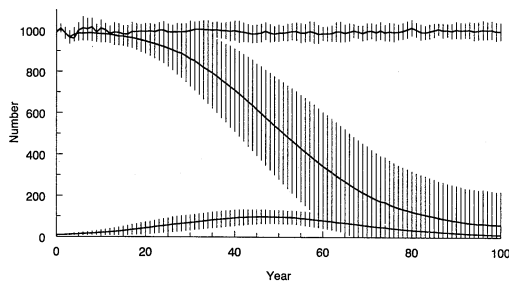
Fig. 2. Total number (mean ± 1 SD) of deer in uninfected (top line) and infected (middle line) populations, as well as the number (mean ± 1 SD) of infectious deer (bottom line) in infected populations; data are from 250 simulations using parameters in Tables 1 and 2. There were nearly equal numbers of infectious and latent deer. Disease did not persist in some very small, infected populations (<10 individuals) following death of all infected deer; data from these small uninfected populations were excluded because they resulted in an abrupt and misleading decline in the average size of uninfected populations in later time periods.

and prevalence changed slowly for an extended period—in some cases more than 40 years. Once CWD was firmly established in the population
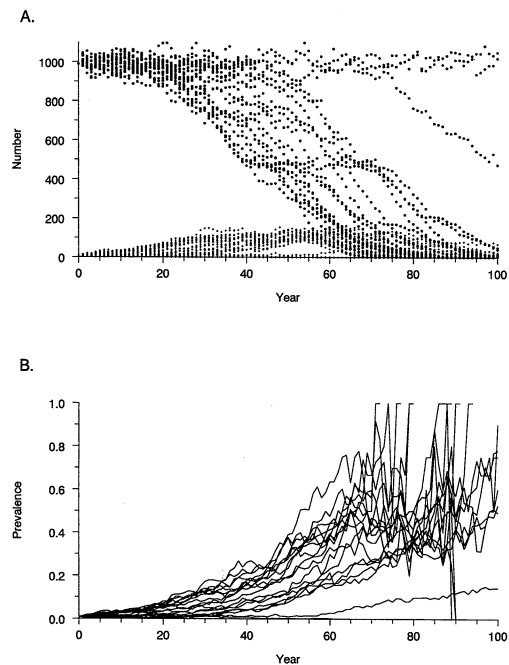

Fig. 3. (A) Population composition and (B) CWD prevalence in 20 representative simulations for 100 years, using reference parameters. (A) Number of susceptible (dots) and infected deer (+; sum of latent and infectious) in 20 simulations. (B) Change in CWD prevalence over time for the same 20 simulations. High annual variation in prevalence after about year 60 results from loss or addition of infected deer in very small populations. Note high variability in model results.
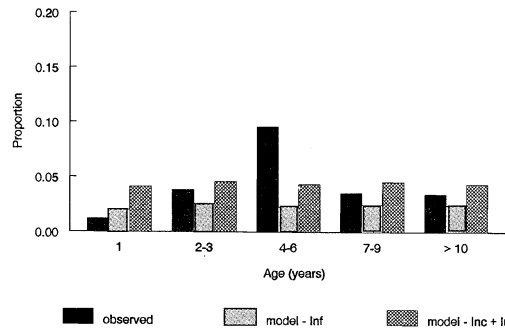

Fig. 4. Observed and simulated age-specific prevalence of CWD in mule deer; observed data are from Miller et al. (2000).

(e.g., prevalence increased to about 2%), the proportion of infectious animals in the population uniformly and rapidly increased and populations declined at a relatively consistent rate (Fig. 3). The proportional increase in infectious animals was largely due to a decline in the number of uninfected (susceptible) deer rather than a large increase in the absolute number of latent and infectious deer (Fig. 3).

