Disease Risk Workshop 2000 II

Disease Risk Workshop II, New Orleans
Report

13–15 September 2000

A contribution of the IUCN/SSC Conservation Breeding Specialist Group.

Sponsored by Omaha's Henry Doorly Zoo, Wildlife Conservation Society and Audubon Zoo.

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Disease Risk Workshop 2000 II

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Disease Risk Workshop 2000 II

Report

Executive Summary

Executive Summary

An international group of about 45 people including zoo and wildlife clinical veterinarians, veterinary pathologists, epidemiologists, and population biologists gathered for a three day workshop, 13-15 September 2000, prior to the AAZV meeting in New Orleans. This workshop was a continuation of the process initiated at the Henry Doorly Zoo in Omaha Nebraska, 30 March – 1 April 2000. The intent is to assemble, develop, and test a tool kit to assist the qualitative and quantitative assessment of disease risk as a part of the decision making process in moving captive or free-ranging animals. The philosophy of zero risk has posed an unattainable goal for needed animal movement actions in wildlife conservation programs. The need for a comprehensive, unified, and broadly applicable set of tools was agreed by all of the participants in both workshops in their stated individual goals for the workshop and was more completely described during the workshop in terms of disease biology, data analysis and decision making tools, and communicating risk analysis information for action.

The pedigree of this process extends back to a May 1991 working group meeting at the National Zoo, which resulted in a more extensive analysis of the problems in 1992 at a workshop in Oakland, and two very recent working group meetings in 1999 at Cincinnati and South Africa. Although some recommendations from the 1991 and 1992 workshops have been implemented, a key recommendation of the 1992 workshop to develop a set of quantitative tools to assist the decision making process was not initiated until the Omaha Workshop.

Workshop Process

Meeting began 8AM Tuesday morning with brief introduction by Doug Armstrong and then going to the two written questions (included with responses in the report). There were about 45 participants. Seal gave a brief opening presentation on CBSG and then we had a series of individual presentations until about 230PM. Doug reviewed the worksheets, which are to be the second task in the process. There were several repeat presentations, with modifications, from the Omaha workshop followed by several new presenters – Travis on Risk Analysis, Hungerford on Stella, and Bright on Precision Tree. We formed 4 working groups with an effort to mix the disciplines and types of work – around 4 designated facilitators who had participated in the Omaha workshop. The first workshop task was a brief 'problems' brainstorming session to establish group processes and the use of the flip charts. Plenary presentations by each group indicated common interests but we did not make an effort to synthesize these reports. Instead they and the introductory statements were printed, copied and distributed for the working groups to use as needed. The next task was the review by each working group of the New Zealand worksheets (in appendix) which had been revised Richard Jakob-Hoff – he could not attend - based on the work at Omaha using species selected from the experience of a group member for the analysis. The species included Attwater's Prairie Chicken (release program), whooping crane (release program) , black and white ruffed lemurs (release program), mountain gorilla (management program), and a population of semi-captive zebras to be moved within Kenya. The groups were asked to make comments and suggest revisions or additions to the worksheets as part of the process. This was a productive process. After a plenary session in which the ideas were presented and discussed, a synthesis group was formed with one person from each working

group to unify these suggestions into a revised Worksheet. All day Wednesday was needed to complete the synthesis and produce a product for review.

Wednesday the groups began the use of the risk analysis development by formulating the hazard identification outlining a flow model and then developing decision tress for each of the species for which the worksheets had been completed plus a few additional examples. They formulated probabilities of the risk at each step of the tree and ultimately of introducing a disease into a destination population. These were reported in plenary. One of the groups also developed cost estimates for all of the procedures and steps and related this to the contribution of the step in reducing the final risk.

Thursday, the groups were asked to develop protocols for the major steps involved. One interesting analysis was for various strategies for protecting the mountain gorilla population from a measles epidemic though exposure from the trackers. They considered diagnostic techniques, vaccination of the trappers, vaccination of their children and those in the towns (the trackers could be carrying fomites rather than having the disease themselves), and direct vaccination of the gorillas. All of these scenarios and the others for the other species are included in the report.

Several of these scenarios were then modeled with STELLA and decision trees were constructed with Precision Tree to start the process of using computer tools to deal with more elaborate or complex scenarios. It is evident that both will be useful. Our challenge will be to develop teaching modules that carry examples from the beginning to the end of the set of tools to allow varying levels of complexity of analysis and to offer the opportunity for interested persons to learn their application.

The revised worksheets were presented to the group and approved. Protocols (teaching modules were developed or started) for several of the tools and will be in the report.

The sequence of events from this point includes:

1) Preparation of the worksheet in Omniform to allow access and use of the form on computers and on a WEB site as well as to prepare a database for compilation and analysis of completed forms.

2) Technical working groups to meet to develop a tool for input of this kind of disease risk information into VORTEX. They will meet in November in Chicago and will include epidemiologists, STELLA and Decision analysis users, with Phil and Bob as the population biologists and Vortex modelers. The US Airforce person from Sandia Laboratories in New Mexico has also agreed to participate. She has access to and is using a range of more elaborate tools including neural nets and AI as part of their program to predict the possible occurrence and timing of ‘natural’ epidemics and for early detection of possible bio-terrorist events. She also uses spatial tools and has agreed to attend the tools workshop. The epidemiologist who uses Stella also plans to attend both meetings. They will be a major addition to expanding our vision.

3) A follow up workshop on this one sometime next year to continue the development of the toolkit. This is not contingent on the availability of a special Vortex module. We still have an

array of other tools, which need to be carried further and develop teaching modules for each of the tools. This next workshop would include a different composition of actors: 10 wildlife vets, 10 wildlife managers, 10 zoo vets, 10 experts in various tools including the epidemiologists and various modelers, and perhaps 10 vets from the Army Veterinary Corps (emergency and disaster response interests globally). They would go through a similar process of evaluation of the workbook and the several tools developed in this workshop and the several computer applications. We hope by then to add a spatial component from the work at the CBSG Tools workshop.

4) An acquaintance and training workshop for one day at the zoo vets meeting 21 September next year at Disney This workshop has already been arranged with Amand, Jansen, Junge,, and Lamberski to be the conservation day and will especially target the vet TAG advisors but be open. One intention is to use the TAG advisors to begin building the database of diseases by taxonomic group and location.

5) An acquaintance and training and testing workshop 22-24 July in Costa Rica for Latin American vets. This will be organized by Danilo Oleander, veterinarian at the Simon Bolivar Zoo (he was at the Omaha workshop) under the umbrella of CBSG Mesoamerica.

6) Several potential workshops with Federal and State wildlife veterinarians.

Working Groups Summaries

Group 1: Madagascar Ruffed Lemur Release Program

Question #1: What is the likelihood (risk) of introducing a hazard into the Madagascan lemur population and becomes endemic in the whole ecosystem (whole island) ??

Question #2: What is the likelihood of introducing TB into lemurs into Betampona given that the current population is TB-free?

CONCLUSIONS:

Probability of Release based on prevalence estimate of 0.001 = 0.0000033

Probability of Release assuming one infected animal that is shipped is 0.0033

As a result of low likelihood of release, the decision was made to not pursue further studies of exposure and consequences.

Concluding Remarks

- In this model, the disease prevalence in the source population is the most important factor followed by test sensitivity.
- Resources should be allocated to ensure minimal likelihood of disease introduction during transport.
- Determining prevalence of important hazards should be a high research priority.
- Multiple testing methods should be considered to maximize sensitivity estimates within the model.
- More work is needed on modeling the probability of introducing disease during transport and at quarantine facilities.
- Further work on exposure and consequence assessments is needed to answer Question 1.

PROTOCOL DEVELOPMENT FOR DISEASE RISK ANALYSIS FOR ANIMAL MOVEMENT

(Refer to Black and white ruffed lemur example for clarification)

Section 1: Define the Problem/Policy

Step 1: Summarize the issues surrounding the entire process.

Step 2: Define the question.

Step 3: Outline the pathway completely.

Step 4: Identify and list all *potential hazards* (This will vary depending on the specific risk assessment).

Section 2: Risk Assessment

Step 4: Define specific concerns.

Step 5: Outline specific pathways and identify important steps known as *critical control points* (CCP).

Step 6: Build a model from these critical control points.

Step 7: Qualitative test model

Step 8: Quantitative assessment

Step 9: Describe uncertainty of process.

GROUP 2: DECISION TREE COST ANALYSIS

Human ⇐ Gorilla Measles

Description and Interpretation

Three scenarios were assessed. The first involved an assumed prevalence in the in-contact human population of 10% and screening for the disease in these individuals is conducted by cursory inspection and observation of clinical signs only. The sensitivity of this method was assumed to

In the second scenario the screening test method used was a hypothetical PCR of clinical samples from every in-contact human. The sensitivity of this method was assumed to be 99%.

The third scenario implemented vaccination of the in-contact humans. Vaccine efficacy was assumed to be 99% and therefore prevalence dropped to 1%. Testing was limited to inspection

Recommendations

Based on these data and models it is clearly more cost beneficial to vaccinate the in-contact humans, however the use of PCR as screening test reduces risk of measles introduction five-fold. These conclusions appear to differ from those obtained using the Stella model, however, this disparity may be due to the complexity of the Stella model, that is- the addition of temporal considerations and additional variables which may effect the outcome.

Decision Tree Cost Analysis- *Capillaria* ⇐ Cranes

The originally presented decision tree was expanded to include all possible animal treatment/test groups and their associated probabilities. Also to calculate the number of animals that are eligible for release in each scenario and associated costs.

Assumptions:

- Capture/handling costs = $610 (60 hours effort)
- Fecal sedimentation = $10/tst x 24 = $240
- Re-testing has same sensitivity and specificity as initial
- Treatment = $3/ bird x 24 = $72
- Re-treatment has same efficacy as original
- No mortality due to handling the birds

GROUP 3: DECISION TREE ANALYSIS

This group worked through an exercise of the Quarantine and Health Screening Worksheet for Animal Movements, using translocation of whooping cranes as our example. After filling out this worksheet we took the example of *Capillaria* in the birds to be moved and applied a Decision Tree Analysis.

Our goal was to take the initial Decision Tree and turn it into a Decision Analysis process using the computer program Precision Tree.

The question the decision analysis is designed to answer is: What is the probability of introducing the exotic *Capillaria* species present in the captive population at the release site in Florida?

We performed a simplified form of decision analysis in which a set of decisions has already been made, thus we are modeling the risk associated with those predetermined decisions, and not evaluating which decision to make.

Advantages of a formal decision analysis compared to informal (simplified) decision tree:

- Ability to alter assumptions and alter assigned probabilities to see how these changes affect outcomes.
- Ability to incorporate stochastic parameters (uncertainty) into the model. For example, if we were uncertain about the sensitivity of the fecal sedimentation test to detect *Capillaria*, we could quantify that uncertainty by creating a distribution of sensitivity values centered on our estimate of the mean sensitivity of 60%.
- Allow the user to formulate additional questions and modify the model to answer that question—comparison of scenarios rapidly. For example, we could examine if changing the current testing protocol significantly affects the risk of introducing an infected bird.
- Ability to incorporate financial costs into the analysis and ability to compare costs of different management situations.
- Increased ability to model more complex situations more accurately

On the contrary, formalized decision analysis may be an unnecessarily labor intensive tool, depending on the complexity of the question one is trying to address, and the available time and resources for addressing the question.

Group 4: Stella Working Group Summary of Diagram

We developed this model as a working draft to allow the group to become familiar with the Stella program.

Set up:
Modeled as transmission of disease among gorillas, transmission among children of trackers, transmission among other children in the village, trackers used as route of exposure of measles to the gorillas.

Assumptions:
1. Gorilla contract measles (from humans and each other)
2. Humans act as fomites for the measles virus
3. Trackers developed immunity to measles as adults
4. Naive populations = all but trackers
5. Negligible impact of transmission tracker to tracker.
6. Closed populations
7. Random contacts
8. Random dispersal
9. Human adults that are not trackers are irrelevant (only trackers have contact with gorillas)
10. That all people infected recovered to immunity.

Identifying data:
Other kids = 5000
Trackers kids = 700
Trackers = 110
Gorilla population = 320
Noncontact gorillas = 60
Contact gorillas = 260
Vaccine programs as 98% efficacy for gorillas and people
Contact rate sick child to child of 1:10
Contact rate for trackers to gorillas in contact groups of 1:20
Contact rate for noncontact gorillas to contact gorillas of 1:2

Run and evaluate scenarios:
1. Measles goes through the population
2. Vaccinate just the trackers children
3. Vaccinate all children
4. Vaccinate gorillas only

Results of simulations:
Vaccinating the gorillas only was the most effective way to minimize the incidence of measles in the gorilla population.
Reevaluate model again, and again and again.....

Summary:

Process of developing the model:

Identification of the problems to address.
Assemble a group individuals with diverse experience and training.
Employ someone who has a clue about Stella.
Begin to draw a conceptual picture of the problems you are addressing.
Develop assumptions.
Determine control points of the model.
Input data into the model (if possible real data used and otherwise bet estimates).
Run the model.
Evaluate the data, model and graphs resulting.
Reevaluate the appropriateness of the data entered and the relationships created.
Continue to refine and improve the model (to infinity).

Question:

Does this approach provide benefit in exploring a complex problem?

Answer:

Yes, it allows you to visualize the process, identify critical control points, and identify relationships that may not have been obvious, clearer idea of information needed to acquire.

Question:

Can this approach give you a quantitative answer?

Answer:

With more refinement and enough good data it may give you quantitative answers.

GROUP 5: REVISED WOPRKSHEET

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached explanatory notes before completing this Worksheet)

1. SPECIES TO BE MOVED:

2a. FROM:_____ **2b. TO:**_____

3a. Are other source institutes involved? If yes, list:

3b. Are other destination institutes involved? If yes, list:

4. TOTAL NUMBER OF ANIMALS:_____

5. ANIMAL IDENTIFICATION:

ID NUMBERS*	ID TYPES	ANIMAL ORIGIN**	DOB/AGE EST	SEX***	MED Hx (Y/N)	COMMENTS

Attach additional sheet if needed.
*Large groups or colonies not individually identified may be given a single group name or number
List animal origin as **W=wild, **C**=captive, **U**=unknown, **B**=both (may be used only for groups)
***List sex as **M**=male, **F**=female, **U**=unknown, **B**=both (may be used only for groups)
Comments should include pertinent information on individual animals/groups (eg. significant disease history, contraceptive implants, neutered, etc.)

6. ANIMAL MOVEMENT CATEGORY: ☐ Wild to wild ☐ Wild to captivity

☐ Captivity to wild ☐ Captivity to captivity

7a. PROJECT MANAGER: _____ Tel:_____
b. TITLE, INSTITUTION: _____ Email:_____
8. PROJECT VETERINARIAN:_____ Tel:_____
Email:_____

9.POTENTIAL DISEASES AND OTHER MEDICAL CONCERNS (comprehensive list based on source and destination animals including wildlife, domestic animals, and humans. Veterinary assistance is strongly advised in the development of this list.)

DISEASE/MEDICAL PROBLEM	SOURCE	DESTINATION	JUSTIFICATION*	REQ
	Yes, **N**o, **U**nknown	**Y**es, **N**o, **U**nknown		

*Justification includes animal disease implications, public health impacts, legal requirements, etc.

10. DISEASES AND OTHER MEDICAL PROBLEMS OF CONCERN FOR THIS ANIMAL MOVEMENT
(Include all listed as required above)

DISEASE/MEDICAL PROBLEM	RECOMMENDED TEST	TESTING LOCATION*	SAMPLE AMOUNT

*****If multiple source/destination institutions are involved, be sure that samples are sent to the same testing facilities.

11. DIAGNOSTIC SAMPLES

Diagnostic samples to be collected (check)	Collection dates	Date results received	Pass or Fail?*
Physical exam, body weight and measurements			
Feces			
Blood smear, hematocrit and total protein			
Whole blood, serum or plasma (max. volume/animal =)			
Fresh fecal or rectal swab for culture			
Choanal or oral swab for culture			
Ectoparasites			
Other (specify based on diseases of concern):			
Serum banking (if yes, please attach inventory, including location of storage)			

*If there are test failures, please explain in the assessment section.

12. TREATMENTS / VACCINATIONS AND DATES (Please list any adverse reactions to medications. For documentation, refer to individual animal records):

13. ADDRESSES AND CONTACT PERSON(S) FOR TESTING LOCATIONS (Attach additional sheets if necessary)**:**

Quarantine Details

14. LOCATION OF QUARANTINE: ☐ Source ☐ Destination ☐ Both
(if both, duplicate quarantine sheet)

15. FACILITY:_____

16. QUARANTINE DURATION BASED ON ANIMAL MANAGEMENT AND DISEASE CRITERIA (specify reason for the duration):

Begins:_____Ends: _____Total Days:_____

17. PERSON SUPERVISING QUARANTINE: _____Tel:_____
Email:_____
_____

18. DATE OF TRAINING/BRIEFING FOR SUPERVISOR:_____

19. QUARANTINE EQUIPMENT AND SETUP:

☐ "Quarantine – no unauthorized entry" sign	☐ Protective clothing	☐ Feeding, watering and cleaning utensils
☐ Insect/rodent traps/ screens/baits	☐ Cage furniture appropriate to the species	☐ Animal capture / restraint equipment
☐ Diagnostic sample collection, storage and transport	☐ Animal record forms, pens	☐ Quarantine register
☐ Lock for facility	☐ Bags for waste disposal	☐ Keeper health check
☐ Footbath/boot changes	☐ Other:	

20. BUDGET

Personnel hours _____@_____ _____
Equipment costs _____

Feed costs	_____
Lab costs	_____
Courier fees	_____
Veterinary fees	_____
Other (specify)	_____
TOTAL COST	_____

Budget Code _____

Assessment

21. INTERPRETIVE SYNTHESIS OF PHYSICAL EXAM AND DIAGNOSTIC TEST FINDINGS (Include explanation of any failed tests):

Recommendation

22a. Healthy and minimal threat to destination populations ☐ OK to move

22b. Healthy but there is a significant threat to source animals ☐ Delay move
☐ Cancel move

22c. Unhealthy or threat to destination populations ☐ Delay move
☐ Cancel move

23. EXPLANATION AND JUSTIFICATION FOR ANIMAL MOVEMENT RECOMMENDATIONS:

24. FOLLOW UP ACTIONS (eg. long-term monitoring, repeat testing):

25. PERMITS FOR ANIMAL MOVEMENT RECEIVED: Yes No (circle one)
(List all permits)

Signature, Project Manager _____ Date _____

Signature, Project Veterinarian _____ Date _____

Disease Risk Workshop 2000 II

Report

Problems, Needs, and Common Interests

Disease Risk Workshop Plenary Session 13 September 2000

Participant expectations and challenges anticipated regarding disease risk issues over the next five years.

1. "My expectations for the workshop are to learn more about the necessary tools needed to evaluate disease risk in populations (and how they can be applied to field conservation)"

"I think the most important disease challenge we may face is the introduction and transport of new diseases to naïve populations through human-induced environmental modifications. How disease relates to altering ecology."

2. "Open forum to discuss and learn techniques about disease monitoring assessment and hopefully prevention from a generalized perspective."

"With the extreme human population expansion and corresponding agriculture needs and general consumption, there will be increased interaction between wildlife human and livestock. This will also increase the probability of disease spread. Our challenge is to recognize this quantitatively and control it to the best of our ability."

3. "To learn new techniques for risk assessment of animal moves between populations."

"Improvement of diagnostic tools for health assessments."

4. "Ability to objectively determine risk of a particular disease to a population. Better understanding of "risk assessment" in general."

"Lack of understanding of a particular disease/disease process y individuals involved. Diagnostic challenges. Lack of information from free-living population."

5. "Expect to have a tool that might use with the wildlife I am working with."

"Disease in the mountain gorillas that would likely to be transmitted from humans."

6. "Learn more about and contribute to a process for standardizing disease risk assessments for conservation programs. I would like to see a practical tool or product come from this workshop."

"Having the ability to identify infections agents before we know much about their significance (i.e., what their disease causing potential is for that host or other hosts)."

7. "To learn from the expertise of people to better handle disease and outbreak in the wild."

"What to do and improve in disease knowledge in order to help decision making and conservation management."

8. "To gain a better perspective on the conventional wisdom surround global animal movements."

"Emerging diseases as yet uncharacterized. That is the lack of knowledge. Management of uncertainty, standardization."

9. "Gain a greater understanding of risk assessment for captive and free-ranging populations."

"Retroviruses"

10. "Meet people. Learn where conservation communication is at in risk analysis and assessment."

"Most important disease challenge: TB – directly; emerging diseases."

11. "Learn more about developing a quantitative risk assessment for moving animals into and out of captivity. To be able to provide some hard data to people making restoration/recovery decisions on disease risk."

"Protecting wild populations and people against movement of pathogenic organisms. This statement is brief as we face new and emerging issues daily and each day brings a more complicated problem. Additionally changing attitudes and affecting political climates will be most difficult."

12. "Identify field survey assessment tools."

"Identify human – domestic animal – wildlife disease inter-relations. Develop predictive assessment tools for managing these inter-relationships better."

