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Research Article

Ecoepidemiological Model and Analysis of Prey-Predator System

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In this paper, the prey-predator model of five compartments is constructed with treatment given to infected prey and infected predator. We took predation incidence rates as functional response type II, and disease transmission incidence rates follow simple kinetic mass action function. The positivity, boundedness, and existence of the solution of the model are established and checked. Equilibrium points of the models are identified, and local stability analyses of trivial equilibrium, axial equilibrium, and disease-free equilibrium points are performed with the method of variation matrix and the Routh-Hurwitz criterion. It is found that the trivial equilibrium point E_o is always unstable, and axial equilibrium point E_A is locally asymptotically stable if $\beta k - (t_1 + d_2) < 0$, $qp_1k - d_3(s+k) < 0$ and $qp_3k - (t_2 + d_4)(s+k) < 0$ conditions hold true. Global stability analysis of an endemic equilibrium point of the model has been proven by considering the appropriate Lyapunov function. The basic reproduction number of infected prey and infected predators are obtained as $R_{01} = (qp_1 - d_3)^2 k\beta d_3 s^2/(qp_1 - d_3)\{(qp_1 - d_3)^2 ks(t_1 + d_2) + rsqp_2(kqp_1 - kd_3 - d_3 s)\}$ and $R_{02} = (qp_1 - d_3)(qp_3 d_3)k + \alpha rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2(t_2 + d_4)k$, respectively. If the basic reproduction number is greater than one, then the disease will persist in the prey-predator system. If the basic reproduction number is one, then the disease is stable, and if the basic reproduction number is less than one, then the disease dies out from the prey-predator system. Finally, simulations are done with the help of DEDiscover software to clarify results.

1. Introduction

Mathematical modeling of prey-predator systems of interaction of species have a long history since the original remarkable work done by the Lotka-Volterra Model in the 1920s [1–4], and the SIR model compartment of systems of population is another vital area of research after the pioneering work of Kermack and Mckendrick [1–9]. Anderson and May were the first who combined these two modeling systems, while Chattopadhyay and Arino were the first who used the term "ecoepidemiology" for such models [2, 3, 6]. The dynamics of disease in prey-predator systems now become an interesting area of research due to the fact that prey-predator interaction is rich and complex in nature [4, 6, 10–13]. Several mathematical models have been proposed and studied on prey-predator systems [1–6, 8–12]. Many studies focused on the study of disease in prey only [1–3, 5, 6, 10, 12, 14–20], other researchers were interested in the study of disease within the predator population only [18, 21], and there are also some studies on diseases in both prey and predators [4, 8, 11]. In this paper, we proposed and studied infectious disease in both prey and predator interaction of species with treatment given to infected prey and infected predator.

2. Mathematical Model Formulation and Assumptions

In this paper, the prey-predator population is divided into five compartments. Let us denote $X(t)$ as the susceptible prey, $W(t)$ as the infected prey, $Y(t)$ as the susceptible predator, $Z(t)$ as the infected predator, and $H(t)$ as both infected prey and infected predator population under treatment. In the absence of infectious disease, the susceptible prey population grows logistically with intrinsic growth rate r and environmental carrying capacity k, and only susceptible prey can reproduce. In the presence of infectious disease, susceptible predators become infected predators when they come into contact with infected predators, susceptible prey become

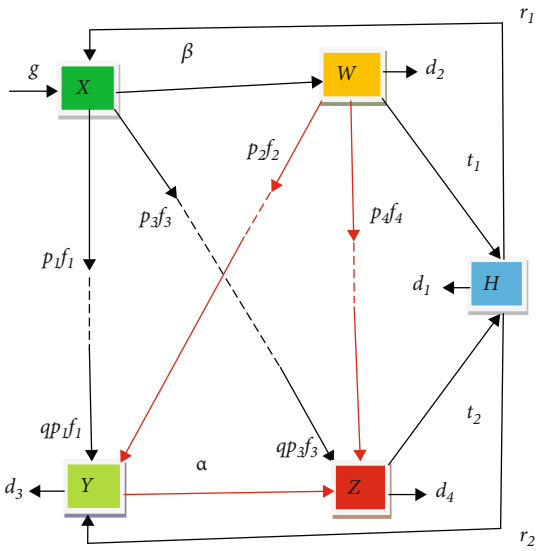

Figure 1: Model diagram.