Model results closely matched independent field observations of age-specific prevalence rates and the ratio of latent to infectious deer (Fig. 4), especially for older age classes. Simulated prevalence in young deer exceeded observations, but this discrepancy may be due to inability to detect CWD in brain tissue early in latency (Sigurdson et al. 1999, Miller et al. 2000). Simulated prevalence estimates included all latent and infectious animals, and the disparity in prevalence estimates in younger age classes between modeled and field data likely arose because these classes contain a higher proportion of individuals in early (i.e., non-detectable) stages of disease. Existing field data that base detection on examination of brain tissue will invariably underestimate true prevalence (Miller et al. 2000), particularly in fawns and yearlings where virtually all infected individuals are latent and many are not identifiable via available diagnostic methods.

Growth and productivity of infected populations were profoundly influenced by even low rates of infection (Fig. 5). Sizes of diseased populations initially declined because harvest rates were adjusted to maintain populations with close to 1,000 deer, and the rate of harvest did not respond to population size until there were fewer than 500 deer. A small decline in female survival due to disease-caused mortality (Table 1) resulted in annual growth rates of <1.0 (Fig. 5) and declining
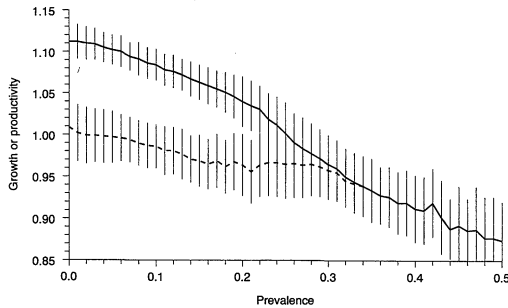
Fig. 5. Growth rate (dashed line) and productivity (solid line) of simulated deer populations infected with CWD. Growth rate is calculated from uncorrected population size while productivity is corrected for animals removed by harvest. In general, no deer were harvested from populations when prevalence exceeded about 0.25 because size of these populations fell below the threshold size for harvest (Table 2).

population sizes. The combination of smaller population size and decreased per capita productivity resulted in a rapid decline in the number of animals harvested as prevalence increased. In populations of >500 deer (populations harvested at a normal or high level; Table 2), this decline was linear (number harvested = 103 – 262 × prevalence; $P < 0.0001$), resulting in an average reduction in harvest of about 25% when CWD prevalence reached 10%.

Management of CWD

Efforts to control CWD are limited to activities that may reduce the number of infected animals in a deer population or otherwise alter the rate of transmission. Specific actions undertaken include culling and removal of obviously sick deer (when reported or observed) and enforcing regulations that prohibit feeding of big game species; in addition, policies and regulations have been established to preclude translocation of deer and elk from endemic areas.

Rates of increase in CWD prevalence and persistence in simulated populations were highly sensitive to small changes in transmission rates (Fig. 6). A 10% decrease in transmission rate resulted in a 3-fold increase in the likelihood that CWD would be eliminated from the population within 50 years, as well as a dramatic reduction in the rate of growth of CWD in the population. Rates of transmission higher than our reference parameter resulted in a rapid disappearance of the disease after about 50 years (Fig. 6), but this apparent reduction in persistence was due to the extinction of many infected populations. When we used the highest transmission parameter simulated

(0.80; Fig. 6), more than 90% of all infected populations were either extinct or had eliminated the disease (i.e., the few infected individuals in a very small population died) by the eightieth year of simulation. Under these conditions, CWD persisted to year 100 in only 2 of 250 simulations. The extinction of most infected populations resulted in highly variable rates of prevalence after about year 60, particularly in simulations with a high transmission rate (i.e., > 0.7 contacts per period; Fig. 6B).