13. "My expectations are to gain clearer understanding of risk assessment, and improving my ability to make management decisions that are both cost-effective and protective of native fish populations."

"Finding ways to determine the probable consequence of movement of non-indigenous pathogens into native populations for recovery and restoration."

14. "Develop and gain experience with risk assessment tools and learn how to use them in practical applications."

"Determining "acceptable risk" for disease for animal relocations."

15. "To continue to develop practical tools for addressing disease risk and to learn more about the subject."

"Human population."

16. "My first workshop – experience how these function and learn various approaches to disease concerns in populations."

"First – human overpopulation (happens so fast), and second – mycobacteria (happens so slowly)."

17. "To gain a clearer understanding of how to assess and mitigate disease risks of translocating and reintroducing wild animals. Take away some practical recommendations."

"Knowing what diseases are relevant and important to wildlife populations and what impact we might have."

18. "Integrate tools and thoughts from experts in a variety of disciplines to build solid approaches to evaluating risk in implementing policy."

"Designing something generic and flexible enough to deal with emerging and not yet diagnosable or recognized health threats. Quantifying critical steps."

19. “Curious to see if we can implement anything from the Omaha meeting.”
“”TB, Brucellosis”

20. “To develop tool accepted by reintroduction biologists to assess risk of disease transmission when moving animals. Easy to use and understood by clinical veterinarians. Giant panda reintroduction: infectious diseases in captivity? Wild? (Impact on).”
“Laboratory diagnosis and interpretation.”

21. “Build on what was started/compiled in Omaha, further refining tools developed, integrate more examples to “proof” tools.”
“Determination of definition of “acceptable” risk that vets and management can agree on and the calculation/estimation of that risk using imperfect/incomplete information.”

22. “To become familiar with the considerations for and limitations of our current methods of disease risk assessment and to participate in discussions regarding modeling approaches. Assumptions and limitations of our data.”
“Currently, the increase in international movements of animals (both domestic and wildlife) and people, poses increased risk along with re-emergence of diseases once thought to be controlled, combined with population growth and environmental alteration.”

23. “I’d love to walk out of here as a master of Vortex, but realistically I’d like to gain a better understanding of the capabilities and limitations of the program with respect to both general population modeling and the inclusion of infectious disease impact.”
“The most important disease challenge in my opinion remains the ability to gather enough information about the natural history of various pathogens to make meaningful and realistic predictions about pathogen behavior as it relates to wildlife conservation (also the political difficulties related to the presence or absence of certain pathogens).”
24. “Explore the details of risk assessment and determine the possibility of broader population/genetics/immunological testing to determine more general disease risk.”
“Mycobacteriosis of emerging diseases.”

25. “Better understanding of disease risk considerations when planning wildlife translocations.”
“Emerging diseases in the field due to climate change or human intervention. How best to monitor or track.”

26. “Simple, realistic framework for making decisions regarding disease risk associated with translocation and reintroduction of wildlife and with metapopulation management. Applicable to “real world”.”
“Disease risks associated with reintroducing wildlife to their former range. IN particular, in the Midwest the effect of P. tenuis infection on reintroduced herds of native cervidae; or disease risks faced by rhinos leaving the USA being returned to Africa (e.g., trypanosomiasis).”

27. “To see whether tools from workshop are appropriate for the real world.”

"Disease interactions/transmission between domestic animals, humans and free-ranging wildlife. Gain better understanding which should help implement strategies."

28. "To learn more about the important issues and problems in disease risk assessment especially from an epidemiological point of view, and the actual process or "nuts and bolts" of dealing with those issues."

"Tuberculosis; compilation of disease risk information in a workable accessible database."

29. "Achieving a realistic, practical, acceptable and sustainable protocol for addressing the risks inherent in animal movements."

"Creating excessively complex guidelines that may be unacceptable to the multi-disciplinary conservation community and thereby encourage non-compliance. We started talking in 1992 in Oakland and we are in danger of being left behind – or out of the loop."

30. "To know more about risk assessment of diseases in wildlife. My experience so far is on clinical risk assessment."

"Spread of parasitic zoonotic diseases."

31. " My expectations for this disease risk assessment workshop are to get knowledge and scientific tools to be able to make decisions in relation to reintroduction of captive species into natural habitats and to evaluate the health status between captive and wildlife species in there natural habitats."

AS SUMMARIZED ON FLIP-CHART:

1. To meet people (with similar concerns). Find out where others "are at"
   TB Problems, emerging infections.
2. Work in epidemiology risk assessment
   Qualitative assessment.
3. Continue tool development (from March workshop).
   Human population (encroachment).
4. Where are we at?
   General probes for disease; mycobacterium probes.
5. Translocation activities and risks.
   Emerging diseases; climate changes; monitoring.
6. How to use tools?
   Acceptable risks
7. Learn
   Parasitic diseases
8. Simple tools
   Emerging. Reintroductions of cervidae and P. tenuis; rhino relocations.
9. Objective evaluation, learn
   Diagnosis. Uninformed participants in translocations
10. How to do assessments
    Mt gorillas, potential impact

11. Culling impacts on population genetic diversity using repro technology
12. Knowledge of risk assessment and how to do it.
13. Open forum; human populations effects on mt gorilla
14. Learn about tools, field applications
    Ecological changes affects on disease
    Natural history
15. Test tools
    Disease interactions between major sources
16. Simple, acceptable protocols, get on with it, be left behind.
17. Standardized tools, identify agents in advance
18. Learn
    Fish interests, management consensus
    Recognize restoration; acceptable heads of risk
19. Lean about quantitative tools
    Attitudes about disease. Political
20. Lean vortex model, people
21. Lean where we are at, Need practical tools
    Increased animal and people movements
    Human pop effects
22. test March tools, refine
    Acceptable risks?
23. Acceptable tools, for moving animals.
    Pop effects
    Interpretation of lab findings
24. What has happened since March
    TB and Brucellosis
25. Use of tools and integration
    Critical point identification
26. Learn, practical.
    People, mycobacterium,
27. Mitigate risks
    Which diseases most important
28. Use tools in Army applications
    Interactions with human. Wildlife, domestics
29. Tools to use
30. How little we know
    Latin America – confiscation problems
    Pragmatic normalized guidelines
    Biodiversity
31. Animal movements
    Ecosystems context
    Chronic wasting disease
32. Lean about issues Process
    TB, how to compile information into database
33. How to assess acceptable risks
    Zoos, retroviruses

34. How to measure response to outbreak
    Knowledge
35. Global animal movements
    Management of uncertainly
36. Leaning how to assess
37. Tools. No zero risk
38. Learn, workbook , self-regulations

Disease Risk Workshop 2000 II

Report

Working Group 1:
Ruffed Lemurs; Models and Protocol

Group 1 Participants: Terry Norton, Sharon Deem, Mike Cranfield, Nadine Lamberski, Ana Arnizaut, Dominic Travis, Mark Atkinson, Randy Junge, Naida Loskutoff

Problems and Concerns for Risk Assessment and Model Formulation

1. Workshop discussions need to move from the theoretical to direct field applications.

2. Assess and factor in the true "benefits" along with the risks in animal movement.

3. Need to make a comprehensive disease assessment of the wild population(s). Difficulties in obtaining data needed (samples) to make quantitative assessments.

4. For free-ranging populations, knowing enough about what parameters are pertinent to the disease risks. Knowing disease ecology before trying to start with designing the appropriate models (specific question needed to address problem).

5. Utilization of existing data and how it might apply in "real world" situations.

6. Need a comprehensive method to be made available for collecting and cataloging data to make it meaningful for later analysis (or standardization of certain protocols for later comparison).

7. Need to explore the validity and interpretation of diagnostic tests.

8. Make protocols for risk assessment and analysis simple and easy to use so as to be applicable to and used by people worldwide.

9. A universal, common format(s)/tool(s) is(are) needed for disease assessment and an effective method to disseminate and to communicate.that information.

10. A method/protocol is needed to determine what an "acceptable" risk is.

Summarization, Prioritization and Grouping of Suggestions

1, 4 and 5: Sample collection

Background on Animal Movement

Project started 1995, involved North American and Betampona reserve in Madagascar (2500 ha East Coast – island pop) – carrying capacity of 60 (only 25-30 exist). Population modeling showed not sufficient genetic diversity to sustain long-term (however, can increase long-term genetic health if add 20+ animals).

Move animals within Madagascar (but sub-speciation and behavioral abnormalities of pets a major concern). Therefore, decision made to move captive animals from zoos in N. American and European zoos. Interest to see if released zoo animals would work. Ingrid Porton selects animals by SSP pedigree – only represented blood lines, and would include extensive medical examinations, animals must have reproduced, be young adults (2-3 years) ideally (for long breeding life). The original plan was to release pairs or breeding groups.

Randy Junge is the veterinary advisor to look at medical concerns. Shipment in 1997 (n=5), 1998 (n=4), 5/9 now dead. Pre-release training on St. Catherine's Island and Duke University – adds other disease risk issues. Released animals are radio-collared and tracked by field biologists (predation by fossa, injury and one disappeared).

Ideally 6 month pre-release training, but actually 2-3 months, then another very short pre-release in reserve before actual release. Suggest (Terry) longer pre-release training would be better (up to a year). Next release scheduled this Fall (5 total, but one already died). Release during dry season – easier for biologists to tracking.

Potential Benefits of Animal Movement

To reach carrying capacity and increase genetic diversity in the wild population for long-term genetic health. Lost 5 out of 9 already – not known if this rate is higher than natural occurrence. Some released animals have already integrated into natural groups, others are alone or are making new groupings. Two released pairs have reproduced, one reproduced with a wild lemur. Two surviving offspring have been produced from the translocated animals.

Agricultural development around reserve (fragmentation) thought to cause original reduction in population. Last 10 years, increase in management of reserve, guards, increased research component, lots more activity and interest – seems to be secure at this time. Other benefits – flagship species to help protect reserve, and to continue interest in Madagascar and their own people and students. Two other projects this year – research station (with a manager) initiated. Now other projects come in as a result. Ecotourism not in this reserve. Permits available for research only.

Approached this project (disease risk) – literature search, surveyed animals in zoos in Madagascar to see major disease problems (found few). Added some more based on research and review.

Initially 13 animals identified for movement – but some found not acceptable for various reasons (results of initial screening). Veterinarians need to be involved in those initial screenings

and decisions. Vet needs to be involved in captive to captive movement decisions – could also be common sense that is not caught by SSP – overall heath, age, conditions, etc. All these animals should be placed on worksheet (pre-quarantine sheet in deciding first step). This information important for overall risk assessment and standardization of information necessary for future continuity.

Suggested Changes to Existing Worksheets

Need to include a description of assumptions and benefits of the diseases of concern at start (ages of the animals, medical concerns, etc.).

Animal Identification

Should require two forms of ID (e.g., studbook plus transponder) or perhaps multiple ID (e.g., plus ear tag). Need some expansion.

Outcome Category

Should be clarified that a 1-4 code should be use as directed, then that this category should be filled out at the completion of the worksheet.

Diseases of Concerns

What diseases could be present in Madagascar that the released lemurs could potentially transmit to the reserve (most of the diseases tested for are not a real concern for lemurs).

Diseases of concern list should be expanded for a comprehensive, all inclusive (to include general health screen, previous history – to include all diseases to affect health) list in the beginning but then prioritize of what the veterinarian in charge would like to see addressed. Should include a justification of why the diseases should be looked at.

Concern voiced for sending animals that are completely parasite free (e.g., strongyloides) that will be susceptible to indigenous forms

Add an additional section for the medical staff to justify diseases of concern – make the most complete form, then biologists can extract bits of information of interest. Suggest change points 8 and 9 into a more organized table with column headings such as:

8A. Diseases and Other Medical Concerns or Hazards

Disease/Medical Problem	Justification	Required?

8B. Diseases of Major Concern

Disease of Concern	Recommended Test	Testing Location	Sample Amount	Results
Hep A	Sero			
Hep B	Sero			
Herpes Simplex	Sero			
Cytomeg virus	Sero			
Epstein Barr	Sero			
Measles	Sero			
Salmonella	Fecal x 3			
Shigella	Fecal x 3			
Campylob	Fecal x 3			
Yersinia	Fecal x 3			
TB	ID skin			
Toxo	Sero			
T. cruz	Cult + Sero			
Cutarebra	P. Ex			
Strongyloides	Fecal x 3			
Entamoeba	Fecal x 3			
Lyme's	Skin biopsy			
Ehrlichia	Sero (PCR)			
RMSF	Sero (PCR)			
gEctos (ticks)	P Ex			
Other				

Routine Screening/Diagnostic Samples

Insert additional columns to right of "Dates/Results": Acceptable and Not-Acceptable so as to flag vet abnormal results.

Expand the "Other" section based on the comprehensive "Potential Hazard. . ." list above (8A).

Collection date, date results, then add columns for "Acceptable" and "Not Acceptable".

For Example:

Collection Dates	Dates Results Received	Acceptable	Not-Acceptable

☐ Other: _____

_____

_____

_____

Quarantine Section

Need to expand this section to include more details for two separate quarantine sites (i.e., quarantine when entering facility, then months later – quarantine pre-release).

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet)

1. SPECIES TO BE MOVED: Black & White Ruffed Lemur (*Variecia veriagata*)

2a. FROM: North American and European Zoos **2b. TO:** St. Catherine's Island

3. TOTAL NUMBER OF ANIMALS: 4

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS
SB 1382	Studbook	5 years	Female		
SB 1383	Studbook	4	Male		
SB 1384	Studbook	3	Female		
SB 1385	Studbook	6	Male		
SB 1386	Studbook	7	Female		
SB 1387	Studbook	3	Male		

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY:

Wild to wild	☐	Wild to captivity	☐
Captivity to wild	☐	Captivity to captivity	X

6a. PROJECT MANAGER: Ingrid Porton Tel. E-mail:

6b. TITLE, INSTITUTION: Curator of Primates, St. Louis Zoo Tel.

7. PROJECT VETERINARIAN: Dr. Randy Junge, DVM, St. Louis Zoo E-mail:

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references.

Hepatitis A, B, Herpes simplex, cytomegalo virus, Epstein Barr virus, measles.
Rectal culture for Salmonella,Shigella, Campylobacter and Yersinia.
Tuberculosis; Toxoplasmosis antibody.; Trypanosoma cruzi serology.
Endoparasites, enteric parasites, Cutarebra
Lyme, Erlichia, Rocky Mountain spotted fever

9. SPECIFIC DIAGNOSTIC TESTS

For documentation refer to individual animal records

See comments by group to modify sections 8, 9 and 10.

Hepatitis A
Hepatitis B
Herpes Simplex
CM Virus

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records

Diagnostic samples to be collected: *(Check)*

	Collection Dates	Dates results received
☐ **Physical exam, body weight and measurements**		
☐ **Faeces**		
Blood smear, haematocrit and total protein		
☐ **Whole blood, serum or plasma (max volume/animal = ml)**		
☐ **Fresh faecal or rectal swab for culture**		
☐ **Choanal or oral swab or culture**		
☐ **Ectoparasites**		
☐ **Other:** Group faecals 2 weeks after treatment		

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

1. 10 day Fenbendazole SID PO (Strongyloides) based on results of 3 x fecals.
2. Frontline (and/or) Interceptor)
3. Rabies and Tetanus vaccination.

12. SAMPLES TO BE FORWARDED TO:

Quarantine Details

13. LOCATION: St. Catherine's Island

14. FACILITY: Cage in net kraal

15. QUARANTINE DURATION: **Begins** *(date)* 14 September 2000 **Ends** *(date)* 14 October 2000

Total days: 30 If less than 30 days specify reason(s) below

16. PERSON SUPERVISING QUARANTINE: Dr. Terry Norton

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? **YES** *NO*

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT:

- ☐ **"Quarantine - No Unauthorized Entry Sign"**
- ☐ **Insect/rodent traps/screens/baits**
- ☐ **Diagnostic sample collection, storage and transport equipment**
- ☐ **Lock for facility**
- ☐ **Footbath/boot changes**
- ☐ **Protective clothing**
- ☐ **Cage furniture as appropriate for species**
- ☐ **Animal record forms, pens**
- ☐ **Bags for waste disposal**
- ☐ **Feeding, watering and cleaning utensils**
- ☐ **Animal capture and restraint equipment**
- ☐ **Quarantine register**
- ☐ **Animal caregiver personal health check**
- ☐ **Other:** _____
- ☐ **Other:** _____
- ☐ **Other:** _____

19. BUDGET:

Personnel hours **hrs @** _____ **.....** _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments **.....** _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move ☐

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

21. FOLLOW UP ACTIONS:

22. PERMITS TO MOVE ANIMALS RECEIVED? **YES** **NO**

23. SIGNED OFF BY: _____ Project Manager

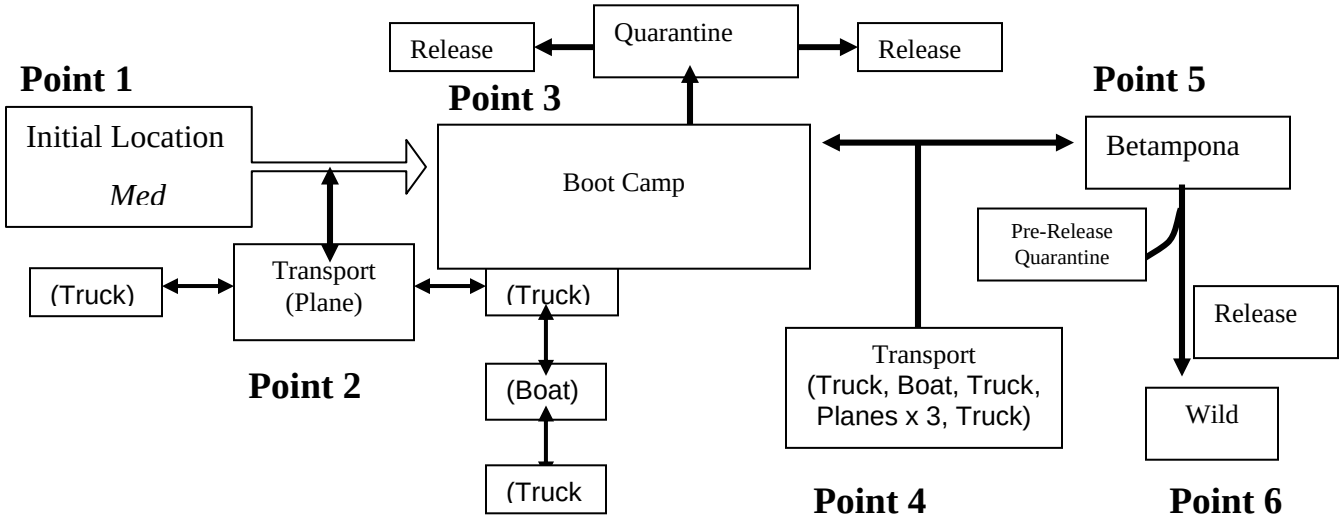
DATE: _____

_____ Veterinarian

Madagascar Ruffed Lemur Release Program

Question #1: What is the likelihood (risk) of introducing a hazard into the Madagascan lemur population and becomes endemic in the whole ecosystem (whole island) ??

Question #2: What is the likelihood of introducing TB into lemurs into Betampona given that the current population is TB-free?



Model Formulation:

Point 1: Probability of animal x leaving the zoo infected with disease y
- Probability of an infected animal
- Probability of not detecting (FN) before it moves on (1-Se)
- Can assume an infection (1) or use prevalence estimate
- *[Skin test and radiograph, CBC and physical exam for cumulative sensitivity of 0.85]*
- 0.001 (prevalence est) 3pos/5000 animals in 25 years
- 1-.5 = .5 (p)FN

Point 2: Probability of previous infection surviving transport or introduction of agent during transport.
- Probability of host survival
- Probability of agent survival
- Probability of introduction during transport
- Assume that no agent introduced and agent survives

Point 3: Probability that infectious animal gets out of boot camp.
- Prob. of FN on initial exam/quar
- Prob of FN on final quar exam
- Prob of introduction of new infection and FN test
- 2 tests X .5 p(FN) = 0.25
- .000001 chance

Point 4: Transport #2: Probability of previous infection surviving transport or introduction of agent during transport from GA to Madagascar.

Probability of host survival
Probability of agent survival
Probability of introduction during transport
Assume that no agent introduced and agent survives

Point 5: Probability of release in Madagascar at release site (no testing) or introduction of agent before release.

0.001 chance based on human prevalence and wild (guestimate)

CONCLUSIONS:

Probability of Release based on prevalence estimate of 0.001 = 0.0000033

Probability of Release assuming one infected animal that is shipped is 0.0033

As a result of low likelihood of release, the decision was made to not pursue further studies of exposure and consequences.

CONCLUDING REMARKS

- In this model, the disease prevalence in the source population is the most important factor followed by test sensitivity.
- Resources should be allocated to ensure minimal likelihood of disease introduction during transpsort.
- Determining prevalence of important hazards should be a high research priority.
- Multiple testing methods should be considered to maximize sensitivity estimates within the model.
- More work is needed on modeling the probability of introducing disease during transport and at quarantine facilities.
- Further work on exposure and consequence assessments is needed to answer Question 1.

