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Research paper

Modelling fungal growth with fractional transport models

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ABSTRACT

Due to the network-shaped colony formed by the filamentous fungi, fractional operators are likely to capture the time-evolution of their biomass distribution. In this paper, a generalised fractional transport model is developed to simulate the colony growth of a wood-rot fungus, *Postia placenta*. The colony is described by two variables, active and inactive biomass. The active biomass corresponds to the tips and the "active points", responsible for biomass formation, while the inactive component represents the remaining biomass, which is assumed immobile. The fractional in time and space derivatives are applied to the active biomass to represent the spatial colonisation (i.e., tip movement). The proliferation of biomass (local densification of the network due to branching) is driven by a source term, while a portion of active biomass becomes inactive over time. The model is solved using an extended finite volume discretisation scheme and the accuracy is confirmed by comparison to an analytic solution obtained for the case where the source term is assumed linear. Next, the model parameters are identified for an optimized solution of the model that matches experimental observations well, indicating the suitability of the fractional operators for modelling biomass diffusion in a fungal colony. An interesting finding is that the best results are obtained when only anomalous diffusion in space (not time) is considered, which is probably related to the fractal dimension of mycelia. The spatial fractional–order derivative provides a unique ability to capture the non-local biomass diffusion of the fungal colony. We postulate that the fractional indices may provide a form of biological marker for the growth characteristics of different fungal species.

1. Introduction

Fungal mycelia are commonly used in solid-state fermentation for a range of diverse applications, such as enzyme, antibiotic or bio-fuel production [1]. They are also the main organisms responsible for the decomposition of wood and wood-based products, resulting in the damage of lumber structures and the reduction of the service life of the building [2]. Whether the concern is related to the optimization of the solid-state fermentation or protection of wood-based products from fungal

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decay, it is essential to estimate or predict fungal biomass growth behaviour, since the rate of degradation or enzyme production is tightly related to the quantity of biomass. However, due to the complex branched structure of the mycelial network, the determination of fungal biomass is challenging and pure experimental approaches can be quite time consuming [3,4]. During recent decades, mathematical models have attracted much attention and have made major contributions towards fungal research, which provides a supplementary and efficient tool for studying fungal development to gain a deeper insight into fungal growth mechanisms.

The continuous approach has been widely used to model spatio-temporal evolution of fungal biomass at the macroscopic scale. Most of the previous models applied normal reaction-convection equations to link fungal development with the behaviour of individual hyphae [5–9]. These models obeyed the fundamental mycelial growth rules, namely: i) a mycelium is formed by filaments called hyphae, which grow strictly through the extension of their apex called tips; ii) as a tip moves, it subsequently leaves an immobile hypha behind it [10]; iii) tips are generated by branching and are eliminated by anastomosis. In these models, tip density was regarded as a key variable to which the convection process and the source term were acted, and the biomass change was approximately proportional to the tip flux. As a result, fungal biomass was tightly related to the tip quantity. Recently, a reaction-diffusion model was proposed by Du et al. 2019 [11] and validated against a discrete model considering the basics strategy of mycelium development : tip elongation, branching, anastomosis [12]. A reaction-diffusion model is more predictive that a reaction-convection model that requires the colonisation direction to be known in advance. However, 3 independent continuous variables were required in Du et al. 2019 [11] for the model to match the results of the discrete model. Some other models have tried to directly calculate the fungal biomass evolution [13,14]. However, it was observed that the spatial biomass distribution was constrained by the normal diffusion process and this led to some significant differences compared with experimental results.

In this paper, a fractional reaction–diffusion model is applied to describe the spatio-temporal evolution of fungal biomass in consideration of the fractal nature of the mycelial networks [15–19]. Fractional calculus has been used in many fields of research to model anomalous diffusion, such as solute transport in porous media or particle diffusion in viscoelastic liquids [20–23]. However, it appears from the literature that relatively little work has been devoted to modelling macroscopic biomass development of fungi using fractional operators. One relevant study is describing fractal structures using a fractional dynamic model to show the impact of fractal dimension on fungal branching patterns [24]. In other biological fields, the fractional derivatives are used to model the anomalous diffusion of signals [25,26] or immune cells [27] in biological tissue characterised by high spatial heterogeneity, such as the human brain and heart. Among these studies, Estrada-Rodriguez et al. [27] related the time and space fractional indices to the levy distributions of the cell run distances and of the cell pause frequency. Another related field is understanding chemotactic aggregation of cellular slime mold by chemical attraction using the well-known Keller–Segel model [28]. This model was extended by Escudero [29] to use a space fractional operator of the Riesz type to describe a cellular population self–interacting chemotactically. The fractional Keller-Segel model was proposed as a way to overcome the inadequacies of the classical model in representing the population dispersal. Atangana and Alkahtabi [30] noted that the original Keller-Segel model was unable to describe memory effects, nor the movement of bacteria within different layers of the medium. This motivated a modification of the system by replacing the standard time derivative with the Caputo–Fabrizio fractional time derivative to overcome the singularity of the kernel. More recently, Azevedo et al. [31] introduced a time fractional variant of the Keller–Segel model. All these researches highlight the applicability of the fractional derivatives in biology.

In this work the suitability of a fractional reaction–diffusion model for simulating fungal biomass evolution is assessed by comparing the results against experimental data measured at the Laboratoire Génie des Procédés et Matériaux, CentraleSupélec. The colony extension of *Postia placenta*, a species of wood-rot fungus, has been observed and visualized using confocal microscopy [32] in Fig. 1. Colony images were obtained using the maximal intensity projection method at the five instants $t = 72,\ 120,\ 168,\ 240$ and $288\,h$ post inoculation in Fig. 1(A). Each colony image was divided into a series of rings with a gap of $60\,\mu m$. The normalized radial biomass density in each ring was calculated by averaging the mycelial network over radial increments. In Fig. 1(B), a small fragment of mycelium has been magnified. The red circles mark the active points on the hyphae at time instant t. As time progresses by an additional Δt, it can be observed that either the hyphae elongate, or new branches emerge from the active points. Note that the normalized biomass density is a dimensionless variable representing the ratio of the space occupied by hyphae to the total space.

The paper is organized as follows. In Section 2 we derive the anomalous transport model in terms of the concept of a fractional potential. The mycelial network is represented by two variables, active biomass that can move and proliferate, and inactive biomass which is assumed immobile and produces no biomass. Thus, the fractional diffusion and the source term apply only on the active biomass. The numerical solution strategy for this model using the finite volume method is described in Section 3 where we present a computational algorithm. To validate this numerical solution strategy, we also derive an approximate analytic solution. In Section 4, the numerical solutions computed from these two methods are compared when applying a linear source term. In Section 5 we compare the results of our model against experimental data, where excellent agreement is observed. The main findings of the work are summarized in Section 6 and future research work is proposed.