

# Dynamic Analysis of an Algae-Bacteria Ecological Model

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## Abstract

In the paper, under the framework of exploring the interaction between algae and bacteria, an algae-bacteria ecological model was established to analyze the interaction mechanism and growth coexistence mode between algicidal bacteria and algae. Firstly, mathematical work mainly provided some threshold conditions to ensure the occurrence of transcritical bifurcation and saddle-node bifurcation, which could provide certain theoretical support for selecting key ecological environmental factors and numerical simulations. Secondly, the numerical simulation work dynamically displayed the evolution process of the bifurcation dynamic behavior of the model (2.1) and the growth coexistence mode of algae and algicidal bacteria. Finally, it was worth summarizing that intrinsic growth rate and combined capture effort of algae population had a strong influence on the dynamic behavior of the model (2.1). Furthermore, it must also be noted that transcritical bifurcation and saddle-node bifurcation were the inherent driving forces behind the formation of steady-state growth coexistence mode between algicidal bacteria and algae. In summary, it was hoped that the results of this study would contribute to accelerating the study of the interaction mechanism between algicidal bacteria and algae.

## Keywords

Algae, Algicidal Bacteria, Transcritical Bifurcation, Saddle-Node Bifurcation, Coexistence Mode

## 1. Introduction

As we all know, algae and bacteria have coexisted ever since the early stages of evolution, algae and bacteria together influence ecosystems as deep seas to lichens and represent all conceivable modes of interactions from mutualism to

parasitism [1]. Furthermore, during the process of algal blooms, there is a dual relationship between algae and bacteria, *i.e.* coexistence of symbiotic and hostile relationships, which may have significant impacts on the physiology of algae and the dynamics of algal blooms [2]. At the same time, in the past 20 years, scientists have explored the dynamic relationship between algae and bacteria from different perspectives, including physical processes, biological processes, environmental processes and chemical processes, and they have sorted out the phenomena and behaviors involved in the relationship between algae and bacteria, including the beneficial side of bacteria to algae, the harmful side of bacteria to algae, and the ways and means of algae responding to bacterial behaviors [3]. Moreover, with the infiltration of mathematics into the ecological environment, it has brought new opportunities for people to understand the relationship between algae and bacteria, and has brought down to observe the dynamic process of the relationship between algae and bacteria [4]. Therefore, explaining the interaction process and mechanism between algae and bacteria from the perspective of population dynamics is worthy of in-depth research, which can provide a theoretical basis for the prevention and control of algal blooms. In a word, the relationship between algae and bacteria in the future will be a stage where chemistry, biology, environmental science, mathematics and computer science are intertwined, and may be a focus of future scientific problems.

Bacteria play a diverse role in the growth process of algae, in addition to exhibiting a beneficial relationship with algae, they also exhibit inhibition or antagonism against algae, mainly manifested in nutrient competition, toxin release, and the production of lysozymes. The paper [5] studied the effects of bacteria on the growth and proliferation of algae under nutritional competition conditions, and found that there are species specificity and differences in the algal inhibition effects of different bacterial species, concentrations and treatment methods. The paper [6] pointed out that the bacteria of *Proteobacteria* and *Bacillota* could secrete thermally unstable substances with molecular weight greater than 10 kDa into the water environment, which can inhibit the growth of *Karenia milkimotoi* and *Gymnodinium catenatum*. The paper [7] confirmed that two types of bacteria (*Ateromonas* sp. and *Cytophaga* sp.) could secrete an algicidal enzyme to inhibit and kill algal cells, and that the bacteria exhibit a population taxis phenomenon. The paper [8] found that the metabolites of 7 bacterial strains have varying degrees of inhibitory effects on the growth of 2 microalgae species and have certain selectivity. Obviously, bacteria can inhibit the growth of algal cells directly or indirectly, thereby effectively controlling the outbreak of algal blooms and maintaining the balance of algal ecology. In summary, the interaction mechanism between algae and bacteria can naturally degrade pollutants in the aquatic environment within a certain time range, maintain the relative stability of the aquatic natural ecological chain, improve the utilization efficiency of nutrients in the water, and even build an efficient ecosystem.

Algicidal bacteria are bacteria that directly or indirectly dissolve and destroy

the structure of algal cells or inhibit algal growth, the use of algicidal bacteria to control algal blooms has the advantages of being fast, simple, drug-free, low energy consumption, safe, and non-secondary pollution [9]. The paper [10] analyzed the algicidal mode, algicidal characteristics of algicidal bacteria (WJ6) on *Microcystis aeruginosa*, and the effects of different culture periods, different concentrations of bacterial solution and different environmental factors on the algicidal effect, and discussed its possible algicidal mechanism. The paper [11] showed that the bacterium *Phaeobacter inhibens*, a well-studied member of the *Roseobacter* group, intimately interacts with *E. huxleyi*, and while attached to the algal cell, bacteria initially promote algal growth but ultimately kill their algal host. The paper [12] reported the algicidal mechanism of prodigiosin from *Hahella* sp. KA22 against *Microcystis aeruginosa*, and revealed the multiple toxicity mechanisms of PG on *M. aeruginosa* and its potential for controlling the occurrence of *M. aeruginosa* blooms in lakes. The paper [13] pointed out that a new freshwater bacterial strain with strong algicidal activity, GLY-2107, was isolated from Lake Taihu and identified as *Aeromonas* sp., which could produce two algicidal compounds: 2107-A (3-benzyl-piperazine-2,5-dione) and 2107-B (3-methylindole), and both compounds exhibited potent algicidal activities against *Microcystis aeruginosa*. In summary, these studies indicate that the mechanism of controlling and killing algae by algicidal bacteria may have potential use for the development of a novel control strategy for harmful cyanobacterial blooms.

With the gradual deepening of mathematical and simulation techniques into the study of the dynamic relationship between algae and bacteria, the use of mathematical model and numerical simulation to study the dynamic relationship between algae and bacteria has received increasing attention and achieved some good research results [14]-[20]. The paper [14] obtained a quadratic polynomial model of the removal rate of Chl.-a and the initial concentration of algicidal bacteria (*Chryseobacterium* sp.S7), as well as the concentration of Chl.-a in the water body, and the amount of algicidal bacteria added was determined to achieve the most effective control effect based on this model. The paper [15] studied the algal inhibition characteristics of strain 2 - 4 and its secretions through orthogonal experiment and dynamical model, and analyzed the relationship between the ecological toxicity and algal inhibition efficiency of algicidal bacteria, which can provide theoretical reference for biological control practices. The paper [16] constructed an algae-bacteria microecological dynamical model based on the inhibitory effect of algicidal bacteria on algal populations, which could explore the dynamic growth trends and coexistence patterns of algicidal bacteria and algal populations. The paper [17] proposed a mathematical model of algae and bacteria, which mainly studied the effects of physical and chemical parameters on the interaction between algae and bacteria. The paper [18] introduced the FLAM modeling framework to construct an ecological model of algae and bacteria, which could explore the ecological relationship between algae and bacteria. The paper [19] considered autotrophic bacteria and algae in the reactor and constructed an

algae-bacteria coupling dynamical model, they clarified that the maximum specific growth rate of algae and bacteria and the yield coefficient of bacteria are the most sensitive coefficients. The paper [20] proposed an algae-bacteria model composed of autotrophic bacteria, algae, and heterotrophic bacteria, which could describe the dynamic relationship between bacteria and algae, and conduct sensitivity analysis on the algae-bacteria model. In a word, it is worth believing that with the deepening of research on the dynamic relationship between algae and bacteria and the practical need for algal bloom control, the application of mathematical model in the research and application process of algal bloom control by algicidal bacteria will become more and more extensive, and there is a possibility that more excellent research results will emerge.

Based on the above research review, the main purpose of this paper is to propose an algae-bacteria ecological new model, which can characterize the direct process of algal death caused by algal lysing bacteria by dissolving algal cells. At the same time, from the perspective of population dynamics evolution, the internal driving mechanism that can force the dynamic evolution of algae and bacteria will be revealed. Furthermore, an algal dissolution dynamical new equation also will be proposed to elucidate the dissolution dynamical mechanism of algicidal bacteria. Finally, the biological significance represented by some bifurcation dynamics is presented from the perspective of population dynamics evolution.

## 2. Construction of Algae-Bacteria Model

As early as 1924, Geitler reported that a myxobacteria (*Polyangium parasitium*) parasitized on the algae (*Cladophora*), which can cause *Cladophora* to die [21]. Since then, algicidal bacteria have received a lot of attention both domestically and internationally, especially the direct contact between myxobacteria and cyanobacteria cells, which can inhibit or dissolve the growth of algae [22]. Therefore, within the framework of the dynamic relationship between algae and bacteria, we will construct an algae-bacteria ecological model to characterize the inhibition mechanism or dissolution mechanism of algicidal bacteria.

