



## *Project Summary*

# **Sewage Sludge Pathogen Transport Model Project**

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The sewage sludge pathogen transport model predicts the numbers of salmonella, ascaris, and polioviruses which might be expected to occur at various points in the environment along 13 defined pathways. These pathways describe the use of dried or liquid, raw or anaerobically digested sludge as a cropland fertilizer, dried raw sludge as an animal feed supplement, and composted sludge as a residential soil amendment.

The model uses a compartment-vector approach in which a mathematical state represents a discrete point in a treatment or application pathway where pathogen populations are computed as a function of time. Within these compartments, mathematical process functions describe population changes due to environmental factors. Pathogen exchanges between compartments are described by transfer functions. The model permits user specification of various parameters in both process and transfer functions, enabling him to simulate a unique set of environmental conditions. The model has the additional capability of performing exposure risk calculations for environmental compartments specified by the model user at the time of model variable initialization. These calculations are then performed automatically at each hour interval using the pathogen population calculated for the compartment at that time.

The five separate exposure risk calculations provide risk assessment determinations for pathogens associated with airborne particulates, resi-

due and soil, vegetable crops, meat, and milk. Certain of the exposure risk calculations can be modified by the model user to simulate unique exposure conditions. The model can be progressively modified to accommodate new information, thus constantly enhancing its predictive accuracy.

*This Project Summary was developed by EPA's Health Effects Research Laboratory, Cincinnati, Ohio, to announce key findings of the research project that is fully documented in a separate report of the same title (see Project Report ordering information at back).*

### **Introduction**

The constraints imposed on sewage treatment and disposal by clean air and water legislation are increasing the amounts of sewage sludge which a municipality must dispose of while reducing disposal alternatives. Legislation has encouraged waste management procedures which emphasize the recycling and beneficial use of waste materials. At the same time, the consequences of such use are being questioned. Before municipal officials can consider using sludge for beneficial purposes they must decide whether the environmental release of human pathogens inherent in sewage sludge poses an unacceptable risk.

One mission of the Applied Biology and Isotope Utilization Division of Sandia Laboratories is the development of cost-beneficial uses for existing and future supplies of radioactive isotopes. The Waste Resources Utilization Program, a major subprogram of the Bene-

ficial Uses Program, has developed methods, using cesium-137, to reduce the pathogen content of municipal sewage sludge so that the organic and nutrient value of sludge can be used safely and productively. As a result of this effort, a prototype sewage sludge irradiator has been developed which may make this treatment technology available to municipalities.

The extent of the health hazard posed by enteric pathogens in sludge, however, remains an unanswered question. In an attempt to evaluate and possibly quantify this hazard, Sandia Laboratories contracted with the BDM Corporation to accumulate an information base that would include available, relevant data regarding pathogen occurrence in sewage, pathogen survival during common sewage treatment processes, and pathogen movement through the environment as a result of sludge application and use. A computerized library storage and retrieval system was designed to classify and store the abstracts of reviewed literature which constitute the information base. This information base was used to develop a computer model which predicts the numbers of specific pathogens that would be found in sewage sludge at various points during sludge treatment and application. Once the pathogen population estimates are determined for points in the environment, the model has the added capability of assessing the risk to health resulting from human exposure to the pathogens. The model is a first step towards evaluating the potential risk to human health from beneficial uses of municipal sewage sludge.

## Results

The sludge treatment and application alternatives described in the computer model were specified by Sandia Laboratories. These alternatives include the use of cesium-137 gamma irradiation in conjunction with the following sludge uses:

- a. Dried raw sludge applied to cropland as a fertilizer.
- b. Dried, anaerobically digested sludge applied to cropland as a fertilizer.
- c. Dried raw sludge used as a feed supplement for ruminant animals.
- d. Composted sludge used as a soil conditioner by the general public.
- e. Liquid raw or anaerobically digested sludge applied to cropland as a fertilizer.

In designing the computer model, these treatments and applications were divided into 13 separate pathways which describe the major steps in the flow of pathogens through the environment. Figure 1 is a sample illustration of Pathway 6.

Four pathways were developed which describe sludge treatments. Pathway 1, General Sludge Treatment Pathway, describes the treatment of raw or digested sludge for application as cropland fertilizer. Pathway 2, Sludge Treatment Pathway - Animal Feed Supplement, describes the treatment of raw sludge necessary to prepare an animal feed supplement. Pathway 3, Sludge Treatment Pathway - Composting of Raw or Digested Sludge, describes a general composting cycle to render sludge an inoffensive residential soil amendment. Pathway 10, Sludge Treatment Pathway - Liquid Sludge, describes the treatment of either raw or anaerobically digested, liquid sludge intended for application to cropland.

