GLOBAL ANALYSIS OF A SIMPLE PARASITE-HOST MODEL WITH HOMOCLINIC ORBITS

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(Communicated by Yang Kuang)

Abstract. In this paper, a simple parasite-host model proposed by Ebert et al. (2000) is reconsidered. The basic epidemiological reproduction number of parasite infection ($R_0$) and the basic demographic reproduction number of infected hosts ($R_1$) are given. The global dynamics of the model is completely investigated, and the existence of heteroclinic and homoclinic orbits is theoretically proved, which implies that the outbreak of parasite infection may happen. The thresholds determining the host extinction in the presence of parasite infection and variation in the equilibrium level of the infected hosts are found. The effects of $R_0$ and $R_1$ on dynamics of the model are considered and we show that the equilibrium level of the infected host may not be monotone with respect to $R_0$. In particular, it is found that full loss of fecundity of infected hosts may lead to appearance of the singular case.

1. Introduction. Parasites can reduce host density and induce host population extinction in some cases. In order to understand how six microparasites regulate Daphnia populations and drive the populations to extinction, Ebert et al. [1] formulated the following epidemiological microparasite model

\[
\begin{align*}
\frac{dx}{dt} &= a(x + \theta y) \left(1 - \frac{x+y}{K}\right) - bx, \\
\frac{dy}{dt} &= \beta xy - (d + \alpha)y,
\end{align*}
\]

(1)

2000 Mathematics Subject Classification. 92D30, 34C37, 37G35.

Key words and phrases. Parasite-host model, global dynamics, homoclinic orbit, reproduction number.

The first author is supported by the China NSF Grant (No.11071256). The second author is supported in part by the China NSF Grant (No.11171268), the National Megaproject of Science Research of China (No.2012ZX10001-001), and the Fundamental Research Funds for the Central Universities (No. 08143042). The third author is supported by the Nature Science Foundation of Shaanxi Province of China (No. 2012JQ1019).
where $x(t)$ and $y(t)$ represent the densities of uninfected (susceptible) and infected (infective) hosts at time $t$, respectively; $a$ is the maximum per capita birth rate of uninfected hosts; $\theta (0 \leq \theta \leq 1)$ is the relative fecundity of an infected host; $K$ is the carrying capacity of the environment for the host population; $d$ is the parasite-independent host background mortality; $\beta$ is the constant infection rate, and $\alpha$ is the parasite-induced excess death rate.

In model (1), the microparasite transmission is assumed via a mass action process, the fecundity of uninfected host is density-dependent, and the fecundity of infected host may be reduced due to being infected compared with that of uninfected host. Here, $\theta = 0$ means that infected hosts completely lose fecundity; $\theta = 1$ means that the fecundity of infected hosts is not affected by parasite infection; $0 < \theta < 1$ means that the fecundity of infected hosts is reduced, but they still have certain fecundity. For model (1), there is always equilibrium $O(0,0)$, which is a saddle when $a > d$. This implies that extinction of host is impossible when $a > d$, that is, host always persists when $a > d$. But, in [1], the simulation for the stochastic model indicates that extinction of host likely occurs in certain parameter regions.

By carefully examining the infection term $\beta xy$, Hwang and Kuang [2] replaced the mass action incidence function $\beta xy$ with a standard incidence function $\beta xy/(x+y)$, and obtained the following model

\[
\begin{align*}
\frac{dx}{dt} &= a(x + \theta y) \left(1 - \frac{x+y}{K}\right) - dx - \frac{\beta xy}{x+y}, \\
\frac{dy}{dt} &= \frac{\beta xy}{x+y} - (d + \alpha)y,
\end{align*}
\]

where $\beta$ represents the maximum number of infections that an infected host can cause per unit time. Subsequently, based on model (2), some higher dimensional epidemiological models were presented and analyzed[3, 4, 5].

Since model (2) is not differentiable at the origin, Hwang and Kuang [2] initially transformed model (2) into the form of a Gause-type predator-prey system by making the change of variables $(x,y) \rightarrow (u,y)$ with $u = x/y$, and then, by investigating the transformed system, they showed that the transformed system can exhibit the parasite induced host extinction. This theoretically complements the findings in [1]. However, Hwang and Kuang [2] did not consider dynamical behaviors of model (2) directly, some complicated and interesting dynamics of model (2) were missed.

In [6], Berezovsky et al. incorporated the emigration of uninfected hosts into model (2), and then obtained the following model

\[
\begin{align*}
\frac{dx}{dt} &= a(x + \theta y) \left(1 - \frac{x+y}{K}\right) - (d + m)x - \frac{\beta xy}{x+y}, \\
\frac{dy}{dt} &= \frac{\beta xy}{x+y} - (d + \alpha)y,
\end{align*}
\]

where $m$ is the per capita emigration rate of uninfected hosts. They mathematically studied it as an epidemiological model, and found a family of homoclinic orbits by investigating the local dynamics of the model near the origin. But the effect of the related parameters on dynamical behaviors of the model is not discussed completely. In particular, the case $\theta = 0$ is not considered. Note that model (2) and model (3) are dynamically equivalent.

In this paper, we reconsider model (2) by rescaling it and completely analyzing the global dynamics of the rescaled model. The initial objective is to fully understand the asymptotic behavior of model (2) and theoretically prove the existence of its heteroclinic and homoclinic orbits. In particular, we investigate the effect of the basic epidemiological reproduction number of parasite ($R_0$) and the basic demographic reproduction number of infected hosts ($R_1$) on the survival of hosts,
and analyze the change of the level of infected hosts with the basic reproduction number of parasite infection ($R_0$).

The organization of this paper is as follows. In the next section, we initially rescale model (2) and then introduce the primary results on the rescaled system. In Sections 3 and 4, we theoretically analyze the rescaled system with cases $0 < \theta \leq 1$ and $\theta = 0$, respectively, and prove the existence of heteroclinic and homoclinic orbits of the rescaled system. Dynamic behaviors of system (2) are demonstrated in Section 5, where the effect of $R_0$ and $R_1$ on dynamics of the model is investigated. The effect of $R_0$ on the level of infected hosts is also considered in Section 6. We conclude with a discussion of the results in Section 7.