Now some modeling assumptions are given as follows:

1) The growth space of algicidal bacteria and algae is semi-closed water environment, species concentration is always evenly distributed in space and changed instantaneously with time  $t$ ,  $x(t)$  represents the density of the algae population,  $y(t)$  represents the density of algicidal bacteria.

2) It assumes that algicidal bacteria are attached to the algal population and the change in the density of algicidal bacteria depends to some extent on the change in the density of algae population. We assume that the growth function of algae population is logistic mode  $r_1x\left(1-\frac{x}{k}\right)$  with intrinsic growth rate  $r_1$  and maximum environmental capacity  $k$ , then the growth function of algicidal bacteria is quasi logistic mode  $r_2x\left(1-\frac{y}{hx}\right)$  with intrinsic growth rate  $r_2$  and max-

imum environmental capacity  $hx$ .

3) The inhibition or dissolution function of algicidal bacteria on algae is a humped function and declines with the high densities of algicidal bacteria and internal competitive relationship [16]. Thus, we give an inhibition or dissolution function of algicidal bacteria on algal growth  $\frac{cxy}{d+y^2}$  with the half saturation constant  $d$  and the maximum value of the per capita reduction rate  $c$ .

4) Preventing algal blooms from breaking out or rotting later, the algae needs to be salvaged or harvested regularly. Meanwhile, because algicidal bacteria are attached to algae population, the salvage or harvest of the algae will lead to the salvage or harvest of some algicidal bacteria. Thus, we give that the harvesting functions of algae and algicidal bacteria are  $q_1mex$  and  $q_2mey$  respectively, where  $q_i$  is the catchability co-efficient of the  $i$ th species,  $e$  is the combined capture effort used to harvest, and  $m(0 < m < 1)$  is the fraction of the stock available for harvesting [16].

Based on the above assumptions, we will provide an algae-bacteria ecological model, which can be described by the following differential equation:

$$\begin{cases} \frac{dx}{dt} = r_1x\left(1 - \frac{x}{k}\right) - \frac{cxy}{d+y^2} - q_1mex = f(x, y), \\ \frac{dy}{dt} = r_2y\left(1 - \frac{y}{hx}\right) - q_2mey = g(x, y). \end{cases} \quad (2.1)$$

Based on the established model (2.1), we will first conduct theoretical analysis on the existence and stability of equilibrium points, as well as bifurcation dynamics, and provide certain threshold conditions. Secondly, we will conduct numerical simulations of relevant dynamic behaviors to elucidate the characteristics of dynamic evolution. Finally, we will summarize and analyze the theoretical and numerical results to elucidate the relevant biological significance.

### 3. Existence and Stability of All Possible Equilibrium Points

In order to explore the dynamic evolution and growth coexistence mode of algae population and algicidal bacteria, the existence and stability of all possible equilibrium points need to be comprehensively explored. Now, we can obtain all possible equilibrium points of the model (2.1) using the following equation:

$$\begin{cases} r_1x\left(1 - \frac{x}{k}\right) - \frac{cxy}{d+y^2} - q_1mex = 0, \\ r_2y\left(1 - \frac{y}{hx}\right) - q_2mey = 0. \end{cases} \quad (2.2)$$

It is obvious that the model (2.1) has only one possible trivial equilibrium point  $E_0\left(\frac{k(r_1 - q_1me)}{r_1}, 0\right)$  and the equilibrium point  $E_0$  will exist when  $r_1 - q_1me > 0$  from the biological perspective.

The ecologically acceptable coexistence equilibrium points (CEPs) correspond

to the positive solutions of the following algebraic system of equations:

$$\begin{cases} r_1 \left(1 - \frac{x}{k}\right) - \frac{cy}{d + y^2} - q_1 me = 0, \\ r_2 \left(1 - \frac{y}{hx}\right) - q_2 me = 0. \end{cases} \quad (2.3)$$

We can assume that  $E(x^*, y^*)$  is a positive equilibrium point of the model (2.1) with  $x^* = \frac{r_2 y^*}{h(r_2 - q_2 me)}$  and  $r_2 > q_2 me$ , then  $y^*$  is a root of the equation:

$$\begin{aligned} w(y) &= \frac{r_1 r_2}{hk(r_2 - q_2 me)} y^3 - (r_1 - q_1 me) y^2 \\ &\quad + \left( \frac{r_1 r_2 d}{hk(r_2 - q_2 me)} + c \right) y - (r_1 - q_1 me) d \\ &= 0. \end{aligned} \quad (2.4)$$

According to Descartes rule of sign, Equation (2.4) can present conditions in their coefficients that allow us to determine three positive solutions for  $y$ . Equation (2.4) has maximum change of signs, which implies that we can have three positive solutions for  $y$ . At the same time, we can obtain from Equation (2.3) that  $y$  is a positive proportional function of  $x$  when  $r_2 - q_2 me > 0$ .

Obtaining positive roots of Equation (2.4) is a very complex task from the algebraic point of view. However, it is possible to obtain theoretical conditions of positive solutions if we use Shengjin formula. The above algebraic constraints can guarantee the existence of three CEPs.

Under the restriction of  $r_1 - q_1 me > 0$  and  $r_2 - q_2 me > 0$ , we use Shengjin discriminant method to obtain the following theorem.

**Theorem 1.** The existence of internal equilibrium points in the model (2.1) is as follows:

- 1) If  $\Delta > 0$ , then the model (2.1) has one internal equilibrium point  $E_1(x_1, y_1)$ .
- 2) If  $\Delta = 0$ , then the model (2.1) has two internal equilibrium points  $E_{11}(x_{11}, y_{11})$  and  $E_2(x_2, y_2)$ .
- 3) If  $\Delta < 0$ , then the model (2.1) has three internal equilibrium points  $E_{111}(x_{111}, y_{111})$ ,  $E_{22}(x_{22}, y_{22})$  and  $E_3(x_3, y_3)$ .

**Proof.** We can write down Equation (2.4) as follows:

$$w(y) = \rho_1 y^3 + \rho_2 y^2 + \rho_3 y + \rho_4 = 0, \quad (2.5)$$

where  $\rho_1 = \frac{r_1 r_2}{hk(r_2 - q_2 me)}$ ,  $\rho_2 = -(r_1 - q_1 me)$ ,  $\rho_3 = \frac{r_1 r_2 d}{hk(r_2 - q_2 me)} + c$ ,

$\rho_4 = -(r_1 - q_1 me) d$ . It is obvious that  $w(y) = 0$  must have a positive root because  $w(0) = -(r_1 - q_1 me) d < 0$ ,  $\lim_{y \rightarrow +\infty} w(y) = +\infty$  and  $\lim_{y \rightarrow -\infty} w(y) = -\infty$ .

Furthermore, it can be known from Shengjin discriminant method that  $\Delta = B^2 - 4AC$ , where  $A = \rho_2^2 - 3\rho_1\rho_3$ ,  $B = \rho_2\rho_3 - 9\rho_1\rho_4$ ,  $C = \rho_3^2 - 3\rho_2\rho_4$ . After a simple calculation, the following formula is obtained:

$$\Delta = \frac{1}{h^4 k^4 (q_2 m e - r_2)^4} \left[ 12k^4 h^4 (q_1^2 m^2 e^2 d - 2q_1 m e d r_1 + d r_1^2 - 0.25c^2)(q_2 m e - r_2)^4 \right. \\ \times (q_1 m e - r_1)^2 + 60k^3 (q_2 m e - r_2)^3 r_1 r_2 (q_1^2 m^2 E^2 d - 2q_1 m e d r_1 + d r_1^2 - 0.2c^2) c h^3 \quad (2.6) \\ \left. + 24(q_1^2 m^2 e^2 d - 2q_1 m e d r_1 + 1.5c^2)(q_2 m e - r_2)^2 r_1^2 r_2^2 k^2 h^2 d \right. \\ \left. - 36r_2^3 r_1^3 d^2 k (q_2 m e - r_2) c h + 12r_1^4 r_2^4 d^3 \right].$$

At the same time, we will obtain the derivative equation of Equation (2.5):

$$\frac{3r_1 r_2}{hk(r_2 - q_2 m e)} y^2 - 2(r_1 - q_1 m e) y + \left[ \frac{r_1 r_2 d}{hk(r_2 - q_2 m e)} + c \right] = 0. \quad (2.7)$$

It is easy to know that when  $\Delta = 0$ , Equation (2.5) has three real roots, which implies that Equation (2.7) has two real different roots, which means the discriminant of the root of Equation (2.7) is strictly positive, that is  $\delta > 0$ . By the rooting formula, we can calculate the two real roots of Equation (2.7) as follows:

$$\begin{cases} yy_1 = \frac{-b - \sqrt{\delta}}{2a}, \\ yy_2 = \frac{-b + \sqrt{\delta}}{2a}, \end{cases} \quad (2.8)$$

where  $a = \frac{3r_1 r_2}{hk(r_2 - q_2 m e)}$ ,  $b = -2(r_1 - q_1 m e)$ ,

$\delta = \frac{-12r_1 r_2 \left[ \frac{r_1 r_2 d}{hk(r_2 - q_2 m e)} + c \right]}{hk(r_2 - q_2 m e)} + [2(r_1 - q_1 m e)]^2$ . Moreover, it is obvious that

$0 < yy_1 < yy_2$  is true.

