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Estimating Downwind Concentrations of Viable Airborne Microorganisms in Dynamic Atmospheric Conditions

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A Gaussian plume model has been modified to include an airborne microbial survival term that is a best-fit function of laboratory experimental data of weather variables. The model has been included in an algorithm using microbial source strength and local hourly mean weather data to drive the model through a summer- and winter-day cycle. For illustrative purposes, a composite airborne "virus" (developed using actual characteristics from two viruses) was used to show how wind speed could have a major modulating effect on near-source viable concentrations. For example, at high wind speeds such as those occurring during the day, or with short travel times, near-source locations experience high viable concentrations because the microorganisms have not had time to become inactivated. As the travel time increases, because of slow wind speed or longer distances, die-off modulation by sunshine, relative humidity, temperature, etc., potentially becomes increasingly predominant.

For numerous reasons it is useful to estimate the downwind concentration of live airborne microorganisms from certain sources. Mathematical simulation models can make such estimates. A frequently used model, developed by Pasquill (10) and further explained by Slade (13) and Hanna et al. (2), has Gaussian properties that statistically predict dispersed lateral, vertical, and downwind particle concentrations in the plume downwind from an elevated source. This model was first modified and applied to the dispersion and die-off of airborne microorganisms in a plume (3–5) and was later modified to include a microbe settling term (11). This communication explains how the model is changed to include an algorithm with a function(s) modulating airborne microbial death due to temperature, relative humidity (RH), solar radiation, and time in the aerosol, as well as statements defining weather conditions specifying the values for the terms in the above death function and dispersion models. Because complete data for any single microorganism were not available, data from several sources were combined to generate a "composite virus" for illustrative purposes.

MATERIALS AND METHODS

Dispersion model development. Except for the survival function, term D (below), the version of the Gaussian model used here was described in detail by Peterson and Lighthart (11) (see equation 1). Briefly, (i) term A [i.e., $bQ/2\pi\mu(\sigma_y\sigma_z)$] represents the concentration on the mean plume axis at a given distance, x, from the source with no microbial death; (ii) term B [i.e., $\exp(-Y^2/2\sigma_y^2)$] accounts for lateral dispersion; and (iii) term C [i.e., $\Sigma q_i \exp(-\{[H-(V_{s_i}x/\mu)]^2/s\sigma_z^2\})$] accounts for vertical dispersion and differential droplet settling rates. Term C also modifies the formula so that the computed concentration is the ground-level concentration. Term D (i.e., S) takes into account the loss of the airborne microorganisms as a function of the environmental parameters used in a polynomial curve-fit of the organisms to these factors. The two spread factors, σ_y and σ_z, were those used for an ordinary summer day and an overcast, windy winter day (see Table 1 of reference 11).

$$X = (bQ/2\pi\mu\sigma_y\sigma_z)\exp(-Y^2/2\sigma_y^2)\ \Sigma q_i \exp(-\{[H-(V_{s_i}x/\mu)]^2/2\sigma_z^2\})S \quad (1)$$

where X is the mean number of viable microbes per unit volume of air (cubic meters) at ground level and is a function of downwind and lateral distance for the source; b is the number of microbes per unit volume (cubic meters) of effluent at the source; Q is the volume emission rate of effluent (cubic meters per second); μ is the mean wind speed (meters per second; generally a 1-h average) and must be greater than zero for this model to be valid; σ_y is the standard deviation of the horizontal plume spread (meters) and is a function of downwind distance and atmospheric stability; σ_z is the standard deviation of the vertical plume spread (meters) and is a function of downwind distance and atmospheric stability; Y is the lateral distance (meters) from the mean position of the plume axis; q_i is the mass weighted proportion of particles in the ith size category (dimensionless); H is the height above ground (meters) of the plume axis after the initial plume rise; V_{s_i} is the settling speed (meters per second) of an average microbe-containing droplet in the ith size category; x is the downwind distance (meters) from the source along a line parallel to the mean plume axis; S is the percent microbial survival (dimensionless). The surface concentration pattern of particles that the model predicts is shown in Fig. 1.

