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The wood decomposition system and community diversity of fungi

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ABSTRACT

Fungi are critical agents of the global carbon cycle, however, our ability to link fungal community composition to ecosystem functioning is constrained by a limited understanding the wood decomposition rates of fungus. Here we examined the wood decomposition rate of fungus and the impact of fungal community diversity on the wood decomposing. To understand the relationship between the wood decomposition rate and the traits of fungi, we introduced 37 types of fungus into the wood decomposition system and set the growth rate and moisture tolerance of fungus as the explanatory variables. In addition, we constructed the competition, parasitic and symbiotic model based on Malthus-block growth comprehensive to analyze and predict the interactions between different fungus. The entropy weight-TOPSIS model was established to understand the biodiversity of fungus and obtain the relative dominance degree which can reflect the advantages and disadvantages of different fungus. The ARIMA model was used in five different environments to predict the impact of fungal community diversity on the overall efficiency of wood decomposing. Our research can not only help us to better understand the fungus community, but also significant for improving the quality of climate and the carbon cycle.

Keywords: Fungi; Malthus-Retarded growth; Entropy weight-TOPSIS; ARIMA

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1. Introduction

The carbon cycle is a vital component for life on the planet. As the primary decomposers of organic material in ecosystems, fungi are critical agents of the global carbon cycle. However, our ability to link fungal community composition to ecosystem functioning is constrained by a limited understanding of the factors accounting for different wood decomposition rates among fungi. There is still room for us to study the relationship between the traits of fungi and wood decomposing rate as well as the function of diversity of fungi community in the ecosystem.

The author of a recent study on fungal wood decomposition identified the fungal traits that determine the decomposition rate and revealed the relationship with some traits of fungi^[1]. Among these traits, two important traits are moisture tolerance and growth rate. In this paper, we still use these two traits and further study the interaction of different fungi and their sensitivity to the environment. This leads to the study of the decomposition system of wood

fiber by fungi, which is different from animals and plants, fungi are more sensitive to litter and environment, and the information of fungal community is more different from that of animals and plants^[2]. The impacts of community diversity on the wood decomposing and ecosystem are also worth exploring.

In this paper, we focus on the relationship between the traits of fungi and the wood decomposing rate, and impact of the diversity of fungal community on the wood decomposing efficiency. We construct a fungal wood decomposition system to explore the laws and characteristics of fungal decomposition activities, considering the interactions and strains combination. Our research can provide some meaningful reference for studying fungus' traits and their relationship with the wood decomposing rate and the diversity of fungal in the ecosystem, which is important to understand the laws and improve the quality of climate and carbon cycle. The research route of this paper is as given in Fig. 1.

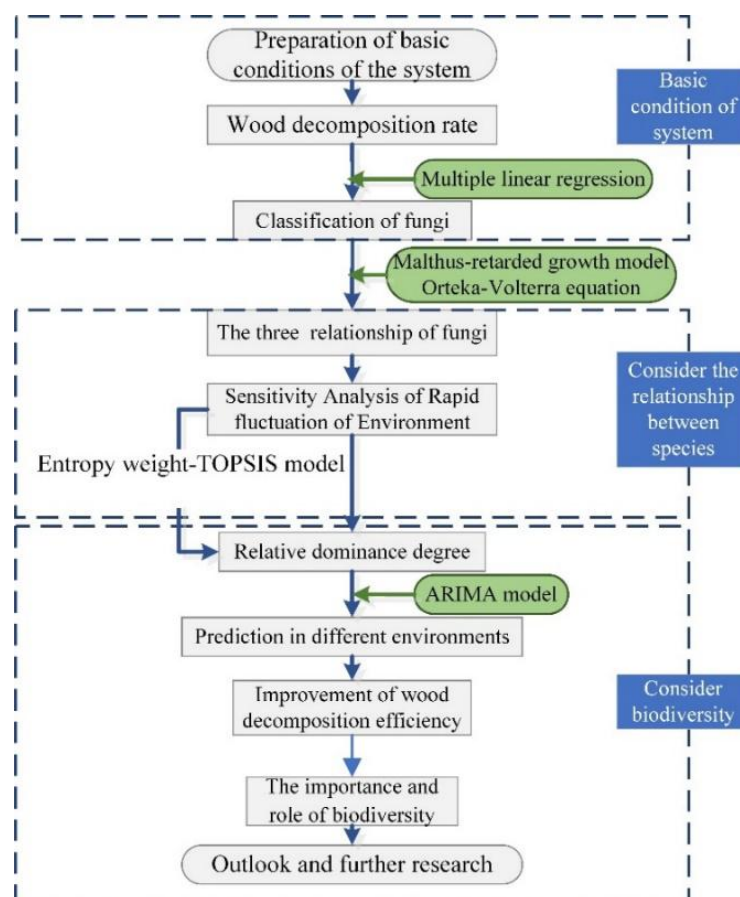


Fig. 1 The research route of this paper

2. Establishment of fungal decomposition system

Based on literature data and theories [3, 4], we converted the relationship between growth rate and moisture resistance and wood decomposition rate into a regression function for solving decomposition rate on different factors such as temperature, humidity, competition

ranking, and water niche width, etc. Then the decomposition rate of wood of various fungi will be calculated and the establishment of the basic decomposition system model will be completed. The input and output factors and the process of establishing the system are shown in the Fig. 2.

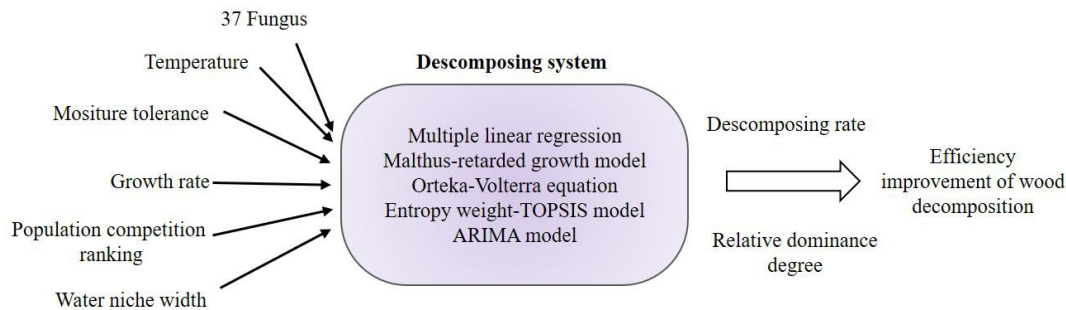


Fig. 2 Wood decomposition system

2.1 Basic conditions of the system

The establishment of any system requires certain conditions, so does the wood decomposition system^[5]. Therefore, we prepared the following basic system conditions to ensure the integrity of the system before building a multi-group fungal decomposition system. The composition of the decomposition system consists of two parts: non-biological components and biological components. Non-biological components refer to non-biological substances and energy such as sunlight, air, moisture and minerals. The biological components include

producers and decomposers. In our paper, the producers are wood and the decomposers are fungus.