2. Rescaling and primary results. Rescaling model (2) by letting

\[
\tilde{x} = x/K, \quad \tilde{y} = y/K, \quad \text{and} \quad \tilde{t} = at,
\]

and removing the bars leads to the rescaled system

\[
\begin{align*}
\frac{dx}{dt} &= (x + \theta y)[1 - (x + y)] - \delta x - \frac{sxy}{x+y} =: P(x, y), \\
\frac{dy}{dt} &= \frac{sxy}{x+y} - (\delta + r)y =: Q(x, y),
\end{align*}
\]

(4)

where

\[
s = \beta/a, \delta = d/a, r = \alpha/a.
\]

It follows from (4) that

\[
\frac{d(x + y)}{dt} = (x + \theta y)[1 - (x + y)] - \delta(x + y) - ry.
\]

Since $0 \leq \theta \leq 1$, then

\[
\frac{d(x + y)}{dt} \leq (1 - \delta)(x + y) \quad \text{for} \quad x \geq 0 \quad \text{and} \quad y \geq 0,
\]

which gives that $\lim_{t \to +\infty}(x(t), y(t)) = (0, 0)$ for $\delta \geq 1$. So, in the rest of this paper, we shall assume $\delta < 1$, which implies that $a > d$ for (2). For convenience of discussion hereafter, we give the following results about (4).

Lemma 2.1. (i) The $x$-axis is an invariant set of (4). And $\lim_{t \to +\infty} x(t) = 1 - \delta$ for the initial value $(x(0), 0)$ with $x(0) > 0$; $\lim_{t \to -\infty} x(t) = 0$ for the initial value $(x(0), 0)$ (where $0 < x(0) < 1 - \delta$).

(ii) The set $D_1 = \{(x, y) \in R^2_+ : x + y \leq 1 - \delta\}$ is always positively invariant to (4).

(iii) The set $D_2 = \{(x, y) \in R^2_+ : \theta y \geq (s - r - 1)x, x + y \leq 1 - \delta\}$ is positively invariant to (4) when $s > r + 1$ and $\theta \neq 0$.

Proof. Lemma 2.1 (i) and (ii) can be proved easily, so we omit it. To prove (iii) we get from (4),

\[
\frac{d}{dt} \left( \frac{y}{x} \right) = \frac{y}{x} \left[ (s - r - 1)x - \theta y + (x + \theta y)(x + y) \right] > \frac{y}{x} \left[ (s - r - 1) - \theta \frac{y}{x} \right], \quad \text{for} \quad x > 0, y > 0,
\]

then $\lim_{t \to +\infty} \frac{y(t)}{x(t)} \geq (s - r - 1)/\theta$ as $s > r + 1$. Hence, the set $\{(x, y) \in R^2_+ : \theta y \geq (s - r - 1)x\}$ is positively invariant to (4) when $s > r + 1$. Therefore, according to Lemma 2.1(ii), the set $D_2 = \{(x, y) \in R^2_+ : \theta y \geq (s - r - 1)x, x + y \leq 1 - \delta\}$ is positively invariant to (4) when $s > r + 1$. \(\square\)
According to Lemma 2.1, we henceforth do our mathematical analysis on the set $D_1$. For the case $s > r + 1$, the feasible region may be limited on the set $D_2 (D_2 \subset D_1)$.

On the other hand, if we choose $B(x, y) = 1/(xy)$ as a Dulac function, it follows from (4) that
\[
\frac{\partial(BP)}{\partial x} + \frac{\partial(BQ)}{\partial y} = -\frac{1}{y} - \frac{\theta(1 - y)}{x^2} < 0, \text{ for } (x, y) \in \text{int}D_1.
\]

Therefore, we have

**Lemma 2.2.** In the interior of the set $D_1$, there is no closed orbit to (4).

3. **Mathematical analysis for system** (4) **with** $0 < \theta \leq 1$. In this section, we consider dynamical behaviors of the rescaled system (4) with $0 < \theta \leq 1$, that is, the infected hosts have certain fecundity.

3.1. **The existence and stability of equilibria.** It is easy to see that $E_0 (1 - \delta, 0)$ is always an equilibrium of system (4). Direct calculation shows that, when $s > \delta + r$ and $\theta(s - \delta - r) > (\delta + r)(s - r - 1)$, system (4) has a unique positive equilibrium $E^* (x^*, y^*)$, where
\[
x^* = \frac{(\delta + r)(\theta(s - \delta - r) - (\delta + r)(s - r - 1))}{s[\theta + (1 - \theta)(\delta + r)]},
\]
\[
y^* = \frac{s(\theta(s - \delta - r) - (\delta + r)(s - r - 1))}{s[\theta + (1 - \theta)(\delta + r)]}.
\]
Here, $E_0$ represents that host has not been infected, $E^*$ implies that host is infected chronically. About the local stability of $E_0$ and $E^*$, we have

**Theorem 3.1.** The boundary equilibrium $E_0$ is locally asymptotically stable on the set $D_1$ if $s \leq \delta + r$, and unstable if $s > \delta + r$. The positive equilibrium $E^*$ is locally asymptotically stable if $s > \delta + r$ and $\theta(s - \delta - r) > (\delta + r)(s - r - 1)$.

**Proof.** From the Jacobian matrices of (4) at $E_0$ and $E^*$, it is easy to know that $E_0$ is locally asymptotically stable on the set $D_1$ for $s < \delta + r$, and unstable for $s > \delta + r$. And the positive equilibrium $E^*$ is locally asymptotically stable if it is feasible.

When $s = \delta + r$, equilibrium $E_0$ is a higher order one. To discuss its locally stability on the set $D_1$, we make the change of variables: $u = x - (1 - \delta)$, $v = y$, which moves $E_0$ in the $xy$-plane to the origin in the $uv$-plane, then (4) becomes
\[
\begin{align*}
\frac{du}{dt} &= -(1 - \delta)u + [(1 + \theta)\delta - 1 - s]v - (u + \theta v)(u + v) + \frac{sv^2}{(1 - \delta) + u + v}, \\
\frac{dv}{dt} &= -\frac{sv^2}{(1 - \delta) + u + v}.
\end{align*}
\] (6)

Letting $w = (1 - \delta)u - [(1 + \theta)\delta - 1 - s]v$, system (6) yields
\[
\begin{align*}
\frac{dw}{dt} &= -(1 - \delta) \left\{ w + \frac{w + (\theta\delta - s)v[2w + (\delta + \theta - 1 - s)v]}{(1 - \delta)^2} - \frac{(s - \theta)sv^2}{(1 - \delta)^2 + w + (\theta\delta - s)v} \right\}, \\
\frac{dv}{dt} &= -\frac{sv^2}{(1 - \delta)^2 + w + (\theta\delta - s)v}.
\end{align*}
\] (7)

It follows from $\frac{dw}{dt} = 0$ that
\[
w + \frac{w + (\theta\delta - s)v[2w + (\delta + \theta - 1 - s)v]}{(1 - \delta)^2} + \frac{(s - \theta)sv^2}{(1 - \delta)^2 + w + (\theta\delta - s)v} = 0.
\] (8)

Direct calculation shows that, for the implicit function $w = w(v)$ defined by (8), $\frac{dw}{dv} |_{(0,0)} = 0$, which implies $w = o(v)$. Substituting it into the second equation of
Proof.