Most simulated selective culling treatments effectively limited the rate of increase in CWD prevalence and eventually resulted in elimination of the disease. Only selective culling treatments that eliminated fewer than 10–20% of infected (latent and infectious) deer failed to eliminate the disease from virtually all populations after 80 years of treatment (Fig. 7). However, even high levels of effort that resulted in
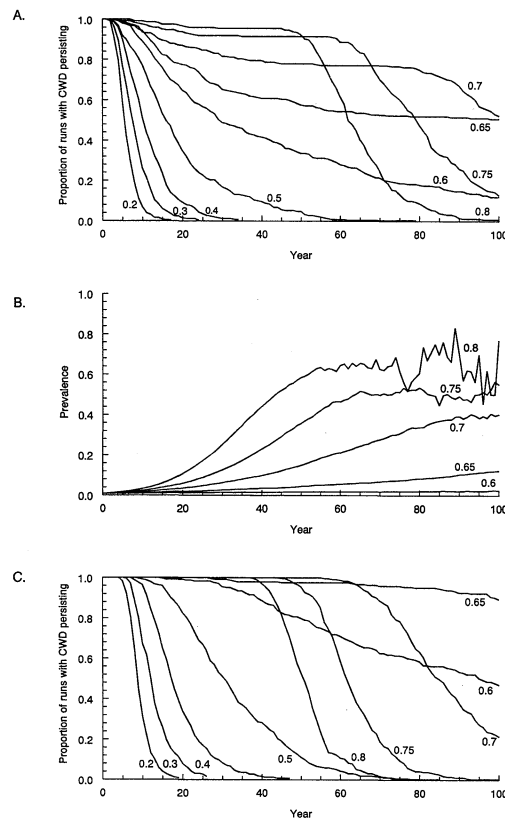

Fig. 6. Effects of a range of values of the CWD transmission parameter (β) on (A) persistence and (B) prevalence of CWD in populations initialized with 4 latent and 4 infectious 2-year-old females, and (C) persistence of CWD in populations with an initial CWD prevalence of 0.05.
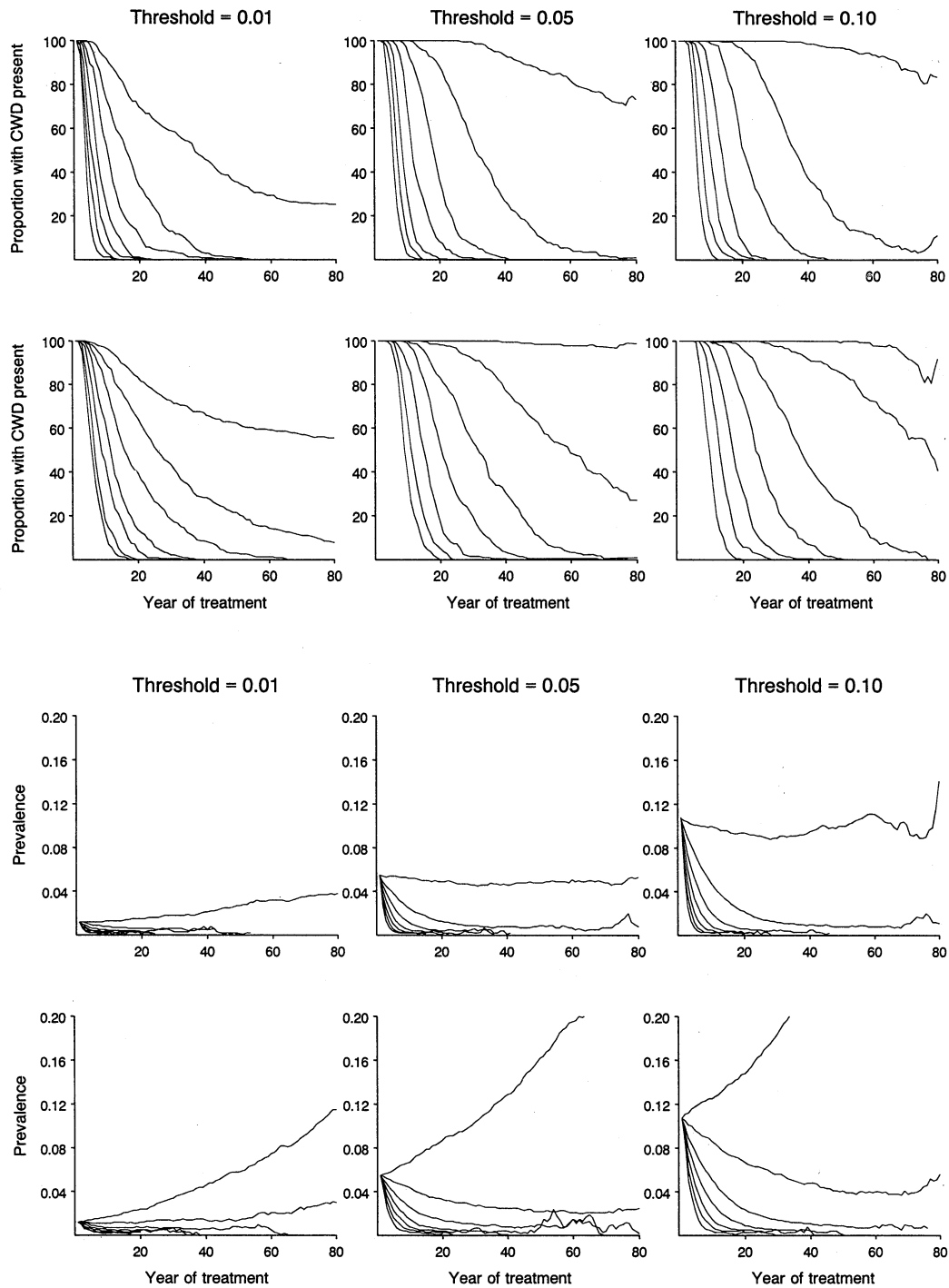
Fig. 7. Effects of test and slaughter programs on persistence of CWD (top 6 graphs) and prevalence (bottom 6 graphs). Simulated test and slaughter treatments were initiated in populations with threshold prevalence rates of 0.01, 0.05, and 0.10, using tests that permitted early identification of infected animals (after 6 months latency; first and third rows of graphs) or detection only of infectious animals (second and fourth rows of graphs). Lines are results from test and slaughter programs that examined 10%, 20%...70% of the entire population. The top 6 graphs show results from simulations in which 70% (left-most line in each graph) to 10% (line furthest to right or top of each graph) of the population was tested. The bottom 6 graphs show results from simulations in which 70% (lowest line of each graph) to 10% (top line of each graph) of the population was tested.