Protocol Development for Disease *Risk Analysis* for Animal Movement
(Refer to Black and white ruffed lemur example for clarification)

***Italicized words defined in glossary*

Section 1: Define the Problem/Policy and Identify Potential Hazards

Step 1: Summarize the issues surrounding the entire process.
Provide background (tell the story)

Step 2: Define the question.
What is the overall policy question that the above story brings out that needs to be evaluated/studied

- Describe the animal move.
- Formulate a broad question.
- List all species of concern from source and destination
    - Human
    - Domestic animals
    - Other wildlife species

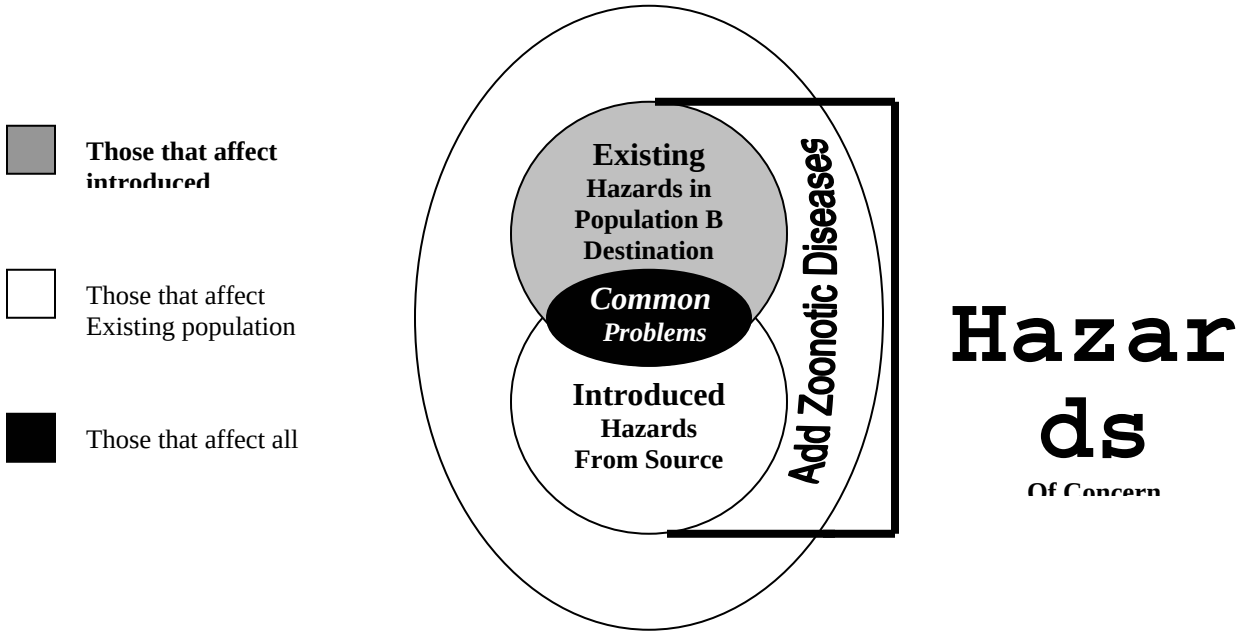
Step 3: Outline the pathway completely.

- Detail all moves and exposure points from point A to point B in box diagram form. This should diagram the entire flow of the process covered in the question above.
- Write a narrative for the flow diagram
- Include such things as
    - Source
    - Quarantine procedures
    - Transport methods
    - Procedures done at all points on diagram
    - End points

Step 4: Identify and list all *potential hazards* (This will vary depending on the specific risk assessment).

- Create a master list(s) of diseases (using disease form from quarantine protocol) that are possible from:
    - PHVA
    - Disease surveys
    - Literature search
    - SSP Veterinary Advisor protocols
- Create specific list for each location (may be the master list or lists may vary depending on regional differences).
    - Identify potential hazards at:
        - Source or point of origin
        - Midpoints along the pathway
        - Destination population

- Don't forget possible zoonoses that can be introduced along the pathway
    - Populations animal may be exposed to during transport (e.g., domestic animals, humans, other species).



Step 5: Create list of *hazards*

- Create hazard list from potential hazard list using *ranking criteria*
    - Define ranking criteria (determined by the risk assessor).
        - Factors that are important in determining if potential hazards should be fully assessed in the *risk assessment* (i.e., potential hazards to *hazards*).
        - Example ranking criteria
        - *Infectivity*
        - *Pathogenicity*
            - Morbidity and mortality
        - *Transmission*
            - Routes and rates
            - Presence of competent vectors
        - *Susceptibility*
            - Species of concern
            - Source and destination
            - Humans
            - Domestic animals
            - Other wildlife species
        - Severity, consequences/outcomes of infection such as:
            - Reproductive effects
            - Morbidity and mortality

    - None (or unknown)
    - Immunosuppression (alter susceptibility)
    - Economic impact
        - Species of concern
        - Ecosystem
        - Humans
        - Domestic animals
- Existing prevalence and incidence

- Should now have a list of hazards that is a subset of potential hazard list
- Each hazard must be assessed in the *Risk Assessment*.

***Section 2*: Risk Assessment**

Step 6: Define specific concerns.
In order to build a model, specific question must be asked. This is usually one of many questions that could be asked under the broad policy question above.

- Formulate a specific question including all or some of the following:
    - Species
    - Source
    - Destination
    - Specific hazard(s)
    - Transport method(s)
    - Pathway

For Example: *What is the likelihood of introducing [species, animal or group] positive for ["x" hazard] from [source] to [destination] via [transport method] on [pathway]?*

i.e. *What is the likelihood of introducing Lemurs positive for TB from Kalamazoo to Timbuktu via the transport route described in the pathway flowchart for reintroduction?*

Step 7: Outline specific pathway that models the question in #4 and identify important steps known as critical control points (CCP).

- A critical control point is any point in the transportation pathway where the hazard may be introduced or released (depending on the question) into or from the pathway. These are subjective and must be chosen by the assessor, these will vary depending upon case scenario.

Step 8: Build a model based on critical control points.

- Make it simple (e.g., by pen and paper or software such as Excel).
- Include all critical control points.
- Each CCP should be a separate input to the model

    - Begin each phrase with: "What is the likelihood of an event happening at a specific CCP. . ." See example.
  - Define qualitative grading scale
- State the *assumptions* used to build the model.

Step 9: Qualitatively test model.

- Qualitatively test the model (based on stated Risk Assessment question)
- Run through example
  - Does it make sense?
  - Does it flow?
  - Are there too many steps?
  - Are there not enough steps?
  - Does it answer the question?

    If yes, congratulations – you have completed your Risk Assessment.

    If no, move on to Step 8 (Quantitative Assessment).

Step 10: Quantitative assessment.

- *Deterministic model*
  - Use point estimates for inputs
    - Number(s), mean, std. deviation etc.
    - Probability
    - Percentages
  - Derive estimates from:
    - Literature
    - Expert opinion (personal communication)
    - Personal experience
    - Specific data

    [Try to avoid guessing if possible – but, sometimes that is all that is available. The lack of information should be described under uncertainty and may also help to guide future research resources and efforts.]

  - Do the math
    - Does it make sense?
    - Does it answer the question?

- *Stochastic model*
  - Incorporates uncertainty
    - Moving from point estimates to the incorporation of ranges or variability in the model. Rarely does a point estimate actually represent the true likelihood of an event. Stochastic modeling allows for variability of the estimate to be incorporated into the model.
    - What are the advantages of using it?
      - Incorporating the use of distributions (e.g., worse versus best scenarios)

    - Easily adaptable/changeable
    - Can perform multiple scenario
    - More rapid, once set
    - Sensitivity analysis
    - Simulations/Monte Carlo
- When is it needed?
    - More detailed knowledge
    - Increases credibility
    - Have to use a range for estimate
    - Have expertise, funds and time
    - Seriousness, complexity of the problem
- Useful tools (e.g., software)?
    - Excel
    - @Risk or Decision Tools (Palisade Co.)
    - Stella
    - Vortex (CBSG)
    - Epi Info (CDC)

Step 11: Describe *uncertainty* of process.
Describe all of the things that you are unsure about in this process. Also describe the degree to which you are unsure. Areas usually included are: the pathway flow diagram, the CCP's used in the model, the data inputs (point estimates etc.)

Glossary:

Acceptable risk: Risk level judged to be compatible with the protection of animal and public health within the pathway of concern.

Assumptions: Properties/characteristics of parameters in a risk assessment, which are fixed within the model and do not change. They may be objective or subjective, but must be explicitly stated in the risk assessment to enhance transparency and risk communication.

Deterministic model: A model whose inputs are completely determined by a given set of conditions resulting in point estimates.

Hazard: A potential hazard that meets the specifications of established ranking criteria and is now considered a high priority potential hazard; all identified hazards must be included in the risk assessment.

Hazard identification: The process of identifying the pathogenic agents, which could potentially be introduced into or released from the reintroduction pathway of concern.

Infectiousness: The ease by which a disease organism is transmitted from one host to another; often used synonymously with transmissibility/communicability.

Infectivity: The characteristic of a microorganism that allows it to infect and subsequently survive and multiply within a susceptible host.

Model: Diagram, flow chart, mathematical or statistical summarization/representation of a complex real-world process.

Pathogenicity: Host-specific ability of an agent to cause disease or otherwise induce pathological change in a susceptible host.

Potential hazard: Any pathogenic agent that could produce adverse consequences on the reintroduction program.

Qualitative risk assessment: An assessment where the outputs on the likelihood of the outcome or the magnitude of the consequences are expressed in qualitative terms such as high, medium, low or negligible.

Quantitative risk assessment: An assessment where the outputs of the risk assessment are expressed numerically.

Ranking criteria: Specific characteristics, properties or attributes of an agent or situation used to differentiate a potential hazard from a hazard during hazard identification; criteria used to decide which potential hazards must be assessed in the risk assessment.

Risk: The likelihood (probability or frequency) and magnitude of the occurrence of an adverse event or hazard; a measure of the probability of harm and the severity of the unwanted adverse effect.

Risk analysis: The process composed of hazard identification, risk assessment, risk management and risk communication.

Risk assessment: The evaluation of the likelihood and consequences of entry, establishment, or spread of a pathogenic agent within the pathway or species of concern.

Risk communication: Risk communication is the interactive exchange of information on risk among risk assessors, risk managers and other interested parties (stakeholders).

Risk management: The process of identifying, selecting and implementing measures that can be applied to reduce the level of risk.

Sensitivity analysis: The process of examining the impact of the variation in individual model inputs on the model outputs in a quantitative risk assessment.

Stochastic/probabilistic model: A model whose inputs represent the inherent variability and uncertainty of the situation; this may be accomplished by incorporating variance and standard deviations around point estimates or by performing multiple iterations of the model using a random number generator.

Susceptibility: The state of being readily affected by a pathogen; a lack of resistance to a pathogen.

Uncertainty: The lack of precise knowledge of the input values which is due to measurement error or to lack of knowledge of the steps required, and the pathways from hazard to risk, when building the scenario being assessed.

Variability: A real-world complexity in which the value of an input is not the same for each case due to natural diversity in a given population.

Virulence: The host-specific ability of an infectious agent to multiply in the host while inducing lesions and disease.

Glossary References:

1. Ahl AS, Acree JA, Gipson PS, McDowell RM, Miller L, McElvaine MD. Standardization of nomenclature for animal health risk analysis. Rev. sci. tech. Off. Int. Epiz. 1993. 12(4): 1045-1053.

2. OIE. 2000. Import Risk Analysis, Section 1.3, International Animal health Code. Office of International Epizootics. Paris, France.

3. Toma B, Vaillancourt JP, Dufour B, *et al*. 1999. Dictionary of Veterinary Epidemiology. Iowa State University Press. Ames, Iowa.

Disease Risk Workshop 2000 II

Report

Working Group 2:
Attwater Prairie Chicken, Cost Analysis

Disease Risk Assessment Workshop- Working Group Two

Mike Ziccardi- Presenter
Tony Allchurch
Jeff Proudfoot
Bill Van Bonn- Recorder
Tony Mudakikiwa
Lisa Done
Robin Radcliffe
Felicia Nutter
Don Janssen- Facilitator

13 September, 2000

Perceived Problems and Questions:

Themes

C= Communication; 1,2,4,7,10,11,12,14,16,26
I= Integrity of data; 3,9,22,23
V= VORTEX and model elements; 6,13,17,18,19,21
A= Application and Implementation; 5,8,10,11,15,20,22,24
+/- a priori decisions

Individual Points

1. Language and terminology to communicate to stakeholders
2. Tools, clear to understand, simple, yet complete
3. Data must be sufficient to make model work; and how to work when data not sufficient.
4. Inclusive, not exclusive approach – rest of world, captive, wild, etc
5. Risk assessment tools – common ground and strengths/weaknesses of each
6. Uncertainty of models- how to address
7. Training needs once tools available
8. Intervention policy- e.g., Mountain gorillas
9. Accuracy and standardization of data
10. Prioritizing risk- some more important
11. Context of risk important (what is acceptable risk for given situation?)
12. Understand what decision makers want before choosing method used, e.g., “low,med,high” vs. %
13. Make disease module flexible in VOTEX for variety of uses needed (e.g., population size- zoo vs. wild)
14. Look at what “market” needs for a product. Product we produce needs to be desired.
15. Tool box- many Risk Assessment (RA) tools for different situations.
16. Difficulty of establishing contingency plan due to gap in information.
17. Need to integrate the cost-benefit into analysis
18. Sensitivity analysis needs to be “visible” and easy in module of VORTEX

19. Should zoonotic concerns be featured into model?
20. Need to prioritize species considered?
21. Is there a way to consider multiple species (domestic/wildlife) disease issue one habitat region?
22. Can data collected on captive populations be applied to models of wild pops?
23. Can you extrapolate information from one disease agent to related agents? (e.g., morbilliviruses)
24. Can we realistically expect to use tool box models on vast variety of taxa?
25. Need change in mindset from individual medicine to population health
26. Tools and information needs to reach stakeholders and decision makers

Worksheet "Problems"

FROM EXAMPLE ONE

1. Animal Origin in #4
2. Differentiate diseases seen in population from all diseases of concern in #6
3. Add "medical procedures" after #11, e.g., transponder implant, etc.
4. Sample banking- e.g., serum bank
5. Are 17a and 17b able to be made more clear?
6. Form designed to be filled out electronically? If so, needs to enable check boxes.
7. Protective clothing- list.
8. Quarantine terminology- same as incoming quarantine, isolated from wild birds, mosquito proof, isolated from other animals, etc? Need Glossary? Need a description of quarantine.
9. Room for comments regarding special considerations (like after #4)
- Medical history

10. Husbandry considerations- diet, predator avoidance, enrichment

From Plenary:

11. Animals from multiple origins to one destination, from one origin to multiple destination and permutations.

FROM EXAMPLE TWO

1. Need place to describe demographics of source and destination populations in order to do risk assessments.
2. What about recommendations for testing destination population? At least a check off that it was considered.
3. Statistical Sampling Plan for large population testing.
4. Suggest Appendix for Power Calculations
5. Need place for sensitivity/specificity of testing method
6. Recommendations (specify)
- Post-release monitoring
- Follow up screening of population
- Habitat assessment (e.g., C.C.)

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet)

1. SPECIES TO BE MOVED: ATTWATER PRAIRE CHICKEN *Tympanunchus cupido attwateri* **EXAMPLE ONE**

2a. FROM: FOSSIL RIM 159, HOUSTON ZOO 15, SAN ANTONIO ZOO 25, ABILENE 19, SEA WORLD 3

2b. TO: APC NATIONAL WILDLIFE REFUGE, NATURE CONSERVANCY LANDS, (FEW OTHERS)

3. TOTAL NUMBER OF ANIMALS: 236 (200) AVAILABLE

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY:

Wild to wild	☐	Wild to captivity	☐
Captivity to wild	x	Captivity to captivity	☐

6a. PROJECT MANAGER: USFWS BIOLOGIST (RECOVERY TEAM) Tel. _____ E-mail: _____

6b. TITLE, INSTITUTION: USFWS Tel. _____

7. PROJECT VETERINARIAN: J. FLANAGAN E-mail: _____

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references.

Dispharynx	Avian Cholera
Capillariaosis	Newcastle's
Coccidiaosis	REV
Salmonellosis	Pox
Mycoplasmosis	
AV Influenza	

9. SPECIFIC DIAGNOSTIC TESTS

For documentation refer to individual animal records

Fecal parasite screen
CBC / Chemistries
Serology- A.I., A.C., Mycoplasma, *Salmonella pullorum*, S. *typhimurium*, Newcastle's
PCR- REV
Cloacal culture (Salmonellosis)

---

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records

Diagnostic samples to be collected: *(Check)*

		Collection Dates	Dates results received
☒	**Physical exam, body weight and measurements**		
☒	**Faeces**		
	Blood smear, haematocrit and total protein		
☒	**Whole blood, serum or plasma (max volume/animal = ml)**		
☐	**Fresh faecal or rectal swab for culture**		
☐	**Choanal or oral swab or culture**		
☒	**Ectoparasites**		
☐	**Other:** Group faecals 2 weeks after treatment		

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

Routine: Ivemectin and fenbendazole
Dipharynx: multiple treatments q2wk with ivermectin, move to clean area and control pill bugs

---

12. SAMPLES TO BE FORWARDED TO:

TVMDL- most samples, serology, cultures
Tavleton State- REV

Quarantine Details

13. LOCATION: Intensive Management Area

14. FACILITY: Fossil Rim

15. QUARANTINE DURATION: **Begins** *(date)* _____ **Ends** *(date)* _____

Total days: 60 If less than 30 days specify reason(s) below

Testing period = 60 day

16. PERSON SUPERVISING QUARANTINE: Radcliffe (veterinarian), Avian Coordinator

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? **YES** NO

X

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT:

- ☐ **"Quarantine - No Unauthorized Entry Sign"**
- ☒ **Insect/rodent traps/screens/baits**
- ☒ **Diagnostic sample collection, storage and transport equipment**
- ☒ **Lock for facility**
- ☒ **Footbath/boot changes**
- ☒ **Protective clothing**
- ☒ **Cage furniture as appropriate for species**
- ☒ **Animal record forms, pens**
- ☒ **Bags for waste disposal**
- ☒ **Feeding, watering and cleaning utensils**
- ☒ **Animal capture and restraint equipment**
- ☐ **Quarantine register**
- ☐ **Animal caregiver personal health check**
- ☐ **Other:** _____
- ☐ **Other:** _____
- ☐ **Other:** _____

19. BUDGET:

Personnel hours **hrs @** _____ **.....** _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments **.....** _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move ☐

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

21. FOLLOW UP ACTIONS:

22. PERMITS TO MOVE ANIMALS RECEIVED? YES NO

23. SIGNED OFF BY: _____ Project Manager **DATE:** _____

_____ Veterinarian

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet)

1. SPECIES TO BE MOVED: BLACK LION TAMARIN *Leontopithiecus chrysopygus*

2a. FROM: JERSEY ZOO **2b. TO:** CPRJ (RID Primate Center)

3. TOTAL NUMBER OF ANIMALS: 2Γ,E

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS
All microchipped					

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY:

Wild to wild	☐	Wild to captivity	☐
Captivity to wild	☐	Captivity to captivity	☒

6a. PROJECT MANAGER: Director Zoo Programs Tel. E-mail:

6b. TITLE, INSTITUTION: Jersey Zoo Tel.

7. PROJECT VETERINARIAN: T. Allchurch E-mail:

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references.

Yersinia pseudotuberculosis	EMC
Campylobacteriosis	LCM
Sallmonellosis	Other primate diseases
Shigellosis	
M. Tb complex	
Nematodiasis	
Cestodiasis	
External parasites	

9. SPECIFIC DIAGNOSTIC TESTS

For documentation refer to individual animal records

Fecal culture for Yersinia + Salm,Shig,Camp
Tb testing- chest, ID, avian/mammalian
Fecal parasitology
Serology- hepatitis, herpes
PCR feces for Yersinia (in development)

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records

Diagnostic samples to be collected: *(Check)*	**Collection Dates**	**Dates results received**
☒ **Physical exam, body weight and measurements**		
☒ **Faeces**		
Blood smear, haematocrit and total protein		
☐ **Whole blood, serum or plasma (max volume/animal = ml)**		
☒ **Fresh faecal or rectal swab for culture**		
☐ **Choanal or oral swab or culture**		
☐ **Ectoparasites**		
☒ **Other:** radiology, (Px is under anesthesia)		

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

No vaccination
FBZ routine

12. SAMPLES TO BE FORWARDED TO:

In-House- CBC, Chem, fecals
Serology- UK, needs CITES

Quarantine Details

13. LOCATION: separate room- isolation

14. FACILITY: Veterinary Hospital- Jersey

15. QUARANTINE DURATION: **Begins** *(date)* _____ **Ends** *(date)* _____

Total days: 30 If less than 30 days specify reason(s) below

6 weeks actual

16. PERSON SUPERVISING QUARANTINE: Head of Mammals

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? **YES** NO

X

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT:

- ☒ **"Quarantine - No Unauthorized Entry Sign"**
- ☒ **Insect/rodent traps/screens/baits**
- ☒ **Diagnostic sample collection, storage and transport equipment**
- ☒ **Lock for facility**
- ☒ **Footbath/boot changes**
- ☒ **Protective clothing**
- ☒ **Cage furniture as appropriate for species**
- ☐ **Animal record forms, pens**
- ☐ **Bags for waste disposal**
- ☒ **Feeding, watering and cleaning utensils**
- ☒ **Animal capture and restraint equipment**
- ☐ **Quarantine register**
- ☐ **Animal caregiver personal health check**
- ☐ **Other:** _____
- ☐ **Other:** _____
- ☐ **Other:** _____

19. BUDGET:

Personnel hours **hrs @** _____ **.....** _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments **.....** _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move ☐

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

21. FOLLOW UP ACTIONS:

22. PERMITS TO MOVE ANIMALS RECEIVED? YES NO

23. SIGNED OFF BY: _____ Project Manager **DATE:** _____

_____ Veterinarian

Decision Tree Cost Analysis- Human ⇐ Gorilla measles

Description and Interpretation

Three scenarios were assessed. The first involved an assumed prevalence in the in-contact human population of 10% and screening for the disease in these individuals is conducted by cursory inspection and observation of clinical signs only. The sensitivity of this method was assumed to be 50%. The cost was assumed to be zero.