(7) gives \( \frac{dv}{dt} = -sv^2/(1-\delta) + o(v^2) \). Thus, according to Theorem 7.1 in [7], \( s/(1-\delta) > 0 \) implies that \( E_0 \) is locally asymptotically stable on the set \( D_1 \) for \( s = \delta + r \).

To consider the global stability of \( E_0 \) and \( E^* \) of (4) on the positively invariant set \( D_1 \), we first need to discuss the dynamical behaviors of (4) near the origin in the first quadrant since it may be complex.

Lemma 3.2. (i) When \( s \leq r + 1 \), orbits of system (4) starting from near the origin in the interior of \( D_1 \) move away from the origin as \( t \) increases;

(ii) When \( s > r + 1 \) and \( \theta(s-\delta-r) > (\delta + r)(s-r-1) \), orbits of system (4) initiating from near the line \( \theta y = (s-r-1)x \) sufficiently close to the origin, we have

\[
\frac{dx}{dt} \bigg|_{\theta y = (s-r-1)x} = \frac{x \{[\theta(s-\delta-r) - (\delta + r)(s-r-1)] - (s-r)(x+y)\}}{s + \theta - r - 1} > 0,
\]

and

\[
\frac{dy}{dt} \bigg|_{\theta y = (s-r-1)x} = \frac{y}{s + \theta - r - 1} [\theta(s-\delta-r) - (\delta + r)(s-r-1)] > 0.
\]

Thus, according to dependence relationship of solutions of (4) on the initial values, orbits of (4) initiating from near the line \( \theta y = (s-r-1)x \) sufficiently close to the origin move away from the origin. And, for points in the interior of \( D_2 \), the inequality \((s-r-1) \cos \varphi < \theta \sin \varphi\) always holds, which implies \( G(\varphi) < 0 \). Similar to the case \( s \leq r+1 \), (9) has no characteristic direction in the interior of \( D_2 \) for this case. Therefore, when \( s > r+1 \) and \( \theta(s-\delta-r) > (\delta + r)(s-r-1) \), orbits of system (4) starting from near the origin in the interior of \( D_2 \) move away from the origin as \( t \) increases.

\(\square\)
According to Lemma 3.2, when \( s \leq r + 1 \) or \( s > r + 1 \) and \( \theta(s - \delta - r) > (\delta + r)(s - r - 1) \), no orbit of (4) starting from the first quadrant approaches the origin as \( t \to +\infty \).

Notice that when \( \delta + r < s \leq r + 1 \), the inequality \( \theta(s - \delta - r) > (\delta + r)(s - r - 1) \) holds. So equilibrium \( E^* \) exists when \( \delta + r < s \leq r + 1 \). Therefore, according to Lemma 2.2, we have the following conclusion about the global stability of \( E_0 \) and \( E^* \).

**Theorem 3.3.** For system (4), when \( s \leq \delta + r \), equilibrium \( E_0 \) is globally stable on the set \( D_1 \); when \( s > \delta + r \) and \( \theta(s - \delta - r) > (\delta + r)(s - r - 1) \), equilibrium \( E^* \) is globally stable in the interior of the set \( D_1 \).

3.2. **Heteroclinic and homoclinic orbits.** According to the results obtained in Section 3.1, the global dynamical behaviors of (4) have been understood clearly for the following cases:

\[ s \leq \delta + r; \quad s > \delta + r \text{ and } \theta(s - \delta - r) > (\delta + r)(s - r - 1). \]

Notice that the inequality \( \theta(s - \delta - r) > (\delta + r)(s - r - 1) \) always holds for \( \delta + r < s \leq r + 1 \), then, in the following, we consider dynamics of (4) in a case of \( s > 1 + r \) and \( \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \).

We initially discuss the vertical isocline \( L \) of (4). Denote

\[ g(x, y) := (1 - \delta)x^2 + \theta y^2 + (\theta + 1 - \delta - s)xy, \]

then, it follows from \( dx/dt = 0 \) that the vertical isocline \( L \) of (4) is defined by equation

\[ g(x, y) = (x + \theta y)(x + y)^2. \quad (12) \]

Obviously,

\[ \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \iff f(r) := r^2 - (s + \theta - \delta - 1)r + [\delta(1 - \theta) - s(\delta - \theta)] \leq 0. \]

Since \( f(r) \) is a quadratic function of \( r \), then \( f(r) \leq 0 \) implies that the discriminant of equation \( f(r) = 0 \) is positive, that is, \( \Delta := (\theta + 1 - \delta - s)^2 - 4\theta(1 - \delta) \geq 0. \)

Notice that the discriminant of equation \( g(1, u) = 0 \) of \( u \) is also \( \Delta \). On the other hand, from \( \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \) and \( s - \delta - r > s - r - 1 > 0 \), we easily have that \( \theta < \delta + r \), i.e., \( r > \theta - \delta \). So it follows from \( s > r + 1 \) that \( s > \theta + 1 - \delta \), that is, \( \theta + 1 - \delta - s < 0 \). Thus, when \( s > r + 1 \) and \( \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \), equation \( g(1, u) = 0 \) has two distinct positive roots,

\[ k_{\pm} = \frac{(s + \delta - \theta - 1) \pm \sqrt{\Delta}}{2\theta}. \quad (13) \]

Therefore, for this case, \( g(x, y) \) can be rewritten as \( g(x, y) = \theta(y - k_+x)(y - k_-x) \).

Furthermore, (12) can be rewritten as

\[ (y - k_-x)(y - k_+x) = \left( y + \frac{1}{\theta}x \right) (y + x)^2. \quad (14) \]

By applying Lemma 7.1 in Appendix to (14), we have the following Lemma with respect to the vertical isocline \( L \) of system (4).

**Lemma 3.4.** When \( s > r + 1 \) and \( \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \), the vertical isocline \( L \) of (4) defined by (12) (or (14)) consists of two branches, which have the following properties:
Global Analysis of a Parasite-Host Model

(i) The two branches intersect with two coordinate axes at points \((1 - \delta, 0)\) and \((0, 1)\), respectively.

(ii) The two branches are located in the regions \(D_3 = \{(x, y) \in \mathbb{R}^2_+: y < k - x\}\) and \(D_4 = \{(x, y) \in \mathbb{R}^2_+: y > k + x\}\), respectively.

(iii) One of the two branches in the region \(D_3\) is concave down, while the other in the region \(D_4\) is concave left.

According to Lemma 3.4, the two branches of the vertical isocline \(L\) of (4) are shown in Figure 1.

![Figure 1](image1.png)

**Figure 1.** The vertical isocline \(L\) of (4) as \(s > r + 1\) and \(\theta(s - \delta - r) \leq (\delta + r)(s - r - 1)\).