2.1.1 The data of fungus in the system

In order to establish the basic wood decomposition system, we introduced the fungal data based on Daniel S. Maynard's study on the characteristics of saprophytic fungi^[2], which included 23 unique strains of Basidiomycetes (37 isolated fungus) collected from the North America. We number them separately and their stains are as shown in Fig. 3.

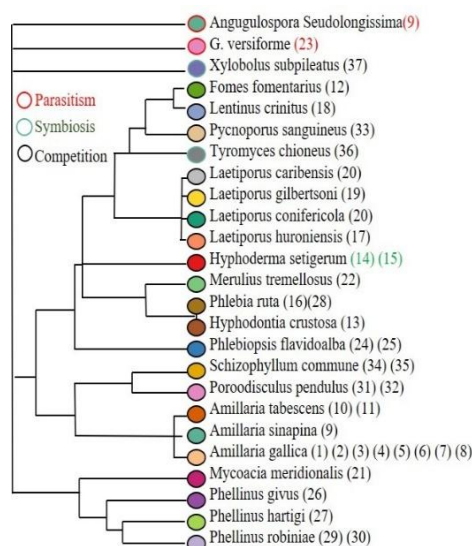


Fig. 3 37 basidiomycetes isolates

2.1.2 Competition resource for fungus

When the supply of resources is limited, the biological competition in the ecosystem is mainly manifested as the competition of resources. In the fungal system, the main competitive resources are single-source bionutrient carbon,

host root and limited space for living [6]. Different fungi form different fungal groups will compete for limited resources. The following diagram shows the competition and interaction of fungi with different traits (Fig. 4).

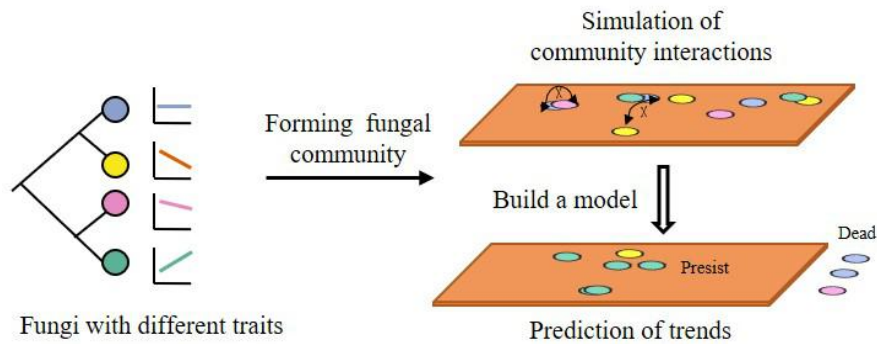


Fig.4 Diagram of the competition and interaction of fungi

2.2 Wood decomposition rate based on multiple regression

The prediction of wood decomposition by fungi can be improved based on the character analysis of fungi, thus the establishment of decomposition system should start with it. We select the moisture tolerance and growth rate as two important traits of fungi and let the decomposition rate of the decomposition

$$\sum_{i=1}^n x_{1,i} = \sum_{i=1}^n f(T_{i,t}, H_{i,t}) \quad (1)$$

Where $T_{i,t}$ is the temperature (°C) and $H_{i,t}$ is the water potential (MPa) of fungi i at time t . The functional relationship between wood

$$D = \sum_{i=1}^n f(x_{1,i}) = \sum_{i=1}^n a(x_{1,i})^b, \text{ where } a \text{ and } b \text{ are constants.} \quad (2)$$

For moisture tolerance, Daniel S. Maynard has defined moisture tolerance as the difference between the competitive ranking R_i of fungi

$$\sum_{i=1}^n x_{2,i} = \sum_{i=1}^n (R_i - W_i) \quad (3)$$

And the relationship between the decomposition rate and moisture tolerance can also be

$$D = \sum_{i=1}^n f(x_{2,i}) = \sum_{i=1}^n px_{2,i} + q, \text{ where } p \text{ and } q \text{ are constants.} \quad (4)$$

Through consulting the data, the decomposition rate of wood is affected by both growth rate and moisture resistance, therefore the growth rate and moisture resistance can be taken as

system be D , which is controlled by the extension rate $x_{1,i}$ ($\text{mm} \cdot \text{day}^{-1}$) and moisture tolerance $x_{2,i}$ of fungi. Where i is the i numbered fungi, $i=1,2,\dots,n$ and n is the number of fungus's strains. According to the characteristics of saprophytic fungi by Daniel S. Maynard, the extension rate is closely related to temperature and humidity, that is:

decomposition rate and growth rate of fungi at different temperatures can be fitted by MATLAB, that is:

and its water niche width W_i , and both values can be normalized, that is:

fitted, that is:

independent variables, and the functional expression of wood decomposition rate can be obtained by using the method of multiple linear regression, that is:

$$D = \sum_{i=1}^n f(x_{1,i}, x_{2,i}) = \sum_{i=1}^n f(T_{i,t}, H_{i,t}, R_i, W_i) \quad (5)$$

The functions of wood decomposition rate on the growth rate and moisture resistance were fitted respectively, that is:

$$D=3.932x_{1,i}^{0.5141}; D=0.8323x_{2,i}+1.882 \quad (6)$$

The relationship between wood decomposition rate (the percentage of mass loss within 122 days after logarithmic conversion) and domi-

nance / moisture tolerance trade-off, and the relationship between extension rate ($\text{mm} \cdot \text{day}^{-1}$) and decomposition rate were plotted (Fig. 5).