Survival model development. The survival function, term D in the dispersion model, accounts for the surviving fraction of the airborne microorganisms as they are affected by the independent variables: atmospheric temperature, RH, solar radiation, and time in the plume. It is assumed that the environmental conditions in the plume remain constant after microbe injection into the atmosphere. Ideally, the term would be used in the form of a single polynomial equation fit to experimental survival data. However, to our knowledge, no such data set exists; therefore, for this analysis two separate sets of virus survival data were combined to simulate a virus. Henceforth, unless indicated, "virus" refers to "composite virus." Thus, the use of two viruses in this presentation is to illustrate the methods with relatively

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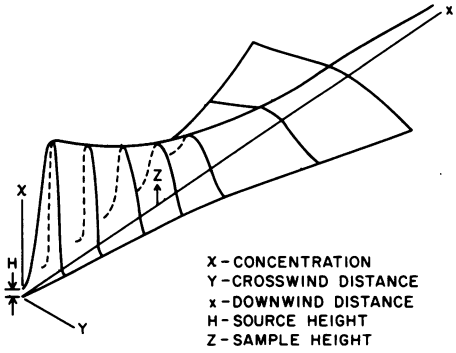

FIG. 1. Surface-concentration pattern downwind from an elevated source (adapted from reference 13).

realistic values, and it should not be inferred that the composite virus would actually respond to any particular set of environmental conditions in the manner to be described. The two data sets of virus were those of Mohr (A. J. Mohr, Ph.D. dissertation, Utah State University, Logan, 1984), who made measurements of the survival of reovirus (type 1, Lang, potentially infectious virus) in a dynamic aerosol toroid as a function of temperature, RH, and time, and Berendt et al. (1), who made similar measurements of Venezuelan equine encephalomyelitis virus survival as a function of solar radiation, RH, and time. The SAS Institute multiple regression program REG (12) was used to calculate a set of polynomial coefficients for the least square fit for each data set. To estimate the composite virus survival due to both polynomial predictors, no interaction was assumed between the functions, and therefore they were simply multiplied together; i.e., the final calculated survivors were those microorganisms that survived the independent effects described by the first polynomial. These survivors were then exposed to the second polynomial (Robert Worrest, personal communication). This approximation, which would not be necessary if a complete data set for one organisms were available, generates a trivial error in the second term in equation 3. This error is <5% for simulations of $<10^3$ s.

Microbial source strength. The strength of the microbial source is computed in term A of the diffusion equation (equation 1). For sources such as cooling towers or certain farming machines, calculations require a knowledge of the concentrations of emitted microorganisms (b) and the volume emission rate (Q) or their product (bQ) in microbes per time within a volume. A knowledge of the flux (number per meter squared per second) and wind speed of airborne microbes over a source such as a plant canopy may also be used (see references 8 and 9). In this report the microbial input source was assumed to be either a constant of 100 virus m^{-2} s^{-1}, or variable as a function of the wind speed. The function is a direct proportion of the midday wind speed to hourly wind speeds, multiplied by the midday mean upward flux of bacteria from a bean field canopy, i.e., 195 CFU m^{-2} s^{-1} (from reference 9). In this presentation the source particles were assumed to be one size class.

Computer algorithm. A program was written in Applesoft BASIC to run on an Apple IIe computer with 128K of memory to compute the viable microbial concentration downwind from a point source. The major elements of the program were (i) temporal weather data input; (ii) calculation of the surviving airborne virus as a function of atmospheric conditions prevailing at a particular place in the downwind plume, using the previously defined polynomial equations; (iii) an estimate of the source strength; and (iv) calculation of the remaining viable virus after particle dispersion, particle deposition, and virus death (Fig. 2). The latter two inputs have been discussed; the former two consisted of weather data collected at the Eugene, Oregon, airport over 16 years starting in 1948. Hourly averages of temperature, RH, wind speed, and solar radiation for the months of July and December were used because these months represent the extremes of these independent variables at this location. These data are available from the Climatic Research Institute at Oregon State University, Corvallis.

RESULTS

The polynomial equations using the coefficients generated from the multiple regression to estimate composite airborne virus survival are given in equation 2 as a function of temperature, RH, and time and in equation 3 for solar radiation, RH, and time. Note that the only parameter common to both polynomial fits except for time, which is assumed identical in both, is RH, and it only expresses independent interactive effects of RH with temperature and solar radiation in equations 2 and 3, respectively. Although cubic terms were attempted in the fit, quadratic fits gave acceptable results with coefficients of determination (r^2) of >0.91.