Scenario one- physical inspection of trackers

COST?	parameter	(p)	value	comment
-	Prevalence	0.1	$0	
+	Test	0.5	$0	Cursory observation for signs of infection
-	Viability	0.01	$0	
-	transmission	0.5	$0	
TOTAL		0.0002	$0	

In the second scenario the screening test method used was a hypothetical PCR of clinical samples from every in-contact human. The sensitivity of this method was assumed to be 99%. Specificity was assumed to be 75%. Additional assumptions were that positive in-contact humans were excluded from the workforce. Based on this specificity the probability of a false positive individual is 0.225. This created the requirement for an additional 25 (rounded) individuals on the workforce and resulting labor cost increases. This was also based on a daily application of the method- may not be realistic at all. The effect of frequency of PCR testing (daily, weekly, quarterly, annually) on the sensitivity value of the method (not of the test) must be considered. The costs incurred were the test costs and the labor costs. The probability of disease (agent) introduction into the gorilla population was reduced to 0.00005 in this model.

Scenario two- PCR testing of trackers

COST?	parameter	(p)	value	comment
-	Prevalence	0.1	0	
+	Test	0.01	25 x 100 75	PCR oronasal swab Labor increase
-	Viability	0.01	0	
-	transmission	0.5	0	
TOTAL		0.00005	2575	Per test application (day?/week/quarter) Need to figure change in sensitivity due to change in testing frequency

Assumptions:

- 100 tracker/guards at $3/day
- PCR test cost = $20
- Increased sensitivity of PCR increases false + % so that (p) = 0.225 therefore workforce required increases

The third scenario implemented vaccination of the in-contact humans. Vaccine efficacy was assumed to be 99% and therefore prevalence dropped to 1%. Testing was limited to inspection for signs and therefore 50% efficacy was assumed. This approach dropped cost to a one-time investment of $2.00 per vaccinate or initial $200 outlay. The risk probability went to 0.000025.

Scenario three- vaccination of trackers

COST?	parameter	(p)	value	comment
-	Prevalence	0.01	200	Vaccine efficacy reduces prevalence to 1%
+	Test	0.5	0	Inspection for signs
-	Viability	0.01	0	
-	transmission	0.5	0	
TOTAL		0.000025	200	One time cost

Assumptions:

- Vaccine cost = $2/dose
- 100 trackers/guards vaccinated
- Vaccination reduces prevalence to 1%

Recommendations

Based on these data and models it is clearly more cost beneficial to vaccinate the in-contact humans, however the use of PCR as screening test reduces risk of measles introduction five-fold. These conclusions appear to differ from those obtained using the Stella model, however, this disparity may be due to the complexity of the Stella model, that is- the addition of temporal considerations and additional variables which may effect the outcome.

Decision Tree Cost Analysis- *Capillaria* ⇐ Cranes

Description and Interpretation

The originally presented decision tree was expanded to include all possible animal treatment/test groups and their associated probabilities. Also to calculate the number of animals that are eligible for release in each scenario and associated costs.

Assumptions:

- Capture/handling costs = $610 (60 hours effort)
- Fecal sedimentation = $10/tst x 24 = $240
- Re-testing has same sensitivity and specificity as initial
- Treatment = $3/ bird x 24 = $72
- Re-treatment has same efficacy as original
- No mortality due to handling the birds

Scenario one- Test, treat all, test: $610+240+240+72		$1162 ($552)*
Release ~19	(p)= 0.024	[$29/bird]

*Capture and handling occurs annually for health screening. Therefore the figure in parentheses excludes this cost and actual cost per bird is based on this figure.

The above scenario represents the current protocol of testing and treatment. This results in approximately 19 birds eligible for release at a cost of $29.00 per bird and a probability that a released bird is Capillaria infested of 0.024 (~2:100).

The probability of false negative birds is calculated as follows. (See Decision Tree)

(p) False Negative = (0.3 x 0.4 x 0.2 x 0.4) + (0.3 x 0.6 x 0.2 x 0.4) = 0.024

The number of release candidates was calculated as follows. (See Decision Tree)

= (true negatives + false negatives)
= [(24 x (0.11+0.45+0.077+0.12)] + [24 x 0.024]

Scenario two- Treat, Test: $610+240+72		$922 ($312)
Release ~ 19	(p)= 0.024	[$16.42/bird]

Scenario two modifies the decision tree by excluding the first test requirement. This collapses the second decision node (i.e., eliminates the first test-decision point) and results in the same probability that a released bird is Capillaria infested for a lower cost. The probability is the same because no management decision is made based on the first test.

Scenario three- Test, treat+, retest+: $610+21+240+70		$941 ($331)
Release ~ 23	(p)= 0.12	[$14.39/bird]

This scenario assumes only those birds testing positive on the first test are treated and re-tested. This ends the branching of the decision tree at all negative test levels. Therefore, the result is an increase in the number of release candidates, however, the probability of false negatives increases as well. As a result the cost per release candidate is further reduced.

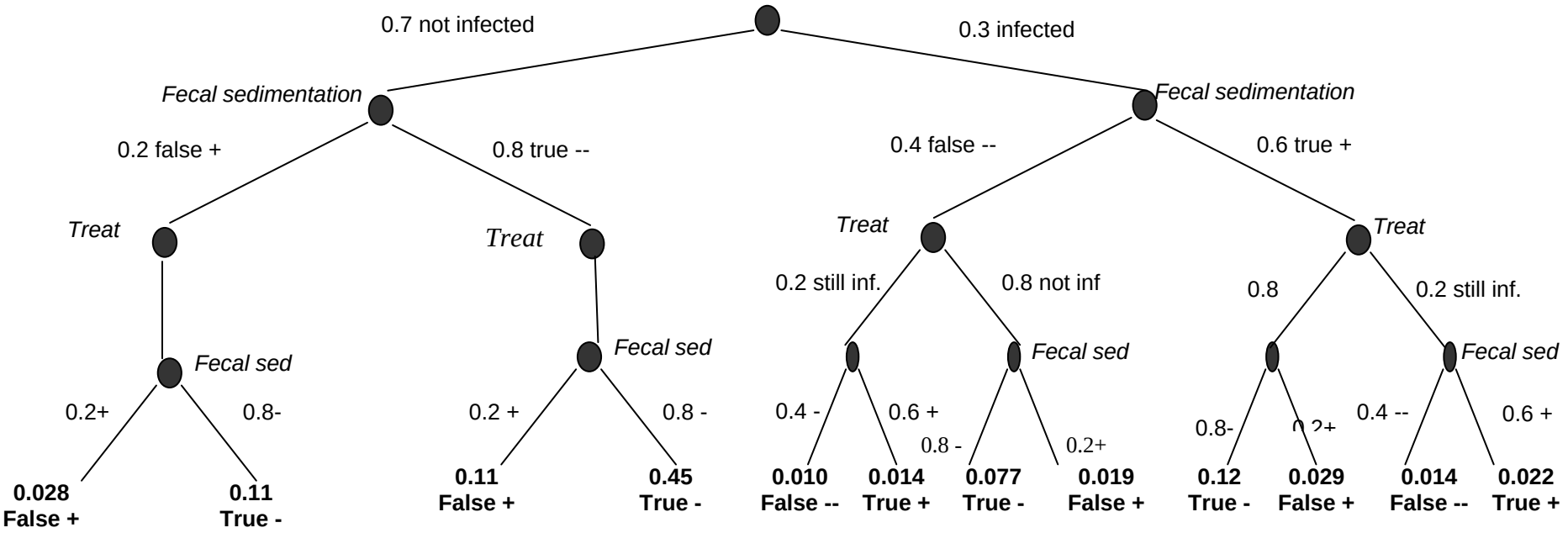
Scenario four- Treat only: $610+72		$682 ($72)
Release ~ 24	(p)=0.06	[$3/bird]

The treatment-only scenario simplifies decision tree analysis by eliminating all test nodes. The number of release candidates is maximized, the cost per candidate is minimized but the probability of releasing an infested bird is 2.5 times greater than scenarios one and two.

Scenario five- Treat x 2: $610+610+72+72		$1364 ($72)
Release ~ 24	(p)=0.012	[$31.41/bird]

Scenario five illustrates the effect of adding a second treatment. The cost increases because of the additional handling required but risk decreases five-fold. It should be noted that twice the handling increases health risk for the birds. The added handling cost could also be eliminated by treatment at time of release.

Concluding Comments: The costs incurred in the above scenarios should be kept in perspective of the overall cost of the program estimates of $40,000/ bird. Costs due to other disease management will be incurred as well.



Decision tree analysis for Whooping crane – *Capillaria spp.*

Risk of releasing *Capillaria spp* infested birds.

Disease Risk Workshop 2000 II

Report

Working Group 3:
Whooping Crane; Decision Tree Analysis

Group 3 (Barrie)

Issue / Problem Generation – Day 1 (13 September 2000)

Mike Barrie, Deana Fritcher, Bruce Rideout, Rani Thiyagarajah, Scott Citino, Vince Mudrak, John-Bosco Nizeyi, Julie Langenberg, Phil Miller, Patti Bright, Jode Garbie

Information Needs

- How much disease information is enough? How do we obtain the relevant information to make better decisions?
- What are the pitfalls of semi-quantitative v. qualitative methods for assessing risk?
- How do we decide which risk assessment tool is appropriate for a given scenario or set of resource availability (e.g., captive-to-captive transfer, release of captive animals to wild populations, etc.)?
- What are the precise mechanisms by which uncertainty is included in risk assessment models?
- Which diagnostic tests are appropriate for a given scenario?
- Where do we find assistance, expertise and funding in the development and interpretation of disease risk assessment models?
- How do we link in the quantitative epidemiological community and the wildlife population community? What are the opportunities for collaboration?
- What are the sample sizes necessary to effectively test for specificity, incidence, etc.?
- What are the factors that need to be identified to perform an effective risk assessment?
- Consideration of real costs into the larger diagnostic testing and risk assessment process

Risk Analysis Results Interpretation

- How do we identify the context of risks of our decisions on associated activities? Risk from one activity being focused upon v. risk from another activity (e.g., botulism risk in carcass placement for CA condor program)
- How do we determine “high” v. “low” risk, given the intrinsic variability (mutation, etc.) of many pathogens? Can we successfully define these categories quantitatively?
- Which diagnostic tests are appropriate for a given scenario?
- How do we interpret results from a given diagnostic test?

Risk Communication

- Who are the stakeholders that must be involved in the development and application of disease risk assessment tools?
- What are the relative contributions of biology v. policy in determining acceptable levels of risk?
- What are the pitfalls of semi-quantitative v. qualitative methods for assessing risk?
- How do we link in the quantitative epidemiological community and the wildlife population community? What are the opportunities for collaboration?

Decision Analysis I: Salmonella in Whooping Cranes

Situation

A total of 8 out of 24 captive birds came back positive for Salmonella: six with one strain and two with another. These birds would be used as stock to move to Florida as part of the recovery effort.

A larger-scale analysis is required to qualitatively evaluate risk of introducing this Salmonella strain to Florida. Specifically, does introduction of the organism to Florida pose a risk to:

- The ecosystem? NO
- The destination crane population? NO
- Local domestic animals? NO
- Humans? NO

The conclusion from this qualitative analysis: This serotype of Salmonella is not a significant risk factor for this particular movement action (because there is documentation that this serotype already exists in the Florida avifauna). Consequently, formal decision/risk analysis is not warranted in this case.

Decision Analysis II: EEE in Whooping Cranes

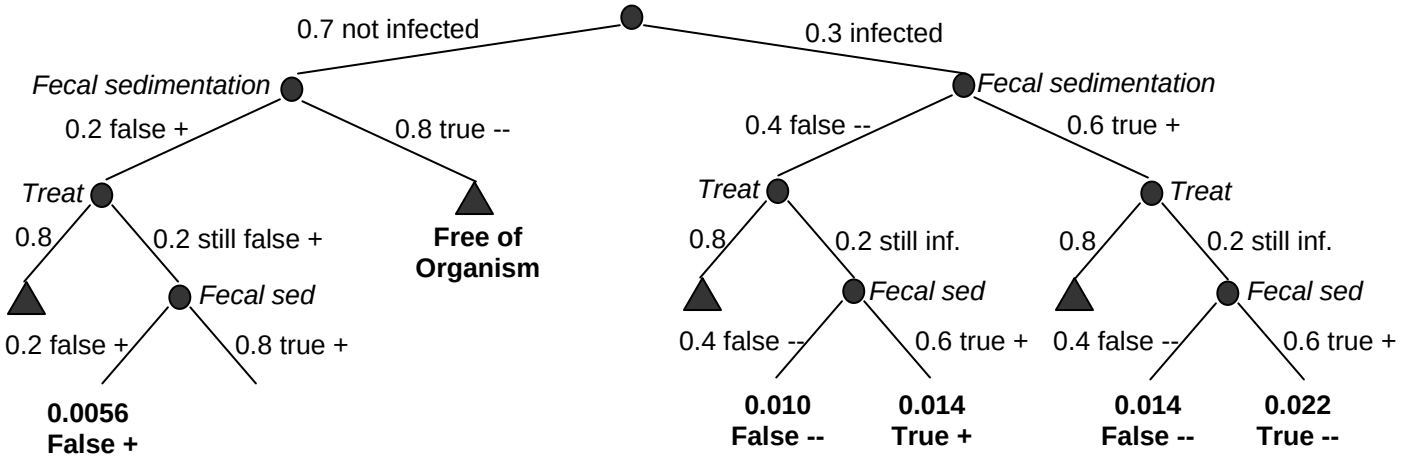
EEE is an endemic disease of birds in Florida. It has also occurred as a clinical disease at one whooping crane captive breeding center, with apparently very high mortality in whooping cranes. There is some evidence from release birds in Florida that EEE is not lethal as some released birds have shown titers and survived. Incubation period is around 2 weeks, and birds typically die before they show a titer in captivity. Consequently, our question is:

> What is the risk to newly translocated animals of contracting EEE from birds already resident in Florida?

The group concluded that this type of question is best answered by a STELLA – type epidemiological model incorporating factors such as transmission biology, prevalence, general ecology, etc.

Decision Analysis III: Capillaria infestation in Whooping Cranes

What is the risk of introducing a non-North American Capillaria species into Florida from released captive birds?



Definition of a False + : Bird infected with the NORTH AMERICAN species of Capillaria, not the foreign species for which we are evaluating risk.

Comments on plenary:

- Non-independence of iterative testing – is the probability of false negatives the same each time you test a given animal?
- What about evaluating the efficacy (financial?) of just treating everybody regardless of testing? This could be evaluated using financial payoff (costs) in a formal decision analysis.

Decision Tree Analysis

This group worked through an exercise of the Quarantine and Health Screening Worksheet for Animal Movements, using translocation of whooping cranes as our example. After filling out this worksheet we took the example of *Capillaria* in the birds to be moved and applied a Decision Tree Analysis.

Our goal was to take the initial Decision Tree and turn it into a Decision Analysis process using the computer program Precision Tree.

The question the decision analysis is designed to answer is: What is the probability of introducing the exotic *Capillaria* species present in the captive population at the release site in Florida?

We performed a simplified form of decision analysis in which a set of decisions has already been made, thus we are modeling the risk associated with those predetermined decisions, and not evaluating which decision to make.

Advantages of a formal decision analysis compared to informal (simplified) decision tree:

- Ability to alter assumptions and alter assigned probabilities to see how these changes affect outcomes.
- Ability to incorporate stochastic parameters (uncertainty) into the model. For example, if we were uncertain about the sensitivity of the fecal sedimentation test to detect *Capillaria*, we could quantify that uncertainty by creating a distribution of sensitivity values centered on our estimate of the mean sensitivity of 60%.
- Allow the user to formulate additional questions and modify the model to answer that question—comparison of scenarios rapidly. For example, we could examine if changing the current testing protocol significantly affects the risk of introducing an infected bird.
- Ability to incorporate financial costs into the analysis and ability to compare costs of different management situations.
- Increased ability to model more complex situations more accurately

On the contrary, formalized decision analysis may be an unnecessarily labor intensive tool, depending on the complexity of the question one is trying to address, and the available time and resources for addressing the question.

For example, the pen and paper decision tree created by our group the previous day was adequate to answer the initial question "what is the probability of releasing a Capillaria infected whooping crane at the Florida release site?" Furthermore, the initial decision tree was modified by group #2 to incorporate costs. Although both of these decision trees produced quantitative answers, many assumptions were made to simplify the tree so that it could be analyzed without computer assistance.

Limitations of using Precision Tree to perform a decision analysis

- Training is necessary
- Increased time needed to design tree and input data
- Cost of the software/ computer access needed (impractical in remote field situation)
- The program cannot determine what is an acceptable level of risk.
- If we wanted to assess what may happen if this organism is released in the environment, an epidemiologic/ecologic model that is more appropriate could be applied (ex. STELLA).

General Conclusions

Decision analysis can be a useful tool for assessing risk in animal movements. The complexity of the analysis will depend on the availability of resources and the question that is to be answered. In some situations other methods of risk assessment will be more appropriate or more useful.

Decision Analysis I: Salmonella in Whooping Cranes

Situation

A total of 3 out of 24 captive birds came back positive for *Salmonella muenchen*. These birds would be used as stock to move to Florida as part of the recovery effort.

A larger-scale analysis is required to qualitatively evaluate risk of introducing this Salmonella strain to Florida. Specifically, does introduction of the organism to Florida pose a risk to:

- The ecosystem?
- The destination crane population?
- Local domestic animals?
- Humans?

The conclusion from this qualitative analysis: This serotype of Salmonella is not a significant risk factor for this particular movement action (because there is documentation that this serotype already exists in the Florida avifauna). Consequently, formal decision/risk analysis is not warranted in this case.

Decision Analysis II: EEE in Whooping Cranes

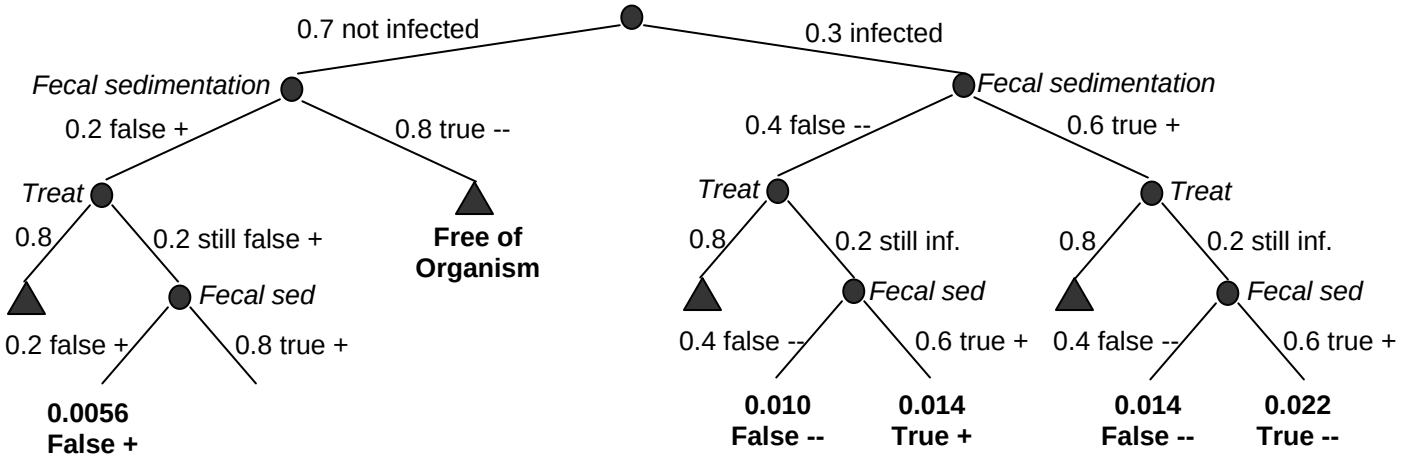
EEE is an endemic disease of birds in Florida. It has also occurred as a clinical disease at one whooping crane captive breeding center, with apparently very high mortality in whooping cranes. There is some evidence from release birds in Florida that EEE is not lethal as some released birds have shown titers and survived. Incubation period is around 2 weeks, and birds typically die before they show a titer in captivity. Consequently, our question is:

> What is the risk to newly translocated animals of contracting EEE from birds already resident in Florida?