![Figure 2](image2.png)

**Figure 2.** The heteroclinic and homoclinic orbits of (4). The thick closed curve is a heteroclinic closed orbit, the thin curves surrounded by the closed curve are all homoclinic orbits. Here, \(\theta = 0.2, \delta = 0.4, r = 0.5, \) and \(s = 1.8\). All the orbits of (4) starting from the first quadrant approach the origin along the direction \(\varphi = \arctan 1.5\) as \(t\) tends to positive infinity.
Theorem 3.5. When $s > r + 1$ and $\theta(s - \delta - r) \leq (\delta + r)(s - r - 1)$, for (4) we have the following results:

(i) There is a heteroclinic closed orbit of (4) on the set $D_1$;
(ii) There is a family of homoclinic orbits of (4), which are full of the domain surrounded by the heteroclinic closed orbit (Fig. 2);
(iii) All the orbits of (4) starting from the first quadrant approach the origin along the direction $\varphi = \arctan(s - r - 1)/\theta$ as $t$ tends to positive infinity.

Proof. (i) We initially prove that there is a heteroclinic orbit $L_1$ of (4) in the interior of $D_1$, where $\lim_{t \to +\infty}(x(t), y(t)) = (0, 0)$ and $\lim_{t \to -\infty}(x(t), y(t)) = (1 - \delta, 0)$ for $(x(t), y(t)) \in L_1$.

Since $s > r + 1$ implies $s > \delta + r$, it follows from the Jacobian matrix of (4) at $E_0$ that $E_0$ is a saddle. Hence, there is a saddle separatrix $L_1$ of $E_0$ in the first quadrant, whose slope at $E_0$ is

$$k_1 = \frac{(1 - \delta) + (s - \delta - r)}{(1 + \theta)\delta - 1 - s}. \quad (15)$$

It is easy to know that $L_1$ is an unstable manifold of $E_0$, that is, $\lim_{t \to -\infty}(x(t), y(t)) = E_0$ for $(x(t), y(t)) \in L_1$.

By Lemma 3.4, the vertical isocline $L$ of (4) passes through $E_0$. And direct calculation shows that the tangential slope of $L$ at $E_0$ is

$$k_2 = \frac{1 - \delta}{(1 + \theta)\delta - 1 - s}. \quad (16)$$

Using $\theta(s - \delta - r) \leq (\delta + r)(s - r - 1)$ yields

$$(1 + \theta)\delta - 1 - s \leq -\frac{T}{s - \delta - r},$$

where $T = (s - r - 1)^2 + (1 - \delta)[(\delta + 3 + r)(s - r - 1) + (2 + r - \delta)]$. Obviously, $T > 0$ for $s > r + 1$. So $(1 + \theta)\delta - 1 - s < 0$. Thus, it follows from (15) and (16) that $-1 < k_1 < k_2 < 0$, which implies that the separatrix $L_1$ near $E_0$ is located between the line $x + y = 1 - \delta$ and the vertical isocline $L$.

According to Lemma 2.1, when $s > r + 1$, the separatrix $L_1$ must pass through the line $y = (s - r - 1)x/\theta$ and enter the region $D_2$ in a finite time. Again, $s > r + 1$ and $\theta(s - \delta - r) \leq (\delta + r)(s - r - 1)$ imply $0 < k_2 < \frac{-\delta - \delta + r}{\delta + r} \leq \frac{\delta - r - 1}{\delta + r} < k_1$, so it follows from Lemma 3.4 that system (4) has no equilibrium in the set $D_2 \setminus \{O\}$, then $L_1$ must approach the origin as $t$ tends to positive infinity, that is, $\lim_{t \to +\infty}(x(t), y(t)) = O$ for $(x(t), y(t)) \in L_1$.

The above inference shows that $L_1 \subset D_1$ is a heteroclinic orbit of (4) connecting equilibrium $E_0$ and the origin $O$.

On the other hand, by Lemma 2.1 (i) the line segment $L_2 = \{(x, y) : 0 < x < 1 - \delta, y = 0\}$ is also a heteroclinic orbit of (4) connecting $E_0$ and $O$, and $\lim_{t \to -\infty}(x(t), y(t)) = O, \lim_{t \to +\infty}(x(t), y(t)) = E_0$. Therefore, the closed curve consisting $L_1, L_2, E_0$ and $O$ is a closed heteroclinic orbit of (4) on the set $D_1$.

(ii) Since (4) has no positive equilibrium in the set $D_1$ and $\varphi = 0$ is a characteristic direction of (4) according to expression (11), it is easy to know that there is a family of homoclinic orbits of (4) full of the interior of the heteroclinic closed orbit.

(iii) To further understand dynamics of (4) for $s > 1 + r$ and $\theta(s - \delta - r) \leq (\delta + r)(s - r - 1)$, by introducing the change of variables $(x, y) \to (x, u)$ for (4), where $u = y/x$, then (4) becomes
4. Mathematical analysis for system (4) with $\theta = 0$. In this section, we consider dynamical behaviors of the rescaled system (4) in the case $\theta = 0$, which implies that the fecundity of infected hosts is completely lost.

When $\theta = 0$, system (4) becomes
\[
\begin{aligned}
\frac{dx}{dt} &= x \left( (1 - \delta) - (x + y) - \frac{sx}{x+y} \right), \\
\frac{dy}{dt} &= y \left( \frac{sx}{x+y} - (\delta + r) \right).
\end{aligned}
\]  

Similar to the previous argument for the case of $0 < \theta \leq 1$, for system (18) the first two items of Lemma 2.1 hold true, and so is Lemma 2.2. With respect to the existence and stability of equilibria of system (18), we have the following results.

**Theorem 4.1.** System (18) always has the infection-free equilibrium $E_0(1 - \delta, 0)$, which is globally stable on the set $D_1$ when $s \leq \delta + r$; when $\delta + r < s < r + 1$, system (18) has a unique positive equilibrium $E_1^*(x_1^*, y_1^*)$, which is globally stable in the interior of the set $D_1$, where
\[
x_1^* = \frac{(\delta + r)(r + 1 - s)}{s}, \quad y_1^* = \frac{(s - \delta - r)(r + 1 - s)}{s}.
\]
Notice that both $x$-axis and $y$-axis are solution curves of system (18). For system (18) we can have the following results similar to Theorem 3.5.

**Theorem 4.2.** When $s \geq r+1$, system (18) has a heteroclinic closed orbit on the set $D_1$, and a family of homoclinic orbits is full of the interior the heteroclinic closed orbit (Figure 3).

