Models of the rhizosphere

II. A quasi three-dimensional simulation of the microbial population dynamics around a growing root releasing soluble exudates

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Abstract

A mathematical model is outlined which is capable of simulating the radial and vertical distribution of soluble carbon, and of microbial biomass and necromass around a root growing through the soil. An alternating-direction implicit finite difference method is used to simulate the movement of soluble C by diffusion and convection in the rhizosphere cylinder surrounding the root. Results are presented which suggest that microbial populations in the rhizosphere of a growing root may vary considerably with distance along the root with the precise distribution of soluble C and biomass depending on the pattern of exudate release along the root length.

Introduction

Any root growing in soil is surrounded by a cylinder of soil in which the microbial biomass is higher than that in the surrounding soil, with root-derived C, either in the form of soluble exudates, sloughed cells, or senescent root tissue, fuelling the biomass increase (Curl and Truelove, 1986). Because it is likely that the concentration of this C decreases with distance from the root surface, a similar gradient of microbial biomass is thought to exist across the rhizosphere. One of the most fundamental objectives in rhizosphere research is to estimate the diameter of the rhizosphere and the abundance and distribution of microbial biomass within it. Simulation models have been developed (Newman and Watson, 1977; Darrah, 1991) which suggest that the rhizosphere surrounding an individual segment of root is a very dynamic entity, with its diameter changing considerably during the lifetime of the root and with very marked changes occurring in both the total amount and distribution of microbial biomass within the rhizosphere.

The survival of individual species of microorganism within this immensely competitive and dynamic region is of great importance for the plant as some components of the rhizosphere microflora may be involved in mutualistic associations with the root, may be potentially pathogenic, or may affect the uptake of essential mineral nutrients from the soil. The success of many microbial inocula designed to affect the performance of the plant also depends to a large extent on their ability to colonize and survive in the rhizosphere, and it is therefore vital that our understanding of rhizosphere population dynamics is improved. The abundance of an individual microbial species within the rhizosphere may depend on a whole host of factors such as the spectrum and availability of C compounds re-
leased by the root, the organisms' competitive ability in using these compounds, the organisms' ability to migrate towards or along the growing root to maintain itself in an optimum environment, modifications to the physico-chemical environment induced by the root, and the number and selectivity of predatory species. To date no simulation models have attempted to simulate the rhizosphere in such detail.

The existence of the rhizosphere depends on the increased availability of C derived from the root and it would therefore seem reasonable to assume that the abundance and distribution of microorganisms will be controlled by the abundance and distribution of available C around the root. Therefore, one pre-requisite of any rhizosphere model has to be the ability to simulate changes in the radial and vertical distribution of root-derived C so that the distribution of the dependent microbiota along and around a length of root can be simulated. This type of three-dimensional model would also be necessary for predicting the chemotactic response of motile bacteria moving towards and along the root following a soluble C gradient (Gaworzewska and Carlile, 1982), or the migration of microbial predators feeding along a microbial biomass gradient in the rhizosphere (Clarholm, 1981).

Existing simulation models only simulate the changes in plant-derived and biomass C occurring with time in a single horizontal plane through the soil as the rate of C input into the plane changes during the lifetime of the root and so cannot be used to construct an accurate picture of how the rhizosphere changes in time and space.

The objective of this work was to develop a mathematical model which could simulate the dynamics of rhizosphere development around an individual growing root both in time and in space, and which would be capable of serving as a framework for the ultimate development of species-specific models of the rhizosphere.

**Development of the model**

The physical system simulated by the model consists of a isotropic cylinder of soil of length L, and radius \( r_b \). At the start of the simulation, the tip of a growing root is located at the centre of, and just touching the top of, this cylinder. The root itself is assumed to be a smooth cylinder of constant radius and devoid of root hairs. During the simulation, this root grows through the centre of the cylinder, eventually exiting through the plane at \( x = L \). As the root grows through the cylinder, it releases soluble organic compounds which will diffuse out into the soil and serve as a growth substrate for the native microbial biomass. All the C exuded by the root is assumed to be soluble and to be confined to the soil solution, where its diffusion can be described by a single diffusion coefficient. The rate of exudation is assumed to be concentrically isotropic and therefore the distribution of carbon around the root can be represented by any vertical cross-section taken through the centre of the cylinder. Hence the model is of a quasi 3-dimensional form in that only 2 spatial coordinates are required to simulate the changes occurring in the rhizosphere cylinder.

Figure 1 shows part of an imaginary grid superimposed on such a cross-section through the column, where each nodal point on the mesh represents a spatial position in the cylinder in terms of an i, j coordinate. The model simulates the changes in the C concentration at each of these nodal points. Three carbon pools are considered at each node by the model, comprising a soluble C pool; a biomass C pool; and a necromass C pool. The soluble C fraction is the only