

Assessing Pesticide Risks to Threatened and Endangered Species Using Population Models: Findings and Recommendations from a CropLife America Science Forum

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ABSTRACT

This brief communication reports on the main findings and recommendations from the 2014 Science Forum organized by CropLife America. The aim of the Forum was to gain a better understanding of the current status of population models and how they could be used in ecological risk assessments for threatened and endangered species potentially exposed to pesticides in the United States. The Forum panelists' recommendations are intended to assist the relevant government agencies with implementation of population modeling in future endangered species risk assessments for pesticides. The Forum included keynote presentations that provided an overview of current practices, highlighted the findings of a recent National Academy of Sciences report and its implications, reviewed the main categories of existing population models and the types of risk expressions that can be produced as model outputs, and provided examples of how population models are currently being used in different legislative contexts. The panel concluded that models developed for listed species assessments should provide quantitative risk estimates, incorporate realistic variability in environmental and demographic factors, integrate complex patterns of exposure and effects, and use baseline conditions that include present factors that have caused the species to be listed (e.g., habitat loss, invasive species) or have resulted in positive management action. Furthermore, the panel advocates for the formation of a multipartite advisory committee to provide best available knowledge and guidance related to model implementation and use, to address such needs as more systematic collection, digitization, and dissemination of data for listed species; consideration of the newest developments in good modeling practice; comprehensive review of existing population models and their applicability for listed species assessments; and development of case studies using a few well-tested models for particular species to demonstrate proof of concept. To advance our common goals, the panel recommends the following as important areas for further research and development: quantitative analysis of the causes of species listings to guide model development; systematic assessment of the relative role of toxicity versus other factors in driving pesticide risk; additional study of how interactions between density dependence and pesticides influence risk; and development of pragmatic approaches to assessing indirect effects of pesticides on listed species. *Integr Environ Assess Manag* 2015;11:348–354. © 2015 SETAC

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INTRODUCTION

In 2013, the National Research Council (NRC) published a report on *Assessing Risks to Endangered and Threatened Species*

from *Pesticides* (NRC 2013) that recommended the use of population models. This recommendation sends an important signal to policy makers that effective risk assessments need to be more tightly coupled to protection goals through use of population-level endpoints and that models have an important role to play in this regard. This view corresponds well with recent scientific opinions coming out of Europe in which mechanistic effect models (including organism-level and population models) are increasingly viewed as important tools for ecological risk assessment (EC 2013). Although the NRC

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report likewise recognized the importance of population models for threatened and endangered species risk assessments, the report has raised some concerns among stakeholders, particularly given the large number (>1500) and diversity of species currently listed under the Endangered Species Act (ESA) in the United States. Whether and which existing population models can be applied in practice to different groups of listed species is not clear. In some cases, the large spatial scale over which pesticide risks must be assessed raises challenges, as does the lack of demographic and ecological data for many listed species. To explore these and other issues, CropLife America sponsored a 2-day Science Forum on 8–9 April 2014, in Washington, DC, to bring together a panel (i.e., the coauthors of this paper) consisting of population modelers with expertise in terrestrial and aquatic plants, vertebrates, and invertebrates and industry representatives having expertise in listed species risk assessments. This brief communication provides an overview of the panel's main findings and recommendations for future actions.