For system (18), function $G(\phi)$ defined in (11) becomes

$$G(\phi) = \rho(s-r-1) \sin \phi \cos \phi (\cos \phi + \sin \phi),$$

then, when $s > r+1$, $\phi = 0$ and $\phi = \pi/2$ are the characteristic directions of system (18); when $s = r+1$, $G(\phi) \equiv 0$, which is the singular case. Therefore, for dynamics of system (18) near the origin $O$ we have

**Corollary 1.** When $s > r+1$, any orbit of system (18) starting from the first quadrant approaches the origin along the $y$-axis as $t$ tends to positive infinity, and any orbit leaving the origin moves along the $x$-axis as $t$ increases (Figure 3(a)); however, when $s = r+1$, along any direction except for $\phi = \arctan \frac{s-\delta}{\delta+r}$, there is a unique orbit of system (18) which either tends to or leaves the origin (Figure 3(b)) as $t$ increases.

![Figure 3](image-url)

**Figure 3.** The heteroclinic and homoclinic orbits of (18). The thick closed curve is a heteroclinic closed orbit, the thin closed curves surrounded within the heteroclinic closed orbit are all homoclinic orbits. Figure 3(a) corresponds to the case $s > r+1$, where $\delta = 0.4$, $r = 0.5$, and $s = 1.8$. Figure 3(b) corresponds to the case $s = r+1$, where $\delta = 0.4$, $r = 0.5$, and $s = 1.5$.

5. **Dynamic behaviors of system (2).** In sections 3 and 4, we have completely analyzed the rescaled system (4). In this section, we will discuss dynamical behaviors of model (2) according to the above results, and explain these results epidemiologically.

We first summarize the main results on system (4) in Table 1, which shows that system (4) has four types of dynamical behaviors:
For Case (C1) defined in Table 1, the global stability of the origin $O$ implies that hosts (including uninfected and infected hosts) go to extinction eventually. The host extinction in such case is not due to the parasite infection but demographic decline feature of hosts themselves.

For Case (C2), the global stability of $E_0$ implies that parasite infection dies out eventually in the host population, while uninfected host population approaches a positive constant as $t$ tends to infinity.

For Case (C3), the parasite infection keeps present persistently. The sizes of both uninfected and infected hosts stabilize to positive constants eventually as $t$ tends to infinity.

For Case (C4), the parasite infection leads to host extinction due to parasite regulation, whereas hosts do not extinct in the absence of parasite infection, which is different from Case (C1). Here, the existence of homoclinic orbits shows that the outbreak of parasite infection is possible. Whether the infected hosts can reproduce may lead to various phenomena. For $\theta \neq 0$, that is, the infected hosts can certainly reproduce, by Theorem 3.5 we have $\lim_{t \to \infty} y(t)/x(t) = (s - r - 1)/\theta$, which implies that in the process of host extinction the ratio between sizes of infected and uninfected hosts tends to a constant. However, for $\theta = 0$, that is, the infected hosts can not reproduce, the change of the ratio is complex according to Corollary 1.

To describe the obtained results with the original parameters in model (2) and demonstrate them epidemiologically, we introduce three new parameters with the original parameters:

$$R_0 = \frac{\beta}{d + \alpha}, \quad R_1 = \frac{\theta a}{d + \alpha}, \quad R_2 = \frac{a}{d}.$$  

Since $1/d$ and $1/(d + \alpha)$ are the average periods that the uninfected and infected hosts stay in their compartments, respectively. $a$ and $\theta a$ are the per capita maximum birth rates of uninfected and infected hosts, respectively. Then $R_0$ is referred to as the basic epidemiological reproduction number of parasite infection, that is, average of number of secondary infections induced by a single infected host in a whole susceptives during infectious period. Whereas, $R_1$ and $R_2$ are the basic demographic reproduction numbers of infected and uninfected hosts, respectively.

For simplicity, we define the following two parameters

$$\gamma = \frac{d}{d + \alpha}, \quad \hat{R}_0 = \begin{cases} 
1 + \frac{\gamma(R_2 - 1)}{1 - R_1}, & \text{for } R_1 \neq 1; \\
+\infty, & \text{for } R_1 = 1,
\end{cases}$$

where $\gamma$ represents the ratio between the average life spans of infected and uninfected hosts, $\hat{R}_0$ is a threshold determining the existence of hosts in the presence of parasite, which will be understood in the following discussion.

By using expressions (5) and the new parameters defined above, the inequality $\theta(s - \delta - r) > (\delta + r)(s - r - 1)$ is equivalent to the inequality

$$(R_2 - 1)\gamma > (R_0 - 1)(1 - R_1). \quad (19)$$

Obviously, (19) holds true for $R_0 > 1$ and $R_2 > 1$ when $R_1 \geq 1$. However, when $R_1 < 1$, from (19) we have

$$R_0 < 1 + \frac{\gamma(R_2 - 1)}{1 - R_1} = \hat{R}_0.$$  

Notice that, $R_1$, $R_2\gamma$ and $R_2$ satisfy the relations $R_1 \leq R_2\gamma < R_2$ since $\theta \leq 1$. Thus, Table 1 can be re-expressed with Table 2, in which Case (C3) in Table 1 is
\( \delta \geq 1 \quad O \) is globally stable.
\( \delta < 1, \ s \leq \delta + r \quad E_0 \) is globally stable.
\( \delta < 1, \ s > \delta + r, \ \theta(s - \delta - r) > (\delta + r)(s - r - 1) \quad E^* \) is globally stable.
\( \delta < 1, \ s > \delta + r, \ \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) \quad O \) is globally attractive, and there are a family of homoclinic orbits of system (4).

<table>
<thead>
<tr>
<th>Cases</th>
<th>Conditions</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>(C1)</td>
<td>( \delta \geq 1 )</td>
<td>( O ) is globally stable.</td>
</tr>
<tr>
<td>(C2)</td>
<td>( \delta &lt; 1, \ s \leq \delta + r )</td>
<td>( E_0 ) is globally stable.</td>
</tr>
<tr>
<td>(C3)</td>
<td>( \delta &lt; 1, \ s &gt; \delta + r, \ \theta(s - \delta - r) &gt; (\delta + r)(s - r - 1) )</td>
<td>( E^* ) is globally stable.</td>
</tr>
<tr>
<td>(C4)</td>
<td>( \delta &lt; 1, \ s &gt; \delta + r, \ \theta(s - \delta - r) \leq (\delta + r)(s - r - 1) )</td>
<td>( O ) is globally attractive, and there are a family of homoclinic orbits of system (4).</td>
</tr>
</tbody>
</table>

\( R_2 \leq 1 \quad O \) is globally stable.
\( R_2 > 1, \ R_0 \leq 1 \quad E_0 \) is globally stable.
\( R_2 > 1, 1 \leq R_1 \leq R_2 \gamma, \ R_0 \geq 1 \quad E^* \) is globally stable.
\( R_2 > 1 > R_1, R_1 \leq R_2 \gamma, \ 1 < R_0 < R^*_0 \quad E^* \) is globally stable.
\( R_2 > 1 > R_1, R_1 \leq R_2 \gamma, \ R_0 \geq R_0 \quad E^* \) is globally stable.