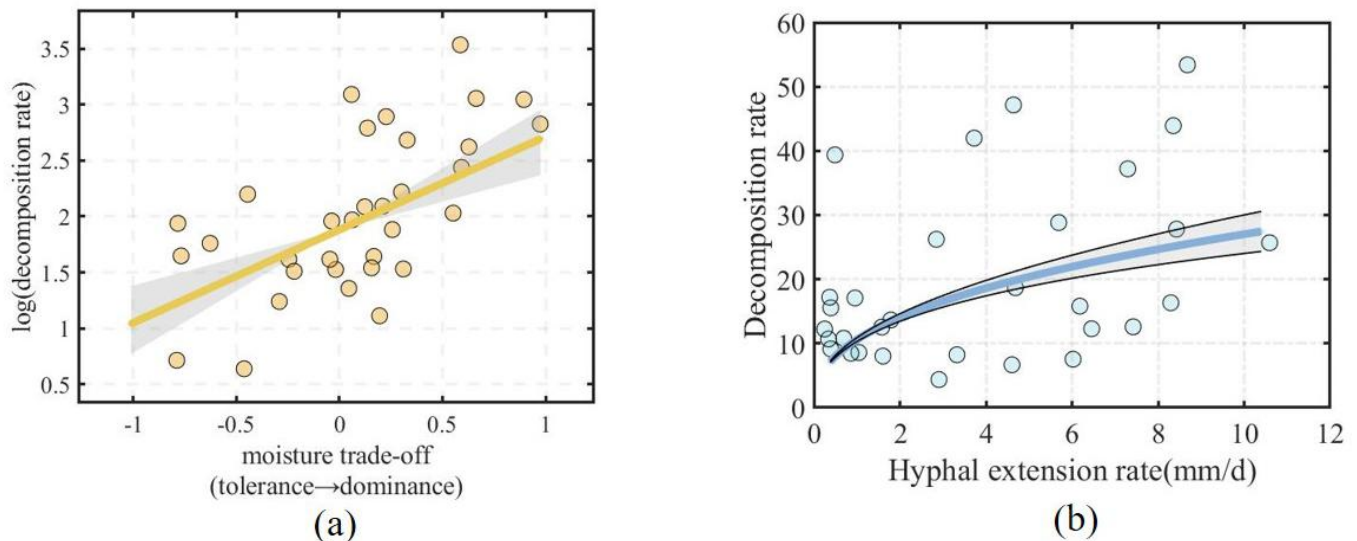


Fig. 5 (a) The relationship between wood decomposition rate and dominance / moisture tolerance trade-off, (b) The relationship between extension rate ($\text{mm} \cdot \text{day}^{-1}$)

3. The correlation between populations

In view of the specific environment in the decomposition system, we combine the relevant characteristics of 37 strains of fungi and consider the relationships of competition, parasitism and symbiosis as shown in the Fig. 6. The models based on the change of the number of fungus were established respectively,

and then the effect of interspecific relationship was determined. We considered the dynamic change of the interaction of fungus and introduced the fluctuating environmental variables in the short-term and long-term trends, and the corresponding weather patterns and atmospheric trends.

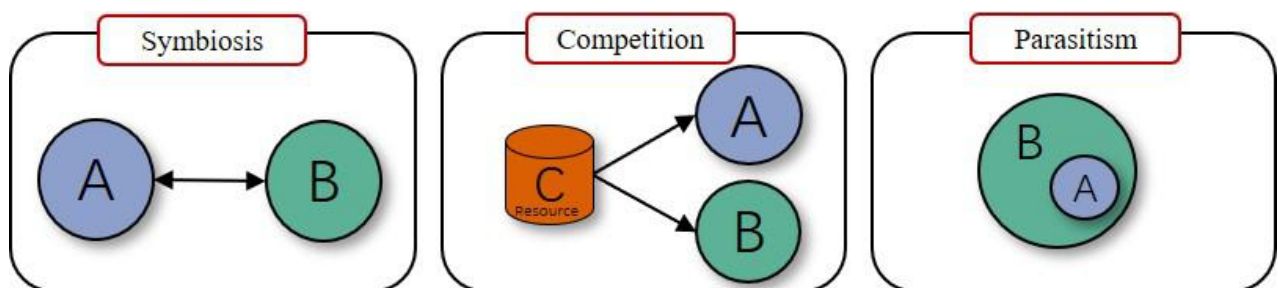


Fig. 6 The three relationships of fungi

3.1 Systematic clustering of fungal populations

In order to examine the interaction of fungus with different traits in the decomposition system, we focused on the growth rate and moisture

tolerance of fungus, which were used as variables for systematic cluster analysis of 37 strains of fungi. We use the SPSS software to solve the cluster pedigree, which is as given in Fig. 7.