**Item 1.** When  $\Delta > 0$ , Equation (2.5) has a real root  $y_1$  and a pair of conjugate complex roots  $y_2^*$  and  $y_3^*$ . The relationship between the roots of a univariate cubic equation and its coefficients is the following equation:

$$y_1 y_2^* y_3^* = \frac{(r_1 - q_1 m e)(r_2 - q_2 m e) d h k}{r_1 r_2} > 0. \quad (2.9)$$

Thus, it is obvious that the model (2.1) has one internal equilibrium point  $E_1(x_1, y_1)$  if  $\Delta > 0$ . Furthermore, we can obtain  $yy_2 < y_1 < \frac{hk(r_2 - q_2 m e)}{r_2}$  or  $0 < y_1 < yy_1$ .

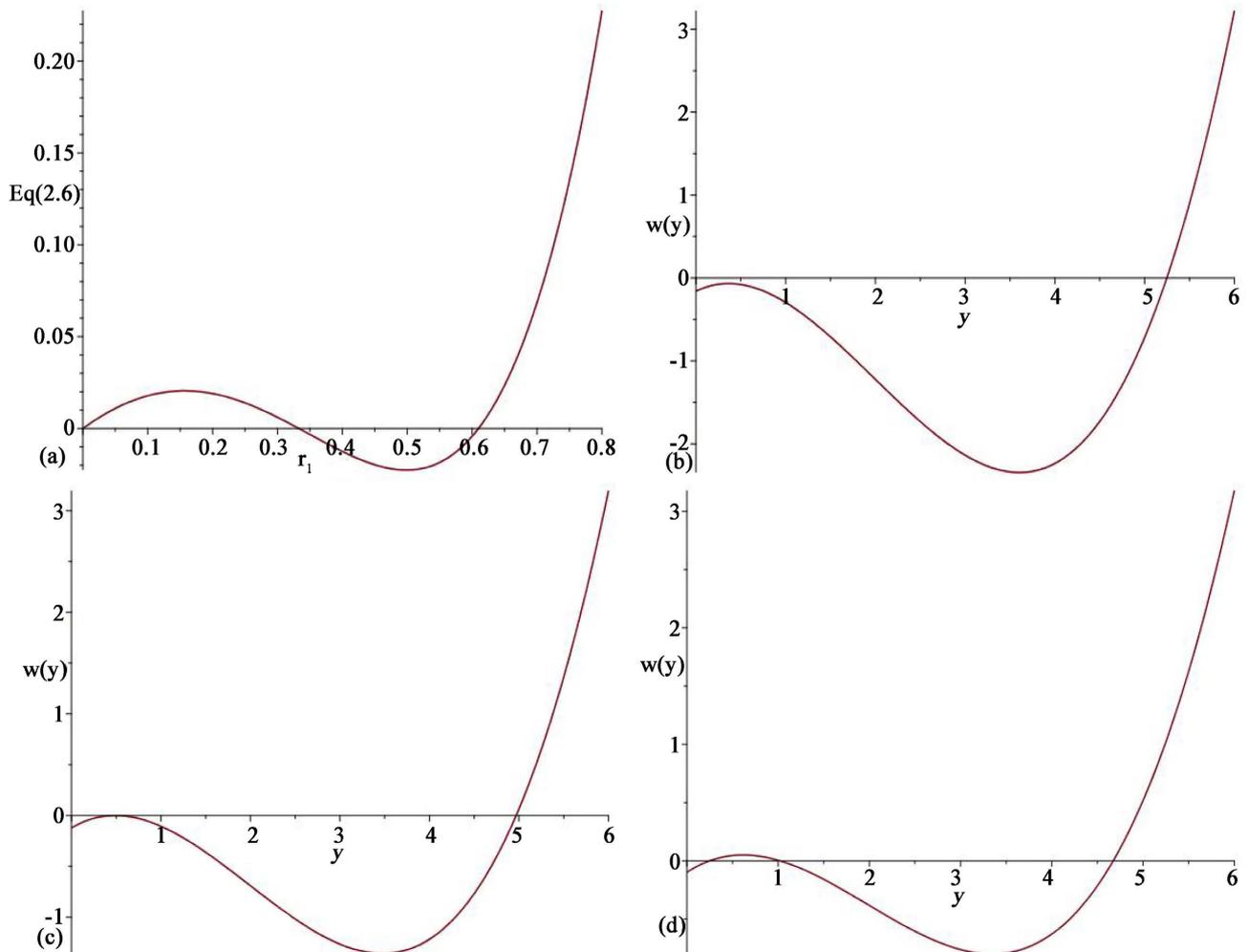
**Item 2.** When  $\Delta = 0$ , Equation (2.5) has three real roots and two of them are equal. As we know from Item 1, the product of three roots of Equation (2.5) is strictly positive, which means that Equation (2.5) has one positive root and two equal negative roots or three positive roots, two of which are equal.

Based on the knowledge of algebra and geometry, we can conclude that Equation (2.5) has three positive roots. Thus, we can know that when  $\Delta = 0$  the model (2.1) has two internal equilibrium points  $E_{11}(x_{11}, y_{11})$  and  $E_2(x_2, y_2)$  with  $y_{11} = yy_1$  or  $y_{11} = yy_2$ . At the same time, it is easy to know that

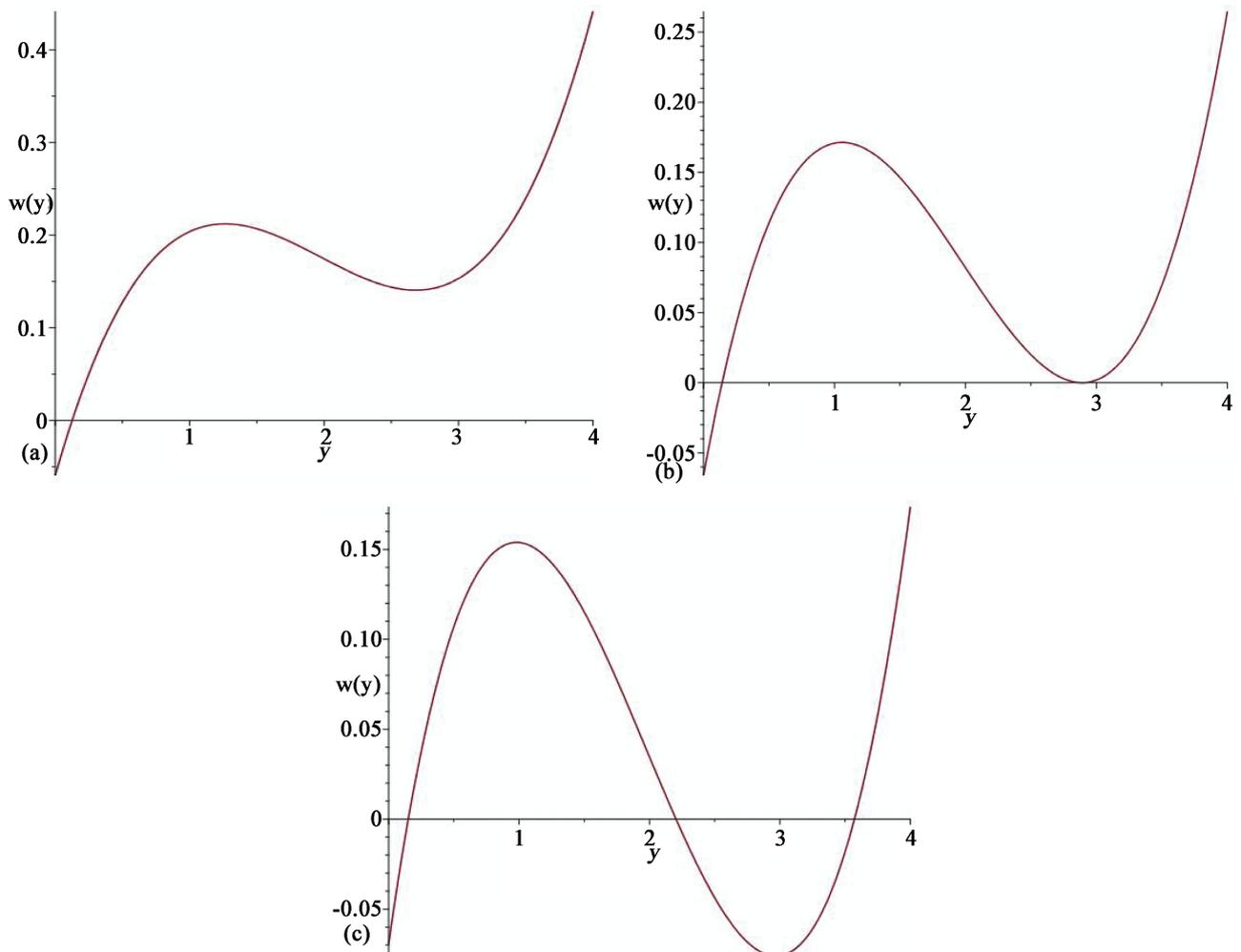
$$yy_2 < y_2 < \frac{hk(r_2 - q_2me)}{r_2} \text{ or } 0 < y_2 < yy_1 < y_{11}.$$

**Item 3.** When  $\Delta < 0$ , Equation (2.5) has three different real roots. Based on the proof process of Item 2, we can obtain that if  $\Delta < 0$ , the model (2.1) has three coexistence internal equilibrium points  $E_{111}(x_{111}, y_{111})$ ,  $E_{22}(x_{22}, y_{22})$  and  $E_3(x_3, y_3)$  with  $0 < y_{111} < yy_1 < y_{22} < yy_2 < y_3$  or  $0 < y_3 < yy_1 < y_{22} < yy_2 < y_{111}$ .