<table>
<thead>
<tr>
<th>Cases</th>
<th>Conditions</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>(C1)</td>
<td>( R_2 \leq 1 )</td>
<td>( O ) is globally stable.</td>
</tr>
<tr>
<td>(C2)</td>
<td>( R_2 &gt; 1, \ R_0 \leq 1 )</td>
<td>( E_0 ) is globally stable.</td>
</tr>
<tr>
<td>(C3)</td>
<td>( R_2 &gt; 1, 1 \leq R_1 \leq R_2 \gamma, \ R_0 \geq 1 \quad E^* ) is globally stable.</td>
<td></td>
</tr>
<tr>
<td>(C4)</td>
<td>( R_2 &gt; 1, R_0 \geq 1 + \gamma(R_2 - 1) )</td>
<td>( O ) is globally attractive, and there are a family of homoclinic orbits of system (18).</td>
</tr>
</tbody>
</table>

\( R_2 \leq 1 \) implies that the basic demographic reproduction number of uninfected hosts is not greater than 1, then, corresponding to Case (C1), the extinction of hosts is natural in the absence of parasite infection. Therefore, in the following we only discuss the case \( R_2 > 1 \), which implies that hosts can persist forever in the absence of parasite infection.

In order to understand the dependence of dynamics of model (2) on the parameters \( R_0 \) and \( R_1 \) for the given parameters \( R_2 \) (\( R_2 > 1 \)) and \( \gamma \) (\( \gamma < 1 \)), we partition the feasible regions of \( R_0 \) and \( R_1 \) into some subregions according to Table 2. These
regions are shown in Figure 4. Figure 4(a) and (b) correspond to two cases: \(R_2 \gamma \geq 1\) and \(R_2 \gamma < 1\), respectively.

In Figure 4(a) we define the region \(\Omega_2 = \{(R_1, R_0) : 0 \leq R_1 \leq R_2 \gamma, 0 < R_0 \leq 1\}\) corresponding to Case (C2), the region \(\Omega_3 = \{(R_1, R_0) : 1 \leq R_1 \leq R_2 \gamma, R_0 > 1\}\) corresponding to Case (C3), the region \(\Omega_{32} = \{(R_1, R_0) : 0 \leq R_1 < 1, 1 < R_0 < R_0^*\}\) corresponding to Case (C32), and the region \(\Omega_4 = \{(R_1, R_0) : 0 \leq R_1 < 1, R_0 \geq R_0^*\}\) corresponding to Case (C4). In Figure 4(b), Case (C31) does not exist for \(R_1 \leq R_2 \gamma < 1\). The region \(\Omega'_2 = \{(R_1, R_0) : 0 \leq R_1 \leq R_2 \gamma, 0 < R_0 \leq 1\}\) is associate with Case (C2), the region \(\Omega'_{32} = \{(R_1, R_0) : 0 \leq R_1 \leq R_2 \gamma, 1 < R_0 < R_0^*\}\) is associated with Case (C32), and the region \(\Omega'_4 = \{(R_1, R_0) : 0 \leq R_1 \leq R_2 \gamma, R_0 \geq R_0^*\}\) is related to Case (C4).

![Figure 4](image-url)

**Figure 4.** The division of the feasible region of \(R_0\) and \(R_1\) corresponding to the different dynamics of model (2), where the curve \(l_1 : R_0 = 1 + \gamma (R_2 - 1)/(1 - R_1) (= R_0^*); l_2 : R_1 = R_2 \gamma; l_3 : R_1 = 1\); and \(l_4 : R_0 = 1\). Here, Figure 4(a) corresponds to the case \(R_2 \gamma \geq 1\); Figure 4(b) corresponds to the case \(R_2 \gamma < 1\).

In the region \(\Omega_2\) (or \(\Omega'_2\)), the basic reproduction number of parasite infection \(R_0\) is less than unity, which implies the parasite infection dies out eventually in the host population. The uninfected host population tends to \(K(a - d)/a\) as \(t\) tends to infinity.

In the regions \(\Omega_3, \Omega_{32}\) and \(\Omega_4\) (or \(\Omega'_{32}\) and \(\Omega'_4\)), the basic reproduction number of parasite infection is greater than 1, which indicates that the parasite infection keeps persistently. However, for the different values of \(R_1\), there are some essential differences between the associated dynamical behaviors of (2).

In the region \(\Omega_3, R_1 \geq 1\) implies that infected hosts can reproduce sufficient uninfected hosts to maintain the supply of uninfected hosts being infected. In such case, parasite infection can not regulate the host population even if \(R_0\) is sufficiently large. Whereas, in \(\Omega_{32}\) (or \(\Omega'_{32}\)), \(R_1 < 1\) implies that infected hosts’ reproduction is not large enough to induce various dynamics, depending on relation of \(R_0\) and \(R_1\). In such scenario, parasite infection can not regulate the host population unless \(R_0 \geq R_0^*\).

In the region \(\Omega_4\) (or \(\Omega'_4\)) where \(R_0 \geq R_0^*\) and \(R_1 < 1\), a combination of large epidemiological reproduction number and small demographic reproduction number...
of infected hosts results in ultimate extinction of both uninfected and infected hosts due to parasite regulation. However, according to Theorem 3.5 and Corollary 1, the trend of the extinction of uninfected and infected hosts is different for the cases \( R_1 \neq 0 \) and \( R_1 = 0 \). When \( R_1 \neq 0 \),

\[
\lim_{t \to \infty} \frac{y(t)}{x(t)} = \frac{1}{R_1} [R_0 - 1 - \gamma(R_2 - 1)],
\]

which implies that the extinction of uninfected and infected hosts is along certain direction. Whereas, when \( R_1 = 0 \), the limit (i.e., the direction of extinction) depends on the initial values of (2).

We initially consider the effect of \( R_0 \) on dynamics of the system for various \( R_1 \). When \( R_1 < 1 \), the dynamics of system (2) go through extinction of parasite infection (i.e., global stability of disease-free equilibrium for \( R_0 \leq 1 \)), persistence of both parasite infection and host population (i.e., global stability of the endemic state for \( 1 < R_0 < R_0^* \)), and hosts extinction while infection persistence (i.e., global attractiveness of the origin for \( R_0 \geq R_0^* \)) as the epidemiological reproduction number \( R_0 \) increases. Whilst \( R_1 \geq 1 \), the first two kinds of dynamics of system (2) certainly occur, but the third kind - parasite regulation does not happen. For fixed \( R_0 \) (either \( R_0 < 1 \) or \( 1 < R_0 < 1 + \gamma(R_2 - 1) \)), global extinction or persistence of parasite infection is independent on \( R_1 \). However, for relatively large \( R_0 \) (\( R_0 \geq 1 + \gamma(R_2 - 1) \)), increasing \( R_1 \) would change the dynamics of system (2) from host extinction to host persistence while keeping infection present.