The group concluded that this type of question is best answered by a STELLA – type epidemiological model incorporating factors such as transmission biology, prevalence, general ecology, etc.

Decision Analysis III: Capillaria infestation in Whooping Cranes

What is the risk of introducing a non-North American Capillaria species into Florida from



released captive birds?

All numbers used in this Decision Tree are best guesses based on the experience of the whooping crane program and input from the group members.
-It was estimated, based on WC flock history, that there is a 30% infection rate of this capillaria in release age birds.
-It was GUESSED that the fecal sedimentation test used will pick up 60% of infected birds.
-It was estimated that treatment with ivermectin and fenbendazole is 80% successful.

Definition of a False + : Bird infected with the NORTH AMERICAN species of Capillaria, not the foreign species for which we are evaluating risk.

Conclusion: There is a 0.024 (0.010 + 0.014 false negatives) probability of introduction of the non-North American capillaria when these birds are moved.

Comments from other working groups:

- Non-independence of iterative testing – is the probability of false negatives the same each time you test a given animal?
- What about evaluating the efficacy (financial?) of just treating everybody regardless of testing? This could be evaluated using financial payoff (costs) in a formal decision analysis.

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet) **– Need Date added to top of form**

1. SPECIES TO BE MOVED: Whooping Crane (*Grus americana*)

2a. FROM: Patuxent, Maryland **2b. TO:** Wild population in Florida

3. TOTAL NUMBER OF ANIMALS: 24

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS
1 – 24	Chips, leg bands	6 mos.	12.12		

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY:

Wild to wild	☐	Wild to captivity	☐
Captivity to wild	X	Captivity to captivity	☐

6a. PROJECT MANAGER: Julie Langenberg

Tel. _____

E-mail: _____

6b. TITLE, INSTITUTION: _____

Tel. _____

7. PROJECT VETERINARIAN: Patti Bright

E-mail: _____

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references. **Veterinary assistance advised (required?)**

(How far do you extend your search – taxonomically, geographically? Do you project some time into the future in terms of these diseases, or do you look just at today? The general group conclusion is to initially take a focused approach in terms of these considerations, and then perhaps broaden the scope at a later date.)

"Short list" includes:

Avian TB; Salmonella; IBDC; EEE /WEE; WNV; Coccidiosis; Capillaria; Ascarids; Cyathostoma; Feather lice; Hexamita; Metal ingestion; developmental abnormalities (angular limb deformities, tracheal shortening); Newcastle virus, Avian influenza

- Worksheet does not specify source versus destination populations
- Also consider separating "legal" v. "biological" types of concern?

9. SPECIFIC DIAGNOSTIC (SCREENING?) TESTS

For documentation refer to individual animal records

(Comments on specific test – percentage of false negatives, etc. -- should be made on a preliminary worksheet.)
If you're testing a larger population in which only a sample of individuals will be tested, some guidelines should be given on sample size needs)

Perhaps consider flock / herd history as a means for identifying disease history and risks

Coccidiostat; serology for IBDC, EEE, WEE, WNV; parasites, 2 fecals; feather lice, PE; TB and Salmonella, fecal culture; metal ingestion, rads; developmental abnormalities, PE and rads

---

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records – **multiple sample dates make this limiting →**

Diagnostic samples to be collected: *(Check)* **What about banking serum?**

	Collection Dates	Dates results
☐ **Physical exam, body weight and measurements**		
☐ **Faeces**		
Blood smear, haematocrit and total protein		
☐ **Whole blood, serum or plasma (max volume/animal = ml)**		
☐ **Fresh faecal or rectal swab for culture**		
☐ **Choanal or oral swab or culture**		
☐ **Ectoparasites**		
☐ **Other:** _____		

Significant test results:
IBDC All negative
EEE All Negative
WEE "
WNV "
Feather lice Neg
Mycobacterium neg
No developmental abnormalities
Fecal exam 30% positive for capillaria
Fecal culture *Salmonella muenchin* 3 birds positive
Radiographs 2 birds with metallic foreign bodies (one with sharp fragments, lead and zinc levels run on second bird- normal levels

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

Ivermectin
EE Vaccination
Fenbendazole – some birds appeared to develop negative reaction (specific details unclear)

(Need to capture complications so that future actions can be based on past experience)
Endoscopic removal of metallic foreign bodies.

---

12. SAMPLES TO BE FORWARDED TO:

IBDC – EEE – WNV: National Wildlife Health Center
Salmonella culture, TB culture: University of Wisconsin Veterinary Diagnostic Lab
-- REWORK SECTION TO SOMEWHERE INCLUDE SUMMARY OF SIGNIFICANT RESULTS. NEEDS TO BE INCLUDED BEFORE SUMMARY OF MOVEMENT RECOMMENDATIONS

Quarantine Details

13. LOCATION: Patuxent, Maryland

14. FACILITY: Quarantine pens

15. QUARANTINE DURATION: **Begins** *(date)* _____ **Ends** *(date)* _____

Total days: 30 If less than 30 days specify reason(s) below

_____

_____

_____

16. PERSON SUPERVISING QUARANTINE: Patti Bright

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? YES **NO**

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT: (PHYSICAL DESCRIPTION OF QUARANTINE FACILITY?)

- ☐ "Quarantine - No Unauthorized Entry Sign"
- ☐ Insect/rodent traps/screens/baits
- ☐ Diagnostic sample collection, storage and transport equipment
- ☐ Lock for facility
- ☐ Footbath/boot changes
- ☐ Protective clothing
- ☐ Cage furniture as appropriate for species
- ☐ Animal record forms, pens
- ☐ Bags for waste disposal
- ☐ Feeding, watering and cleaning utensils
- ☐ Animal capture and restraint equipment
- ☐ Quarantine register
- ☐ Animal caregiver personal health check
- ☐ Other: _____
- ☐ Other: _____
- ☐ Other: _____

19. BUDGET:

Personnel hours **hrs @** _____ ..... _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments ..... _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move X

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

The following significant results were evaluated using a risk assessment process (Decision Tree Analysis) attached.

1. Salmonella. Decision Analysis I
This serotype of salmolella is not a significant risk factor for this particular movement because there is evidence that this already exists in Florida avifauna.

2. EEE. The birds were all vaccinated to protect them at the release site.

3. Capillaria Decision Analysis III 30% of birds were infected with a species of capillaria not indigenous to North America. All were tested and treated reducing the parasite burden as illustrated in decision tree III. Based on this decision analysis there was an estimated 0.024 probability of introducing the organism into the release environment. Data of previously released birds show that this species of capillaria is already present at the release site. There is minimal additional risk of introducing these individuals.

4. Heavy metals. Risk of disease was addressed by removal of sharp metallic foreign body from one bird, lead and zinc levels of second bird were normal.

---

21. FOLLOW UP ACTIONS:

Released cranes and native birds should be monitored for nonindigenous capillaria.
Efforts to reduce exposure to metallic objects should be addressed at source facility.
Continue to investigate risks of EEE to birds at release area.

---

22. PERMITS TO MOVE ANIMALS RECEIVED? **YES** X **NO**

23. SIGNED OFF BY: Project Manager **DATE:**

Veterinarian

Note: Tasks that must be completed prior to decision analysis: Identification of source /destination populations, generation of disease matrix, identification of diseases of concern, identification of sources of information regarding disease.

STEPS FOR DESIGNING A DECISION ANALYSIS MODEL FOR DISEASE RISK ASSOCIATED WITH ANIMAL MOVEMENT

EXAMPLE ISSUE: Evaluation of the probability of accurately detecting a parasitic infection (of a foreign capillaria species) in captive whooping cranes slated for introduction into the wild.

Part I.

1. Determine the question(s) to be answered:

a) What is the probability that a captive bird will be incorrectly identified as non-infected (false negative), leading to potential introduction of the capillaria into the destination population?

b) What is the probability that a captive bird will be incorrectly identified as infected (false positive), leading to its exclusion from the reintroduction program?

(Note: Correctly identifying the question(s) is crucial. Selection of the wrong question may lead to the user addressing a different problem with different outcomes that will impact the ultimate decision…this is an issue that will need to be expanded upon and clearly explained in our final product…)

2. Determine process to be evaluated:

Evaluation of the current testing and treatment protocol for foreign capillaria species for whooping cranes in captivity. Current protocol requires that a bird have 2 consecutive negative test results in order to be eligible for release.

3. Define the process that is to be evaluated:

a) All birds in the captive (source) population are tested prior to treatment

b) All birds receive first treatment, regardless of test results

c) All birds are tested a second time.
   Those birds that test negative and now have 2 consecutive negative test results are categorized as birds to be released. These birds will receive one more treatment but will not be tested again.
   Those birds that test negative, but do not have 2 consecutive negative test results will be treated again and tested a third time.
   Birds that test positive will be treated a second time and re-tested.

d) All birds receive a second treatment

e) Treatment of any birds that do not have 2 consecutive negative test results
Those birds that test negative and now have 2 consecutive negative test results are categorized as birds to be released. These birds will receive one more treatment but will not be tested again.
Those birds that test negative, but do not have 2 consecutive negative test results will be treated again and tested a fourth time.
Birds that test positive will be treated a third time and tested.

f) Need to verify what happens

Note we'll need to have Julie Langenberg to review this procedure for accuracy

4. Identify outcomes of interest:

a) Proportion of birds that test false negative.
b) Proportion of birds that test false positive
c) Economic costs associated with current testing protocol. (to include financial costs associated with FP and FN outcomes)

5. Generate a list of variables that affect the outcome(s) of interest:

Variables (%) that influence the proportion of birds testing FN	**Variables (%) that influence the proportion of birds testing FP**
❑ Prevalence of disease (infected vs. non infected) ❑ Sensitivity of the first diagnostic test- True Negatives (TN) Vs False Negatives (FN) ❑ Efficacy of the first treatment ❑ Sensitivity of the second diagnostic test *(*consider: potential reduced sensitivity with serial testing)* ❑ Efficacy of the second treatment *(*consider -potential reduced efficacy with serial treatments)* ❑ Sensitivity of the third diagnostic test ❑ Efficacy of the third treatment	❑ Prevalence of disease (infected vs. non infected) ❑ Specificity of the first diagnostic test- True Positives (TP) Vs False Positives (FP) ❑ Efficacy of the first treatment ❑ Specificity of the second diagnostic test *(*consider-potential reduced specificity with serial testing)* ❑ Efficacy of the second treatment *(*consider-potential reduced efficacy with serial treatments)* ❑ Specificity of the third diagnostic test ❑ Efficacy of the third treatment

6. Generate a list of decisions that affect the outcome(s) of interest ;

a) Decision to test all the animals initially (Y/N)
b) Decision to treat the animals (Y/N)
   If yes, determine which animals to treat:
   - all animals
   - only those that previously tested positive
c) Decision to test animals a second time (Y/N)
   If yes, determine which animals to test:
   - all animals
   - only those that previously tested positive
d) Decision to administer a second treatment (Y/N)
   If yes, determine which animals to treat:
   - all animals
   - only those that do not have 2 consecutive negative test results
e) Decision to test animals a third time (Y/N)
   If yes, determine which animals to test:
   - all animals
   - only those that do not have 2 consecutive negative test results
f) Decision to administer a third treatment (Y/N)
   If yes, determine which animals to treat:
   - all animals,
   - only those that do not have 2 consecutive negative test results

7. Generate a list of probabilities and distributions for the variables listed in question #4

NOTE:

- Probabilities may be estimated based on published literature, medical records, anecdotal information.
- Distribution type can be selected from one of 30 listed in the @Risk program (we may need to provide guidelines for the user on selecting appropriate distribution) Riskview can also help users make the correct selection
- To maintain transparency the sources of the information need to cited. If the information is based on the users best guess or extrapolated from another species that should be clearly stated
  in the Source of Information column

Variable	***Probability-minimum***	***Probability-mean***	***Probability maximum***	***SD***	***probability distribution***	***Source of information***
Sensitivity of 1st fecal sediment test for foreign capillaria	Note: #s used here are Hypothetical				normal	Journal X, dated, Vol. Pg.
Specificity of 1st fecal sediment test						
Efficacy of 1st treatment (% treated successfully)						Drug manufacturer pers. comm 10/99
Sensitivity of 2nd fecal sediment test for foreign capillaria						
Specificity of 2nd fecal sediment test						
Efficacy of 2nd treatment						
Sensitivity of 3rd fecal sediment test						
Specificity of 3rd fecal sediment test						
Efficacy of 3rd treatment						

Part II
Performing a Sensitivity Analysis

Note: We can use either precision tree for analyzing decision trees or Top Rank to analyze on spreadsheet models….

Part III
Economic Analysis

Additional Notes:

OUTLINE Of Process:

Step 1: Basic model based on variables can be used to evaluate outcomes of current testing/quarantine/treatment protocols

- Outcomes can be used to further evaluate acceptable risk
- Outcomes can potentially be used to generate data for vortex

Step 2. Incorporate "decisions" (i.e. test or not test) to evaluate/ compare outcomes of different protocols

Step 3 Add economic costs to evaluate and compare cost/benefit of different protocols

The DA model is designed to generate quantitative outcomes, but the crucial part of the DA should be the thinking process required by the user. If the model is developed correctly the user should gain an insight and understanding of the advantages and disadvantages of the different testing/treatment different protocols.

Disease Risk Workshop 2000 II

Report

Working Group 4:
Burchell's Zebra; Stella System Model

GROUP 4: African Examples and Stella Modeling

Members:
Suzanne Kennedy-Stoskopf
Laura Hungerford
Tom Meehan
Genny Dumonceaux
Pat Klein
Shirley Llizo
Jim Else
Robert Bakal
Steph Sanderson

Problems:

(1) How do we model the unknown? Examples canine distemper in lions and west Nile disease in New York? How do we factor in disease for which we have little background data?

(2) What is stochastic and is it a good approach?

(3) Can you include the adaptability of animals in modeling? How do we factor in the principle or rate of adaptation in with habitat loss, dietary changes, etc. These can often blow the model apart. Or they may actually make models fail because they are not included?

(4) Determine how we will test and interpret the diagnostic test. Need to understand the disease pathogenesis.

(5) Disease modeling in too much isolation can be a problem if it ignores genetics and other factors.

(6) Host, disease, environment triad is important. Without consideration of the environmental factors the big picture is lost. (9) Are we looking at population estimates, or overall risk of reintroduction for ecosystem or risk for a specific species or particular diseases? Do we want to know impact on just the wild members of a specific species or also want to consider other species in the environment?

(7)Which diseases are significant? Just because you isolate a pathogen doesn't mean that it means anything. (8) Concern that disease risk assessment might be too complicated and take too long to react to real problems.

(10) What is the product we want at the end? List of questions that can be asked with models, but what are the key questions? People want hard data and are uncomfortable with speculation... even informed speculation. So how does this balance fit in modeling? Model should make clear where it comes from as far as assumptions.

(11) How do we build partnership with the public into the model? If you ignore the public response/human component/perception, the ultimate outcome may be different. How do you get the public to participate in the process? How do the model results get to the policy maker? Reach them in time and also inform the decision and also be practical? Conservation needs to make explicit that there are direct human health benefits of saving wildlife and the environment. The public needs to see the direct cost or benefit of conservation to them. Focus on the direct benefit to those who are local.

(12)Animal handling and the risk for human disease. How to put the zoonotic risks associated with different activities in context. Zoonotic risk for disease with Canada geese versus food safety issues.

(13) How much does the model fit with the use of the model? If the audience doesn't want to hear what you say, maybe you asked the wrong range of outcomes in the model.

(14) Does Vortex determine carrying capacity?

(15) How do consider natural extinction rate and what should and shouldn't go extinct? In a multispecies model, some may have to go extinct in order to save others or saving some may save them all. Or if you fail with the charismatic species, then will they all be lost because there is no other interest. Should pathogens be protected as well from extinction?

Themes:

Public - 11,12, 13
- Inclusion of all stakeholders in the process
- impact of conservation to public and public health concerns
- relative importance of zoonotic concerns

Models - 1, 2, 3, 8, 10, 13, 14
- User friendly and usable
- are they comprehensible enough
- do they address the right questions

Diseases - 4, 5, 7, 15
- significance of disease component within the risk assessment

Population - 6, 9, 15
- are we limited to considering a population of a single species

Problems Encountered in Using the Sheet:

Problems of preshipment versus postshipment quarantine

Issue of place of this form in the risk assessment process

Need of information on health/exposure history of herds (captive/wild) involved

How would this apply to animals too small to do extensive testing

Issue of animals captively bred in 150 sites across the country without health, disease, necropsy information

How to handle situation when those involved in program won't do the tests that are recommended due to time or cost

Need to know how many animals to sample to screen for some of these agents - possibly using EpiTable, Pepi, etc.

Modeling Infectious Disease Risk with STELLA®

Laura L. Hungerford, DVM, MPH, PhD
Great Plains Veterinary Educational Center, University of Nebraska

Risk assessment is a theoretical approach for making decisions when information about the decision process or possible outcomes is uncertain. Scientific data and estimates about the likelihood that certain things will happen are combined to model the situation and predict outcomes. This approach to decision making has already become wide spread in other fields, and continues to grow as a method for dealing with complicated human and animal health issues. Modeling infectious disease helps us conceptualize and summarize the risk of disease introduction and transmission.

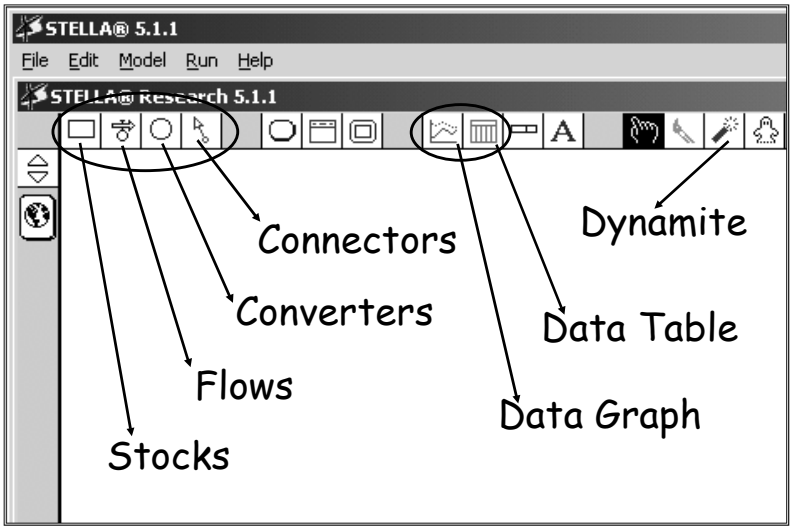
One advantage of modeling is that it creates an explicit, visual picture of our current beliefs and understanding about a problem. If we use modeling software, like STELLA®, to compose this picture, we can then simulate and predict the logical outcomes from this vision. If these results don't match field observations, it shows us that either our model needs to be revised or that our real world data are biased. The conceptual model may highlight critical information that is currently unknown and needs to be collected before solving the problem. Sensitivity analysis of the model identifies the factors that most strongly influence outcomes. If very contentious points have little impact on final outcomes, this can help build consensus. Models can, additionally, be used to predict consequences, compare potential programs or policies, and quantify efficacy of interventions. Prediction of consequences and evaluation of the effectiveness of interventions are major goals of disease risk assessment.

The reason we are now seeing so many risk assessment and other types of computer models is that they provide a way to address issues that are perceived as "bombs waiting to go off". You can't generally know, from past experience, **exactly** what will happen in the future, especially if you are considering doing something that has never been done before. You can use existing data to try to predict, but you can't know for sure until it happens. Models provide a way of making educated predictions resulting in decisions when there is uncertainty. They are seen as these magic "black boxes" that give us answers.

Modeling and risk assessment can be accomplished mentally or using pencil and paper. Computer programs are useful tools as problems or potential options grow more complex. There are a number of different computer programs that can facilitate this process. STELLA® is a commercial software program designed for modeling complex problems, made by High Performance Systems, Inc. Information is available at the website: http://www.hps_inc.com/edu/stella/stella.htm. It is a graphically oriented program, which allows a diagram of the problem to be made, then the underlying equations to be completed, then the outcomes to be simulated, and parameters varied. Because it is simple to begin using and has a graphical interface, it lends itself very well to modeling problems in groups of experts from diverse fields.

A challenge in constructing a model is finding the appropriate data. Sources may include the scientific literature, field studies, epidemiologic analyses of risk factors, best guesses, etc. Accepting the validity of the data and agreeing on the underlying assumptions is often the most

contentious step in the modeling process. Recognition of specific new data items that need to be collected is a common outcome of the modeling process.



Although STELLA® is very powerful, it uses a simple set of tools that can be learned very quickly.