In order to verify the correctness and effectiveness of the theoretical derivation, we select  $r_1$  as the control parameter with  $r_2 = 0.6$ ,  $h = 0.6$ ,  $k = 10$ ,  $d = 0.2$ ,  $c = 0.5$ ,  $q_1 = 0.15$ ,  $q_2 = 0.12$ ,  $m = 0.1$  and  $e = 0.2$ . It is easy to find from **Figure 1(a)** that  $\Delta$  size varies from positive to negative with the value of  $r_1$  changing, which implies the existence of one root, two roots, and three roots in equation 2.6, the detailed numerical simulation results are shown in **Figures 1(b)-(d)** and **Figures 2(a)-(c)**. Obviously, these numerical simulation results not only validate the feasibility of Theorem 1, but also point out that the



**Figure 1.** (a) The sign of  $\Delta$  changes with  $r_1$ . (b) The equation  $f(y)$  has a positive root with  $r_1 = 0.80$ . (c) The equation  $f(y)$  has two positive roots with  $r_1 = 0.60968293633525798911$ . (d) The equation  $f(y)$  has three positive roots with  $r_1 = 0.50$ .



**Figure 2.** (a) The equation  $f(y)$  has a positive root with  $r_1 = 0.333006785365646689$ . (b) The equation  $f(y)$  has two positive roots with  $r_1 = 0.333006785365646689$ . (c) The equation  $f(y)$  has three positive roots with  $r_1 = 0.35$ .

model (2.1) may have one, two, and three internal equilibrium points.

In this section, we will explore characteristics of some equilibrium points of the model (2.1), which can signify the formation of stable steady-state coexistence mode between bacteria and algae. As we all know, the stability of some equilibrium points can be obtained through the signs of the eigenvalues of Jacobian matrix, hence we can obtain the expression of Jacobian matrix about the model (2.1) as:

$$J_{E(x,y)} = \begin{bmatrix} r_1 - q_1 m e - \frac{2r_1 x}{k} - \frac{cy}{d + y^2} & \frac{cx(y^2 - d)}{(d + y^2)^2} \\ \frac{r_2 y^2}{hx^2} & r_2 - q_2 m e - \frac{2r_2 y}{hx} \end{bmatrix}.$$

Combined with Equation (2.3), we can simplify the Jacobian matrix into:

$$J_{E_{(x,y)}} = \begin{bmatrix} \frac{r_1 x}{k} & \frac{cx(y^2 - d)}{(d + y^2)^2} \\ \frac{h(r_2 - q_2 me)^2}{r_2} & -(r_2 - q_2 me) \end{bmatrix}.$$

By solving Equation (2.3), the model (2.1) only has one boundary equilibrium point  $E_0\left(\frac{k(r_1 - q_1 me)}{r_1}, 0\right)$  with  $r_1 > q_1 me$ , which means that the bacterial population is extinct, but algal populations can survive.

**Theorem 2.** If the equilibrium point  $E_0\left(\frac{k(r_1 - q_1 me)}{r_1}, 0\right)$  exists, then  $E_0$  is a saddle when  $e < \frac{r_2}{q_2 m}$ , while  $E_0$  is a stable node when  $e > \frac{r_2}{q_2 m}$ .

**Proof.** The Jacobian matrix about the equilibrium point  $E_0$  is:

$$J_{E_0} = \begin{bmatrix} -(r_1 - q_1 me) & \frac{-ck(r_1 - q_1 me)}{r_1 d} \\ 0 & r_2 - q_2 me \end{bmatrix},$$

and its eigenvalues are  $\lambda_1 = -(r_1 - q_1 me)$  and  $\lambda_2 = r_2 - q_2 me$ . It is obvious that  $\lambda_1$  is negative since  $r_1 - q_1 me$  is strictly positive. Therefore, when  $e > \frac{r_2}{q_2 m}$ , the two eigenvalues of are both negative, then the equilibrium point  $E_0$  is stable node, while the equilibrium point  $E_0$  is an unstable saddle if  $e < \frac{r_2}{q_2 m}$ . Furthermore, this result shows that the mode (2.1) can exhibit a transcritical bifurcation at the equilibrium point  $E_0$  when the value of  $e$  crosses a critical threshold  $\frac{r_2}{q_2 m}$ , and this is characterized by a transition between a saddle and a sink.

**Theorem 3.** 1) If  $\Delta > 0$ , the model (2.1) has only one internal equilibrium point  $E_1(x_1, y_1)$ , and the stability analysis of the equilibrium point  $E_1(x_1, y_1)$  is as follows with  $T$  and  $D$ ,  $T$  and  $D$  are respectively the trace and determinant of  $J_{E_1}$ :

a) When  $D > 0$  and  $T^2 - 4D > 0$ , the equilibrium point  $E_1(x_1, y_1)$  is a stable node.

b) When  $D > 0$  and  $T^2 - 4D = 0$ , the equilibrium point  $E_1(x_1, y_1)$  is a stable degenerate node.

c) When  $D > 0$  and  $T^2 - 4D < 0$ , the equilibrium point  $E_1(x_1, y_1)$  is a stable focus.

d) When  $D < 0$ , the equilibrium point  $E_1(x_1, y_1)$  is a saddle.

e) When  $D = 0$ , the equilibrium point  $E_1(x_1, y_1)$  is a saddle-node point.

2) If  $\Delta = 0$ , the model (2.1) has two internal equilibrium points namely  $E_{11}(x_{11}, y_{11})$  and  $E_2(x_2, y_2)$ , and their stability analysis is as follows:

a) The stability analysis of  $E_{11}(x_2, y_2)$  can be summarized to **Item 1** of this

theorem.

b)  $E_2(x_2, y_2)$  is an attracting saddle-node.

3) If  $\Delta < 0$ , the model (2.1) has three internal equilibrium points namely  $E_{111}(x_{111}, y_{111})$ ,  $E_{22}(x_{22}, y_{22})$  and  $E_3(x_3, y_3)$ , and their stability analysis is as follows with  $y_1$  and  $y_2$  are the two positive roots of  $D = 0$  respectively:

a) When  $y_i \in (y_0, y_0^*)$ ,  $E_i(x_i, y_i)$  is a saddle point.

b) When  $y_i \in (0, y_0) \cup (y_0^*, +\infty)$ ,  $E_i(x_i, y_i)$  is a node point.

C) When  $y_i = y_0$  or  $y_i = y_0^*$ ,  $E_i(x_i, y_i)$  is a saddle-node point.

**Proof. Item 1.** The Jacobi matrix of the internal equilibrium points  $E_i(x_i, y_i)$  is:

$$J_{E_i(x_i, y_i)} = \begin{bmatrix} -\frac{r_1 x_i}{k} & \frac{c x_i (y_i^2 - d)}{(d + y_i^2)^2} \\ \frac{h(r_2 - q_2 m e)^2}{r_2} & -(r_2 - q_2 m e) \end{bmatrix}.$$

Apparently, the Jacobi matrix of  $J_{E_i}$  has two characteristic roots,

$$\lambda_1 = \frac{-r_1 x_i}{k} + \frac{c h x_i (y_i^2 - d)(r_2 - q_2 m e)}{r_2 (d + y_i^2)^2}, \quad \lambda_2 = -(r_2 - q_2 m e).$$

From the relationship between eigenvalue, determinant and trace, we have  $\lambda_1 + \lambda_2 = T$ ,  $\lambda_1 \lambda_2 = D$ . The following equation is calculated:

$$D = \frac{r_2 y}{h} \left[ \frac{r_1}{k} + \frac{c h (r_2 - q_2 m e)(d - y^2)}{r_2 (d + y^2)^2} \right]. \tag{3.1}$$

Combined with Jacobian matrix, we know that  $T < 0$ . Then, when  $D < 0$ , the two characteristic roots are one positive and one negative, hence  $E_1(x_1, y_1)$  is a saddle. When  $D = 0$ , the two characteristic roots are one positive and zero,  $E_1(x_1, y_1)$  is a saddle-node point. When  $D > 0$ , both characteristic roots are negative,  $E_1(x_1, y_1)$  is a node point.