6. The effect of \( R_0 \) on the equilibrium level of infected hosts. For classical parasite-host models, virus dynamical models and epidemic models, the level of infected hosts (virus, individuals) often increases with increase of the associated basic reproduction number when the positive equilibrium is feasible. But, for system (2) the dependence of the level of infected hosts on the associated basic reproduction number is not such simple. In the following we consider the change of the equilibrium level of infected hosts with the basic reproduction number of parasite infection(\( R_0 \)).

To show the dependence of the level of infected hosts \( y^* \) on \( R_0 \), we denote \( y^* = y^*(R_0) \), then direct calculation shows that

\[
\frac{dy^*}{dR_0} = \frac{K\phi(R_0)}{R_0^2 [R_1(R_0 - 1) + R_2\gamma]^2},
\]

where

\[
\phi(R_0) = c_0(R_1)R_0^2 + c_1(R_1)R_0 + c_2(R_1),
\]

\[
c_0(R_1) = R_1^2 - (1 - \gamma)R_1 - \gamma R_2,
\]

\[
c_1(R_1) = 2R_1 [(1 - \gamma) + (R_2\gamma - R_1)] > 0,
\]

\[
c_2(R_1) = (\gamma R_2 - R_1) [(1 - \gamma) + (R_2\gamma - R_1)] > 0,
\]

with \( R_1 \leq R_2\gamma \) and \( \gamma < 1 \) being used. It is easy to see that there exists a unique positive zero of quadratic function \( c_0(R_1) \), \( R_1 = [(1 - \gamma) + \sqrt{(1 - \gamma)^2 + 4R_2\gamma}]/2 \), such that \( c_0(R_1) < 0 \) as \( 0 \leq R_1 < \bar{R}_1 \) and \( c_0(R_1) > 0 \) as \( R_1 > \bar{R}_1 \). Since \( c_0(1) = \gamma(1 - R_2) < 0 \) for \( R_2 > 1 \), it follows that \( \bar{R}_1 > 1 \).

Further, \( c_1(\bar{R}_1) > 0, c_2(\bar{R}_1) > 0, \) and \( \phi(\bar{R}_0) \) is a quadratic function of \( R_0 \), then, when \( c_0(\bar{R}_1) \geq 0, \phi(\bar{R}_0) > 0 \) for \( R_0 > 1 \); when \( c_0(\bar{R}_1) < 0 \), function \( \phi(\bar{R}_0) \) has a unique zero \( \bar{R}'_0 \) greater than 1 since \( \phi(1) = (R_2 - 1)R_2\gamma^2 > 0 \) for \( R_2 > 1 \), which implies that \( \phi(\bar{R}_0) > 0 \) for \( 1 < R_0 < \bar{R}'_0 \) and \( \phi(\bar{R}_0) < 0 \) for \( R_0 > \bar{R}'_0 \). Therefore, according to the sign of function \( c_0(R_1) \), we have that, when \( R_1 \geq \bar{R}_1 \), \( dy^*/dR_0 > 0 \)
for $R_0 > 1$; when $0 < R_1 < \bar{R}_1$, $dy^*/dR_0 > 0$ for $1 < R_0 < \bar{R}_0$, and $dy^*/dR_0 < 0$ for $R_0 > \bar{R}_0$.

On the other hand, $c_0(R_2) = R_2(2(\gamma - 2))$, then $\bar{R}_1 \leq R_2 \gamma$ as $R_2 \gamma + \gamma - 2 \geq 0$, and $\bar{R}_1 > R_2 \gamma$ as $R_2 \gamma + \gamma - 2 < 0$. Since the existence of the positive equilibrium $E^*$ corresponds to cases (C3$_1$) and (C3$_2$) in Table 2, then, for $R_0 > 1$ and $R_2 > 1$, we list a table (Table 4) to classify the feasible regions of parameters and the associated effect of $R_0$ on the level of infected hosts which are shown in Figure 5. Figure 5(a) shows the fact that $y^*$ increases for $1 < R_0 < \bar{R}_0$, and decreases for $\bar{R}_0 < R_0 < \bar{R}_0 < +\infty$, and $\lim_{R_0 \to \bar{R}_0} y^* = 0$; Figure 5(b) is similar to Figure 5(a), but the limit of $y^*$ as $R_0 \to \bar{R}_0$ is $K(R_1 - 1)/R_1$; Figure 5(c) represents that $y^*$ increases monotonously, and $\lim_{R_0 \to \infty} y^* = K(R_1 - 1)/R_1$.

Comparing Figures 5(a), (b) and (c) suggests the common feature is that the equilibrium level of the infected host ($y^*$) increases monotonously as $R_0$ increases initially. This can be easily understood epidemiologically. However, as $R_0$ keeps increasing various trends of $y^*$ can observed, depending on $R_1$. In fact, Figures 5(a), corresponding to $R_1 < 1$, shows the more $R_0$ and the less the equilibrium level of the infected hosts. That is because the size of uninfected hosts reproduced by infected ones is small, which leads to the shortage of uninfected hosts. Then large $R_0$ causes more infected hosts and consequently more disease-induced death, and hence host extinction due to parasite infection may happen. For large $R_1$ ($R_1 \geq \bar{R}_1$), the infected hosts can reproduce sufficient uninfected ones to not only maintain supply of resource being infected but also balance disease-induced death, which suggests that $y^*$ persistently increases and stabilizes at a fixed level with increasing $R_0$, as shown in Figures 5(c). For middle values of $R_1$ ($1 \leq R_1 \leq \min \{2 \gamma, \bar{R}_1\}$), the equilibrium level of the infected hosts initially reaches a maximum and then decline to a certain level as $R_0$ increases. In addition, it follows from Figure 5(a) and (b) that $\bar{R}_0$ is a threshold in the sense of monotonicity of $y^*$.

### Table 4. Classification of the existence of $E^*(x^*, y^*)$ and the effect of $R_0$ on $y^*$.

<table>
<thead>
<tr>
<th>regions of parameters</th>
<th>existence of $y^*$</th>
<th>effect of $R_0$ on $y^*$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$R_1 \leq R_2 \gamma &lt; 1$</td>
<td>$R_1 &lt; 1$</td>
<td>Case (C3$_2$)</td>
</tr>
<tr>
<td>$1 \leq R_2 \gamma &lt; 2 - \gamma$</td>
<td>$1 \leq R_1 \leq R_2 \gamma$</td>
<td>Case (C3$_1$)</td>
</tr>
<tr>
<td>$R_2 \gamma \geq 2 - \gamma$</td>
<td>$R_1 &lt; 1$</td>
<td>Case (C3$_2$)</td>
</tr>
<tr>
<td>$R_1 \leq R_1 &lt; R_2 \gamma$</td>
<td>Case (C3$_1$)</td>
<td></td>
</tr>
</tbody>
</table>

7. Conclusion and discussion. In this paper, by rescaling parasite-host model (2), we mathematically analyzed the global dynamics on the feasible region, and theoretically proved the existence of heteroclinic and homoclinic orbits which implies that the infection may break out in the process of host extinction.