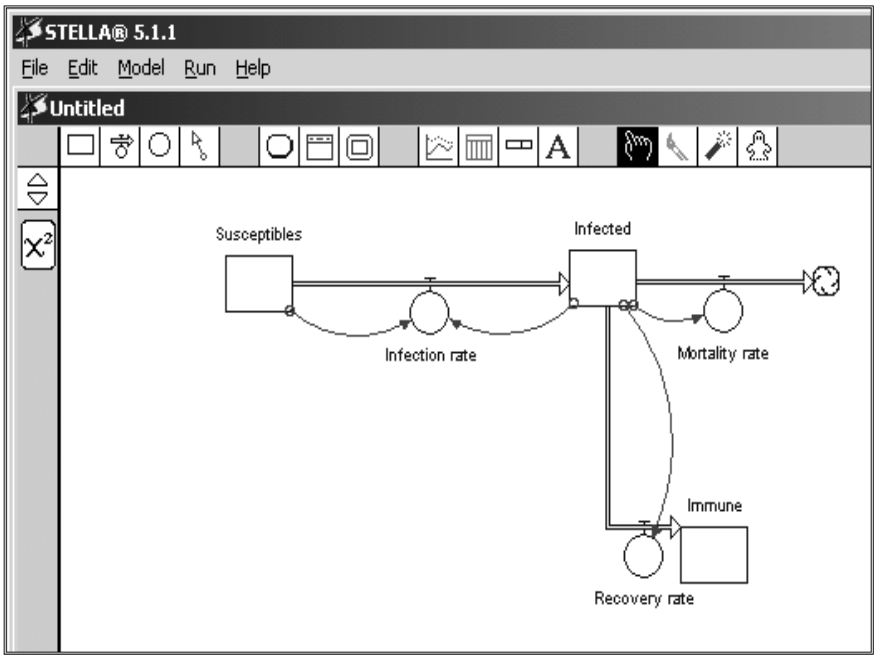
Stocks are used to accumulate numbers of things. In disease modeling, this is usually numbers of animals in different stages of disease. Susceptible, infected, and immune subpopulations would be examples of potential stocks in a model.

Flows are used to model the movement between stocks. A flow would allow susceptible animals to become infected at some rate that would be specified in the flow.

Converters hold information that stays constant or that is needed to modify the flows in the model. These are a convenient way to represent data that are not the actual numbers of animals, but affect the way animals move between the subpopulations in the model.

Connectors illustrate the links between parts of the model, aside from the movements of animals. All of the factors that go into calculating the rate at which animals move between stocks are linked to the flow rate calculation through connectors.

Dynamite is used to "blow-up" unwanted components when building a model. It is equivalent to the delete key in other software programs.



Data graph and **data table** provide a means to visualize the results of a model. The icon is selected to create a new graph or table on the model sheet. Double clicking on the graph or table opens a menu box where variables for the table or graph and other specifics of its appearance can be specified.

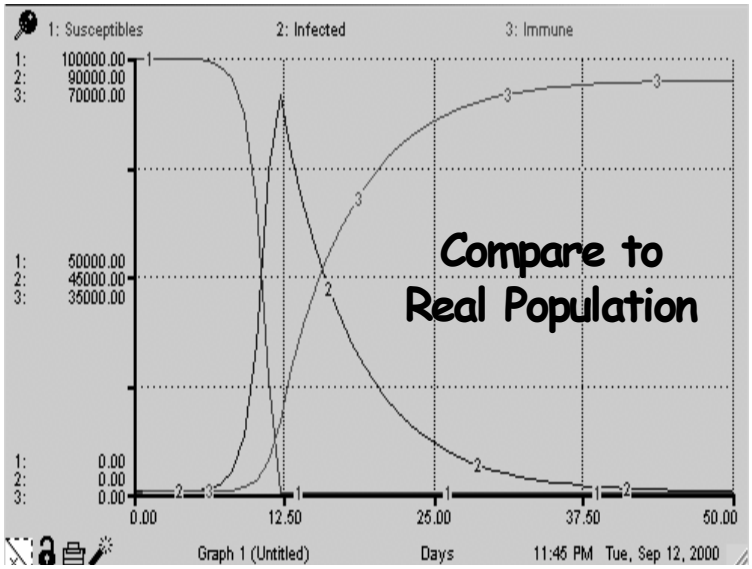
An example of a simple epidemic model would be stocks for susceptible,

infected and immune animals with flows between them for infection, recovery and death. This models the introduction of an agent or infected animal into a population.

After such a base model is begun, additions and enhancements, specific to a disease can be added to make the model more realistic. The risk of that introduction occurring and preventive measures can also be included.

This visual representation is the first step in creating a quantitative model that can generate numerical predictions about disease patterns, transmission and risk. But, in many cases, just the process of specifying the model gives insights. It provides a visual summary of what we believe the relationships to be within a complex situation. This can allow us to recognize relationships that were not previously apparent and also stimulate discussion about the problem being modeled between people from disparate backgrounds.

Once the basic structure of the model has been constructed, double-clicking on a flow or stock opens a window where the values, relationships and equations can be defined. Data for this aspect of the model can come from review of the scientific literature, field studies, epidemiologic studies, expert opinion, and modeling short-cuts which produce a specific pattern. If some of these data are less than satisfactory, they can be modified later to substitute other values and see if the model predictions are sensitive to these changes.



The final steps in creating a model are verifying and validating the model. Verifying includes careful assessment of correctness of the relationships and numbers in the model. Models are then validated by generating predictions and comparing them to actual data to see how well the model mimics reality. If predictions and reality are far apart, this may illustrate a gap in our knowledge about the problem and lead to modifications of the model. Importantly, if the model is the logical expression of our understanding of the system and it doesn't lead to realistic conclusions, then our view of the problem may need to be adjusted.

STELLA® or other similar modeling programs can help us visualize a problem for discussion, quantify relationships, and generate predictions. We can link together and make explicit what we know, believe and perceive about a problem. This provides a valuable tool for addressing complex risk assessment problems, comparing alternative actions and aiding decision making. The ease of use allows content experts, intimately involved with the problem, to create and modify models rather than to rely on external modeling specialists.

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet)

1. SPECIES TO BE MOVED: Springbok (*Antedorcas marsupians*)

2a. FROM: California **2b. TO:** Florida

3. TOTAL NUMBER OF ANIMALS: 1 ☒ **PRESHIPMENT** ☐ **POSTSHIPMENT**

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS
103478	Ear tag	subadult	M	moved	Brought in paratuberculosis

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY: Wild to wild ☐ Wild to captivity ☐ Captivity to wild ☐ Captivity to captivity ☒

6a. PROJECT MANAGER: Tel. E-mail:

6b. TITLE, INSTITUTION: Tel.

7. PROJECT VETERINARIAN: E-mail:

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references.

Johnes, TB, brucellosis, blue tongue, nematodes, cestodes, trematodes, protozoa, ectoparasites, Salmonella, Clostridium, leptospirosis, Anaplasmosis,

9. SPECIFIC DIAGNOSTIC TESTS

For documentation refer to individual animal records

TB – intradermal test
Johnes – fecal culture, 3 samples within 10 days
Brucellosis – serology
Bluetongue – serology (acute)
Nematodes – direct fecal and Baeremanns
Cestodes – direct fecal and Baeremanns
Trematodes – direct fecal and Baeremanns
Protozoa – direct fecal and Baeremanns
Ectoparasites – physical exam
Salmonella – fecal culture, 3 samples within 10 days
Clostridium – rectal swab/scrapping anaerobic culture
Leptospirosis – serology
Anaplasmosis – serology

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records

Diagnostic samples to be collected: *(Check)*	**Collection Dates**	**Dates results received**
☒ **Physical exam, body weight and measurements**		
☒ **Faeces**		
Blood smear, haematocrit and total protein.....CBC		
☒ **Whole blood, serum or plasma (max volume/animal = ml)**		
☒ **Fresh faecal or rectal swab for culture**		
☐ **Choanal or oral swab or culture**		
☒ **Ectoparasites**		
☐ **Other:** Group faecals 2 weeks after treatment		

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

Rabies
Clostridium 7 way
Tetanus
Treatment for parasites if positive for anything

12. SAMPLES TO BE FORWARDED TO:

Appropriate diagnostic labs

Quarantine Details

13. LOCATION: California

14. FACILITY: _____

15. QUARANTINE DURATION: **Begins** *(date)* _____ **Ends** *(date)* _____

Total days: 30 If less than 30 days specify reason(s) below

_____

_____

_____

16. PERSON SUPERVISING QUARANTINE: Hoofstock manager

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? **YES** NO

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT:

- ☐ **"Quarantine - No Unauthorized Entry Sign"**
- ☒ **Insect/rodent traps/screens/baits**
- ☐ **Diagnostic sample collection, storage and transport equipment**
- ☐ **Lock for facility**
- ☐ **Footbath/boot changes**
- ☐ **Protective clothing**
- ☐ **Cage furniture as appropriate for species**
- ☐ **Animal record forms, pens**
- ☐ **Bags for waste disposal**
- ☐ **Feeding, watering and cleaning utensils**
- ☐ **Animal capture and restraint equipment**
- ☐ **Quarantine register**
- ☐ **Animal caregiver personal health check**
- ☐ **Other:** _____
- ☐ **Other:** _____
- ☐ **Other:** _____

19. BUDGET:

Personnel hours **hrs @** _____ **.....** _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments **.....** _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move ☒

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

21. FOLLOW UP ACTIONS:

22. PERMITS TO MOVE ANIMALS RECEIVED? YES NO

23. SIGNED OFF BY: _____ Project Manager **DATE:** _____

_____ Veterinarian

DECISION TREE ANALYSIS

Group 4 day two

Example: Burchell's Zebra, translocation of 200 animals into Meru NP ecosystem, 117 existing animals

1. Introduce or not?

2. Where to introduce?

3. Do we treat diseases?

4. Are diseases of concern (worth worrying about)?

5. Do we test for disease? Which ones?

6. Diseases of concern :

Equine herpesvirus

AHS

Equine encephalosis virus

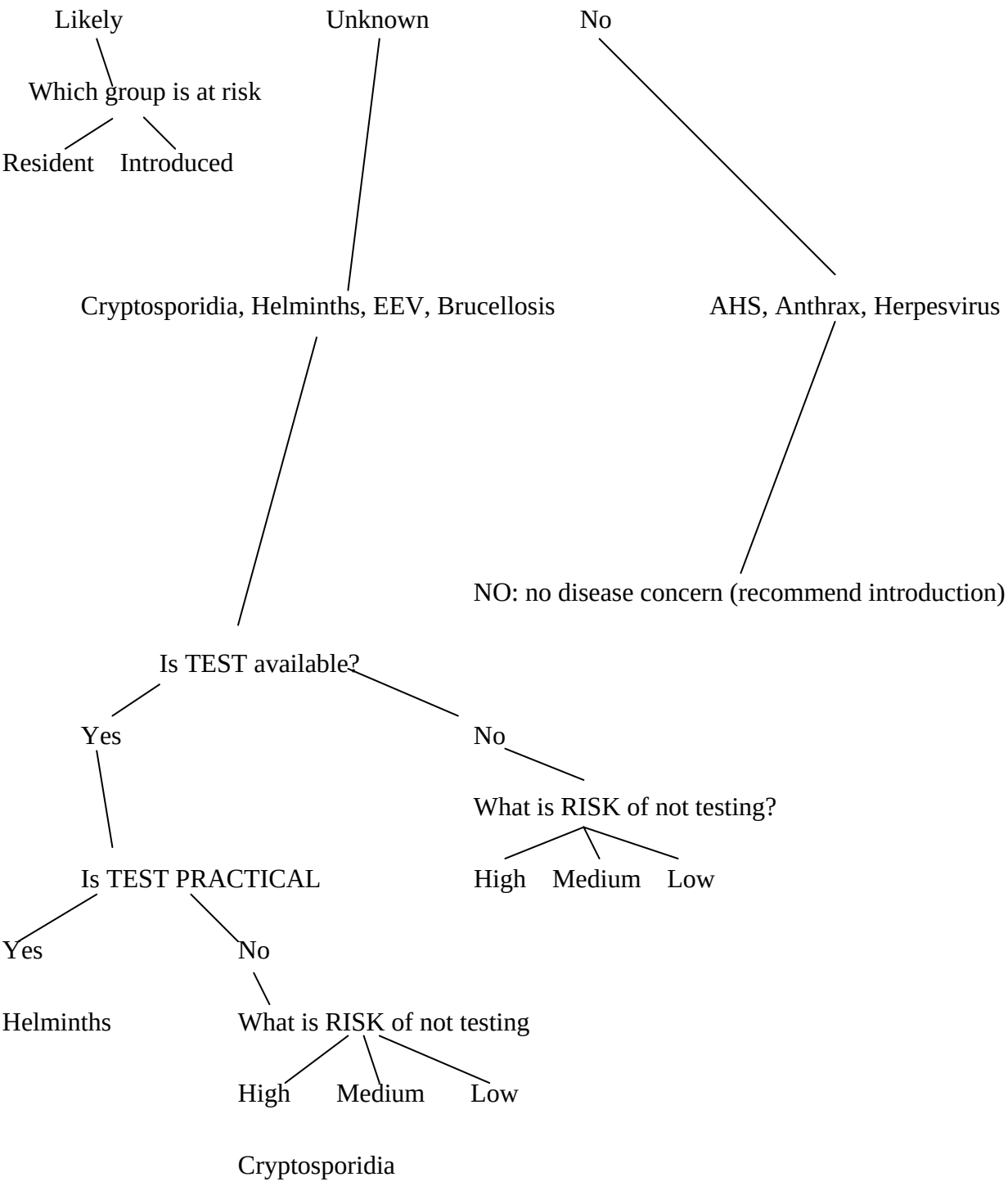
Brucellosis

Anthrax

Helminthes

Cryptosporidia

Qn: Is there a discrepancy in the prevalence from wild to captive? Or are the diseases worth worrying about?



Decision Tree Analysis Process

- We felt that we had the most data regarding the zebra translocation into Meru.
- The original four questions were taken from the March 2000, Omaha meeting decision tree analysis
- When listing diseases we originally listed Tuberculosis but later removed it from consideration due to the fact that domestic cattle migrating through the park would pose a much greater risk.
- We recognized that a simple yes and no choice was not sufficient in answering the question " Is there a discrepancy in the prevalence from wild to captive?" and "Are the diseases worth worrying about?" Therefore we put Likely, Unknown and No as our choices.
- We made the assumption that "No discrepancy" meant there was no disease concern.
- We recognized that a discrepancy in incidence of a disease could pose a risk to either the resident population or the introduced population.
- We discussed the relative importance of the survival of the resident vs. introduced population.
- We assumed that if the discrepancy was "Unknown", we needed to do disease testing on either the resident or introduced groups.
- We discussed the availability of tests as opposed to the practicality of tests in a field situation. E.g. lab availability, sample preservation, sample transport, etc.
- We recognized that we might not have to test all of the animals in question. If the permissible lower limit of disease prevalence can be estimated, Epi Table can be used to determine the number of animals that need to be tested. This software is available as free download software.
- We determined that even if a test was impossible or impractical we needed to consider the risk involved in not doing the test.
- Due to the fact that the risk of not testing was not precisely known, the risk was categorized as high, medium or low.
- Due to lack of information, we did not complete the evaluation, but felt that the decision tree was complete.

Stella Working Group Summary of Diagram

We developed this model as a working draft to allow the group to become familiar with the Stella program.

Set up:
Modeled as transmission of disease among gorillas, transmission among children of trackers, transmission among other children in the village, trackers used as route of exposure of measles to the gorillas.

Assumptions:
1. Gorilla contract measles (from humans and each other)
2. Humans act as fomites for the measles virus
3. Trackers developed immunity to measles as adults
4. Naive populations = all but trackers
5. Negligible impact of transmission tracker to tracker.
6. Closed populations
7. Random contacts
8. Random dispersal
9. Human adults that are not trackers are irrelevant (only trackers have contact with gorillas)
10. That all people infected recovered to immunity.

Identifying data:
Other kids = 5000
Trackers kids = 700
Trackers = 110
Gorilla population = 320
Noncontact gorillas = 60
Contact gorillas = 260
Vaccine programs as 98% efficacy for gorillas and people
Contact rate sick child to child of 1:10
Contact rate for trackers to gorillas in contact groups of 1:20
Contact rate for noncontact gorillas to contact gorillas of 1:2

Run and evaluate scenarios:
1. Measles goes through the population
2. Vaccinate just the trackers children
3. Vaccinate all children
4. Vaccinate gorillas only

Results of simulations:
Vaccinating the gorillas only was the most effective way to minimize the incidence of measles in the gorilla population.
Reevaluate model again, and again and again.....

Summary:

Process of developing the model:

Identification of the problems to address
Assemble a group individuals with diverse experience and training.
Employ someone who has a clue about Stella.
Begin to draw a conceptual picture of the problems you are addressing.
Develop assumptions.
Determine control points of the model.
Input data into the model (if possible real data used and otherwise bet estimates).
Run the model.
Evaluate the data, model and graphs resulting.
Reevaluate the appropriateness of the data entered and the relationships created.
Continue to refine and improve the model (to infinity).

Question:

Does this approach provide benefit in exploring a complex problem?

Answer:

Yes, it allows you to visualize the process, identify critical control points, identify relationships that may not have been obvious, clearer idea of information needed to acquire.

Question:

Can this approach give you a quantitative answer?

Answer:

With more refinement and enough good data it may give you quantitative answers.

Disease Risk Workshop 2000 II

Report

Presentations

Incorporating Epidemiological Models of Disease into Models of Wildlife Population Viability Using *VORTEX*[1]

Philip S. Miller, Conservation Breeding Specialist Group
Robert C. Lacy, Department of Conservation Biology, Brookfield Zoo
Jonathan D. Ballou, National Zoological Park / Smithsonian Institution

An Introduction to Population Viability Analysis

Under almost any set of circumstances, wildlife populations will fluctuate in size over time (Figure 1). These fluctuations result from random variation acting on a set of processes that, acting together, determine the dynamics of population growth. Numbers of individuals comprising a given population are determined largely by specified rates of reproduction, survival, and dispersal in addition to the ecological limitations of habitat carrying capacity. Variation in these rates is influenced by processes both intrinsic (demographic stochasticity, genetic drift and/or inbreeding depression, or deviations in age or social structure) and extrinsic (environmental variation and catastrophic events) to the population (Shaffer 1981).

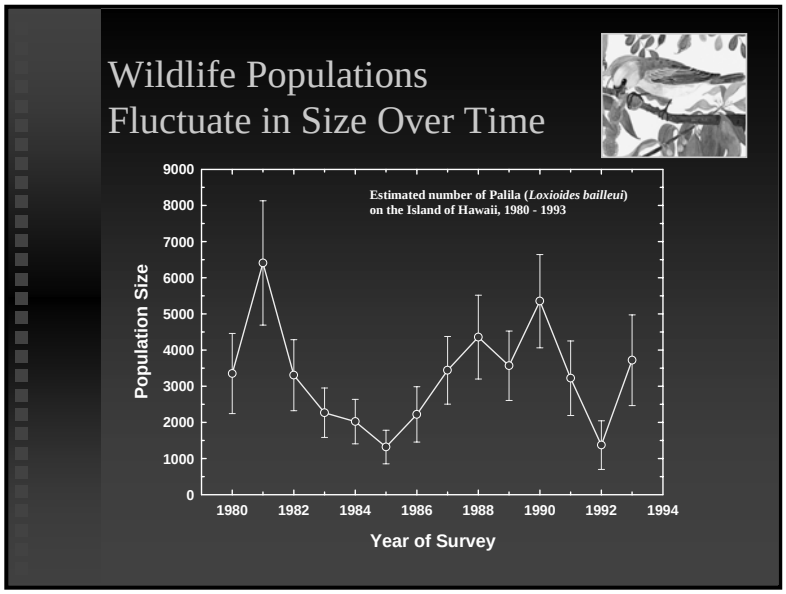


Figure 1. Census data showing annual fluctuations in estimated population size for Hawaii's palila, *Loxioides bailleui*. Figure adapted from ( ).

Disease can be an important force in modulating many of the processes that drive wildlife population dynamics. Diseases can directly survival and reproductive success, and they can also be a major influence in the specification of annual variation in demographic rates. Perhaps more subtly, disease can influence growth dynamics by altering the genetic, social, and age structures of populations.

[1] Revised and updated based on Lacy, R.C. 2000. Integrating considerations of disease into population viability analysis with *VORTEX*, in *Disease Risk Workshop Final Report* (D. Armstrong and U.S. Seal, editors). Apple Valley, MN: Conservation Breeding Specialist Group (SSC/IUCN).

While random fluctuations in size are a normal part of wildlife population dynamics, reductions in mean population size brought about by human activities can result in a greatly increased risk of extinction through the action of stochastic variation in demographic rates. This synergistic interaction between population size and stochastic extinction risk is summarized in the "extinction vortex" concept of Gilpin and Soulé (1986). Population Viability Analysis (PVA) is a technique for applying the extinction vortex concept by examining the threats to persistence of wildlife populations (Boyce 1992; Lacy 1993/4; Groom and Pascual 1998). PVA starts with a model of the forces that drive population change and then assesses population performance under a specified set of conditions (Figure 2). PVA can use empirical, analytical, or simulation methods, but most PVAs rely on simulation to assess the interacting affects of a large number of complex processes. The primary use of PVA is to estimate the probability of extinction of a population, the mean time to extinction, or other measures of population performance such as growth rate, stability, or genetic diversity. A comparison of such measures of population viability for a variety of different scenarios then allows analysis of which threats are most important. In addition, management alternatives can be compared to determine the most effective conservation strategies.