**Item 2.** When  $\Delta = 0$ ,  $E_2(x_2, y_2)$  is the multiple root. From Shengjin Formula, we have:

$$\begin{cases} y_1 = \frac{-\rho_2}{\rho_1} + K, \\ y_2 = y_3 = \frac{-2}{K}, \end{cases}$$

where  $K = \frac{B}{A}$ ,  $A \neq 0$ . See above for  $\rho_1, \rho_2, A, B$ . Easy to get:

$$y_2 = -\frac{(r_1 - q_1 m e)(r_2 - q_2 m e)[8r_1 r_2 d - c h k (r_2 - q_2 m e)] k h}{2(r_1 - q_1 m e)^2 (r_2 - q_2 m e)^2 k^2 h^2 - 6r_1 r_2 c k h (r_2 - q_2 m e e) - 6r_1^2 r_2^2 d}. \tag{3.2}$$

Simultaneous Equation (2.6), Equation (3.1) and Equation (3.2), we get a common factor for  $D$  and  $\Delta$ , which is recorded as  $M$ . Where

$$\begin{aligned}
M = & k^4 h^4 \left( q_1^2 m^2 e^2 d - 2q_1 m e d r_1 + d r_1^2 - \frac{1}{4} c^2 \right) (q_2 m e - r_2)^4 (q_1 m e - r_1)^2 \\
& + 5k^3 (q_2 m e - r_2)^3 r_1 r_2 \left( q_1^2 m^2 e^2 d - 2q_1 m e d r_1 + d r_1^2 - \frac{1}{5} c^2 \right) c h^3 \\
& + 2 \left( q_1^2 m^2 e^2 d - 2q_1 m e d r_1 + d r_1^2 + \frac{3}{2} c^2 \right) (q_2 m e - r_2)^2 r_1^2 r_2^2 k^2 h^2 d \\
& - 3r_2^3 r_1^3 d^2 k (q_2 m e - r_2) c h + r_1^4 r_2^4 d^3
\end{aligned}$$

Therefore,  $D = 0$ ,  $E_2(x_2, y_2)$  is a saddle-node point.

**Item 3.** When  $\Delta < 0$ , For the analysis of the stability of each equilibrium point  $E_i(x_i, y_i)$ , we use Equation (3.1) to study. Since all parameters are strictly positive, we only need to analyze:

$$P(y) = \frac{r_1}{k} + \frac{ch(r_2 - q_2 m e)}{r_2} \cdot \frac{d - y^2}{(d + y^2)^2}.$$

First, we take the derivative of  $P(y)$  and get:

$$P'(y) = \frac{6chy(r_2 - q_2 m e) \left( \frac{y^2}{3} - d \right)}{r_2 (y^2 + d)^3}.$$

It is not difficult to find that  $P(y)$  has an extreme value at  $\sqrt{3d}$  and  $P'(y)$  is a quadratic function of one variable with respect to  $y$ . According to the analysis of **Item 2** in **Theorem 3**,  $P(y)$  must be strictly negative when  $y = \sqrt{3d}$ . Next, we set  $T = y^2$  and get:

$$P(y) = \frac{r_1}{k} + \frac{ch(r_2 - q_2 m e)}{r_2} \cdot \frac{d - T}{(d + T)^2}.$$

When  $P(y) = 0$ ,  $P(y)$  has two zero points  $T_0$  and  $T_0^*$ . Furthermore,  $P(y)$  are two real zeros  $y_0$  and  $y_0^*$ . Let's assume that  $y_0 < y_0^*$ .

To sum up, When  $y_i \in (y_0, y_0^*)$ ,  $D < 0$ , that is the sign of characteristic value of  $J_{E_i(x_i, y_i)}$  is opposite. So  $E_i(x_i, y_i)$  is a saddle point. When  $y_i = y_0$  or  $y_i = y_0^*$ , and  $D = 0$ , that is the characteristic value symbols of  $J_{E_i(x_i, y_i)}$  is a negative number and a zero. So  $E_i(x_i, y_i)$  is a saddle-node point. When  $y_i \in (0, y_0) \cup (y_0^*, +\infty)$ ,  $D > 0$ , that is two characteristic value symbols of  $E_i(x_i, y_i)$  are the same. So  $E_i(x_i, y_i)$  is a node.

## 4. Local Bifurcation Analysis

In this section, we will choose parameter  $e$  and  $r_1$  as critical bifurcation control parameter to investigate the bifurcation dynamics evolution characteristics of the model (2.1), and give the threshold conditions for transcritical bifurcation and saddle-node bifurcation of the model (2.1).

### 4.1. Transcritical Bifurcation

**Theorem 4.** The model (2.1) undergoes a transcritical bifurcation at the equi-

brium point  $E_0\left(\frac{k(r_1 - q_1 m e)}{r_1}, 0\right)$  when  $e = e_{TC} = \frac{r_2}{q_2 m}$ .

**Proof:** On the basis of Theorem 2, when  $e = e_{TC} = \frac{r_2}{q_2 m}$ , the Jacobi matrix of the equilibrium point  $E_0$  is:

$$J_{E_0} = \begin{bmatrix} -\frac{r_1 q_2 - r_2 q_1}{q_2} & -ck(r_1 q_2 - r_2 q_1) \\ 0 & r_1 q_2 d \end{bmatrix}.$$

We assume that  $V$  and  $W$  respectively are eigenvectors of  $J_{(E_0;e)}$  and  $J_{(E_0;e)}^T$  with respect to eigenvalue zero, which means:

$$J_{(E_0;e)} V = 0, J_{(E_0;e)}^T W = 0.$$

Thus, we can get:

$$V = \begin{bmatrix} v_1 \\ v_2 \end{bmatrix} = \begin{bmatrix} 1 \\ -r_1 d \\ ck \end{bmatrix}, W = \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} 0 \\ 1 \end{bmatrix},$$

where  $F$  is

$$F(x, y) = \begin{bmatrix} f(x, y) \\ g(x, y) \end{bmatrix}.$$

Then,

$$W^T F_e(E_0; e) = (0 \ 1) \begin{bmatrix} -q_1 m x \\ 0 \end{bmatrix}_{(E_0;e)} = (0 \ 1) \begin{bmatrix} \frac{q_1 m k (r_2 q_1 - r_1 q_2)}{r_1 q_2} \\ 0 \end{bmatrix} = 0,$$

$$W^T [DF_e(E_0; m) V] = (0 \ 1) \begin{bmatrix} -q_1 m e & 0 \\ 0 & -q_2 m e \end{bmatrix}_{(E_0;e)} \begin{bmatrix} 1 \\ -r_1 d \\ ck \end{bmatrix} = \frac{r_1 r_2 d}{ck} \neq 0,$$

and then

$$\begin{aligned} & W^T [D^2 F(E_0; e)(V, V)] \\ &= (0 \ 1) \begin{bmatrix} f_{xx} & f_{xy} & f_{yx} & f_{yy} \\ g_{xx} & g_{xy} & g_{yx} & g_{yy} \end{bmatrix}_{(E_0;e)} \begin{pmatrix} v_1 v_1 \\ v_1 v_2 \\ v_2 v_1 \\ v_2 v_2 \end{pmatrix} \\ &= \frac{2r_2 q_2 r_1^3 d^2}{hk^3 (r_2 q_1 - r_1 q_2) c^2} \neq 0. \end{aligned}$$

According to Sotomayors theorem [23], when  $e = e_{TC} = \frac{r_2}{q_2 m}$ , then the model (2.1) undergoes a transcritical bifurcation at the equilibrium point  $E_0$ .

### 4.2. Saddle-Node Bifurcation

According to Theorems 1 and 3, it can be inferred that  $r_1$  has two different real

values such that  $\Delta = 0$ , let's assume that  $r_{1_{SN}}$  and  $r_{1_{SN}}^*$ , as well as  $r_{1_{SN}}^* < r_{1_{SN}}$ . Furthermore, the expression of  $r_{1_{SN}}$  and  $r_{1_{SN}}^*$  cannot be written specifically, then we will give it in the numerical simulation section. At the same time, we have:

$$y_{11} = -\frac{(r_1 - q_1 me)(r_2 - q_2 me)[8r_1 r_2 d - chk(r_2 - q_2 me)]kh}{2(r_1 - q_1 me)^2 (r_2 - q_2 me)^2 k^2 h^2 - 6r_1 r_2 chk(r_2 - q_2 me) - 6r_1^2 r_2^2 d},$$

$$x_{11} = \frac{r_2 y_{22}}{h(r_2 - q_2 me)}.$$

**Theorem 5.** Saddle-node bifurcation takes place in the model (2.1) when  $r_1 = r_{1_{SN}}$  under the conditions of:

- 1)  $r_1 > q_1 me$ ,  $r_2 > q_2 me$ .
- 2)  $\Delta = 0$ .