IMPROVEMENTS TO CURRENT PRACTICE ARE NEEDED

The assessment of pesticide risks to threatened and endangered species under US legislation is under revision. An interim approach has been proposed by the involved Federal agencies; however, final guidance has not yet been developed. This type of risk assessment is particularly complex because of the large number of statutes and agencies involved in the process. The Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA) regulates the sale, distribution, and use of pesticides in the United States. As part of the pesticide registration process, the United States Environmental Protection Agency (USEPA) is responsible for ensuring that pesticide use does not cause any unreasonable adverse effects on the environment, including listed species and their critical habitats. At the same time, the ESA regulates the listing of species as threatened or endangered and the designation of critical habitat on which the species depend. Implementing this statute is the responsibility of the US Fish and Wildlife Service (FWS) and the National Oceanic and Atmospheric Administration National Marine Fisheries Service (NMFS), “the Services.” The USEPA (and all federal agencies) is required to ensure that its actions (e.g., registering a pesticide) are not likely to jeopardize the continued existence of listed species or result in the destruction or adverse modification of designated critical habitat. To meet the standard under ESA, the USEPA must assess the impacts of its actions, and as necessary consult the Services. Under the ESA, direct, indirect, and cumulative effects on listed species must be considered. Under FIFRA, the social and economic benefits of pesticide use, as well as costs to human health and the environment, are considered. The ESA, however, is focused on ensuring that listed species are not jeopardized. Whereas assessments conducted under ESA are geographically focused (i.e., defined by the location and habitat of the species under consideration), pesticide registrations conducted under FIFRA are generally at the national level. If the USEPA determines that a pesticide is likely to adversely affect one or more listed species, the Services must be formally consulted to decide whether the pesticide is likely to jeopardize the continued existence of the listed species or result in the destruction or adverse modification of its critical habitat. As a result of the differences in approaches and perspectives of FIFRA and ESA highlighted previously, the

USEPA and the Services often have not been able to reach consensus on the methods and results of their assessments of the risks of pesticides to listed species. In response, the National Research Council was asked by the Federal Family (USEPA, FWS, NMFS, and US Department of Agriculture) to examine the scientific and technical issues involved in risk assessments of listed species. The resulting report (NRC 2013) provides an extensive list of recommendations.

THE NATIONAL RESEARCH COUNCIL RECOMMENDS POPULATION MODELING

An important conclusion of the NRC report was that “the risk-assessment paradigm, as reflected in the ERA process, is a scientifically credible basis of a single, unified approach for evaluating risks to listed species posed by pesticide exposure under FIFRA and the ESA” (p. 44). The report recommended that a common approach, based on this paradigm, be used across agencies. The framework for ecological risk assessment (ERA) includes problem formulation, exposure and effects analysis, and risk characterization. The ERA framework is incorporated into the 3-step tiered process recommended by the NRC Panel for assessments of pesticide risks to listed species. At step 1, a determination is made as to whether the pesticide “may affect” one or more listed species. If the answer is yes, step 2 determines whether the pesticide is “likely to adversely affect” the listed species. If the answer is yes, step 3 makes an assessment of whether the continued existence of listed species is in “jeopardy.” The phases in the ERA framework are repeated and refined in each of the 3 ESA steps, with the focus switching to meet the objective of each step. In keeping with the tiered philosophy of risk assessment, this process starts with more general information and conservative assumptions at step 1 and proceeds with more specific information and realistic assumptions at steps 2 and 3.

With regard to effects assessments, the USEPA primarily uses organism-level attributes (i.e., survival, growth, or reproduction of individuals) to infer population-level impacts (Suter et al. 2005) and assumes that at the earliest tiers in the assessment, the protection of individuals ensures protection of the population. In contrast, the Services have made use of population models to make the link between individual-level effects and population-level impacts explicit (NMFS 2008, 2009). The NRC report concurs that only those effects resulting in a change in survival or reproduction should be considered relevant for determining population-level impacts of pesticides but recommends that population models be used to integrate effects on survival and reproduction to quantify population-level impacts. The report does not recommend specific models or modeling approaches but notes that sometimes species-specific models may be used, whereas in other cases simple generic models are the only option. The report recommends that population models incorporate spatial structure, temporal variability, and density dependence if possible. Whereas the NRC conclusions and recommendations are helpful in providing general guidance for improving the risk assessment process, more detailed consideration of the applicability and regulatory integration of existing models and future research needs are required.