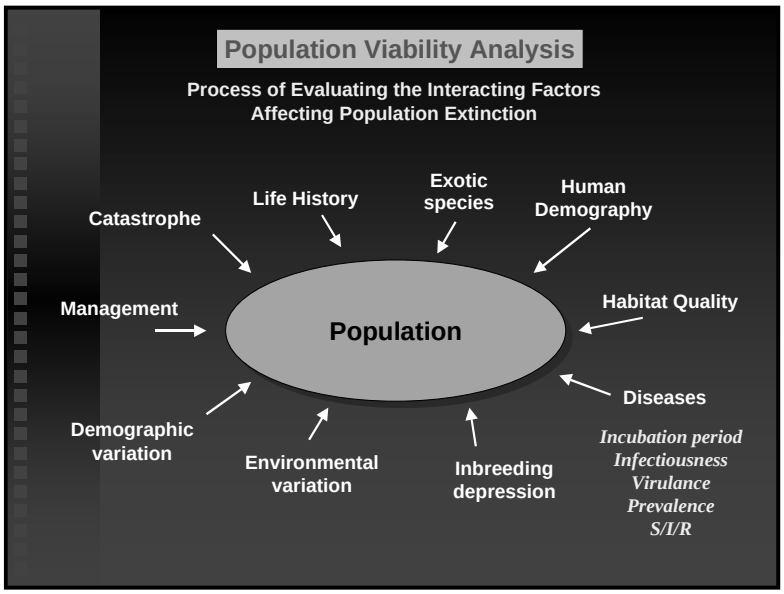


Figure 2. Generalized diagram of the forces shaping population dynamics and their inclusion in population viability analysis.

One widely used PVA model is *VORTEX* (Miller and Lacy 1999; Lacy 2000)[2]. *VORTEX* is an individual-based simulation, which requires highly specific and detailed data on a variety of demographic and other population parameters. It considers mean demographic rates for reproduction, survival, and dispersal; random variation among individuals that experience demographic events; variation in population-wide rates over time; episodic catastrophes that impact survival and/or reproduction; changes in and effects of genetic diversity; breeding systems; habitat limitations; dispersal among local populations; and managed harvest, supplementation, or translocation. Almost all rates in *VORTEX* can be constant over time, can

[2] *VORTEX* is available from CBSG (http://www.cbsg.org ; office@cbsg.org) or from R.C. Lacy (http://www2.netcom.com/~rlacy)

change over time, or can be specified to be functions of population density, age, sex, inbreeding, or other characteristics of individuals or the population.

Modeling Disease in *VORTEX*

Before we discuss the mechanisms by which the effects of disease on population viability can be incorporated into population viability analysis, a brief digression on the general nature of disease modeling in PVA is warranted. In general, opinions differ widely on how disease is to be considered in models of wildlife population viability – or whether it is to be handled at all. For example, in a recent workshop on mountain gorilla population viability and conservation (Werihke et al. 1998), wildlife veterinarians predicted that the remnant populations may be subjected to several kinds of disease: an influenza-like disease that occurs in 10% of the years and causes 5% mortality; a severe viral disease that has a frequency of 10% and causes 25% mortality and a 20% reduction in breeding for the year; and a cyclic viral disease of the reproductive system that has a frequency of 4% and causes 25% mortality and total breeding failure. The PVA showed that the hypothesized diseases would substantially threaten the long-term prospects for gorilla population persistence. As a consequence of this finding, recommended conservation actions included measures to reduce the probability of disease spreading from ecotourists to the gorillas, and increased surveillance for disease.

In contrast, a PVA workshop on the Florida panther (Seal and Lacy 1989) represents the opposite extreme (but perhaps a more typical case) in how disease can be considered in wildlife risk assessment processes. Workshop participants reached a consensus that "Disease epidemics are possible, … but we have no data that would allow estimation of the probability. … Thus, we have omitted any consideration [of disease] … from our modeling." However, the omission of disease from consideration was further justified by: "It is unlikely that the subspecies would survive a catastrophe that caused substantial mortality." It is clear that including processes that are only partially understood and/or quantified will lead to a less precise prediction of future population performance. By the same token, their inclusion into models of the extinction process can help to foster a better understanding of the population data in hand. Perhaps more importantly, comparative simulation modeling of alternative scenarios can be a valuable tool to help biologists make better population management decisions in the face of uncertain knowledge and limited resources. PVA practitioners are faced with choosing how to use the available tools on a case-by-case basis.

The effects of diseases on population viability can be integrated into the *Vortex* PVA modeling system in a variety of ways and at various levels. Disease can be modeled as a static effect on demographic rates, as a cause of variation in rates (including episodic catastrophes), as a cause of trends in rates over time, as a dynamic process in which the impacts are functions of population or individual characteristics, or as an infectious process in which the probability of an individual becoming diseased is a function of the number of other diseased individuals.

<u>Disease as a static effect on population dynamics</u>

When considered simply as a static effect in the PVA model, disease mortality may be one component of the mean "natural" or "baseline" mortality. Similarly, disease may be one determinant of the baseline reproductive rates (e.g., disease can be one cause of breeding failure). Disease may also be a mechanism of inbreeding depression (e.g., if inbred individuals are more

likely to die of disease), or of density dependent breeding or survival. Incorporation of the impacts of disease into a PVA model as a static effect does not require that disease be identified as a cause of the natural rates. But it does require that the "baseline" rates used in a PVA model are estimated under conditions that are likely to prevail into the future, and assumes that there will be constant risks of and effects of disease. Consideration of disease as a static effect in a PVA model may be appropriate for endemic diseases that are always present as a risk in the population.

Disease as a source of variation in demographic rates

Disease that is episodic over time can be incorporated into PVA models as a contributing cause of either random variation in demographic rates over time (environmental variation) or periodic catastrophes in which survival or reproduction are temporarily impacted. For example, Figure 3 shows an example of a simulation produced by *Vortex* for a population that normally has a high potential growth rate (due to high reproduction and low mortality), but which is subjected to catastrophes that occur randomly in 2% of the years and cause 25% mortality. To analyze the effects of a disease causing such a pattern, the simulation would be repeated 100s of times, and the mean result and range of results tallied.

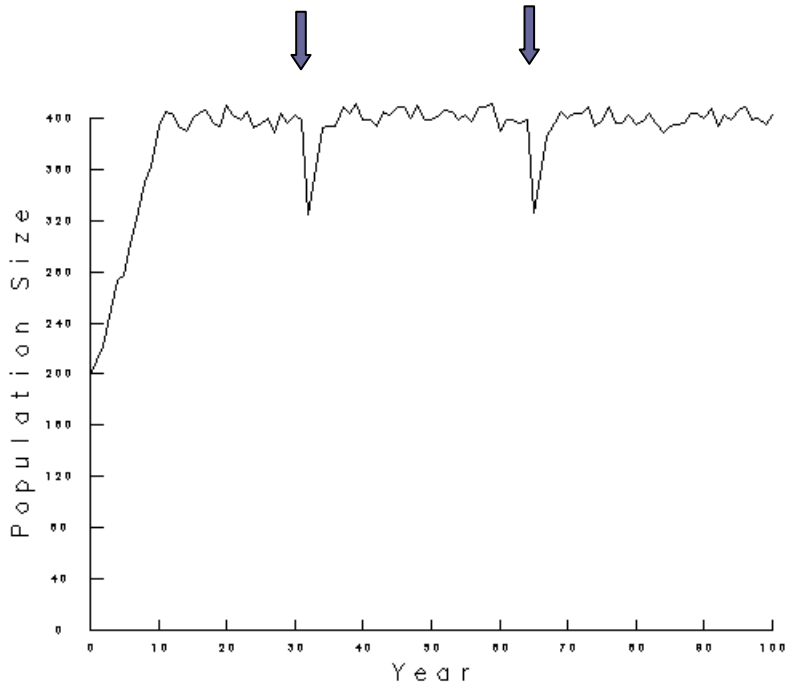


Figure 3. A simulated population subjected to a disease epidemic with a 2% annual probability of occurrence that causes an additional 25% mortality across all age classes. Arrows indicate incidence of epidemics.

Within *VORTEX*, the probability of and impacts of a disease catastrophe can be specified to be a function of population characteristics. As an example, Figure 4 shows the results of a simulation in which the effects of a catastrophe on survival are a function of population density: survival

drops steeply when the population size approaches the ecological carrying capacity of the habitat.

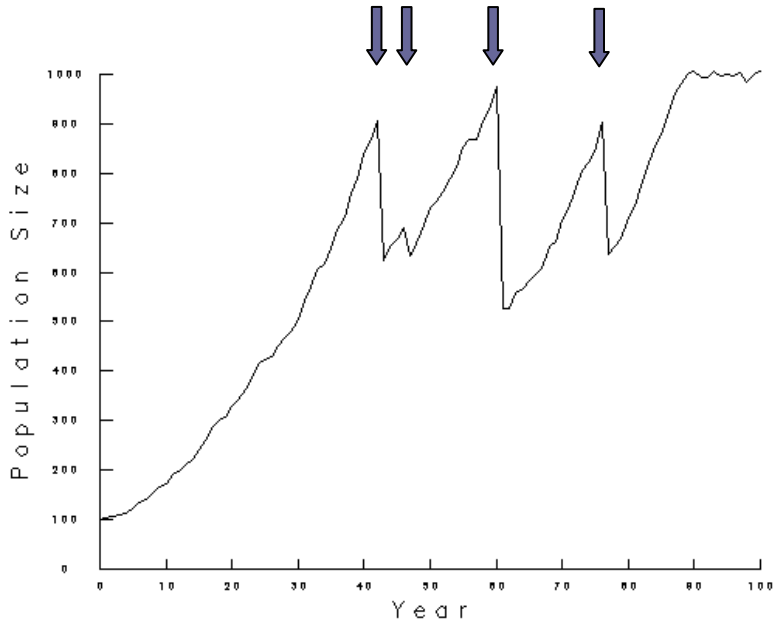


Figure 4. A simulated population subjected to a disease epidemic in which individual survival is a function of population density. Arrows indicate incidence of epidemics.

Disease as a driver of temporal trends

Epidemiological models can generate predictions for cyclical or other temporal patterns for disease (Grenfell and Dobson 1995; Scott and Duncan 1998). With this type of information at the user's disposal, *VORTEX* can model the consequent temporal trends in demographic rates. The trends might be linear (due to increasing disease prevalence), cyclical, or follow some other specified time course. Figure 5 shows a trajectory for a simulated population that is impacted by a disease that occurs are regular 10-year intervals and reduces survival by an additional 20% over "baseline" values.

Incorporating a temporal pattern of disease into a PVA requires prior development of a model of the dynamics of the disease. The time series or pattern of disease outbreaks generated by the epidemiological model then must be used to specify the temporal trend in affected demographic rates. This approach would be appropriate for modeling the impacts on population viability of a disease that follows a known and regular time course. For example, outbreaks of smallpox caused a 5-year cycle in mortality in rural England from 1557 to 1812, and whooping cough mortality in London showed a 3-year cycle with increasing amplitude from 1700 to 1812 (Scott and Duncan 1998).

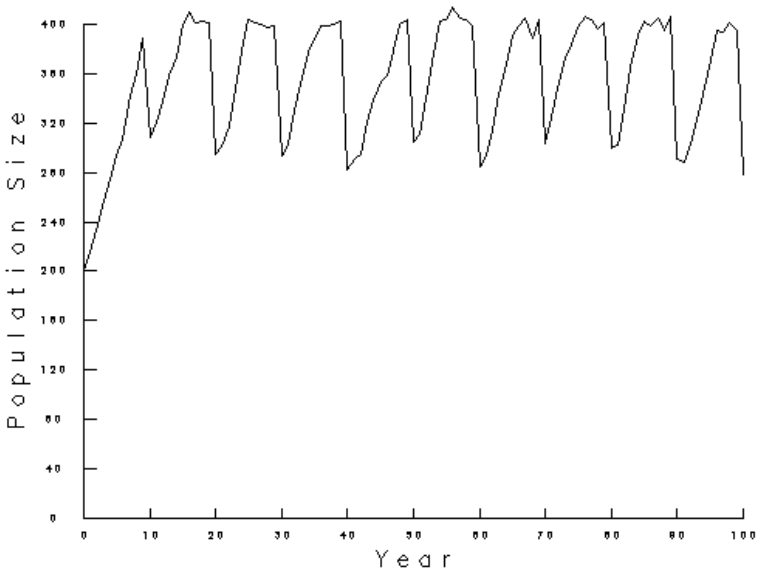


Figure 5. A simulated population trajectory in which disease epidemics occur at 10-year intervals.

Disease as an infectious process

The prevalence of infectious disease is obviously dependent on the number of already infected individuals, as well as on the numbers of susceptible and resistant individuals. To model infectious processes, the state (e.g., susceptible, latent infection, active infection, recovered, or resistant) of each individual would be tracked, and the probabilities of transition among states would be specified as functions of the numbers of individuals currently in each state (Figure 6). Transition probabilities may also be dependent on other individual characteristics, such as sex, age, inbreeding or specific genotypes. The demographic rates would then be specified to be functions of the state of the individual. For example, infected individuals may suffer 50% higher mortality or depressed breeding rates.

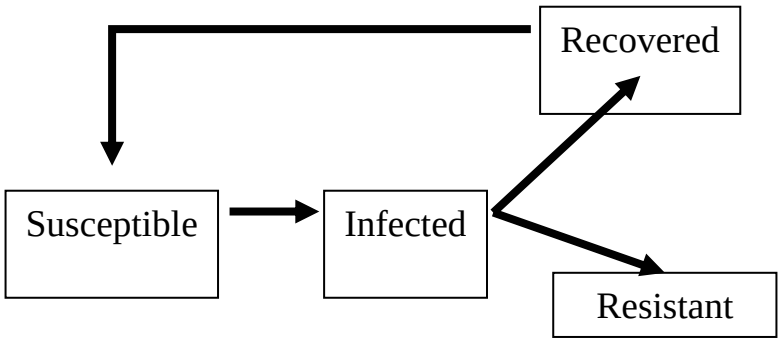


Figure 6. The S-I-R-R model of disease epidemiology. Individuals move from one state to another over time with defined probabilities. Resistant individuals are those who are no longer susceptible to re-infection. Recovered individuals are no longer infected, but can be re-infected.

In order to incorporate an infectious disease process into methods for population viability analysis, there must first be developed a model of disease transmission and recovery. The likelihood of transmission under various conditions must be known (or estimated), as well as the likelihood of recovery and the development of resistance. Unlike the simpler methods of modeling disease in PVA described above, infectious processes cannot yet be incorporated into *VORTEX* simulations (as of version 8). Further modifications of the *VORTEX* program could provide such modeling capabilities.

Preliminary Ideas for a *VORTEX* Disease Module

At the first installment of this disease risk workshop series (Armstrong and Seal 2000), we began to explore ways in which the current implementation of *VORTEX* could be expanded to include more complex models of disease. As the software is currently undergoing a major revision to a MS Windows® interface, we thought that this workshop provided an excellent opportunity to explore how we might sketch out a module for describing the general biology of any diseases known to impact the population of concern, and the specific means by which the disease compromised the population's demographic or genetic integrity.

Before outlining the structure of such a module, it is important to list some important assumptions that guide our thinking:

- We are working with the effects of a particular disease on the individuals in a strictly defined population. Thus, we are not evaluating the effects of the disease on other animals, the environment, local human populations, or domestics. We are focusing on the single threatened species of concern.
- A detailed list of "diseases of concern" have already been identified, using decision tree analysis of similar techniques.

The current version of *VORTEX* consists of a series of screens through which the user moves to input data on the demographic and genetic characteristics of the species and the nature of the

surrounding habitat. We propose that the user would invoke the new disease module by answering:

Do you want to model disease and its impacts on wildlife population viability?

If the user answers **Yes** to this question, *VORTEX* would open a new window that would guide the user through the entry of input data describing the characteristics of each of the diseases of concern. As presented below, we have initially divided disease types into genetic diseases and infectious diseases.

Are there any genetic diseases of concern?

For each genetic disease:

What is the mode of expression? Is it recessive, dominant, or incomplete?

What is the effect of this disease on survival?

X% reduction in survival for individual with trait

Age and sex-specific?

What is the effect on reproduction?

X% reduction in the probability of breeding

X% reduction in fecundity (clutch/litter size)

X% increase in breeding age

What is the frequency of the disease allele in carriers?

Are they homozygote, or heterozygote?

How many carriers are in the population?

Are the carriers in the source or destination population?

Is this disease new to the destination population? If new,

What is the frequency in the source population?

What is the probability of detecting the allele?

Are there any infectious diseases of concern?

For each infectious disease:

We would base our epidemiological model on the familiar Susceptible – Infected – Resistant Model, using the basic algorithms originally proposed by Anderson (1982) and May (1986).

Disease prevalence (source and destination)

Proportion of population now Susceptible

Proportion of population now Infected

Proportion of population now Resistant

Modes of disease transmission

Probability of becoming infected

Probability of becoming resistant (vs. dead or remaining infected)

Probability of becoming susceptible again

What is the effect of this disease on survival?

X% reduction in survival for individual with trait
Age and sex-specific?

What is the effect on reproduction?
X% reduction in the probability of breeding
X% reduction in fecundity (clutch/litter size)
X% increase in breeding age

Does the mode of transmission or nature of impact depend on other factors?
Environmental factors: seasonality, etc.
Population factors: density, inbreeding

VORTEX Disease Module Output

Once the information for the disease module is entered, the remainder of the model parameterization is completed as normal and the model runs the specified number of iterations. In particular, the output from a *VORTEX* disease risk model would include:

- Population growth rate
- Probability of population extinction within the specified time interval
- Changes in allele frequencies over time (if modeling a genetic disease)
- Changes in numbers of susceptible, infected, and resistant individuals over time (if modeling an infectious disease)

In order to specifically evaluate the impact that a given disease would have on population stability, the output from a disease model should be compared to a similar model in which the disease module is not included. This disease-free model could be run prior to the development of the disease model so that, using the graphical capabilities already found in the current modeling package, the results from this simple type of sensitivity analysis can be compared quickly and easily.

Moreover, a broader sensitivity analysis can be developed to explore the consequences of alternative measures of disease control and intervention such as vaccination, treatment, etc. For example,

- What are your options for reducing prevalence in source?
- How much does this reduce prevalence?
- What are your options for reducing impacts?

By using the disease module to formulate specific detailed scenarios with modified disease prevalences and/or impacts, any number of conservation mitigation actions could be evaluated to determine the most effective course of action when faced with unacceptable disease risks.

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Evaluating Animal Health within an Ecosystem: Lessons from the Chesapeake Bay

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The Chesapeake Bay is the largest estuary in the United States providing habitat for more than 3600 species of plants and animals. Over 100,000 streams and rivers drain into the Bay from a watershed that includes Maryland, Virginia, Pennsylvania, West Virginia and New York. A little over 15 million people live in the Chesapeake watershed, with 3 million more projected by 2020. In the late 1970's, a scientific study was conducted to evaluate the status of the Chesapeake Bay. Three areas of concern were identified: nutrient over-enrichment, toxic pollution, and dwindling underwater grasses which covered up to 600,000 acres in the 1930's and were down to 41,000 acres in 1978. As a result of this investigation, the Chesapeake Bay Program was started in 1983. This unique partnership between federal and state governments became the working model for the National Estuary Program in 1987. The goal of these programs is to restore and protect significant estuaries of the United States.

In the case of the Chesapeake Bay, particular emphasis was placed on restoration of its living resources. The vascular underwater plants protect shorelines from erosion, trap sediments, remove excess nutrients, produce oxygen, and provide critical habitat to aquatic organisms. In the early 1900's, oyster beds were so extensive that they posed navigational hazards. The Bay's oyster population could filter the estuary's entire water volume every 3-4 days. By the late 1970's, the population was so reduced that it took a year to filter.

After nearly two decades of efforts to restore the Chesapeake Bay, the underwater grass acreage has nearly doubled and point sources of pollution have substantially declined. However, nitrogen and phosphorus loading, both organic and inorganic, have steadily increased in certain rivers and streams despite the Chesapeake Bay Agreement of 1987 to reduce nutrient loads by 40% by the year 2000. Part of the increased levels is attributed to intensive agricultural practices in the lands forming the eastern shore of the Bay.

So what is the health status of the fish that live in the Chesapeake Bay? In early August of 1997, 10-15,000 fish were found dead in the lower Pocomoke River in association with blooms of *Pfiesteria piscicida*. *Pfiesteria piscicida* and *Pfiesteria*-like organisms have been associated with fish kills in estuaries along the East coast since the early 1990's. The organism that has been variously classified as a microscopic algae, dinoflagellate, and protist was first identified in a tributary of the Chesapeake in 1992 but not in association with any fish deaths. The role *Pfiesteria* plays in fish mortalities remains controversial and highly political. Fish mortalities were occurring in the Pocomoke River in late 1996 and spring of 1997. No *Pfiesteria* was detected at those times. Studies to evaluate water quality eliminated heavy metals and pesticides as potential causes but noted an increase in acidity and low salinity as a consequence of above average rainfall. These conditions favor the replication of *Aphanomyces* spp., oomycetes responsible for a fish disease recognized world-wide as ulcerative mycosis. Fish dying in the Pocomoke River, with or without the presence of *Pfiesteria,* had deep ulcers around

the anal pore and caudal trunk from which *Aphanomyces* were eventually detected by a variety of diagnostic methods (1).