infected prey when they come into contact with infected prey, and the contact process is assumed to follow bilinear functional with convolution rate α, β, respectively. The predation functional response of predator towards the prey is assumed to follow a different Holling type II functional response form with p_1, p_2 respective predation coefficients of $X(t)$, $W(t)$ due to susceptible predator, and p_3, p_4 respective predation coefficient of $X(t)$, $Y(t)$ due to infected predator. Suppose consumed prey converted into predator with efficiency q and also half-saturated constants. It is also assumed that infected prey $W(t)$ and infected predator $Z(t)$ can only recover through treatment and are treated at a treatment rate of t_1, t_2, respectively. The prey-predator population $H(t), W(t), Y(t)$, and $Z(t)$ suffers from infectious disease with death rate d_1, d_2, d_3, and d_4, respectively. Moreover, assume that all variables and parameters used in the model are nonnegative.

According to the above assumption, we have the following model flow diagram.

From the model flow diagram in Figure 1, we have the following set of differential equations:

$$\frac{dX}{dt} = g(X, W) + r_1 H - \beta XW - p_1 f_1(X, Y) - p_3 f_3(X, Z), \tag{1}$$

$$\frac{dW}{dt} = \beta XW - t_1 W - d_2 W - p_2 f_2(W, Y) - p_4 f_4(W, Z), \tag{2}$$

$$\frac{dY}{dt} = qp_1 f_1(X, Y) + qp_2 f_2(W, Y) + r_2 H - \alpha YZ - d_3 Y, \tag{3}$$

$$\frac{dZ}{dt} = qp_3 f_3(X, Z) + qp_4 f_4(W, Z) + \alpha YZ - t_2 Z - d_4 Z, \tag{4}$$

$$\frac{dH}{dt} = t_1 W + t_2 Z - d_1 H - r_1 H - r_2 H, \tag{5}$$

with initial conditions $X(0) \geq 0$; $W(0) \geq 0$; $Y(0) \geq 0$; $Z(0) \geq 0$; $H(0) \geq 0$; and $p_i > 0$, $i = 1, 2, 3, 4$, and $0 < q \leq 1$.

Depending on the assumptions of per capita growth of function $g(X, W)$ for susceptible prey, and different type II functional responses f_i, $i = 1, 2, 3, 4$, we have a more feasible model (8) emanating from model (3) as

$$\begin{aligned}\frac{dX}{dt} &= rX\left(1 - \frac{X + W}{k}\right) + r_1 H - \beta XW - \frac{p_1 XY}{s + X} - \frac{p_3 XZ}{s + X} \\ &= f(X, W, Y, Z, H),\end{aligned} \tag{6}$$

$$\begin{aligned}\frac{dW}{dt} &= \beta XW - t_1 W - d_2 W - \frac{p_2 WY}{s + W} - \frac{p_4 WZ}{s + W} \\ &= g(X, W, Y, Z, H),\end{aligned} \tag{7}$$

$$\begin{aligned}\frac{dY}{dt} &= q\frac{p_1 XY}{s + X} + q\frac{p_2 WY}{s + W} + r_2 H - \alpha YZ - d_3 Y \\ &= h(X, W, Y, Z, H),\end{aligned} \tag{8}$$

$$\begin{aligned}\frac{dZ}{dt} &= q\frac{p_3 XZ}{s + X} + q\frac{p_4 WZ}{s + W} + \alpha YZ - t_2 Z - d_4 Z \\ &= i(X, W, Y, Z, H),\end{aligned} \tag{9}$$

$$\frac{dH}{dt} = t_1 W + t_2 Z - d_1 H - r_1 H - r_2 H = j(X, W, Y, Z, H), \tag{10}$$