**Proof.** The equilibrium point  $E_{11}(x_{11}, y_{11})$  exists under the above two conditions according to Theorem 1, and the Jacobian matrix at  $E_{11}(x_{11}, y_{11})$  when  $r_1 = r_{1_{SN}}$  can be written as:

$$J_{E_{11}} = \begin{bmatrix} \frac{-r_{1_{SN}} x_{11}}{k} & cx_{11}(y_{11}^2 - d) \\ \frac{h(r_2 - q_2 me)^2}{r_2} & -(r_2 - q_2 me) \end{bmatrix}.$$

We assume that  $V$  and  $W$  respectively are eigenvectors of  $J_{E_{11}}$  and  $J_{E_{11}}^T$  with respect to eigenvalue zero, which means:

$$J_{E_{11}} V = 0, J_{E_{11}}^T W = 0,$$

where

$$V = \begin{bmatrix} v_1 \\ v_2 \end{bmatrix} = \begin{bmatrix} 1 \\ \frac{h(r_2 - q_2 me)}{r_2} \end{bmatrix},$$

$$W = \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} 1 \\ \frac{cx_{11}(y_{11}^2 - d)}{(d + y_{11}^2)^2 (r_2 - q_2 me)} \end{bmatrix}.$$

Then, we can get:

$$\begin{aligned} & W^T F_{r_1}(E_{11}; r_{1_{SN}}) \\ &= \begin{bmatrix} 1 & \frac{cx_{11}(y_{11}^2 - d)}{(d + y_{11}^2)^2 (r_2 - q_2 me)} \end{bmatrix} \begin{bmatrix} x_{11} \left(1 - \frac{x_{11}}{k}\right) \\ 0 \end{bmatrix} \\ &= x_{11} \left(1 - \frac{x_{11}}{k}\right) \\ &\neq 0, \end{aligned}$$

$$\begin{aligned}
 W^T \left[ D^2 F(E_{11}; r_{1SN})(V, V) \right] &= [w_1 \quad w_2] \begin{bmatrix} f_{xx} & f_{xy} & f_{yx} & f_{yy} \\ g_{xx} & g_{xy} & g_{yx} & g_{yy} \end{bmatrix} \begin{bmatrix} v_1 v_1 \\ v_1 v_2 \\ v_2 v_1 \\ v_2 v_2 \end{bmatrix} \\
 &= \begin{bmatrix} 1 \\ \frac{cx_{11}(y_{11}^2 - d)}{(d + y_{11}^2)^2 (r_2 - q_2 me)} \end{bmatrix} \begin{bmatrix} \frac{-2r_{1SN}}{k} & \frac{c(y_{11}^2 - d)}{(y_{11}^2 + d)^2} & \frac{c(y_{11}^2 - d)}{(y_{11}^2 + d)^2} & \frac{6cx_{11}y_{11} \left( d - \frac{y_{11}^2}{3} \right)}{(y_{11}^2 + d)^3} \\ \frac{-2r_2 y_{11}^2}{hx_{11}^3} & \frac{2r_2 y_{11}}{hx_{11}^2} & \frac{2r_2 y_{11}}{hx_{11}^2} & \frac{-2r_2}{hx_{11}} \end{bmatrix} \begin{bmatrix} 1 \\ \frac{h(r_2 - q_2 me)}{r_2} \\ \frac{h(r_2 - q_2 me)}{r_2} \\ \frac{h^2 (r_2 - q_2 me)^2}{r_2^2} \end{bmatrix} \\
 &= - \frac{c(d - y_{11}^2) \left[ (h^2 x_{11}^2 - 4hx_{11}y_{11} + 2y_{11}^2)r_2^2 - 2q_2 m e x_{11} (hx_{11} - 2y_{11})r_2 + q_2^2 m^2 e^2 h^2 x_{11}^2 \right]}{x_{11}^2 (y_{11}^2 + d)^2 (q_2 me - r_2) h r_2} \neq 0.
 \end{aligned}$$

According to Sotomayors theorem [23], the model (2.1) will undergo a saddle-node bifurcation at  $E_{11}(x_{11}, y_{11})$  when  $r_1 = r_{1SN}$ . Therefore, it is obvious that the number of internal equilibrium point of the model (2.1) changes from two to three when the value of parameter passes through  $r_1 = r_{1SN}$ . Moreover, the same result is true when  $r_1 = r_{1SN}^*$ .

Based on theoretical analysis, we can provide some threshold conditions for the existence and stability of equilibrium points in the model (2.1), and explore the key conditions for the occurrence of saddle-node bifurcation and transcritical bifurcation in the model (2.1), which can not only supply theoretical support for subsequent numerical simulations, but also clarify the impact mechanism of key ecological environmental factors on the dynamic behavior evolution of the model (2.1).

### 5. Results of Simulation Analysis

In order to better explore the interaction mechanism between algicidal bacteria and algae, we will numerically simulate the dynamic evolution process of the model (2.1), and then reveal the interaction mechanism between algicidal bacteria and algae represented by different dynamic characteristics. Based on the mathematical theory derivation process, we will provide some parameter values as follows:  $r_2 = 0.6$ ,  $h = 0.6$ ,  $k = 10$ ,  $d = 0.2$ ,  $c = 0.5$ ,  $q_1 = 0.15$ ,  $q_2 = 0.12$ ,  $m = 0.1$ . Thus, it is evident that the model (2.1) will undergo a transcritical bifurcation at the equilibrium point  $E_0$  when  $e = e_{TC} = 50$  with  $r_1 = 0.8$ . At the same time, we also can obtain the key values as  $r_1 = r_{1SN}^* = 0.3330067853656466889$  and  $r_1 = r_{1SN} = 0.60968293633525798911$  with the help of  $\Delta = 0$  and  $e = 0.2$ .

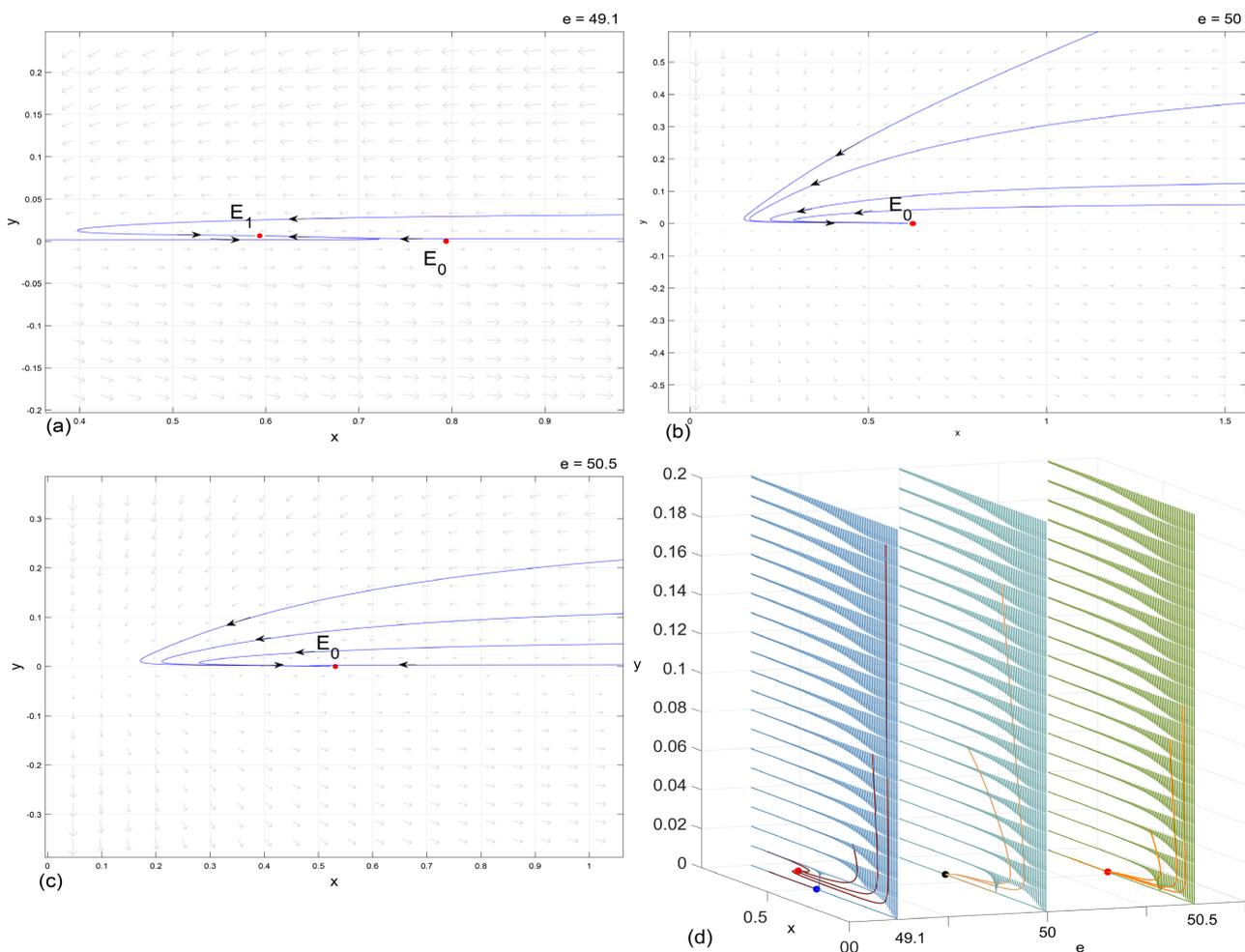
According to Theorems 2 and 4, it can be inferred that the equilibrium point  $E_0$  is stable if  $e > e_{TC} = 50$ , which means that algicidal bacteria will gradually become extinct, and the algal population will gradually increase to its maximum actual environmental capacity. However, when  $e = e_{TC} = 50$ , the model (2.1) will