Three days before the first fish kill in August 1997, the governor of Maryland announced that the increased incidence of skin lesions in fish and fish deaths in the Chesapeake could be attributed to many factors, not necessarily just one. However, with four mortality events occurring within a subsequent five week period associated with *Pfiesteria* blooms and the claims of dire consequences for human exposure to *Pfiesteria*, the governor's earlier statement of multi-factorial causes was quickly lost in rising public hysteria driven by the popular press. All four rivers were closed. The seafood industry in the Chesapeake lost an estimated $43 million, and the impact on recreation and tourism dollars could not even be determined.

As a direct consequence of these fish kills, the U. S. Geological Survey's National Fish Health Laboratory (Kearneysville, WV) and the Maryland Department of Natural Resources (Stevensville, MD) began a broad-base study of fish health. This is an ongoing three to four year study involving a number of Chesapeake Bay tributaries. Selection criteria for rivers include history of recent fish kills, high-levels of nutrient run-offs, exposure to industrialized areas and absence of recorded fish mortalities. Fish are collected three times a year to span the period before and after historical fish kills. White perch (*Morone americana*) are the sentinel species because of their relative abundance in all tributaries to be sampled and their size allows for adequate samples to be collected for immunological studies.

One of the questions being addressed is whether white perch show evidence of compromised immune function prior to or concurrent with morbidity and mortality events in the Chesapeake Bay tributaries. In conjunction with an assay to measure macrophage killing activity, mRNA expression of transforming growth factor-beta (TGF-∃) is evaluated. This molecular-based assay was developed at North Carolina State University College of Veterinary Medicine. It uses a quantitative polymerase chain reaction (PCR) to measure TGF-∃ mRNA from lymphoid cells of a wide variety of teleost fish (2). TGF-∃'s are cytokines with diverse functions affecting cell growth and differentiation, extracellular matrix regulation, wound healing and immune function. TGF-∃ immunoregulatory properties are primarily immunosuppressive. In an experimental setting, there is an inverse relationship between TGF-∃ mRNA levels and macrophage bacteriocidal activity in hybrid striped bass (*M. saxatalis* x *M. chrysops*) treated with a known immunomodulator (3). Field studies provide a more complex setting than the confines of the laboratory to test whether increased TGF-∃ levels correlate with depressed macrophage killing.

Constitutive TGF-∃ production generally increased from June to August and October, 1998, primarily in the Chesapeake Bay Eastern Shore tributaries (4). Macrophage bactericidal activity declined from June to August and October in the same tributaries. The field-based findings of inverse correlation between the two assays, conducted in separate laboratories, indicates the occurrence of immunomodulation consistent with immunosuppression both spatially and temporally in white perch of the Chesapeake Basin.

Biological factors which could alter TGF-∃ mRNA expression include age, sex, and reproductive status. Production of TGF-∃ varies during development and estrogens induce the

production of TGF-∃ in mammals. In this study, the age of the white perch was assessed indirectly by length and weight, which correlate with age in this fish. There were no significant length and weight differences between samplings, and TGF-∃ mRNA did not correlate with either length or weight (4). Likewise, there were no significant differences in sex distribution between samplings, and there was no correlation between TGF-∃ mRNA expression and sex. Further, the sampling period between June and October was after the March to May spawning season so reproductive status was not considered to be a factor.

Physical conditions measured at the sample sites included air temperature, water temperature, pH, depth, salinity and dissolved oxygen (4). Hypoxic conditions have been suggested as a possible factor in the development of menhaden ulcerative lesions as well as other fish morbidity and mortality events in estuarine environments. Dissolved oxygen did not correlate with TGF-∃ or macrophage bactericidal activity. Dangerously low dissolved oxygen (2.4 mg/L) was detected only once in August from a bottom-water sample while the surface water level was an acceptable 5.5 mg/L. Air and water temperatures, pH and depth also did not correlate with TGF-∃ or macrophage bactericidal activity. The estuarine environment is constantly changing with the tides and with river flow rates so that any physical parameter could vary considerably between sampling periods. Further, collected fish might be recent immigrants to a sample site and may have been subjected to different conditions before their capture.

Salinity measurements did correlate with TGF-∃ mRNA expression (4). Osmoregulatory mechanisms, could account, in part, for altered TGF-∃ production by teleost fish responding to salinity changes in estuarine environments. Prolactin and cortisol both play a role in regulating electrolyte flux across gills. In mammals, these two hormones upregulate TGF-∃ expression. Whether interactions between salinity and osmoregulation affect TGF-∃ production of teleost fish will require further investigations in a controlled setting.

No widespread fish mortalities occurred in 1998. The lower macrophage bactericidal activity and higher TGF-∃ mRNA expression measured that year did correlate with the qualitative observations of deep ulcers in menhaden collected in the same areas (4). The temporal and spatial relation between increased TGF-∃ and decreased macrophage killing also coincided with previous fish morbidity and mortality events in the Chesapeake Basin. Whether immune function of white perch is impaired annually in certain rivers at certain times remains to be determined. The importance of this ongoing study is to establish baseline data on a variety of biological parameters in a teleost widely distributed throughout the Chesapeake in order to better understand the pathogenesis of fish mortality events. Further, this ongoing study illustrates the need to evaluate new assays for assessing health of sentinel species in habitats at risk.

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Disease Risk Workshop 2000 II

Report

Worksheet Synthesis Group

Worksheet Revision – Participants: Sharon Deem, Jode Garbe, Felicia Nutter, Suzanne Kennedy-Stoskopf

Comments for Worksheet Revision

Each participant in the worksheet revision group brought suggestions from their individual working group (included at the end of this document). After the suggestions were articulated and discussed, similarities and redundancies were identified and then assessed for relevance to the intended use of the worksheet. The actual changes made in the worksheet based on suggestions are enumerated below in order of occurrence within the sheet.

- Included a specific place to list other source and destination institutions, so that animal movement and testing may be better coordinated among institutions.
- Animal identification table was expanded to address multiple ID types, individual and group identification, reporting of either estimated age or DOB, availability of medical histories, and animal origin.
- Throughout the worksheet, we incorporated explanatory footnotes to aid in proper completion of the form. Given that all of the working groups ignored the printed admonishment at the top of the form to "read the attached explanatory notes before completing the worksheet, " we felt it was important to make the document as stand-alone as possible.
- The single section for listing diseases of concern was split into two sections, to allow initial development of a comprehensive disease list for the species involved, followed by reduction of that list to only those disease of concern for this particular animal movement.
  - ⇒ The comprehensive disease list was expanded to include columns for indicating whether each disease was known to be present in the source and destination populations. A column was added for justifying the inclusion of each disease on the list (animal disease implications, public health impacts, legal requirements, etc.). The final column is for indicating if the disease is "required" for inclusion on the list of diseases of concern for this particular animal movement.
  - ⇒ The list of diseases of concern for this particular animal movement includes columns for the recommended test for each disease, testing locations, and sample amount needed.
- The diagnostic sample section was modified to include a check box for serum banking, and a column for indicating whether animals passed/failed examination and testing (failures must be explained in the assessment section). Space was also provided for listing samples to be collected for specific tests based on the list of diseases of concern for this particular animal movement.
- A request to list any adverse reactions to handling, treatment, vaccination, etc. was added to the treatment/vaccination section.
- A request for contact persons for each testing location was added.
- Quarantine details were amended to include check boxes to indicate where quarantine would occur (source, destination, both). The quarantine sheet should be duplicated if quarantine is to occur at both locations.
- Training/briefing of the quarantine supervisor was made mandatory.

- An assessment section was added between quarantine and recommendations, to clarify the process of interpreting and synthesizing exam and test results.
- Instead of indicating if permits have been received, all permits should be listed.
- Many suggestions that were common to several groups could not easily be incorporated directly on the worksheet, but we felt strongly that they should be available as brief, user-friendly appendices.
  - ⇒ Appendix I: Recommendations for determining diseases of concern (source and destination populations. This should include basic instructions for how to do appropriate lit searches, suggested databases, as well as instructions for risk analysis. **NB: this may need to be two separate appendices – a quick and dirty "how to do a lit search" and a more thorough "how to do a risk analysis".
  - ⇒ Appendix II: Sample size determination for diagnostic testing, surveys of disease prevalence, etc. Tables are available and a variety should be included (disease screening, introduction risk, etc.).
  - ⇒ Appendix III: Sensitivity/specificity and predictive value of diagnostic tests. This should include examples of how variation in sens/spec and predictive value can affect risk analysis.
- Several suggestions were made that we modify the worksheet to more easily handle large groups of animals that are not individually identified (eg fish). Comments have been received that groups may be mixed in origin and sex, and we added a "B=both" category for each of those columns. People with more experience in colony or group movements should have increased input in refining the sheet for that purpose.

Group 1 Suggestions

1. Animal ID (4) need to have DOB or DOH instead of age or in addition to age.
2. Multiple origin and/or multiple destination sites.
3. Colony animal issues (eg, how to develop sample size and sample id)
4. Diseases of concern – any recommendations on how this data is acquired (eg, data on ecosystem); differentiate the diseases of concern based on origin or destination population.
5. Categorize screening vs confirmation tests.
6. Recommendation that a veterinarian is involved.
7. Comments on diagnostic tests – sensitivity / specificity / predictive values.
8. Number 9 should be screening tests and combine 9 + 10
9. Disease history is included
10. Add compilation of significant results for data analysis for vet to take into account for coming to final move/don't move recommendation.
11. Section of adverse reactions to Rxs
12. Serum banking section.
13. Briefing / training date for supervisor mandatory

Group 2 Suggestions

1. Assumptions and benefits need to be addressed pre-worksheet
2. ID types need to be expanded to include space for 2 id types
3. Outcome and comments on the front page but it is related to the end result
4. Number 8 needs to be 2 part with
   -Potential hazards as a comprehensive list of diseases in table form that shows justification and whether is a REAL hazard for your move
   -Title: Hazards of concerns (diseases and other medical problems)
   -Headings to include: Disease of concern rec test test location sample amount
5. Diseases of concern for this animal movement should be a separate category (table), based on the subset of all potential hazards that Number 10 changes
   Diagnostics section (10) expanded on the other section based on hazards of concern to include the other section with diseases taken from hazards of concern
   -Third column with accepted and non-accepted
6. Quarantine details section needs to address the situations when two quar periods may occur for one animal movement

Group 3 Suggestions

1. Multiple sources of origin and destination may be involved in an AM so need a way to be standardized.
2. More animal information under animal ID section (4) to include animal origin based on a code (Wild; Captive; Unknown)
3. Separate number 8 into potential disease and disease of concern for this AM
4. Include an appendix for performing power calculations and for determining sampling size for screening large populations
5. Make recommendations for determining disease prevalence in destination populations.
6. Some preliminary description of source and destination of population demographics to help with risk assessment.
7. Indicate sensitivity and specificity of diagnostic tests.
8. Place to make additional comments for individual or population information (eg, significant disease exposure, contraceptive or telemetry implants)
9. Place to indicate any history on population of origin or destination
10. Some place to list sample bank.
11. List the permits needed.
12. Protective clothing list

Group 4 Suggestions

1. Define what this sheet is addressing (eg, preshipment or postshipping sheet)
2. Check off list of medical history that is available - falls between numbers 5 and 6 or added to number 4
3. Serum banking needs to be recorded

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached explanatory notes before completing this Worksheet)

1. SPECIES TO BE MOVED:

2a. FROM:_____ **2b. TO:**_____

3a. Are other source institutes involved? If yes, list:

3b. Are other destination institutes involved? If yes, list:

4. TOTAL NUMBER OF ANIMALS:_____

5. ANIMAL IDENTIFICATION:

ID NUMBERS*	ID TYPES	ANIMAL ORIGIN**	DOB/AGE EST	SEX***	MED Hx (Y/N)	COMMENTS

Attach additional sheet if needed.
*Large groups or colonies not individually identified may be given a single group name or number
List animal origin as **W=wild, **C**=captive, **U**=unknown, **B**=both (may be used only for groups)
***List sex as **M**=male, **F**=female, **U**=unknown, **B**=both (may be used only for groups)
Comments should include pertinent information on individual animals/groups (eg. significant disease history, contraceptive implants, neutered, etc.)

6. ANIMAL MOVEMENT CATEGORY: ☐ Wild to wild ☐ Wild to captivity

☐ Captivity to wild ☐ Captivity to captivity

7a. PROJECT MANAGER: _____ Tel:_____
b. TITLE, INSTITUTION: _____ Email:_____
8. PROJECT VETERINARIAN:_____ Tel:_____
Email:_____

9.POTENTIAL DISEASES AND OTHER MEDICAL CONCERNS (comprehensive list based on source and destination animals including wildlife, domestic animals, and humans. Veterinary assistance is strongly advised in the development of this list.)

DISEASE/MEDICAL PROBLEM	SOURCE	DESTINATION	JUSTIFICATION*	REQ
	Yes, **N**o, **U**nknown	**Y**es, **N**o, **U**nknown		

*Justification includes animal disease implications, public health impacts, legal requirements, etc.

10. DISEASES AND OTHER MEDICAL PROBLEMS OF CONCERN FOR THIS ANIMAL MOVEMENT
(Include all listed as required above)

DISEASE/MEDICAL PROBLEM	RECOMMENDED TEST	TESTING LOCATION*	SAMPLE AMOUNT

*****If multiple source/destination institutions are involved, be sure that samples are sent to the same testing facilities.

11. DIAGNOSTIC SAMPLES

Diagnostic samples to be collected (check)	Collection dates	Date results received	Pass or Fail? *
Physical exam, body weight and measurements			
Feces			
Blood smear, hematocrit and total protein			
Whole blood, serum or plasma (max. volume/animal =)			
Fresh fecal or rectal swab for culture			
Choanal or oral swab for culture			
Ectoparasites			
Other (specify based on diseases of concern):			
Serum banking (if yes, please attach inventory, including location of storage)			

*If there are test failures, please explain in the assessment section.

12. TREATMENTS / VACCINATIONS AND DATES (Please list any adverse reactions to medications. For documentation, refer to individual animal records):

13. ADDRESSES AND CONTACT PERSON(S) FOR TESTING LOCATIONS (Attach additional sheets if necessary)**:**

Quarantine Details

14. LOCATION OF QUARANTINE: ☐ Source ☐ Destination ☐ Both
(if both, duplicate quarantine sheet)

15. FACILITY:_____

16. QUARANTINE DURATION BASED ON ANIMAL MANAGEMENT AND DISEASE CRITERIA
(specify reason for the duration):

Begins:_____ Ends: _____ Total Days:_____

17. PERSON SUPERVISING QUARANTINE: _____Tel:_____
Email:_____

_____

18. DATE OF TRAINING/BRIEFING FOR SUPERVISOR:_____

19. QUARANTINE EQUIPMENT AND SETUP:

□ "Quarantine – no unauthorized entry" sign	□ Protective clothing	□ Feeding, watering and cleaning utensils
□ Insect/rodent traps/ screens/baits	□ Cage furniture appropriate to the species	□ Animal capture / restraint equipment
□ Diagnostic sample collection, storage and transport	□ Animal record forms, pens	□ Quarantine register
□ Lock for facility	□ Bags for waste disposal	□ Keeper health check
□ Footbath/boot changes	□ Other:	

20. BUDGET

Personnel hours _____@_____	_____
Equipment costs	_____
Feed costs	_____
Lab costs	_____
Courier fees	_____
Veterinary fees	_____
Other (specify)	_____
TOTAL COST	_____

Budget Code _____

Assessment

21. **INTERPRETIVE SYNTHESIS OF PHYSICAL EXAM AND DIAGNOSTIC TEST FINDINGS** (Include explanation of any failed tests):

Recommendation

22a. Healthy and minimal threat to destination populations ☐ OK to move

22b. Healthy but there is a significant threat to source animals ☐ Delay move
☐ Cancel move

22c. Unhealthy or threat to destination populations ☐ Delay move
☐ Cancel move

23. EXPLANATION AND JUSTIFICATION FOR ANIMAL MOVEMENT RECOMMENDATIONS:

24. FOLLOW UP ACTIONS (eg. long-term monitoring, repeat testing):

25. PERMITS FOR ANIMAL MOVEMENT RECEIVED: Yes No (circle one)
(List all permits)

Signature, Project Manager _____ Date _____

Signature, Project Veterinarian _____ Date _____

NEEDED APPENDICES

APPENDIX I: Recommendations for determining diseases of concern (source and destination populations)

APPENDIX II: Sample size determination (tables are available for incorporation)

APPENDIX III: Sensitivity/specificity of diagnostic tests – include positive/negative predictive value

Disease Risk Workshop 2000 II

Report

Participants

Disease Risk Assessment Workshop
New Orleans, LA
September 13- 15, 2000

Participants

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Disease Risk Workshop 2000 II

Report

Appendix:
New Zealand Revised Worksheet and Manual
May 2000

Quarantine and Health Screening Worksheet for Animal Movements

(Please read the attached Explanatory Notes before completing this Worksheet)

1. SPECIES TO BE MOVED: _____

2a. FROM: _____ **2b. TO:** _____

3. TOTAL NUMBER OF ANIMALS: _____

4. ANIMAL IDENTIFICATION:

ID NUMBER	ID TYPE	AGE	SEX	OUTCOME	COMMENTS

Attach additional sheet if needed

5. ANIMAL MOVEMENT CATEGORY: Wild to wild ☐ Wild to captivity ☐ Captivity to wild ☐ Captivity to captivity ☐

6a. PROJECT MANAGER: _____ Tel. _____ E-mail: _____

6b. TITLE, INSTITUTION: _____

7. PROJECT VETERINARIAN: _____ Tel. _____ E-mail: _____

8. DISEASES OF CONCERN (Relevant to source and destination animals - including wildlife, domestic animals and humans). If more space is needed attach additional sheets to this Worksheet and include references.

9. SPECIFIC DIAGNOSTIC TESTS

For documentation refer to individual animal records

10. ROUTINE SCREENING/DIAGNOSTIC SAMPLES

For results refer to individual animal records

Diagnostic samples to be collected: *(Check)*

	Collection Dates	Dates results received
☐ **Physical exam, body weight and measurements**		
☐ **Faeces**		
Blood smear, haematocrit and total protein		
☐ **Whole blood, serum or plasma (max volume/animal = ml)**		
☐ **Fresh faecal or rectal swab for culture**		
☐ **Choanal or oral swab or culture**		
☐ **Ectoparasites**		
☐ **Other:** Group faecals 2 weeks after treatment		

11. TREATMENTS/VACCINATIONS AND DATES

For documentation refer to individual animal records

12. SAMPLES TO BE FORWARDED TO:

Quarantine Details

13. LOCATION: _____

14. FACILITY: _____

15. QUARANTINE DURATION: **Begins** *(date)* _____ **Ends** *(date)* _____

Total days: 30 If less than 30 days specify reason(s) below

_____

_____

_____

16. PERSON SUPERVISING QUARANTINE: _____

Tel. _____ E-mail _____

17a. BRIEFING NEEDED FOR SUPERVISOR? **YES** NO

17b. DATE OF BRIEFING, IF NEEDED: _____

18. QUARANTINE EQUIPMENT:

- ☐ **"Quarantine - No Unauthorized Entry Sign"**
- ☐ **Insect/rodent traps/screens/baits**
- ☐ **Diagnostic sample collection, storage and transport equipment**
- ☐ **Lock for facility**
- ☐ **Footbath/boot changes**
- ☐ **Protective clothing**
- ☐ **Cage furniture as appropriate for species**
- ☐ **Animal record forms, pens**
- ☐ **Bags for waste disposal**
- ☐ **Feeding, watering and cleaning utensils**
- ☐ **Animal capture and restraint equipment**
- ☐ **Quarantine register**
- ☐ **Animal caregiver personal health check**
- ☐ **Other:** _____
- ☐ **Other:** _____
- ☐ **Other:** _____

19. BUDGET:

Personnel hours **hrs @** _____ **.....** _____

Equipment costs..... _____

Animal feed costs..... _____

Lab. costs..... _____

Courier fees..... _____

Veterinary fees..... _____

Other Parasite Treatments **.....** _____

TOTAL COST: ..... _____

Budget code: | | | | |

Movement Recommendation

20a. Healthy and minimal threat to destination populations..... O.K. to move ☐

20b. Healthy but there is a significant threat to source populations..... Delay move ☐

Cancel move ☐

20c. Unhealthy or threat to destination populations..... Delay move ☐

Cancel move ☐

Explanation and justification for recommendations:

21. FOLLOW UP ACTIONS:

22. PERMITS TO MOVE ANIMALS RECEIVED? YES NO

23. SIGNED OFF BY: _____ Project Manager **DATE:** _____

_____ Veterinarian