According to the obtained results on model (2), we demonstrated the effect of the basic epidemiological reproduction number ($R_0$) and the demographic reproduction number of infected hosts ($R_1$) on the dynamics of the model and the level of infected hosts. Here, we obtained two new findings: one is that a combination of $R_0$ and $R_1$ may cause the complexity of dynamics of the model, the other is that, for the different range of $R_1$, variation in the equilibrium level of the infected host ($y^*$) with

...
Figure 5. Variation in the equilibrium level of the infected hosts $y^*$ with $R_0$ for (a): $R_1 < 1$; (b): $1 \leq R_1 < \min \{R_2\gamma, \bar{R}_1\}$; (c): $R_1 \geq \bar{R}_1$.

$R_0$ may not be monotone, which is different from the classical models accepted by mathematicians and epidemiologists. In addition, when the fecundity of infected hosts is lost fully (i.e., $\theta = 0$), the appearance of the singular case implies that the trends of host extinction may depend on the initial state of the model.

Note that in our model the standard incidence function $\beta xy/(x+y)$ plays an important role in coming up with rich dynamics from the point view of mathematics. In fact, standard incidence is indeed based on the epidemiological meanings, where finite contacts of an individual making in a unit time are observed due to finite and often slow movement in large populations, and more details can be found in [2]. We model the growth of host population with logistic growth function to describe the density-constraint growth within host population (or intra-species competition for resources). Hence, our model is reasonable to describe the realities in both biology and epidemiology. Further, our main results show that parasite infection could die out or persist in certain conditions, which is similar to those for other simple models [8]. However, it is interesting to note that our model (2) exhibits some novelties because of introduction of standard incidence. In particular, host extinction can be induced by either demographic decline feature of hosts themselves or parasite regulations. During host going to extinction parasite infection may outbreak and persist eventually, which is different from that for the models with bilinear incidence. Hence, the model examined here describes biological/epidemiological phenomena more reasonably and our conclusions show the dynamics and the biological implications more extensively.

Appendix.

Lemma 7.1. For $m > n > 0$ and $p > 0$, the part of curve $\bar{L}$ in the first quadrant defined by equation

$$\begin{align*}
(y - nx)(y - nx) = (y + px)(y + x)^2
\end{align*}$$

(20)

consists of two branches, which are in the regions $\bar{D}_1 = \{(x, y) \in R^2_+ : y < nx\}$ and $\bar{D}_2 = \{(x, y) \in R^2_+ : y > mx\}$, respectively. Except for the origin, the two branches intersect with two coordinate axes at points $(mn/p, 0)$ and $(0, 1)$, respectively. One
of the two branches in the region \( D_1 \) is concave downwards, the other in the region \( D_2 \) is concave leftwards.

**Proof.** From (20), the polar coordinates equation of the curve \( L \) is given by

\[
\rho = \frac{(\sin \varphi - m \cos \varphi)(\sin \varphi - n \cos \varphi)}{(\sin \varphi + p \sin \varphi)(\sin \varphi + \cos \varphi)^2}.
\]

Since polar radius is nonnegative, then, it is easy to see that in the first quadrant \( L \) consists of two branches, which correspond to \( 0 < \varphi < \arctan n \) and \( \arctan m < \varphi < \pi/2 \), respectively. \( \varphi = \arctan n \) and \( \varphi = \arctan m \) represent two straight lines \( y = nx \) and \( y = mx \), respectively, so the two branches are located in the regions \( D_1 \) and \( D_2 \), respectively.

Direct calculation shows that, except for the origin, the two branches intersect with two coordinate axes at points \((mn/p, 0)\) and \((0, 1)\), respectively.

Using Maple software, the second derivative of implicit function \( y = y(x) \) defined by (20) is given by

\[
\frac{d^2y}{dx^2} = -\frac{2mn-2y-2px-4(y+x)p}{y-nx-2(y+x)(y+p-2x)(y+x)^2} + 2\frac{m(y-nx)+y+2(y+x)p}{2(2y-nx-2(y+x)(y+p-2x)(y+x)^2)} - 2\frac{m(y-nx)+y+2(y+x)p}{2(2y-nx-2(y+x)(y+p-2x)(y+x)^2)}(1-3y-px-2x),
\]

From (20), we have

\[
p = \frac{1}{x} \left[ \frac{(y-mx)(y-nx)}{(y+x)^2} - y \right].
\]

Substituting it into the second derivative yields

\[
\frac{d^2y}{dx^2} = \frac{2(y+x)(y-mx)(y-nx)T_2}{x^2T_1^3},
\]

where

\[
T_1 = (y+x)^3 - x[(1+m)(y-nx) + (1+n)(y-mx)],
T_2 = x(y+x)^3 [(1+m)(y-nx) + (1+n)(y-mx)] - (y-mx)(y-nx) [(1+m)(1+n)x^2 - (y+x)(2y-mx-nx)] - (y+x)^2 [(y-mx)^2 + (y-nx)^2].
\]

\( n < m \) implies that \( y < mx \) as \( y < nx \), so \( T_1 > 0 \) and \( T_2 < 0 \) for \( y < nx \). Hence, \( d^2y/dx^2 < 0 \) for \( y < nx \). This implies that the part of the curve \( L \) in the region \( D_1 \) is concave downwards.

To show that the part of the curve \( \bar{L} \) in the region \( D_2 \) is concave leftwards, we make the change of variables:

\[
x = \frac{mn}{p}v, \quad y = \frac{mn}{p}u,
\]

then (20) becomes

\[
(v - \frac{u}{m})(v - \frac{u}{n}) = (v + \frac{u}{p})(v + u)^2.
\]

(21)

Since \( 1/n > 1/m \), then, according to the above inference for the case \( y < nx \), the part of the curve \( \bar{L}' \) defined by (21) in the region \( D'_2 = \{(u, v) \in R^2_+: v < u/m\} \) is concave towards the \( u \)-axis.
Notice that \( v < u/m \) is equivalent to \( y > mx \), then the region \( D_2' \) on the \((u,v)\)-plane corresponds to the region \( D_2 \) on the \((x,y)\)-plane. Thus, the part of the curve \( L \) in the region \( D_2 \) is concave leftwards.

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Received January 19, 2012; Accepted May 14, 2012.

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