Nine pathways describe the applications of the sludge that could follow the defined treatment alternatives. Pathway 4, Sludge Application Pathway - Fertilizer for Crops Destined for Human Consumption, and Pathway 11, Sludge Application Pathway - Liquid Sludge Used as a Fertilizer for Crops Destined for Human Consumption, describe the environmental flow of pathogens after sludge is applied to cultivated farm land producing common vegetable crops. Pathway 5, Sludge Application Pathway - Fertilizer for Pasture Crops, and Pathway 12, Sludge Application Pathway - Liquid Sludge Used as Fertilizer for a Grazed Pasture, describe the use of treated sludge on a grazed field, while Pathway 6, Sludge Application Pathway - Fertilizer for Crops That Are Processed Prior to Animal Consumption, and Pathway 13, Sludge Application Pathway - Liquid Sludge Used as a Fertilizer on Crops That Are Processed Prior to Animal Consumption, describe the use of treated sludge on field crops harvested for animal consumption. Pathway 7, Sludge Application Pathway - Animal Feed Supplement, is designed to evaluate the use of herbivore feeds containing sludge such as those prepared in Pathway 2. Pathways 8 and 9, Sludge Application Pathway - Residential Garden Soil Amendment and Sludge Application Pathway - Residential Lawn Soil Amendment, respectively, describe the application of composted sludge to

home vegetable gardens and in the establishment of a new lawn.

Considering modern disposal practices, any pathogenic organism can be found in municipal sewage. It would be difficult to design a model which could accurately simulate the survival and environmental movement of more than a few specific organisms. Three organisms were selected to represent the enteric pathogens most commonly found in sludge. These organisms were chosen because each causes significant disease in the general population; there was more information available concerning these organisms than for other members of the principal pathogen groups; and each is exceptionally hardy, surviving longer than average outside the human body. *Salmonella* species were used to represent the bacteria; *Ascaris* species were used to represent parasites, both the helminths and the protozoa; and polioviruses were used to represent all enteric viruses. No representative for the fungi was selected because not enough information is available on this group as a whole or on any individual member of the group to support the type of decision making which is the foundation of environmental modeling.

The possible growth, inactivation, and movement of each of the three selected pathogens, *Salmonella*, *Ascaris*, and poliovirus, were analyzed for each compartment and transfer of the 13 defined pathways which constitute the sewage sludge pathogen transport model. The model uses the state-vector approach. A state or compartment is a discrete point along a pathway where the pathogen population is computed as a function of time. Compartments are indicated in the pathway illustrations as boxes labeled to indicate what processes are acting on the pathogen populations. Within each compartment, first-order, linear, differential equations are derived to compute the rate and direction of change in the pathogen population and the effect that any subprocesses in a compartment may have on that population. The process functions which describe population changes are vectors including parameters to account for time, temperature, moisture content, nutrients, etc. The transfer of pathogens between compartments is described by a set of ordinary differential equations derived using conservation principles, environmental parameters, and relationships developed from data obtained in the literature review. These equations are then integrated to determine the