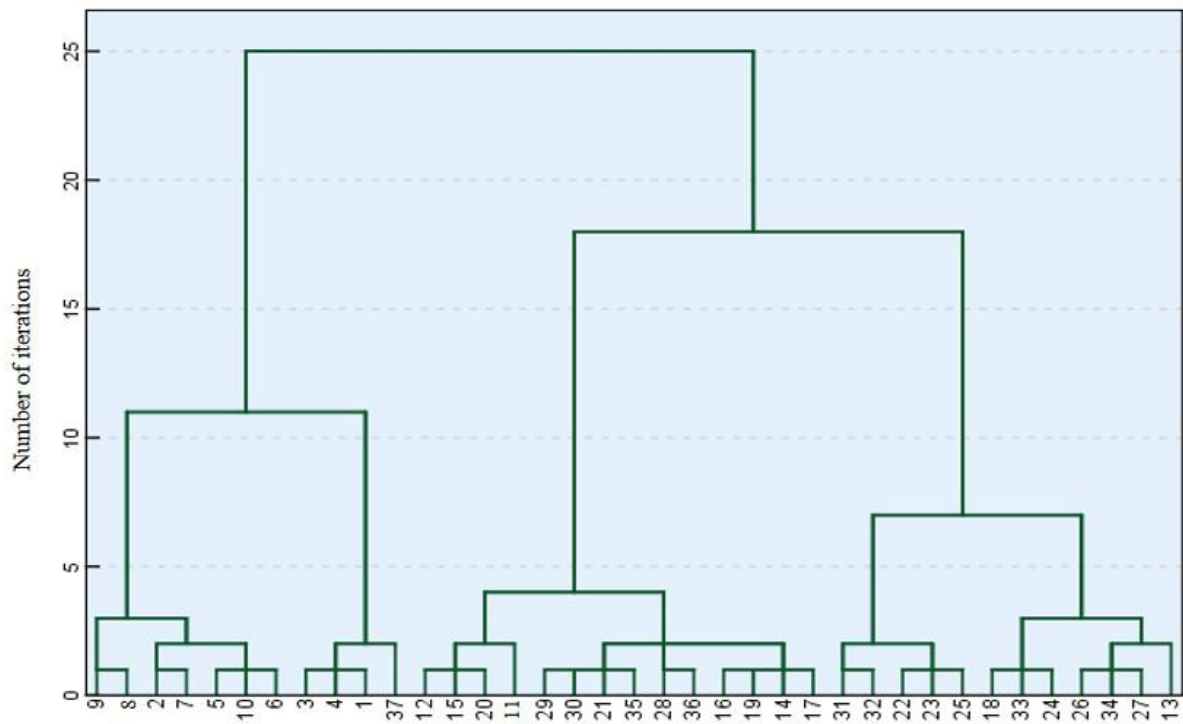


Fig. 7 The cluster pedigree of 37 strains of fungi

The clustering results showed that the strains of fungus numbered 1-10 and 37 were clustered into the first group, and the others were the second group. Combined with the extension rate (growth rate) and moisture tolerance (mapping the data to $[-1, 1]$ interval, the closer

to -1, the better the moisture resistance, the better the moisture resistance, the worse the moisture resistance), the classification and traits of both groups can be analyzed and compared as the following Fig. 8.

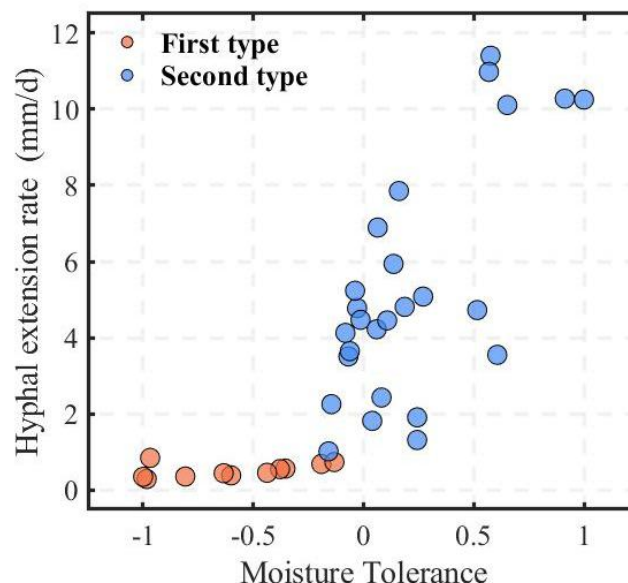


Fig. 8 The scatter comparison diagram of clustering results

The first group of fungus has higher moisture tolerance and lower growth rate, while the second type has lower moisture tolerance and higher growth rate. Combined with the previous research [7, 8], the first type of fungus have

higher decomposition rate of wood, stronger ability to obtain resources and stronger relative competitiveness. Therefore, we can call the first type of fungi as “the strong competitive fungus” and the second type of fungi as “the weak

competitive fungus”.

3.2 The Malthus-blocking growth comprehensive prediction

In view of the relationship of the number of fungus in the decomposition system and the influence of short-term trend and long-term trend, the Malthus-blocking growth comprehensive model was established.

$$\begin{cases} \frac{dp_i(t)}{dt} = r_i p_i(t) \\ p_i(t_0) = N_{i,0} \end{cases} \quad (1)$$

Where r_i , $p_i(t)$, $N_{i,0}$ is the daily growth rate of fungi i , the population number of fungi i at time t and the initial population number of fungi i at time t_0 .

3.2.2 Retarded growth model

The retarded growth model, also known as the logistic model, was proposed by the Dutch

3.2.1 Malthus model

Malthus population model, also known as exponential growth model, is suitable for the prediction of short-term trends [9]. If the model assumes that the growth rate of the first strain remains unchanged, the specific model is as follows:

biological mathematician Verhulst in the middle of the 19th century [10]. It can generally describe the changing law of population and the number of many strains, and is suitable for long-term prediction. If r_i' is the daily growth rate of the number of fungi, the specific model is as follows:

$$\begin{cases} \frac{dp_i(t)}{dt} = r_i' \left(1 - \frac{p_i(t)}{N_{i,m}}\right) p_i(t) \\ p_i(t_0) = N_{i,0} \end{cases} \quad (1)$$

Where $N_{i,m}$ is the maximum number of fungi that can be accommodated by fungi i under natural resources and environmental conditions.

3.2.3 Malthus-retarded growth comprehensive prediction model.

Then combine above two models and Malthus and blocking growth models are used for long-term prediction, G is the time discontinuity point, in which the prediction of Malthusian model is equal to that of blocking growth model. The number of fungal strains before the time break point G is predicted by Malthusian model

while the number of fungal strains after the break point G is predicted by blocking growth model.

3.3 Competitive relationships among populations

In view of the change of the number of fungus in the population competition, the idea of interspecific competition can be introduced based on the blocking growth model. Assuming that the two populations A (numbered A) and B (numbered B) in the system are interspecific competition, the population growth models of populations A and B are as follows:

$$\begin{cases} \frac{dp_A(t)}{dt} = r_A' \left(1 - \frac{p_A(t)}{N_{A,m}} - \frac{\sigma_B p_B(t)}{N_{B,m}}\right) p_A(t) \\ p_A(t_0) = N_{A,0} \end{cases} \quad (1)$$

$$\begin{cases} \frac{dp_B(t)}{dt} = r_B' \left(1 - \frac{p_B(t)}{N_{B,m}} - \frac{\sigma_A p_A(t)}{N_{A,m}}\right) p_B(t) \\ p_B(t_0) = N_{B,0} \end{cases} \quad (2)$$

Where $\frac{\sigma_B p_B(t)}{N_{B,m}}$ is the amount of food consumed by population B, which is σ_B times as the amount of food consumed by population A. $\frac{\sigma_A p_A(t)}{N_{A,m}}$ is the amount of food consumed by

population A, which is σ_A times as the amount of food consumed by population B.