testing a large proportion of the population would require a program sustained for many years to ensure elimination of CWD, despite a very rapid initial decline in prevalence. A dramatic decline in the effectiveness of a specific selective culling strategy to eliminate CWD occurred when the program was initiated at a prevalence of 0.05 compared to 0.01.

The apparent effort necessary to eliminate CWD in infected populations clearly motivates efforts to determine the potential efficacy of actions that may reduce the likelihood of spread of the disease into uninfected populations. Population reductions may lower overall rates of dispersal or movements of infected animals into adjacent, uninfected populations. If movement rates and/or prevalence is low, simulations suggested that reducing the number of potentially infectious animals that can establish CWD in an uninfected population can have a large effect on reducing the proportional risk of transmission (Fig. 8). Our simulations suggest that efforts to prevent spread by reducing dispersal will require that the number of animals dispersing from infected populations must remain very low.

DISCUSSION

Chronic wasting disease appears to be an emerging epidemic among mule deer populations in northeastern Colorado and southeastern Wyoming (Miller et al. 2000); both its origins and its future remain uncertain. Because the magnitude and severity of this epidemic were recognized only recently, long-term trends in CWD dynamics have not been observed. Our model projections are generally consistent with the few estimated parameters from field data that are available for comparison. Modeled stage- and age-specific prevalence, as well as rates of change in prevalence over time, are all consistent with estimates derived from studies of affected deer populations (Miller et al. 2000). To the extent that modeled mechanisms of CWD transmission appear to offer at least a reasonable approximation of disease processes occurring in nature, it follows that this model provides plausible forecasts of future epidemic trends. The projected trends are, to say the least, unsettling. Left unmanaged, our model forecasts 2- to 4-fold increases in CWD prevalence over the next several decades with disease abating only with the extinction of infected deer populations. In light of an observed 10-fold increase in CWD cases among captive mule deer over a 4-year period (M. W.
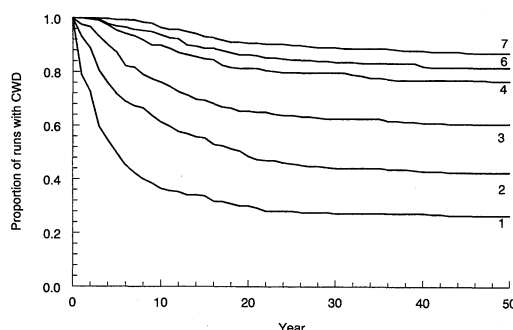

Fig. 8. Persistence of CWD in simulated deer populations as a function of the number of infectious 2-year-old females in the initial population. Numbers adjacent to lines are the number of infectious females used to initialize simulations.