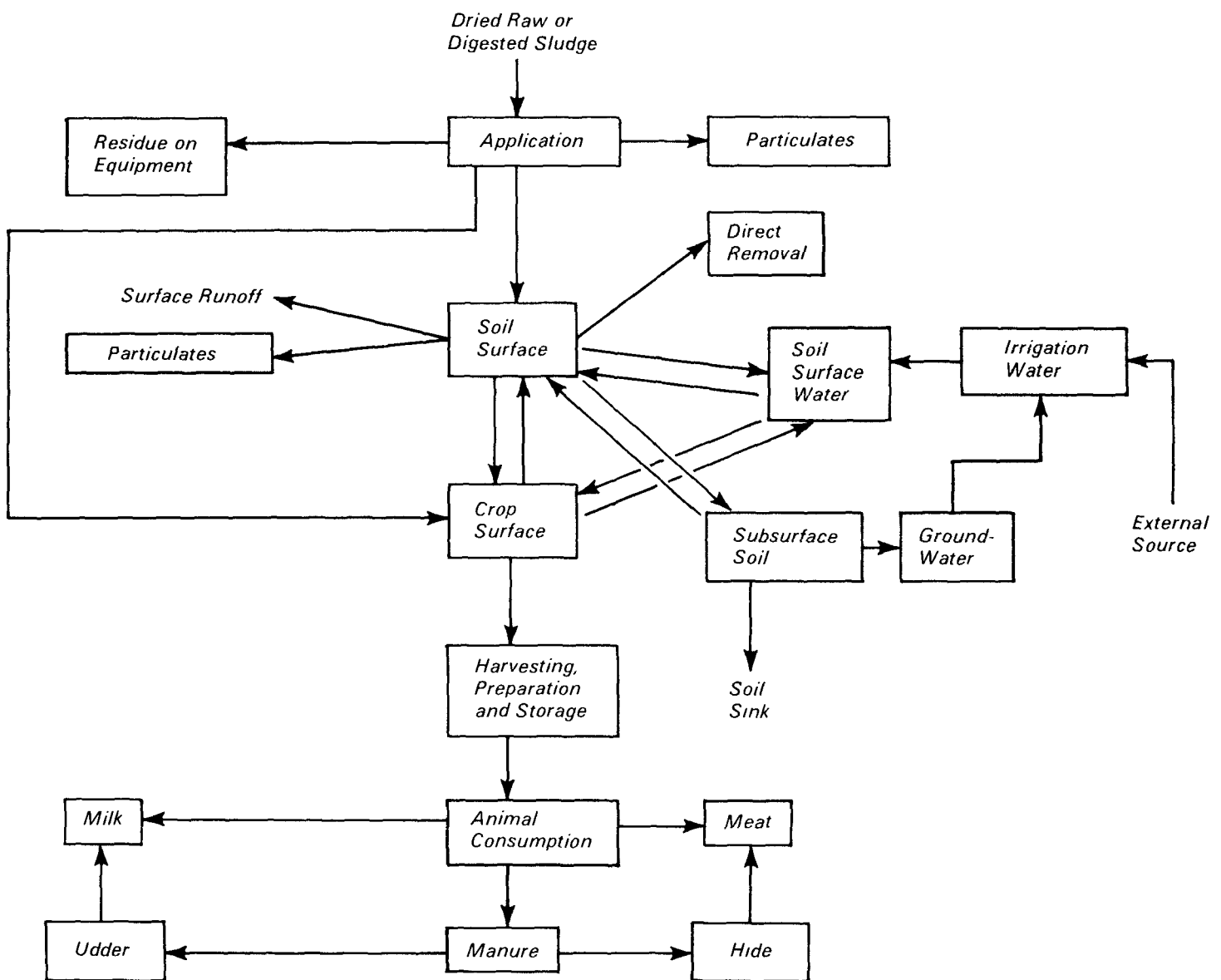


Figure 1. Sludge application pathway—fertilizer for crops that are processed prior to animal consumption (Pathway 6)

pathogen populations in each compartment.

The state-vector approach used to develop the sewage sludge pathogen transport model provides a structure with the capability for supporting both stochastic and deterministic mathematical relationships. It provides a flexibility of model structure which permits addition and/or deletion of pathway compartments and modifications in process and transfer functions. The modeling effort itself has served as a tool to identify areas where data is currently

nonexistent or incomplete and where further research is needed. Informed estimates were incorporated into the model in these less studied areas. As new information becomes available these estimates can be removed from the model and can be replaced with supported data. The model can be progressively modified, thus constantly enhancing its predictive accuracy.

Each of the selected pathogens differs in its response to treatment and environmental processes. Process and transfer functions were developed to

describe each pathogen population separately. The user selects which pathogen will be considered in any particular pathway run. The user may also control the environmental conditions to be simulated in the model by inputting user-selected variables to define duration of compartments, temperature, rainfall, and other parameters. Default values for each parameter are incorporated into the model. These values are based on the extensive literature review which preceded the modeling effort. The decisions which resulted in variable

value determinations are documented in the report. The user may compare the final pathogen populations of one pathogen against another for a particular pathway, or of one pathogen against itself for several different pathways, or may compare the effects of different parameter values on pathogen populations within and between pathways. For example, the default value for ambient temperature in all 13 pathways is 20°C. It is possible to follow all three pathogens through a particular pathway at this temperature. The user may then specify an ambient temperature of 30°C and follow the pathogens through again. Comparison of the six print-outs will show the effects of temperature.

The model pathways were developed using relationships that describe the behavior of representatives of three pathogen classes (bacterial, viral, parasitic) during sewage treatment and in the environment following their dissemination in sludge. The flexible structure of the model and the ample supply of user-specifiable variables will allow an informed user to adapt compartments in any of the pathways to describe the fate of other members of each pathogen class. It must be remembered, however, that even pathogens in the same class may differ widely in their responses to stresses encountered during treatment or in the environment. For example, one might incorporate data describing *Mycobacterium tuberculosis* into the process function associated with one of the compartments in a pathway. The model will function normally with these data incorporated, but it must be remembered when interpreting model output that the relationships in the other compartments of the pathway describe the behavior of salmonella.