$$\% \text{ Reovirus survival} = 0.99556425 + 0.00869311 \times \text{temperature (°C)} + 0.002246044 \times \text{time} - 0.000471046 \times \text{RH} \times \text{temperature} - (2.29743 \times 10^{-4}) \times \text{time} \times \text{temperature} - (2.40529 \times 10^{-4}) \times \text{time} \times \text{RH} - (6.8255 \times 10^{-5}) \times \text{temperature} \times \text{time} - (2.34539 \times 10^{-6}) \times \text{RH}^2 \times \text{time} + (4.88659 \times 10^{-6}) \times \text{temperature}^2 \times \text{time} + (5.22822 \times 10^{-6}) \times \text{RH}^2 \times \text{temperature} + (1.5648 \times 10^{-5}) \times \text{time}^2 \quad (2)$$

and

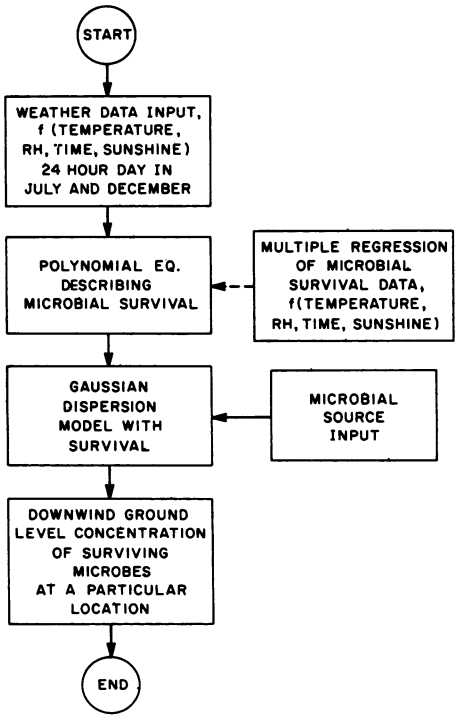

FIG. 2. Flow diagram of the dispersion model algorithm.

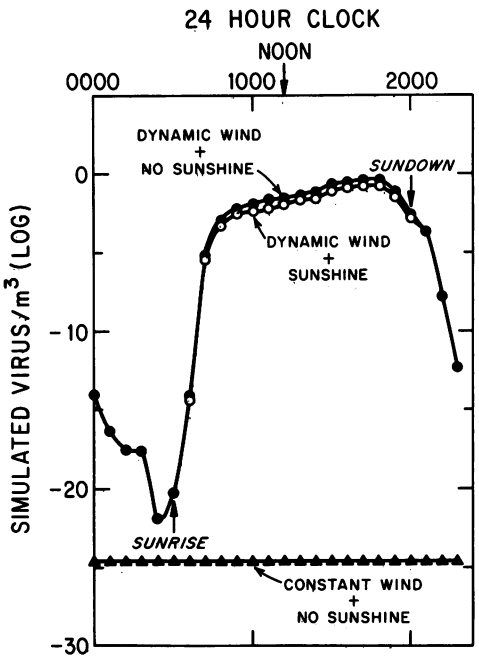

FIG. 3. Atmospheric dispersion model estimation of the concentration of a simulated virus at ground level 20 m downwind from an elevated source (0.1 m) under either dynamic wind speed (1 m s^{-1}) and no sunshine (0 W-h m^{-2} h^{-1}; ●), dynamic wind speed and sunshine (○), or constant wind speed and no sunshine (▲). Inert or nonviable particles plot slightly above points for dynamic wind speed and no sunshine. Environmental variables used to drive the model include 10-year hourly July means for wind speed, RH, temperature, and solar radiation in Eugene, Oregon. Microbial survival factors include RH, temperature, solar radiation, and time (after Mohr [dissertation] and Berendt et al. [1]). Ordinary summer day plume spread factors were used in the model.

$$\% \text{ Venezuelan equine encephalomyelitis virus survival} = 0.99307831 - (4.246503 \times 10^{-3}) \times \text{time} - (1.484 \times 10^{-5}) \times \text{solar radiation} \times \text{RH} - (4.38058 \times 10^{-4}) \times \text{solar radiation} \times \text{time} + (2.52052 \times 10^{-7}) \times \text{RH} \times \text{solar radiation} \times \text{time} + (1.69315 \times 10^{-6}) \times \text{time}^2 \times \text{solar radiation} + (9.82593 \times 10^{-7}) \times \text{solar radiation}^2 \times \text{time} \quad (3)$$

$$\text{Sum \% survival} = \% \text{ Reovirus survival} \times \% \text{ Venezuelan equine encephalomyelitis virus survival} \quad (4)$$

Simulation experiments using the model to compare microbial (virus) concentrations at ground level a constant distance downwind (20 m) from an elevated source, such as a plant canopy (0.1 m), when either wind speed, solar radiation, or virus input was held constant or allowed to vary, show how the atmospheric load could change over a 24-h period (Fig. 3). The dominance of the effect of wind speed for nearby sources is demonstrated by comparing the curves for wind speed held constant at 1 m s^{-1} and all independent variable input as dynamic variables (plots under "dynamic wind + no sunshine" points). The constant wind-speed curve has a lower concentration of virus than does the dynamic curve because the faster daytime wind speeds do not allow time for the virus to become inactivated before it reaches the sample point. The further downwind the sample point, the more travel time will pass and the more virus could be inactivated before sampling. The die-off effect would be magnified as the death rate of the microorganism increases.