For the values of σ_A and σ_B , the following relations can be obtained through simulation training.

$$V_A = \mu_1 \frac{T_{A,t}}{T_{B,t}} + \mu_2 \frac{H_{A,t}}{H_{B,t}}, V_B = \frac{T_{B,t}}{T_{A,t}} + \mu_2 \frac{H_{B,t}}{H_{A,t}} \quad (3)$$

$$\sigma_B = \eta_1 \frac{R_B}{R_A} + \eta_2 V_A + \eta_3 \delta, \sigma_A = \frac{R_A}{R_B} + \eta_2 V_B + \eta_3 \delta \quad (4)$$

Where V_A and V_B are environmental variables, which represent the environmental disturbance effect of fungi A on fungi B and the effect of fungi B on fungi A. $\mu_1, \mu_2, \eta_1, \eta_2, \eta_3$ are different partial coefficients. δ is a

disturbance term of interspecific competition, and its value should consider the following three cases:

Case1: Fungi A and B are highly competitive strains:

$$\delta = 0 \quad (5)$$

Case2: Fungi A and B are weakly competitive strains:

$$\delta = 0 \quad (6)$$

Case3: Fungi A is highly competitive strains, while B is weakly competitive strains, and vice versa:

$$\delta_A = 1.31, \delta_B = 0.76 \quad (7)$$

3.4 Parasitic relationship among populations

In view of the parasitic relationship of the population, the fungi 9 (*Angugulospora Seudolongissima*) and fungi 23 (*G. versiforme*) in the system were taken as examples. In the

parasitic relationship, the fungi 9 is the parasitic fungi and fungi 23 is the parasitic fungi. Based on the retarded growth model, the Lotka-Volterra equation [11] is introduced and the population growth models of fungi 9 and fungi 23 are as follows:

$$\begin{cases} \frac{dp_9(t)}{dt} = r'_9 \left[1 - \frac{p_9(t)}{N_{9,m}} - \lambda_{23} p_{23}(t) \right] p_9(t) \\ p_9(t_0) = N_{9,0} \end{cases} \quad (1)$$

$$\begin{cases} \frac{dp_{23}(t)}{dt} = r'_{23} \left[-1 + \frac{p_{23}(t)}{N_{23,m}} + \lambda_9 p_9(t) \right] p_{23}(t) \\ p_{23}(t_0) = N_{23,0} \end{cases} \quad (2)$$

Where the proportional coefficient λ_{23} is the parasitic destructive ability of fungi 23 to fungi 9, and the proportional coefficient λ_9 is the feeding ability of fungi 9 to fungi 23.

3.5 Symbiotic relationship among populations

According to the parasitic relationship of fungi, the idea of symbiosis among populations can

be introduced based on the retarded growth model. Take fungi 14 and fungi 15 in the system as examples. In this symbiotic relationship, fungi 14 and 15 are white rot fungi (*Hyphoderma setigerum*), so the number growth model under the symbiotic relationship is as follows:

$$\begin{cases} \frac{dp_{36}(t)}{dt} = r'_{36} \left(1 - \frac{p_{36}(t)}{N_{36,m}} + \frac{\sigma_{36} p_{37}(t)}{N_{37,m}} \right) p_{36}(t) \\ p_{36}(t_0) = N_{36,0} \end{cases} \quad (1)$$

$$\begin{cases} \frac{dp_{37}(t)}{dt} = r'_{37} \left(1 - \frac{p_{37}(t)}{N_{37,m}} + \frac{\sigma_{37} p_{36}(t)}{N_{36,m}} \right) p_{37}(t) \\ p_{37}(t_0) = N_{37,0} \end{cases} \quad (2)$$

The above three relationships are based on the blocking growth model, and the Malthus model can also be analyzed in the same way.

3.6 The dynamic characteristics of interacti-

on

The three relationships can be obtained by solving the problem, as shown in the following Fig. 9.

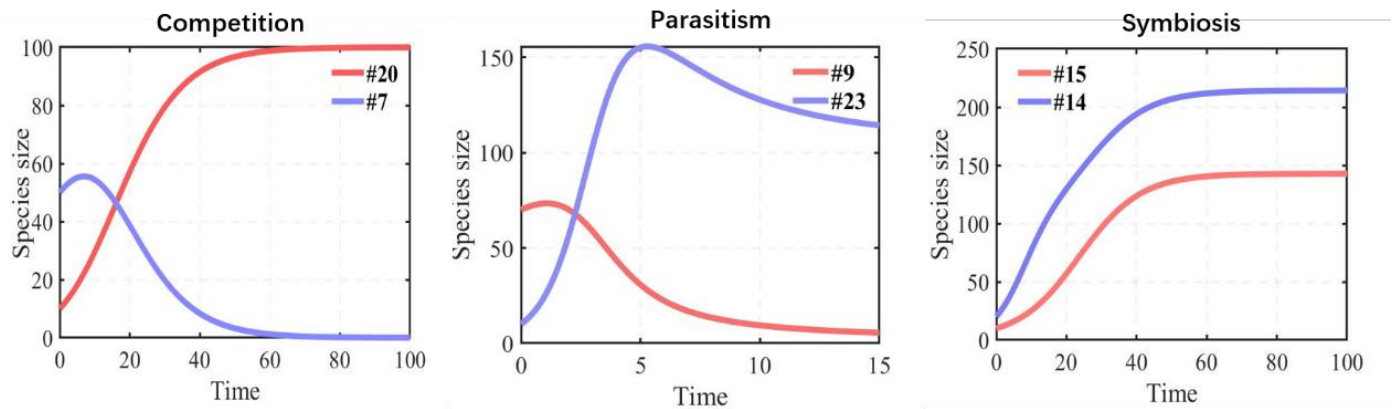


Fig. 9 The relationships of competition, parasitism and symbiosis

For the competitive relationship, there is an equal initial number of strains 20 and 17, and the number of 20 more competitive strains increases over time, and finally reaches the environmental capacity in about 80 days as shown in Fig. 9 (a). On the other hand, the number of strain 7 with relatively poor competitiveness showed an increasing trend in the first 5 days, because strain 7 was less affected by the competition of strain 20 at that time, and then with the increasing number of strain 20, the competitive pressure on strain 7 increased and the number of strain 7 began to decline on the 6th day, and finally went to extinction.

For the parasitic relationship, the number of strain 9 increased in the first 3 days, and then decreased on the 4th day and gradually died out due to the parasitic destruction of strain 23, while strain 23 increased rapidly from the initial number of 12 to a peak of 152 on the 5th day, and then the source of nutritious strains decreased gradually due to the decrease of the number of host strain 9 as shown in Fig. 9 (b).

For the symbiotic relationship, strain 15 and strain 14 grew steadily at first and then tended to be stable, reaching their respective environ-

mental capacity as shown in Fig. 9 (c).