In addition to the 13 sludge treatment and application pathways just described, the model contains five exposure risk calculations. These calculations provide estimates of the risk to human health resulting from exposure to sludge pathogens associated with airborne particulates, soil or residue, vegetable crops, meat, and milk. These calculations are executed automatically when the model user elects to determine the risk associated with the environmental compartment to which the exposure risk calculations are coupled. The exposure risk calculations begin with the number of pathogens present in the selected compartment (e.g., RESIDUE). The pathogen population is then modified based on a series of events that would normally

occur during a human exposure. The final pathogen number is compared with human-dose-response data to provide an estimate of the circumstances that would lead to a human infection. For example, the model would provide the number of vegetable units that would have to be consumed to provide an infectious dose. Certain aspects of these calculations may be modified at the time of model initialization by the model user to enable him to tailor the exposure scenario according to unique conditions.

## Conclusions

The accuracy of this or any other predictive model is directly related to the quality of the quantitative data that is used in the development of the mathematical relationships in the model. Data are available on most aspects of microbial survival during sewage treatment processes. However, most of these data are qualitative in nature and cannot be used directly in the development of quantitative mathematical relationships. Quantitative data available for bacteria are often concerned with the fate of indicator organisms. It was often necessary to extrapolate these data to the less numerous and usually more fastidious pathogenic bacteria. The validity of this extrapolation is subject to the similarities between the pathogens and indicators. Data concerning enteric parasites are usually qualitative in nature, and problems exist in assessing the viability of resistant forms. There is much recent data concerning the survival of viruses during sewage treatment. Most of this information pertains to poliovirus and may not be applicable to other viral pathogens, especially hepatitis A and rotavirus.

Much of the current information on the persistence of pathogens in the environment is also qualitative in nature. Most of the data from laboratory studies lacks confirmation under field conditions. Conversely, descriptive field studies generally do not include laboratory investigation of underlying basic principles. The lack of quantitative information on the relative contributions of interacting environmental parameters such as pH, temperature, microbial antagonism, moisture, toxic substances, ultraviolet radiation, etc. makes it impossible to model the discrete microprocesses that affect environmental survival of pathogens.

The Sewage Sludge Pathogen Transport Model uses general mathematical

descriptions of pathogen behavior during treatment and in the environment. The modular structure of the model allows the easy incorporation of any desired microprocess data as it becomes available. The mathematical relationships in the model were developed using data from three representative pathogens, salmonella, ascaris, and poliovirus. If this caveat is kept in mind, the model can be modified by an informed user to predict the survival and health risks associated with other pathogens.

The risk assessment portion of the model was developed in the absence of information concerning the probability of exposure of individuals to pathogens originating from sludge. Because these data are not available, the risk assessment portion of the model assumes that an individual is exposed to sludge pathogens. The model then provides the user with information about the conditions of exposure that would lead to infection or disease.

As developed, the model will be a useful tool for exploring the relative health risks associated with a variety of user-defined sludge treatment and application scenarios. The value of the model will be its ability to provide rapid comparisons of relative health risks rather than its ability to accurately quantify pathogen survival in the environment.

The Sewage Sludge Pathogen Transport Model was developed on the CDC (Control Data Corporation) 6600 computer at Sandia National Laboratories in Albuquerque, New Mexico. The transportability of the model's FORTRAN code may be limited by characteristics of this computer and its operating system and by the use of several unique system programs in the model.

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***Norman E. Kowal and Gerald Stern** are the EPA Project Officers (see below). The complete report is in two parts, entitled "Sewage Sludge Pathogen Transport Model Project," (Order No. PB 82-109 000; Cost: \$33.50, subject to change) Magnetic Tape (Order No. PB 82-108 994; Cost: \$540.00, subject to change) will be available only from:*

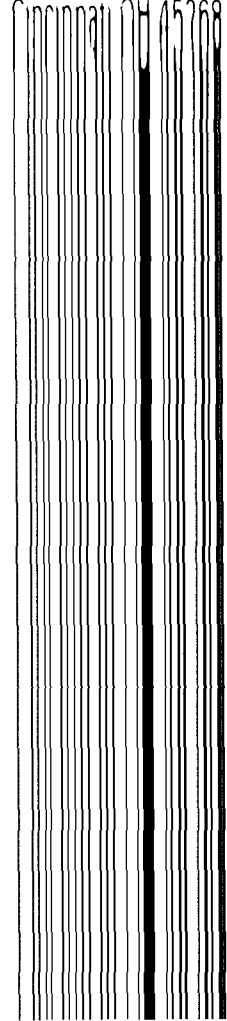
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