In the interim, the Federal Family is developing an implementation plan for the NRC report recommendations. An interim approach has been proposed (<http://www.epa.gov/espp/2013/interagency.pdf>); however, at the time of writing the details of the approach have not been finalized. A

stakeholder workshop was jointly held by the Federal Family on 22 April 2014 (<http://www.epa.gov/espp/2013/nas.html>), and the feedback is being considered. The intent is to improve coordination among agencies and to ensure that each step of the process builds on information used in previous steps. Although population models have the potential to play a key part in the future of pesticide risk assessments for listed species, substantial challenges exist with regard to lack of information on listed species, the large spatial scales required for pesticide risk assessments, the potential for large temporal variability in exposure (e.g., for migratory species), and the need to explicitly consider direct, indirect, cumulative, and habitat effects.

AIMS OF THE SCIENCE FORUM

The overall aim of the 2014 CropLife Science Forum was to gain a better understanding of the current status of population models and how they could be used in pesticide risk assessments for listed species in the United States. The panel considered mechanistic effect models at both the individual and population levels to leverage ongoing developments in European risk assessment (EFSA 2014) and because recent work has demonstrated the advantages of linking the two types of models for improved extrapolation (Gabsi et al. 2014). A key output of the workshop was a list of the panel's recommendations that may assist responsible government agencies in further defining assessment methods that take advantage of population modeling tools. The Science Forum included keynote presentations that provided an overview of current practices, highlighted the main findings of the NRC report and its implications, reviewed the main categories of existing models and the types of risk expressions that can be produced as model outputs, and provided examples of how models are being used in different legislative contexts. The remainder of the Forum consisted of breakout sessions in which a number of questions were discussed and used to develop overall conclusions and recommendations for further action.

THE MODELING TOOLBOX

We considered mechanistic effect models that describe processes occurring at organism (toxicokinetic [TK] or toxicodynamic [TD] and energy budget models) and population levels (scalar, matrix, metapopulation, and individual-based or agent-based models) and explored their advantages and limitations with respect to listed species risk assessments. We included TK, TD, and energy budget models because of their usefulness in extrapolating from simple to more complex exposure scenarios, estimating received dose, in extrapolating individual-level effects across species, and because they can be linked with population-level models to improve mechanistic understanding of toxicant effects. A general advantage of these models is that they add ecological relevance to ERAs by providing outputs that are more directly related to protection goals than the outputs of some other current risk characterization approaches (Galic et al. 2010). The models provide an effective way to integrate effects on multiple organism-level endpoints and to extrapolate from what we typically measure to what we want to protect (Forbes et al. 2008). We intentionally excluded discussion of fate and exposure models, which are already widely used in ERAs, and we believe that coupling these with mechanistic effect models allows a more seamless linkage of exposure and effects information within

the context of spatially and temporally heterogeneous environments than has traditionally been the practice in ERA (Ducrot et al. 2010; Focks et al. 2014). Population models can be linked to exposure via resource selection functions that are proportional to the probability that an area is used by an animal (Boyce and McDonald 1999). They can be interfaced with geographic information systems to estimate the probability that a contaminated area is used by the organism of concern.

When using models in ERA, consideration needs to be given to the choice of population-level endpoints, risk expression(s), and criteria for determining when risks are acceptable or unacceptable. Relevant population-level endpoints include population growth rate, net reproductive rate, population density, total abundance, stage structure, population persistence, and recovery time. These endpoints can be translated into expressions of risk such as risk of (quasi)-extinction, time to extinction, or probability of declining by a specified amount during a given time interval. Like other risk characterization approaches, the population-level outputs and risk estimates derived from them will have some degree of uncertainty, because parameters used in the models have inherent variability or are incompletely known. To the extent possible, these sources of uncertainty should be distinguished and quantified. Nevertheless, as a higher-tier assessment, which considers more data and accounts for the variability and uncertainty of field data, a properly conducted population-level ERA reduces the degree of uncertainty in a risk assessment.