with initial conditions $X(0) \geq 0$; $W(0) \geq 0$; $Y(0) \geq 0$; $Z(0) \geq 0$; $H(0) \geq 0$; $p_1, p_2, p_3, p_4 > 0$, and $0 < q \leq 1$, it is possible to arrange model (6)–(10) and express it in more compact forms with excellent patterns in

$$\frac{dX}{dt} = X\left\{r\left(1 - \frac{X + W}{k}\right) - \left(\beta W + \frac{p_1 Y + p_3 Z}{s + X}\right)\right\} + r_1 H,$$

$$\frac{dW}{dt} = W\left\{\beta X - \left(t_1 + d_2 + \frac{p_2 Y + p_4 Z}{s + W}\right)\right\},$$

$$\frac{dY}{dt} = Y\left\{q\left(\frac{p_1 X}{s + X} + \frac{p_2 W}{s + W}\right) - (\alpha Z + d_3)\right\} + r_2 H,$$

$$\frac{dZ}{dt} = Z\left\{q\left(\frac{p_3 X}{s + X} + \frac{p_4 W}{s + W}\right) + \alpha Y - (t_2 + d_4)\right\},$$

$$\frac{dH}{dt} = t_1 W + t_2 Z - (d_1 + r_1 + r_2)H, \tag{11}$$

with initial conditions $X(0) \geq 0$; $W(0) \geq 0$; $Y(0) \geq 0$; $Z(0) \geq 0$; $H(0) \geq 0$; $p_1, p_2, p_3, p_4 > 0$; and $0 < q \leq 1$.

3. Mathematical Analysis of the Model

In this section, positivity, boundedness, and existence of the solution of the model are checked. This mathematical analysis of the model could be considered as the primary results.

Theorem 1 (boundedness). *All solutions of model (8) are bounded in feasible region* $\mathbb{R}_+^5$.

Proof. Each solution $X(t)$, $W(t)$, $Y(t)$, $Z(t)$, and $H(t)$ of the model is bounded if and only if total population N is bounded. Let total population of prey-predator $N = X + W + Y + Z + H$.

For $\Lambda > 0$ to be constant,

$$\frac{dN}{dt} + \Lambda N = \frac{dX}{dt} + \frac{dW}{dt} + \frac{dY}{dt} + \frac{dz}{dt} + \frac{dH}{dt} + \Lambda N. \quad (12)$$

By substituting all model Equations (8) into (12) and removing all negative terms, we have the following results: $dN/dt + \Lambda N \le rX + q(p_1XY/(s+X)) + q(p_2WY/(s+W)) + q(p_4WZ/(s+W)) + q(p_3XZ/(s+X)) + \Lambda N = \mu$. Then, solving the differential inequality $dN/dt + \Lambda N \le \mu$ yields $N(t) \le (\mu/\Lambda)(1 - e^{-\Lambda t}) + N(0)e^{-\Lambda t}$ for $t \to \infty, N \to \mu/\Lambda$. We know that total prey-predator population is nonnegative, and hence, $0 \le N(t) \le \mu/\Lambda$. So we have invariant feasible region $\Omega = \{(X, W, Y, Z, H) \in \mathbb{R}_+^5 : 0 \le N(t) \le \mu/\Lambda\}$. This proves the theorem and the model is mathematically well posed

Theorem 2 (positivity). *All solutions of model (6)–(10) are positive.*

Proof. To prove Theorem 2, we have to show that variables $X(t)$, $W(t)$, $Y(t)$, $Z(t)$, $H(t)$ of the models (8) are nonnegative $\forall t \ge 0$.