undergo a transcritical bifurcation at the equilibrium point  $E_0$ , which indicates that the boundary equilibrium point  $E_0$  has lost stability, and the coexistence equilibrium point  $E_1$  of algicidal bacteria and algae appears, detailed numerical simulation results can be found in **Figure 3**. Therefore, it is worth emphasizing that transcritical bifurcation can not only promote the transformation of algicidal bacteria from an extinct state to a gradually coexisting existence, but also seriously affect the dynamic behavior of the model (2.1), this also directly indicates that appropriate combined capture effort is beneficial for the long-term coexistence of algicidal bacteria and algae.

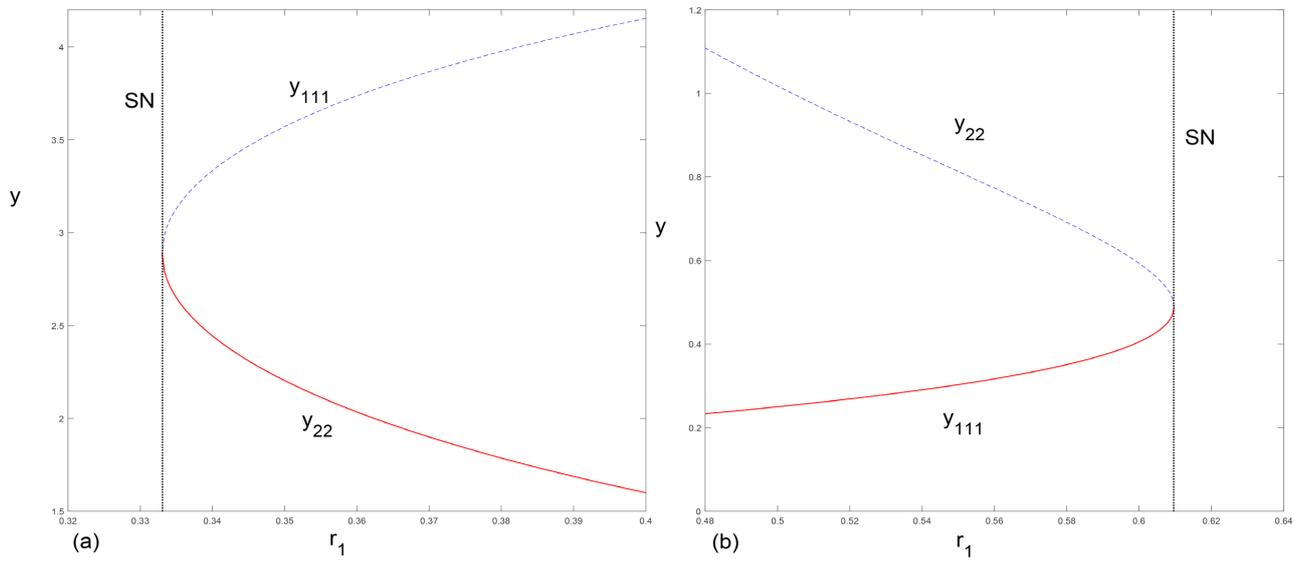
In order to further investigate the impact of algal growth on the interaction between algicidal bacteria and algae, we will choose the intrinsic growth rate  $r_1$  as critical control parameter to simulate the bifurcation dynamics evolution process of the model (2.1). Firstly, it is easy to find from **Figure 4** that the model (2.1) can undergo saddle-node bifurcation when

$$r_1 = r_{1SN}^* = 0.3330067853656466889 \quad \text{and} \quad r_1 = r_{1SN} = 0.60968293633525798911 .$$

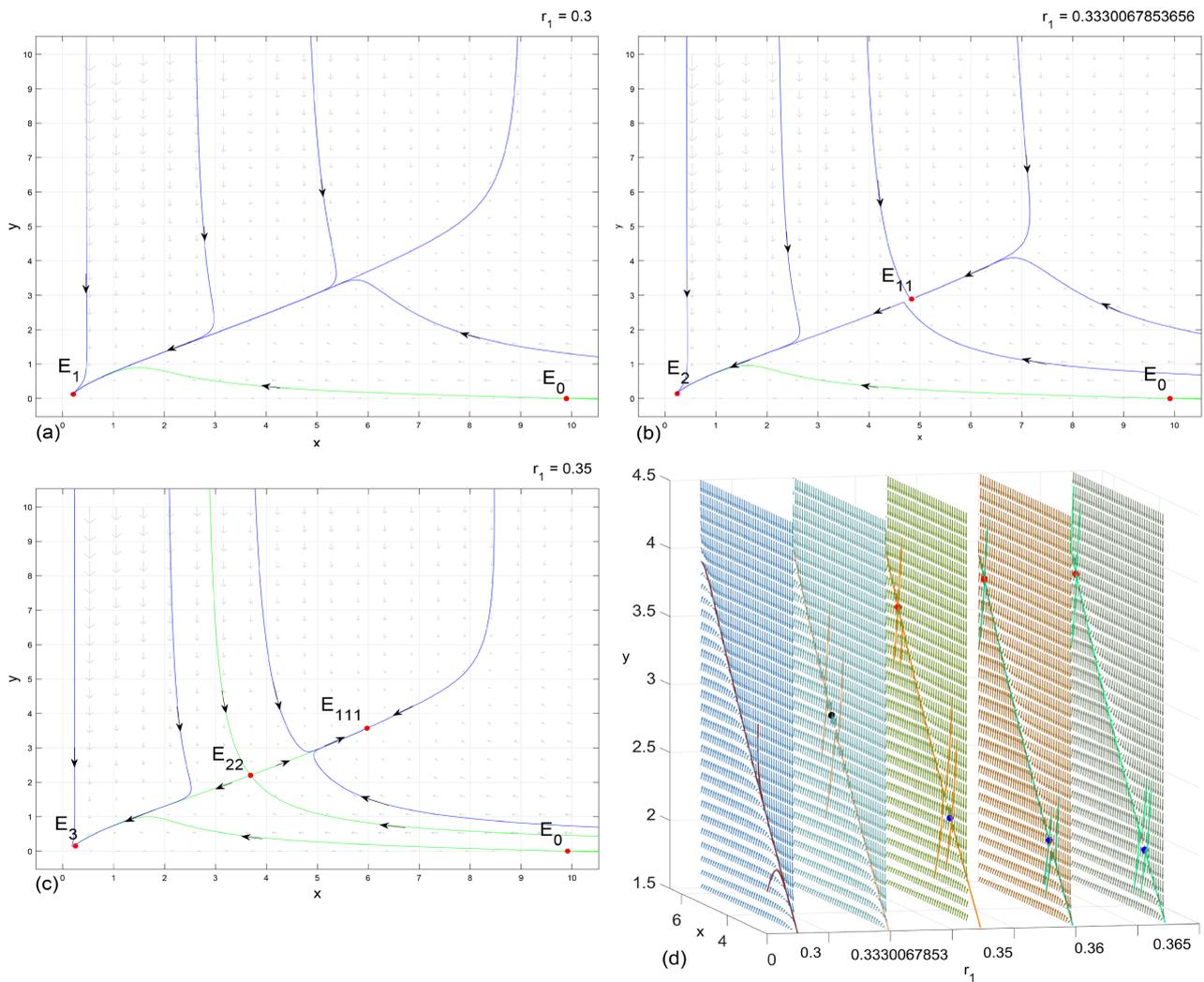
Secondly, it is worth pointing out from **Figure 4(a)** and **Figure 5** that the model (2.1) has only a stable internal equilibrium point  $E_1$  when