Miller, unpublished data), such trends are clearly plausible.

A disturbing result of this modeling exercise was our inability to identify a set of realistic parameters that permits sustained coexistence of CWD in a wild deer population. All parameter sets simulated eventually resulted in extinction of the deer population or eventual loss of CWD from the deer population. CWD was naturally eliminated from simulated populations only under 1 of 2 conditions. In some cases, CWD did not persist in a large population because transmission from infectious individuals was insufficient, due to either a low transmission rate or to the death(s) of the few infectious individuals before transmission occurred. In a few other cases, small remnant populations decimated by disease-caused mortality recovered when the few infectious individuals remaining died before transmitting CWD, simply through chance events. The latter populations subsequently recovered to a large size (i.e., about 1,000) in the absence of CWD.

The slow initial rate of increase in prevalence of CWD and the eventual decimation of infected populations suggest that long-term persistence of CWD is likely to occur as a result of dispersal and the spatial structure of deer populations. Heavily infected populations may die out, while recently infected populations will continue to provide a source of infection and lead to long-term persistence and geographic spread of CWD. In northeastern Colorado, radiomarked deer typically have a high fidelity to seasonal ranges, but ranges used in summer and winter may be separated by >25 km (Siglin 1965; Kufeld et al. 1989; Kufeld and Bowden 1995; M. M. Conner and M. W. Miller, unpublished data); dispersal distances for

fawns may exceed 100 km. The potential for such movement emphasizes the need for coordinated regional plans if CWD is to be effectively managed, reduced, and/or eliminated.

As with any forecasting exercise, we recognize several limitations in our epidemic model of CWD. The biological mechanisms underlying CWD transmission are poorly understood, and as a result model mechanisms are at best a collection of educated guesses. Despite their apparent plausibility, there are undoubtedly other combinations of parameters and processes that could produce results consistent with the few field data available for comparison. In particular, the potential role of environmental contamination in CWD epidemiology warrants further exploration (Miller et al. 1998, 2000). Lack of independent, replicate parameter estimates and data on prevalence trends over time also limits our ability to verify model projections; consequently, we have much greater faith in short-term (10–20 yr) model projections than in those spanning many decades. In light of the limited distribution and recent emergence of CWD, it is not surprising that relatively few data are available for comparison. However, we encourage continued long-term surveillance to provide data on epidemic dynamics and research to improve understanding of CWD transmission. Because the present model included no spatial attributes, potential for and patterns of geographic spread cannot be assessed adequately. This last limitation was largely by design: the model described here is the core for a fully spatial model that we are currently developing to evaluate large-scale control measures and design adaptive management strategies for limiting distribution and prevalence of CWD in free-ranging populations.

MANAGEMENT IMPLICATIONS

Based on model forecasts, effective CWD management in free-ranging deer populations will require a long-term commitment to achieve a reduction in prevalence or eradication. Selective culling may offer the greatest promise of reducing CWD prevalence, particularly when infected populations are detected early in the course of an epidemic and tested aggressively for several decades. As presently applied (e.g., removing clinical cases when noticed or reported by the public), however, selective culling may not be a particularly effective strategy for CWD management. Unfortunately, there are 2 formidable obstacles to large-scale institution of more effec-

tive programs in the foreseeable future. First, practical and reliable tests for detecting preclinical or subclinical CWD under field conditions are lacking; as a further constraint, all antemortem tests currently showing promise require laboratory processing of samples before results are known (Schreuder et al. 1996, O'Rourke et el. 1998). Second, early detection of infected populations is limited by reliance on targeted or harvest-based surveillance programs (Miller et al. 2000), particularly in lightly populated or harvested areas. Without live-animal tests, sampling intensity sufficient to detect disease could rapidly lead to overharvest that would compromise many healthy deer populations. Once antemortem tests do become available, their data should be valuable not only in management programs, but also in improving parameter estimates and refining future modeling efforts.