TK and TD models

Toxicokinetic and toxicodynamic models link exposure and effects through more or less detailed information on the uptake, distribution, biotransformation, elimination (i.e., TK), and interaction of a toxicant with its target site (i.e., TD) in a single mathematical framework (Jager et al. 2011). These models are used to extrapolate toxicity among species and across different exposure scenarios (Kretschmann et al. 2012), to describe the time course of toxicity across a range of exposure concentrations (Nyman et al. 2012), and are recommended as a biologically sound option to evaluate toxicity tests instead of concentration–response relationships (OECD 2006). They also can be used to interpret time-varying exposure patterns, derive time-independent toxicity parameters, and make predictions for other untested situations (Nyman et al. 2012). The TK and TD models provide an effective way to extrapolate from the unrealistic exposure conditions used in standard toxicity studies (e.g., single oral dose for birds or mammals) to more realistic feeding conditions.

Energy budget models

Energy budget models simulate how organisms acquire and allocate energy, can estimate how these processes are changed by toxicants, and can predict impacts of such on organism's growth, survival, and reproduction (Kooijman 2010; Sibly et al. 2013). Energy budget models assume commonalities among organisms in energy acquisition and allocation to, for example, maintenance, growth, and reproduction, and have been used to gain mechanistic insight into effects of chemical and other stressors (Jager et al. 2014). Dynamic Energy Budget (DEB) theory (Kooijman 2010) was originally developed to understand impacts of chemicals on organism metabolism and life history (Kooijman and Metz 1984). DEBtox is the ecotoxicological application of DEB theory and is analogous to a TKTD model.

Responses of individuals, not populations, are the outputs of DEB and other energy budget models, but for population-level ERA, energy budget models can be coupled with scalar or matrix population models or incorporated into individuals in individual-based models (Sibly et al. 2013). In this way, effects of chemicals on energy acquisition and allocation can, through effects on survival and reproduction, be extrapolated to impacts on population dynamics (Martin et al. 2013; Johnston et al. 2014).

Scalar and stage structured models

Scalar population models assume populations are homogeneous in that vital rates such as fecundity and survival are the same for all individuals in the population. Changes in population size over time are determined by the difference in birth and death rates. If vital rates differ between individuals of different stages (e.g., defined by age, size, or developmental phase), then population dynamics also depend on the structure of the population, such as the relative proportion of juveniles and reproductive individuals. Stage structure is most commonly incorporated using matrix models (Caswell 2001) or integral projection models (Easterling et al. 2000). Because over time populations reach a stable stage distribution (e.g., the relative proportion of stages no longer changes), population dynamics of structured models can be approximated with scalar models. However, whenever disturbances disproportionately affect different stages (e.g., if juveniles are more susceptible to pesticide exposure), predictions of scalar and stage structured models may differ considerably. In both types of models, density dependence of vital rates and demographic and environmental stochasticity can be included (Tenhumberg et al. 2008; Rebarber et al. 2012; Townley et al. 2012). Mathematical tools (e.g., sensitivity or elasticity analysis) are available to evaluate the effect of perturbing a single stage of the population on the population growth rate (Caswell 2001). This type of analysis can aid in evaluating the efficiency of different management actions and may be useful for interpreting how impacts (e.g., of chemicals) on the survival and reproduction of individuals are likely to affect population dynamics (Forbes et al. 2010).

Matrix models can be incorporated into a metapopulation framework in which spatially isolated subpopulations are connected via migration (Akçakaya 2000). Commercial metapopulation matrix models are available (e.g., RAMAS Metapop, Applied Biomathematics, Setauket, NY).

Stage structured models have a long history of use in fisheries, invasion ecology, and conservation biology (Morris and Doak 2002), as well as pesticide risk assessment (Stark and Wennergren 1995; Pastorok et al. 2002). The Max Planck Institute for Demographic Research has made freely available a continuously updated database containing matrix models for approximately 900 plants and more than 1200 animal species (http://www.demogr.mpg.de/en/laboratories/evolutionary_biodemography_1171/project/compadre_plant_matrix_database_comadre_animal_matrix_database_1867.htm), which may be useful for listed species assessments. The database also contains taxonomic, phylogenetic, ecological, and biogeographic covariates.