**Figure 3.** The process of transcritical bifurcation of the model (2.1) with control parameter  $e$ .



**Figure 4.** Bifurcation diagrams of the model (2.1) with the previously fixed parameters.



**Figure 5.** The process of saddle-node bifurcation of the model (2.1) with control parameter  $r_1 \in (0.3, 0.365)$ .

$r_1 = 0.3 < r_{1_{SN}}^* = 0.3330067853656466889$ , this indicates that algicidal bacteria and algae can form a steady-state coexistence mode, but their density is low, which is not conducive to long-term survival. When  $r_1 = r_{1_{SN}}^* = 0.3330067853656466889$ , the model (2.1) has a stable internal equilibrium point  $E_2$  and an unstable equilibrium point  $E_{11}$ , however, algicidal bacteria and algae ultimately tend to reach an equilibrium state of low numbers. When

$r_1 = 0.35 > r_{1_{SN}}^* = 0.3330067853656466889$ , the model (2.1) has three internal equilibrium points, and two of them are stable, this indicates that algicidal bacteria and algae can form two steady-state coexistence modes simultaneously. Meanwhile, the population density of a steady-state coexistence mode is relatively high, which is conducive to the long-term coexistence and growth of algicidal bacteria and algae. Finally, it is worth further emphasizing that saddle-node bifurcation not only seriously affects the dynamic behavior of the model (2.1), but also promotes the formation of two steady-state coexistence modes between algicidal bacteria and algae. Moreover, it is easy to discover that the increase in the value of parameter  $r_1$  is beneficial for the long-term coexistence and growth of algicidal bacteria and algae.

We further analyze the impact of the increase in parameter  $r_1$  on the long-term coexistence growth mode of algicidal bacteria and algae, a wonderful result can be discovered from **Figure 4(a)** and **Figure 6**. When

$r_1 > r_{1_{SN}} = 0.60968293633525798911$ , algicidal bacteria and algae can form a steady-state growth coexistence mode, and their population density is relatively high, which is conducive to their long-term good growth. At the same time, the model (2.1) will undergo a saddle-node bifurcation when

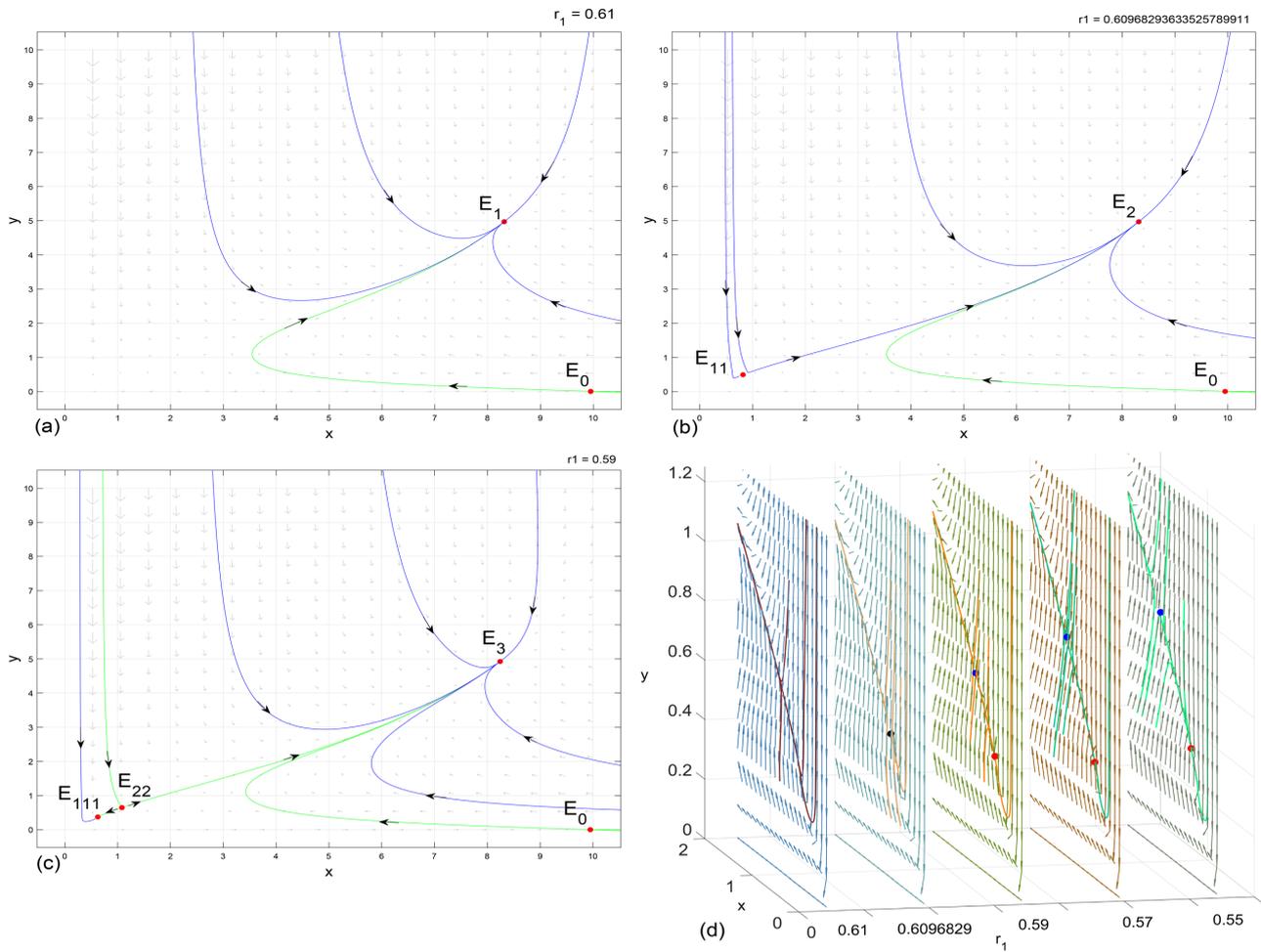
$r_1 < r_{1_{SN}} = 0.60968293633525798911$ . Thus, it must be pointed out that algicidal bacteria and algae can form two steady-state growth coexistence modes when  $0.3330067853656466889 < r_1 < 0.60968293633525798911$ , then algicidal bacteria and algae can form a steady-state growth coexistence mode

$0 < r_1 < 0.3330067853656466889$  or  $r_1 > 0.60968293633525798911$ .

Based on numerical simulation results, it is clearly known that the value of the parameter  $r_1$  not only affects the dynamic behaviors of the model (2.1), but also influences the coexistence mode and the density of algicidal bacteria and algae, and then excessive combined capture effort will lead to the eventual extinction of algicidal bacteria. Therefore, if algicidal bacteria and algae are cultured in the laboratory, it is necessary to increase the self-growth rate of algae in order to form a good algal and bacterial ecosystem.

## 6. Conclusions

Based on the interaction mechanism between algicidal bacteria and algae, an algae-bacteria ecological model was constructed to explore the growth coexistence mode of algicidal bacteria and algae as well as its driving mechanism. Firstly, the mathematical theory work mainly investigated the existence and stability of equilibrium points, and provided threshold conditions for the occurrence of transcritical



**Figure 6.** The process of saddle-node bifurcation of the model (2.1) with control parameter  $r_1 \in (0.55, 0.61)$ .

bifurcation and saddle-node bifurcation in the model, which could not only supply theoretical support for subsequent numerical simulations, but also extract key influencing factors  $r_1$  and  $e$ . Secondly, the relevant dynamic simulation experiments of the model (2.1) were implemented to explore the evolutionary characteristics of some bifurcation dynamics and elucidate the growth coexistence mode and density trends of algalicidal bacteria and algae. Finally, we could conclude that the value of intrinsic growth rate  $r_1$  and combined capture effort  $e$  seriously affected the dynamic behavior of the model (2.1), transcritical bifurcation and saddle-node bifurcation could respectively drive the formation of steady-state growth coexistence mode between algalicidal bacteria and algae.

Specifically, the novelty of this paper lies in the addition of a harvest term to existing models, which can allow for the controllability of algae and algalicidal bacteria. Furthermore, this paper explores the growth coexistence mode of algae and algalicidal bacteria from the perspective of bifurcation dynamics, which will provide a theoretical basis for the cultivation of symbiotic ecology between algae and algalicidal bacteria in the laboratory.

In the follow-up research works, we will continue to investigate the inhibitory

effect of algicidal bacteria on the growth of algal populations and explore the inherent operational characteristics and driving mechanisms of algae-bacteria ecosystems. In a word, it is hoped that the results of this study will contribute to the rapid development of research on the ecological dynamics of algae and bacteria.

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### Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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