(i) *Positivity of* $X(t)$: from the susceptible prey model in (8), $dX/dt = rX(1 - (X+W)/k) + r_1H - \beta XW - p_1XY/(s+X) - p_3XZ/(s+X)$ without loss of generality. After removing all the positive terms from the right-hand side of the differential equation, we have the following differential inequality: $dX/dt \ge -((rX^2 + rXW)/k + \beta XW + (P_1XY + P_3XZ)/(S+X))$ divide both sides by negative yields $-(dX/dt) \le (RX^2 + RXW)/k + \beta XW + (p_1XY + p_3XZ)/(S+X)$. But it is also clear that the following inequality holds: $(rX^2 + rXW)/k + \beta XW + (P_1XY + P_3XZ)/(S+X) \le rX^2 + rXW + \beta XW + p_1XY + p_3XZ = X(rX + rW + \beta W + p_1Y + p_3Z)$. Assume that $rW + \beta W + p_1Y + p_3Z = C$, then the differential inequality is reduced to $-(dX/dt) \le X(rX + C)$. This inequality can be arranged for integration by partial fraction as $\int (1/X(rX+C))dX \ge \int -dt$, integrating the integral inequality $\int ((1/C)/X + (-r/C)/(rX+C))dX \ge -\int dt$ will give us $(1/C)\ln|X| - (1/C)\ln|rX + C| \ge -t + Q$, where Q is integration constant. Using rules of logarithm, the inequality can be written as $\ln|X/(rX+C)| \ge -Ct + CQ$. Finally, solving for X will give us $X(t) \ge ACe^{-Ct}/(1 - rAe^{-Ct})$, for $A = e^{CQ}$. Therefore, $X(t) > 0$ for $1 - rAe^{-Ct} > 0$. That is, $X(t)$ is nonnegative for $t > (1/C)\ln(rA)$.

(ii) *Positivity of* $W(t)$: from the infected prey model in (7), $dW/dt = \beta XW - t_1W - d_2W - p_2WY/(s+W) - p_4WZ/(s+W)$, without loss of original generality, after removing the positive term (βXW). We obtain the following differential inequality: $dW/dt \ge -(t_1W + d_2W + p_2WY/(s+W) + p_4WZ/(s+W))$ if and only if $-(dW/dt) \le (t_1W + d_2W + p_2WY/(s+W) + p_4WZ/(s+W))$. But it is clear that $t_1W + d_2W + p_2WY/(s+W) + p_4WZ/(s+W) \le t_1W + d_2W + p_2WY + p_4WZ = (t_1 + d_2 + p_2Y + p_4Z)W$ holds true. Now assume that $t_1 + d_2 + p_2Y + p_4Z = C$. Then, we have $-(dW/dt) \le CWt$. Now applying integration yield $\ln|W| \ge -Ct + Q$, where Q is the integration constant, then solving for the variable $W(t)$ gives the equation $W(t) \ge e^{-Ct+Q}$ which is the exponential function and positive at all times. Hence, $W(t)$ is positive.

(iii) *Positivity of* $Y(t)$: from the susceptible predator model in (8), $dY/dt = q(p_1XY/(s+X)) + q(p_2WY/(s+W)) + r_2H - \alpha YZ - d_3Y$, without loss of original generality, after removing all positive terms $(q(p_1XY/(s+X)) + q(p_2WY/(s+W)) + r_2H)$, we obtain differential equation $dy/dt \ge -(\alpha z + d_3)y$. Then, applying integration by separation of variable method results, $\ln|y| \ge -(\alpha z + d_3)t + Q$, where Q is integration constant, and solving for variable $Y(t)$,we obtain the solution $|y| \ge e^{-(\alpha z + d_3)t + Q}$. Therefore, $y(t) \ge e^{-(\alpha z + d_3)t + Q}$ is a positive exponential function; hence, $y(t)$ is positive.

(iv) *Positivity of* $Z(t)$: from the infected predator model in (9), $dZ/dt = q(p_2WZ/(s+W)) + q(p_3XZ/(s+W)) + \alpha YZ - t_2Z - d_4Z$ after removing all positive terms $(q(p_2WZ/(s+W)) + q(p_3XZ/(s+W)))$, we obtain the differential inequality $dz/dt \ge -(t_2 + d_4)z$. Applying integration by separation of variable method yields $\ln|z| \ge -(t_2 + d_4)t + Q$ where Q is integration constant by separation of variable method. Then, solving for Z will result in $z(t) \ge e^{-(t_2+d_4)t+Q}$ which is the exponential function that is positive at all time. Hence, $Z(t)$ is positive.