In light of present technological obstacles to detection of both infected animals and infected populations, delays in management intervention appear inevitable. The consequences of such delays, however, may be equally severe. Our model forecasts that allowing prevalence to increase to 0.05 before intervening doubles the time required to have a 50:50 chance of eliminating CWD from the infected population. At prevalence rates currently seen in some affected deer management units in Colorado and Wyoming (Miller et al. 2000), model projections suggest CWD may be essentially unmanageable without substantial investment in selective culling applied to a large proportion of those populations in the very near future.

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LITERATURE CITED

ANDERSON, R. M., AND R. M. MAY. 1991. Infectious diseases of humans: dynamics and control. Oxford University Press, Oxford, England, United Kingdom.

BAER, G. M. 1991. The natural history of rabies. Second edition. CRC Press, Boca Raton, Florida, USA.

BARLOW, N. D. 1996. The ecology of wildlife disease control: simple models revisited. Journal of Applied Ecology 33:303–314.

BARTMANN, R. M., G. C. WHITE, AND L. H. CARPENTER. 1992. Compensatory mortality in a Colorado mule

deer population. Wildlife Monographs 121.

FREDDY, D. J., D. L. BAKER, R. M. BARTMANN, AND R. C. KUFELD. 1993. Deer and elk management analysis guide, 1992–94. Colorado Division of Wildlife, Denver, USA. Division Report 17:1–77.

HOINVILLE, L. J. 1996. A review of the epidemiology of scrapie in sheep. Revue Scientifique et Technique Office International des Epizooties 15:827–852.

HOLLING, C. S. 1978. Adaptive environmental assessment and management. John Wiley & Sons, London, England, United Kingdom.

KUFELD, R. C., AND D. C. BOWDEN. 1995. Mule deer and white-tailed deer inhabiting eastern Colorado plains river bottoms. Colorado Division of Wildlife, Technical Publication Number 41:1–58.

———, D. C. BOWDEN, AND D. L. SCHRUPP. 1989. Distribution and movement of female mule deer in the Rocky Mountain foothills. Journal of Wildlife Management 53:871–877.

MANLY, B. F. J. 1991. Randomization and Monte Carlo methods in biology. Chapman & Hall, London, England, United Kingdom.

MCCARTY, C. W., AND M. W. MILLER. 1998. A versatile model of disease transmission applied to forecasting bovine tuberculosis dynamics in white-tailed deer populations. Journal of Wildlife Diseases 34:722–730.

MILLER, M. W. 2001. Pasteurellosis. Third edition. Pages 330–339 *in* E. S. Williams and I. K. Barker, editors. Infectious diseases of wild mammals. Iowa State University Press, Ames, USA.

———, M. A. WILD, AND E. S. WILLIAMS. 1998. Epidemiology of chronic wasting disease in captive Rocky Mountain elk. Journal of Wildlife Diseases 34:532–538.

———, E. S. WILLIAMS, C. W. MCCARTY, T. R. SPRAKER, T. J. KREEGER, C. T. LARSEN, AND E. T. THORNE. 2000. Epizootiology of chronic wasting disease in free-ranging cervids in Colorado and Wyoming. Journal of Wildlife Diseases 36:676–690.

MORRIS, R. S., AND D. U. PFEIFFER. 1995. Directions and issues in bovine tuberculosis epidemiology and control in New Zealand. New Zealand Veterinary Journal 43:256–265.

O'ROURKE, K. I., T. V. ASZLER, J. M. MILLER, T. R. SPRAKER, I. SADLER-RIGGLEMAN, AND D. P. KNOWLES. 1998. Monoclonal antibody F89/160.1.5 defines a conserved epitope on the ruminant prion protein. Journal of Clinical Microbiology 36:1750–1755.