4. The effect of community diversity

Considering the prediction of the relative advantages and disadvantages of each strains and possible persistent strains combination, we first evaluate the relative advantage of each strains to provide a data basis for the prediction. Meanwhile, the number of stains is an important basis for judging whether fungi is possible to persist, and the combination of strains is considered ^[12]. On this basis, different environmental variables with time are changed to predict in a variety of environments.

4.1 Evaluation of relative dominance of single population

4.1.1 Determination of Indicators

In order to determine the relative advantages and disadvantages of strains or strains combinations, this paper constructs the relative dominance evaluation scores of strains or strains combinations and selects seven indexes, which are competitive ranking, temperature, humidity, moisture tolerance, growth rate, relative population number (the ratio of the number of the population to the number of systematic communities) and the wood decomposition rate (Fig.10).



Fig.10 The indicator selection diagram

4.1.2 Evaluation matrix

Construct an evaluation matrix R with n rows and m columns. The element r_{ij} in the matrix represents the index value of the j -th index

corresponding to the i -th fungus population, where $i=1, 2, \dots, n, j=1, 2, \dots, m; n=37; m=7$, then R is:

$$R = [r_{ij}] = \begin{bmatrix} r_{11} & r_{12} & \cdots & r_{1m} \\ r_{21} & r_{22} & \cdots & r_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ r_{n1} & r_{n2} & \cdots & r_{nm} \end{bmatrix} \quad (1)$$

4.1.3 Normalization and standardization

For the normalization of data, this paper performs normalization processing on the interval index temperature and humidity, that is,

using the matrix normalization processing formula to transform interval data into extremely large data, which can facilitate our unified index evaluation, that is:

$$M = \max\{L - \min\{r_{ij}\}, \max\{r_{ij}\} - H\} \quad (1)$$

$$r_{ij}^{(1)} = \begin{cases} 1 - \frac{L - r_{ij}}{M}, & r_{ij} < L \\ 1, & L \leq r_{ij} \leq H \\ 1 - \frac{r_{ij} - H}{M}, & r_{ij} > H \end{cases} \quad (2)$$

Where L is the lower limit of the optimal temperature or humidity interval and H is the upper limit of the optimal temperature or humidity interval. Here the optimal temperature interval is $[22^\circ\text{C}, 36^\circ\text{C}]$, and the optimal humidity interval is $[-1\text{MPa}, -0.03\text{MPa}]$. $\min\{r_{ij}\}$ is the

maximum value in the j -th index data, r_{ij} is the value of the i -th fungi with the j -th index before normalization and $r_{ij}^{(1)}$ is the value of the i -th fungi with the j -th index after normalization. For data standardization, we use the calculation formula of matrix standardization to standardize

the normalized data to eliminate the influence of different index dimensions on the model, that is:

$$z = \frac{r_{ij}^{(1)}}{\sqrt{\sum_{i=1}^n [r_{ij}^{(1)}]^2}} \quad (3)$$

4.1.4 Entropy weight method

The information entropy of the index reflects the importance of the index in the rating of relative dominance of strains. The greater the entropy value, the greater the amount of information contained and importance in the indicator [13].

$$p_{ij} = \frac{p_{ij}}{\sum_{i=1}^n p_{ij}} \quad (1)$$

Where $i=1, 2, \dots, n; j=1, 2, \dots, m$

Calculate the information entropy e_j , the entropy weight a_j of each indicator, that is: information utility value d_j , and normalize the

$$e_j = -\frac{1}{\ln 37} \sum_{i=1}^{37} p_{ij} \ln(p_{ij}) \quad (2)$$

$$d_j = 1 - e_j \quad (3)$$

$$A_j = \frac{d_j}{\sum_{j=1}^m d_j} = [a_1, a_1, \dots, a_j, \dots, a_m] \quad (4)$$

Where $i=1, 2, \dots, n; j=1, 2, \dots, m$

4.1.5 TOPSIS

Assume the decision matrix is Z , that is:

$$Z = [z_{ij}] = \begin{bmatrix} z_{11} & z_{12} & \cdots & z_{1m} \\ z_{21} & z_{22} & \cdots & z_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ z_{n1} & z_{n2} & \cdots & z_{nm} \end{bmatrix} \quad (1)$$

Where z_{ij} represents the normalized value of under the j -th index.

the corresponding the i -th bacterial strains Define maximum

$$Z^+ = (Z_1^+, Z_2^+, \dots, Z_m^+) = (\max\{z_{11}, z_{21}, \dots, z_{n1}\}, \max\{z_{12}, z_{22}, \dots, z_{n2}\}, \dots, \max\{z_{1m}, z_{2m}, \dots, z_{nm}\})$$

Define minimum

$$Z^- = (Z_1^-, Z_2^-, \dots, Z_m^-) = (\min\{z_{11}, z_{21}, \dots, z_{n1}\}, \min\{z_{12}, z_{22}, \dots, z_{n2}\}, \dots, \min\{z_{1m}, z_{2m}, \dots, z_{nm}\})$$

Define the distance between the $i(i=1, 2, \dots, n)$ numbered strain and the maximum

$$D_i^+ = \sqrt{\sum_{j=1}^m A_j (Z_j^+ - z_{ij})^2}$$

Define the distance between the $i(i=1, 2, \dots, n)$ numbered strain and the minimum

$$D_i^- = \sqrt{\sum_{j=1}^m A_j (Z_j^- - z_{ij})^2}$$

Then the unnormalized relative advantage degree S_i of number $i(i=1, 2, \dots, n)$ can be calculated, that is:

$$S_i = \frac{D_i^-}{D_i^+ + D_i^-} \quad (2)$$

The normalized relative advantage $\hat{S}_i^{(1)}$ is:

$$\hat{S}_i^{(1)} = \frac{S_i}{\sum_{i=1}^n S_i} \quad (3)$$

4.2 Evaluation of relative dominance of strains combination

For strains combinations, we consider the

$$C_k = \{c_k\} \quad (1)$$

Where $\{c_k\}$ is the set of all populations under the combination of those strains. Under the strains combinations of different diversity, we need to consider the discrimination of the

$$B_k = \sum_{t=i}^{50} \left(\int_{t=0}^1 p_k(t) - \int_{t=0}^1 d_k \min \{P_k\} \right) \quad (2)$$

$$\begin{cases} B_k \leq 0, \text{unlikely to persist} \\ B_k > 0, \text{likely to persist} \end{cases} \quad (3)$$

Where B_k is the discriminant variable and $p_k(t)$ is the total number of communities of the k strains combination. d_k is the number of strains in the community and $\min \{P_k\}$ is the number of populations with the smallest number in the community.