Individual-based models (IBMs)

Individual-based models simulate populations or systems of populations as being composed of discrete individual organisms (DeAngelis and Grimm 2014). Each individual has a set of

state variables or attributes, which can include spatial location, physiological traits, growth, reproduction, feeding, dispersal, etc., and which can vary among individuals and change through time. Individuals are allowed to interact with each other and with their environment, and the dynamics of the system (e.g., population growth, density dependence) emerge from the individual-level attributes and the interactions. The IBMs (sometimes referred to as agent-based models) can be particularly useful when variability among individuals, local interactions, or individual adaptive behavior are significant, or for capturing dynamic and spatially varying environmental influences (e.g., resources or contaminants). Individual-based models can be simple and generic, but they find their greatest use for more complex and realistic simulations of ecological systems. Although IBMs can take a long time to develop initially, they are easily adapted to different scenarios or landscapes, offer a multitude of outputs for validation, integrate exposure directly, and use the kinds of data typically collected in laboratory or field studies (i.e., on individuals) for parameterization (Preuss et al. 2010; Wang and Grimm 2010; Johnston et al. 2014). Individual-based models can, to some extent, be based on theory (e.g., allometric or physiological rules), which may be especially useful for listed species for which detailed information may be limited. The development of standard protocols for model development (e.g., transparent and comprehensive ecological modeling; Grimm et al. 2014), testing (e.g., pattern-oriented modeling; Grimm and Railsback 2012), and communication (e.g., overview, design concepts, details protocol; Grimm et al. 2010), as well as the availability of accessible software tools (e.g., NetLogo; Wilensky 1999), are facilitating the growing use of IBMs in population biology and ecological risk assessment (Galic et al. 2010; Schmolke et al. 2010).

SOME QUESTIONS AND ANSWERS

Here we provide some highlights of the breakout group discussions by briefly answering the questions that were posed to participants by the organizers.

1. How does or could population modeling add value to pesticide risk assessments involving listed species? The models are key tools for quantitatively linking ecotoxicological organism-level data to protection goals. They help to organize data and knowledge to communicate risk, integrate the factors affecting risks to population viability, and facilitate quantitative evaluation of input and assumption sensitivity, sources of uncertainty, and the likely effectiveness of risk mitigation actions. The models also can inform decisions on the kind of field data to collect and on toxicity test design.
2. Where does or could the modeling fit into the tiered risk assessment process? The different models can potentially contribute to all phases of ERA. The simplest models can be used to provide a relative ranking of species or life-history vulnerabilities, whereas the more complex models can provide realistic exposure and effects assessments at higher tiers. For listed species assessments, the models are likely to have the most value at step 3 of the ESA process, which requires population-level (jeopardy) assessments for distinct population segments of the species.
3. What scientific criteria need to be fulfilled for a population model to be used for pesticide or ESA risk assessment? The

models have to be sufficiently developed, evaluated, and communicated following principles of good modeling practice (Augusiak et al. 2014; EFSA 2014). The models also should be able to capture the relative contributions of multiple stressors and other factors affecting the baseline condition of listed species.