RUPPRECHT, C. E., J. S. SMITH, M. FEKADU, AND J. E. CHILDS. 1995. The ascension of wildlife rabies: a cause for public health concern or intervention? Emerging Infectious Diseases 1:107–114.

SCHREUDER, B. E. C., L. M. J. VAN KEULEN, M. E. W. VROMANS, J. P. M. LANGVELD, AND M. A. SMITS. 1996. Preclinical test for prion diseases. Nature 381:563.

SCOTT, G. R. 1981. Rinderpest. Pages 18–30 *in* J. W. Davis, L. H. Karstad, and D. O. Trainer, editors. Infectious diseases of wild mammals. Second edition. Iowa State University Press, Ames, USA.

SIGLIN, R. J. 1965. Seasonal movements of mule deer in the Cache la Poudre drainage. Thesis, Colorado State University, Fort Collins, USA.

SIGURDSON, C. J., E. S. WILLIAMS, M. W. MILLER, T. R. SPRAKER, K. I. O'ROURKE, AND E. A. HOOVER. 1999. Oral transmission and early lymphoid tropism of chronic wasting disease PrP^{res} in mule deer fawns (*Odocoileus hemionus*). Journal of General Virology 80:2757–2764.

SPRAKER, T. R., M. W. MILLER, E. S. WILLIAMS, D. M. GETZY, W. J. ADRIAN, G. G. SCHOONVELD, R. A. SPOWART, K. I. O. O'ROURKE, J. M. MILLER, AND P. A. MERZ. 1997. Spongiform encephalopathy in free-ranging mule deer (*Odocoileus hemionus*), white-tailed deer (*Odocoileus virginianus*) and Rocky Mountain elk (*Cervus elaphus nelsoni*) in northcentral Colorado. Journal of Wildlife Diseases 33:1–6.

STARFIELD, A. M. 1997. A pragmatic approach to modeling for wildlife management. Journal of Wildlife Management 61:261–270.

THORNE, E. T., M. S. BOYCE, P. NICOLETTI, AND T. J. KREEGER, editors. 1997. Brucellosis, bison, elk, and cattle in the Greater Yellowstone Area: defining the problem, exploring solutions. Greater Yellowstone Interagency Brucellosis Committee and Wyoming Game and Fish Department, Cheyenne, USA.

U.S. ANIMAL HEALTH ASSOCIATION (USAHA). 1998. Report of the USAHA Captive Wildlife and Alternative Livestock Committee. Accessed 19 August 1999 at http://www.usaha.org/reports98/r98cwal.html.

UNSWORTH, J. W., D. F. PAC, G. C. WHITE, AND R. M. BARTMANN. 1999. Mule deer survival in Colorado, Idaho, and Montana. Journal of Wildlife Management 63:315–326.

WALTERS, C. J., AND C. S. HOLLING. 1990. Large-scale management experiments and learning by doing. Ecology 71:2060–2068.

WHITE, G. C., R. A. GARROTT, R. M. BARTMANN, L. H. CARPENTER, AND A. W. ALLDREDGE. 1987. Survival of mule deer in northwest Colorado. Journal of Wildlife Management 51:852–859.

WILLIAMS, E. S., J. M. KIRKWOOD, AND M. W. MILLER. 2001. Transmissible spongiform encephalopathies. Pages 292–301 *in* E. S. Williams and I. K. Barker, editors. Infectious diseases of wild mammals. Iowa State University Press, Ames, USA.

———, AND S. YOUNG. 1980. Chronic wasting disease of captive mule deer: a spongiform encephalopathy. Journal of Wildlife Diseases 16:89–98.

———, AND ———. 1982. Spongiform encephalopathy of Rocky Mountain elk. Journal of Wildlife Diseases 18:463–471.

———, AND ———. 1992. Spongiform encephalopathies of Cervidae. Revue Scientifique et Technique Office International des Epizooties 11:551–567.

WOOLHOUSE, M. E. J., L. MATTHEWS, P. COEN, S. M. STRINGER, J. D. FOSTER, AND N. HUNTER. 1999. Population dynamics of scrapie in a sheep flock. Philosophical Transactions of the Royal Society London B 354:751–756.