4.3 Prediction of strains superiority and inferiority

Based on the Entropy weight-TOPSIS model, we can calculate the relative dominance of strains combinations under different groups and different diversity of dominance in 50 days, and

$$y_t = u + \sum_{i=1}^p g_i y_{t-i} + \epsilon_t \quad (1)$$

Where y_t is the predicted value of the time series, u is the constant, ϵ_t is assumed to be the random value (the average is equal to 0 and the standard deviation is a constant), and g_i is the correlation coefficient.

By moving average of the error items in the AR

$$y_t = u + \epsilon_t + \sum_{i=1}^q \theta_i \epsilon_{t-i} \quad (2)$$

Where θ_i is the correlation coefficient of MA. After the comprehensive application of the above three methods, we get the model ARIMA. The parameter q in the model can be obtained from the autocorrelation function (ACF) graph, which shows that the data is affected by the

diversity of different strains combinations. Then the k -th strains combination is:

sustainable existence of the strains combination according to the changing trend of the number of strains combinations, that is:

predict the time series. After comprehensive consideration of accuracy and the principle of BIC, the ARIMA model is selected for prediction. The ARIMA model is mainly composed of autoregressive (AR) model, moving average (MA) model [14]. The AR model can describe the relationship between the value of the current time and the value of the historical time, and use the data on the historical time of the variable to predict its current and subsequent time values. The mathematical definition formula of AR model is:

model, the MA model can be calculated, which can effectively eliminate the random fluctuations in the prediction and improve the robustness of the model. The mathematical definition formula of the MA model is:

data between time $t-i$. The parameter d is the difference order of the model, which aims to stabilize the data and extract data features. The parameter p in the model is the autoregressive order, which is obtained by the partial autocorrelation function (PACF) graph.

In summary, ARIMA model converts the non-stationary data into the stationary data on the time series, and then uses the time variables to regress and predict the lag value of the data and the random error term. The mathematical definition of the ARIMA model is:

$$y_t = u + \sum_{i=1}^p r_i y_{t-i} + \epsilon_t + \sum_{i=1}^q \theta_i \epsilon_{t-i} \quad (3)$$

4.4 The effect of environment variables

As fungus are part of the ecosystem, their traits and wood decomposing ability are affected by the environment. Here we considering the difference of environment, especially the difference of environmental variables temperature

and humidity, different environments of arid, semi-arid, temperate, arboreal and tropical rain forest. The predictions of different climate and strains combinations are as shown in Fig. 11 and Fig. 12.

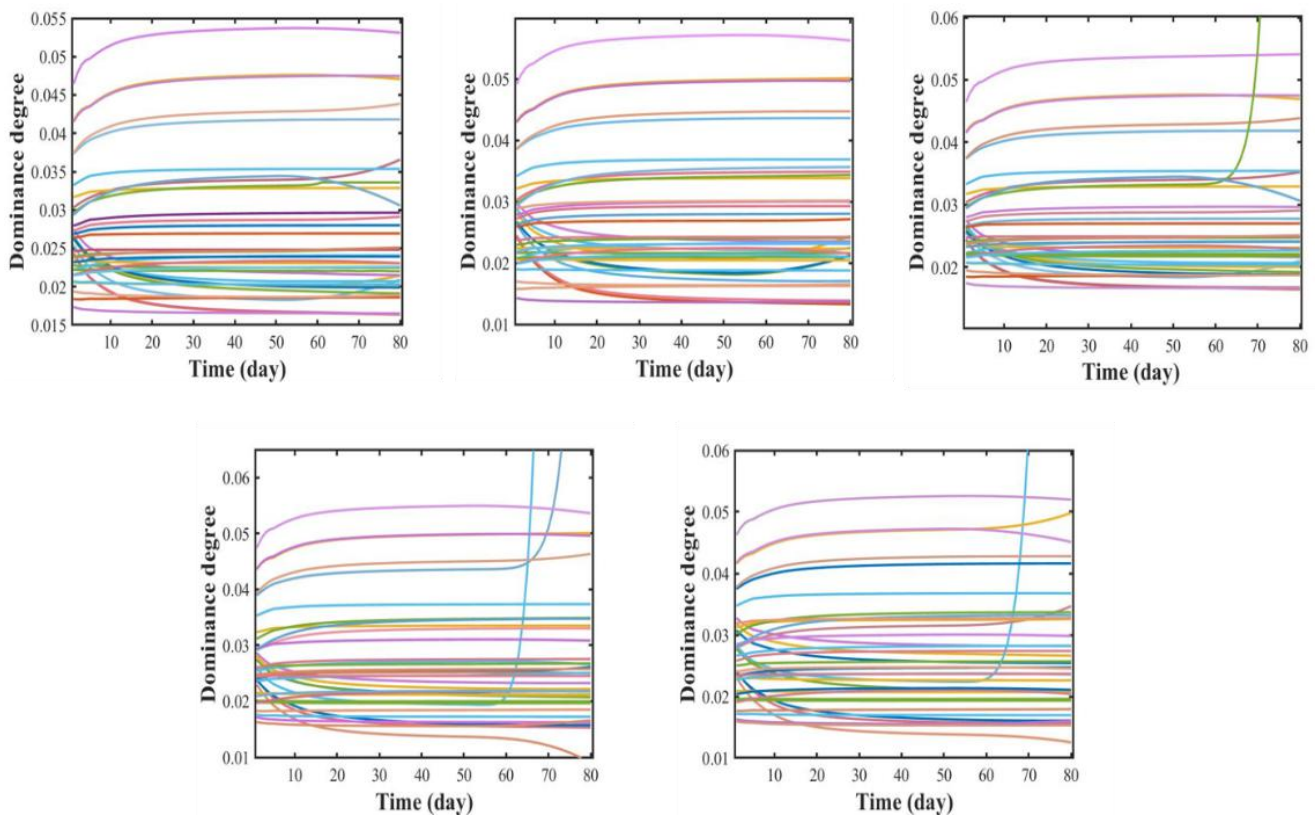


Fig. 11 Prediction of different climates

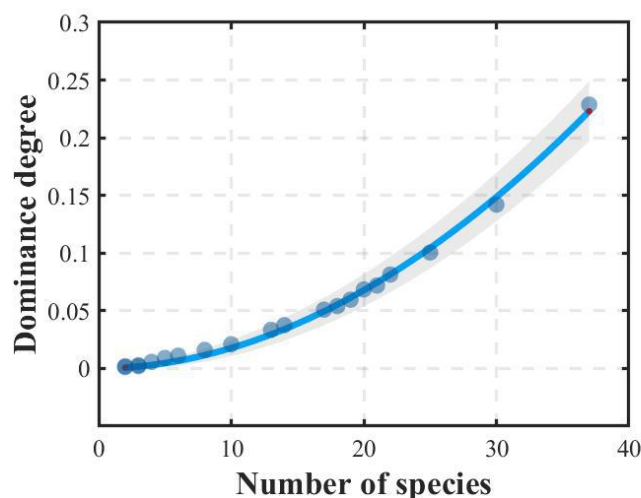


Fig. 12 Prediction of strains combination

4.5 The effect of community diversity

We discussed the evaluation and prediction of the relative dominance of strains combinations under different diversity, one of which is the wood decomposition rate. Here we describe the