4. Given the limited resources available, what is a pragmatic approach for development and use of population models for listed species assessments? For many endangered species matrix models are already available for species with similar life histories (e.g., Max Planck database, mentioned previously) that could be used. For IBMs, a small number of models could be developed for a core set of species that represent larger groups of listed species having similar phylogeny, life history, guild, habitat requirements, and so forth. Both model types, however, do need to be re-parameterized for each species and exposure scenario.
5. What endpoints and risk expressions can be developed from different model(s) or model types? Many population-level endpoints can be produced (e.g., change in abundance, growth rate, risk of decline to low levels), and all may provide useful information for pesticide risk assessment. To determine whether a population is in jeopardy (as in step 3 of the ESA process), risk expressions relating to the probability of quasi-extinction or decline are likely to be most informative.
6. What specific data are needed to parameterize the model(s)? The type and quantity of data needed depend on the model type (described previously), but in general toxicity data in the form of point estimates (e.g., median lethal concentrations, median effective concentrations, lowest observed effect concentrations, and no observed effect concentrations) are not sufficient as input to the models. Likewise, species sensitivity distributions, which are based on these same point estimates, are not useful for population modeling. Because such point estimates, and the distributions created from them, do not take into consideration life history differences among species, they are likely to provide less reliable estimates of population-level impacts than when such factors are taken into consideration (Forbes and Calow 2002). Improved estimates of population-level impacts can be achieved by incorporating data on time-dependent or concentration-dependent effects on survival and reproduction of different life stages. Realistic exposure models or data are needed to link with or be directly incorporated into the effects models. Some baseline (i.e., without pesticide exposure) information on survival and reproduction of field populations is also generally needed.
7. What models are available to translate typical field or laboratory life-history data and toxicity data for input into the model? As described, several types of models are available for these purposes. Some examples of their use can be found in recent issues of *Ecological Modeling* (Grimm and Thorbek 2014) and *Environmental Toxicology and Chemistry* (Galic and Forbes 2014). Also, the USEPA is developing models to translate typical toxicity test results into metrics, such as annual fecundity, that are useful as input to some population models (Etterson and Bennett 2013).
8. What population models, software and datasets or databases would be useful and can be immediately applied to

pesticide or ESA assessments? In addition to the Max Planck database mentioned previously, a large database of matrix models for population viability analysis has been developed in the United States (<http://www.myfwc.com/media/1205682/TR15.pdf>). The Services also maintain databases, and NatureServe (<http://www.natureserve.org/>), Birds of North America Online (<http://bna.birds.cornell.edu/bna/>), and FishBase (<http://www.fishbase.org/search.php>) are examples of other sources of information.

9. What are the most important data gaps and sources of uncertainty for listed species that hinder robust risk assessment? The lack of robust quantitative data on abundance, spatial distribution, life history, and the reasons for why a particular species is listed are common gaps. Formal sensitivity analysis can be used to identify those uncertain input variables to which the model outputs are most sensitive, and these would be defined as the most important to fill. Data on pesticide avoidance or age-specific, species-specific, or habitat-specific sensitivity are often lacking. Lack of detailed life history data for many species may be of less concern, because such data may be available for similar, surrogate species.
10. What options exist for dealing with these sources of uncertainty? The models facilitate the exploration of various “what if” analyses to bound uncertainty. In some cases, theory (e.g., allometric or physiological rules) can be used when data are not available. Toxicity data for listed species often can be extrapolated from other species using TK, TD, and energy budget models. Although reasonable-case conservatism can be used, this should be done with care to avoid compounding multiple conservative assumptions, resulting in unrealistic risk estimates.
11. What options exist for modeling species with limited data or knowledge of the species, for example; life history, diet, range, preferred habitats? One pragmatic approach is to use similar species (e.g., similar life-history traits) for which data are available and to make reasonable assumptions about unknown variables. Population models for various life-history types within different biotic groups (e.g., plants, invertebrates, birds, mammals, reptiles) could be developed based on data for representative species and serve as generic models, whether they be scalar, matrix, or IBMs. Such generic models for classes of populations, such as shorebirds or stream salmonids, could be applied in ranking species vulnerability to prioritize them for risk assessment or jeopardy determinations. However, use of generic models, particularly if they are a composite of data from multiple species within a guild, may not be sufficient for a step 3 jeopardy determination for threatened and endangered species assessments.

KEY RECOMMENDATIONS FOR MOVING FORWARD

The Science Forum reached consensus on the following recommendations for implementing population models to assess the risks of pesticides to listed species.