The effect of the wind alone as a plume dilution factor is indicated by comparing the concentrations of downwind survivors with and without the death function (term D; equation 1) included in the simulations. At 20 m downwind the difference between these two simulations is only fractionally less with the death function included (see legend to Fig. 3).

Comparing the curves for 20 m downwind when solar radiation is dynamic and all other independent variables are held constant, including solar radiation at no sunlight, the model in Fig. 3 indicates that sunshine only slightly decreases the concentration of surviving composite virus during the daylight period. For sampling locations further downwind, travel time would be expected to decrease survival due to longer exposure to sunshine. At night the two curves give the same exposure to sunshine. At night the two curves give the same surviving concentration values. Simulations performed using July (summer) values, when there are few to no clouds at the measurement site, and December (winter) values, when it is almost always cloudy, are shown in Fig. 4. Comparing the curves in Fig. 4A and B shows a marked decrease in the summer versus winter nighttime values, presumably because the slower summertime night winds allow more time for the composite virus to die before reaching any downwind sampling point. Further, for this particular virus the maximum daytime survivor concentration is about the same for summer and winter, although there is a shift from approximately 1800 hours in summer to noon in winter. Both peak values occur at maximum daily wind speeds and where RH and temperature conditions that are similar would result in similar death rates.

DISCUSSION

A Gaussian plume model has been modified so that living particles from an elevated source die in the downwind plume as a result of prevailing dynamic atmospheric conditions at the source site. The model can be modified to include a distribution of particle sizes. The atmospheric conditions

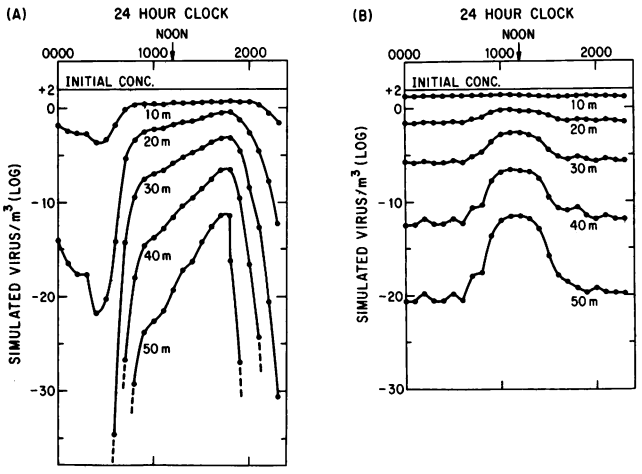

FIG. 4. Summer (A) and winter (B) atmospheric dispersion model estimation of the concentration of a simulated virus at ground level downwind from an elevated (0.1 m) continuous source under real dynamic conditions of wind speed, temperature, RH, solar radiation, and time, and constant virus source strength (100 virus m^{-3} s^{-1}). See the legend of Fig. 1 for details.

driving the variables for the particle survival include temperature, RH, solar radiation, and time in the plume. Other independent variables could easily be included if their mathematical relationships to survival in time were known. These might include gaseous air pollutants (7) such as carbon monoxide (3), sulfur dioxide (6), light wave bands, oxygen, etc.

The model illustrates the potential importance of wind as a dilution and survival factor in understanding the concentration of microbes in the atmosphere at any particular location. Turbulence is a usual characteristic of the atmosphere that dramatically affects the downwind concentration of airborne microbes whether or not their death rate is taken into account. This is very apparent in Fig. 4B, where the calculations indicate the microbes are diluted by a factor of 10,000 in the first 30 m downwind from the source. Furthermore, with respect to the wind as a factor in cell survival measurements, the faster the upwind speed, the less time for the death of cells to occur in their journey to the sampling location; i.e., the faster the wind speed, the more the sample concentration will resemble the source concentration.

Some aspects of the model characteristics and data methods are inadequate, and further research is necessary. It is obvious that data for all the appropriate interacting survival time relationships for any particular microorganism are not available. This information is needed to generate comprehensive polynomial survival equations. For many sources, more measurements must be made of their strengths and the conditions causing strength changes, e.g., weather, microbial variety, location, and phenology effects on plant canopy sources. The model itself needs refinement (i) to provide terms for area sources such as a crop field, (ii) to provide for continuous spread factors that change as weather conditions change, (iii) to increase the time resolution of the model, and (iv) to provide for eddy turbulence and abrasive injection of particles from sources such as plant canopies.

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