$$D = \sum_{i=1}^n D_i' \quad (1)$$

$$Q = \frac{D}{\sum_{i=1}^n D_i} \quad (2)$$

Where D_i' is the decomposition rates of fungi i in consideration of community diversity and D_i is the decomposition rates of fungi i without community diversity, both are the percentage of wood quality loss in 122 days after logarithmic conversion.

These are also important factors that affect the wood decomposition rate of fungi, which can be concluded as follows:

First, the diversity of fungal community has an impact on the decomposition system, especially the overall efficiency of the decomposition of wood. As the community with various strains will bring different species combinations for the population and form large communities or small communities [15]. In this decomposition system, there are three inter-strains relationships: competition, parasitism and symbiosis. Based

efficiency of the decomposition system based on the model. The formulas for calculating the overall efficiency D and the degree of improvement of wood decomposition efficiency Q of the system are:

on these relationships, the growth pattern of each strains has been changed.

Second, the number of the population is an important factor of the relative dominance of the population, which affects the survival advantage and the decomposition rate of the population [16]. It can be seen from the Fig. 13, the decomposition rate of some specific species combinations has been significantly improved.

Third, the environmental variables, such as the temperature and humidity affect the adaptability of different strains and the decomposition rate of wood. Changes in environmental variables increase the fluctuation of environmental variables, promote the coexistence of species, improve the stability of the ecosystem, and thus affect the decomposition rate.

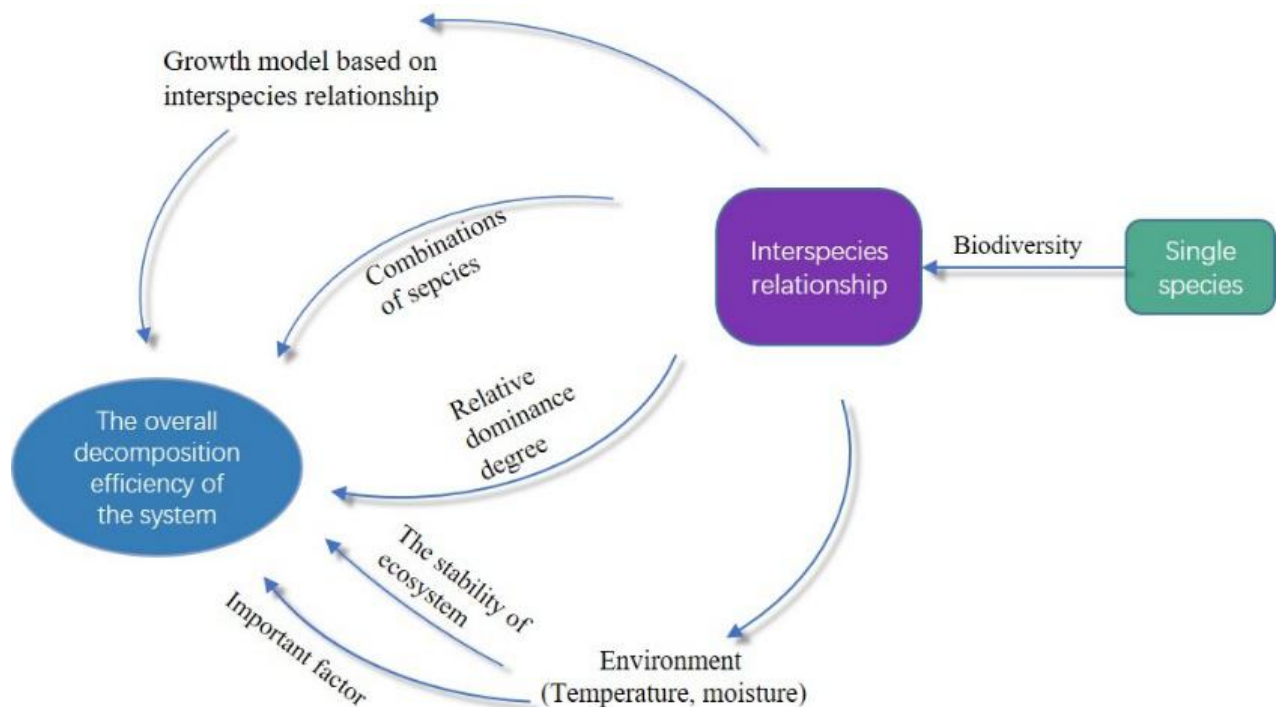


Fig. 13 The influence of community diversity on the overall efficiency of the system

5. Conclusion

The authors in this paper studied the problem of fungal wood decomposition and established the wood decomposing system of fungi based on the data of 37 strains of fungi. The dynamic characteristics of interspecific relationships (competition, parasitism and symbiosis) among fungi are analyzed by the three models based on Malthus-block growth comprehensive prediction. In addition, the relative dominance of various groups and possible persistent strains combinations was evaluated by entropy weight-TOPSIS model to predict the strains combinations. We used the ARIMA model to predict the significance of strains combinations and community diversity to fungal communities.

The results of this paper not only have guiding significance for the study of fungal decomposition and community diversity, but also for improving the quality of climate and the carbon cycle. We found that the traits of fungi are closely related to the wood decomposition rate, the growth rate is positive correlated and the moisture tolerance is negative correlated. Meanwhile, the diversity of fungal community, the number of the population and environmental variables affect the decomposition system, especially the overall efficiency of wood decomposition. However, the predictions of climate and strains combinations in our study are based on the limited assumptions and data, which should be close to practical circumstance, therefore, further studies are necessary to understand the characteristics of fungal community for more accurate modeling.

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