FOR IMMEDIATE ACTION

We recommend that the following actions be immediately implemented:

1. A multipartite advisory committee, representing relevant government agencies, industry, academia, nongovernment

organizations, and multidisciplinary experts including risk assessors, modelers, ecologists, ecotoxicologists, and so forth, should be formed to develop consensus on specific practices and a decision framework for the use of population models for pesticide risk assessment for listed species. This group also could play a key role in reaching decisions on desired model realism, whether and how to add conservatism, and trustworthiness of proposed models as well as consensus on bright-line criteria for making decisions on the basis of probabilistic risk estimates. This advisory committee could be formed under the Federal Advisory Committee Act, or possibly under the NAS, National Research Council or Society of Environmental Toxicology and Chemistry (SETAC) and we recommend a short timeframe for this work (i.e., months to a year).

2. A publicly available database should be created where researchers can contribute specified information useful for modeling populations of listed species. Such a database would not necessarily provide instant data for model input, but it would direct modelers to the relevant primary literature and help identify data gaps.
3. Existing guidance on good modeling practice (Augusiak et al. 2014; EFSA 2014) should be used to provide a basis for appropriate model development and usage. Much progress has been made in this area in recent years, and we conclude that existing guidance is at a sufficient stage of development to be immediately implemented.
4. A comprehensive literature review should be conducted to identify available population models that can be used directly, or with minor modification, in listed species risk assessments.
5. A handful of case studies should be conducted, using readily available models and well-understood species, to demonstrate proof of concept, gain confidence that the models can add value to decision making in real (or realistic) assessments, and identify areas in which further work is needed. The multipartite advisory committee could be responsible for exploring and soliciting potential funding resources for this activity (e.g., from CropLife America, USEPA, FWS, NMFS and so forth).

For improving existing models and their implementation in pesticide ERAs

Recognizing that the effective use of population models in ERAs will be limited primarily by the availability of data for model parameterization and by knowledge of the key processes driving the dynamics of field populations, we recommend that the following issues be given high priority in further developing population models for listed species assessments:

6. Whatever models are used should include realistic variability in environmental and demographic parameters, sensitivity analyses of model input parameters, output for developing quantitative risk estimates, and explicit uncertainty analyses.
7. The models should be demonstrated to be capable of reproducing key processes essential to understanding population dynamics, including how these may be influenced by toxicant effects.
8. The baseline models used to assess risks caused by pesticides should include the relevant factors that have

led the species to be listed (to the extent that these are known) and also should include effects of any management efforts that have been taken in the past.

9. More effort should be given to integrating complex exposure patterns into models for estimating effects of pesticides on population viability.

For future research and development

To further develop the science and ensure that the application of population modeling leads to more robust risk assessments for listed species, we recommend the following:

10. Information on the causes of species decline and listing should be collected and analyzed to categorize species' relative vulnerabilities, and so that modeling efforts can be focused on those species or categories of species that are most likely to be listed.
11. Further research should be conducted to understand interactions of density dependence (and its effects on such things as life history, behavior) and population-level pesticide risks.
12. Further research should be conducted to assess the relative importance of toxicity compared with the other factors (e.g., life history, behavior, geographic distribution, and so forth) influencing population-level risks from pesticides.
13. Further attention should be given to developing pragmatic approaches for assessing indirect effects on listed species. For example, interactions such as predation or competition can sometimes be simulated in single species models by incorporating additional impacts on survival, growth, or reproduction of the listed species, without having to model the interacting species explicitly.

CONCLUSIONS

Population models can make a substantial contribution to pesticide risk assessments for threatened and endangered species. This is particularly true for step 3 of the proposed process (jeopardy determination), but the models also may help in screening-level assessments at steps 1 and 2. Appropriate modeling tools are available for various applications within the 3-step framework being developed by the Federal Family. However, exactly how many existing models can be immediately applied in listed species risk assessments remains to be determined. It is likely that a larger group of models could be adapted to listed species assessments with some modification. We hope that our recommendations can assist in the implementation of population modeling in listed species assessments and can guide future research in this area.

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