Alternative verification: in mode (6)–(10), $dZ/dt = q(p_2WZ/(s+W)) + q(p_3XZ/(s+W)) + \alpha YZ - t_2Z - d_4Z$ Can be written as $dZ/dt = (q(p_2W/(s+W)) + q(p_3X/(s+W)) + \alpha Y - t_2 - d_4)Z$ if only if $(1/Z)dZ = (q(p_2W/(s+W)) + q(p_3X/(s+W)) + \alpha Y - t_2 - d_4)dt$. This equation can be arranged as $\int (1/Z)dZ = \int (q(p_2W/(s+W)) + q(p_3X/(s+W)) + \alpha Y - t_2 - d_4)dt$, which after computing the integration yields, $\ln|Z| = (q(p_2W/(s+W)) + q(p_3X/(s+W)) + \alpha Y - t_2 - d_4)t + Q$, where Q is the integration constant. Thus, $Z(t) = e^{(q(p_2W/(s+W)) + q(p_3X/(s+W)) + \alpha Y - t_2 - d_4)t + Q}$ is the exponential function which is positive, and hence, $Z(t)$ is positive.

Table 1: Partial derivatives.

For f_1:

$$\left|\frac{\partial f_1}{\partial X}\right| = \left|r - \frac{2rx}{k} - \frac{rW}{k} - \beta W - \frac{s(p_1 Y + p_3 Z)}{(s+X)^2}\right| < \infty,$$

$$\left|\frac{\partial f_1}{\partial W}\right| = \left|-\frac{rX}{k} - \beta X\right| < \infty,$$

$$\left|\frac{\partial f_1}{\partial Y}\right| = \left|-\frac{p_1 X}{s+X}\right| < \infty,$$

$$\left|\frac{\partial f_1}{\partial Z}\right| = \left|-\frac{p_3 X}{s+X}\right| < \infty,$$

$$\left|\frac{\partial f_1}{\partial H}\right| = |r_1| < \infty,$$

For f_2:

$$\left|\frac{\partial f_2}{\partial X}\right| = |\beta W| < \infty,$$

$$\left|\frac{\partial f_2}{\partial W}\right| = \left|\beta X - t_1 - d_2 - \frac{s(p_2 Y + p_4 Z)}{(s+W)^2}\right| < \infty,$$

$$\left|\frac{\partial f_2}{\partial Y}\right| = \left|-\frac{p_2 W}{s+W}\right| < \infty,$$

$$\left|\frac{\partial f_2}{\partial Z}\right| = \left|-\frac{p_4 W}{s+w}\right| < \infty,$$

$$\left|\frac{\partial f_2}{\partial H}\right| = 0 < \infty,$$

For f_3:

$$\left|\frac{\partial f_3}{\partial X}\right| = \left|\frac{sqp_1 Y}{(s+X)^2}\right| < \infty,$$

$$\left|\frac{\partial f_3}{\partial W}\right| = \left|\frac{sqp_2 Y}{(s+X)^2}\right| < \infty,$$

$$\left|\frac{\partial f_3}{\partial Y}\right| = \left|\frac{qp_1 X}{s+X} + \frac{qp_2 W}{s+W} - \alpha Z - d_3\right| < \infty,$$

$$\left|\frac{\partial f_3}{\partial Z}\right| = |-\alpha y - d_3| < \infty,$$

$$\left|\frac{\partial f_3}{\partial H}\right| = r_2 < \infty,$$

For f_4:

$$\left|\frac{\partial f_4}{\partial X}\right| = \left|\frac{sqp_3 Z}{(s+X)^2}\right| < \infty,$$

$$\left|\frac{\partial f_4}{\partial W}\right| = \left|\frac{sqp_4 Z}{(s+W)^2}\right| < \infty,$$

$$\left|\frac{\partial f_4}{\partial Y}\right| = |\alpha Z| < \infty,$$

$$\left|\frac{\partial f_4}{\partial Z}\right| = \left|\frac{qp_3 X}{s+X} + \frac{qp_4 W}{s+W} - \alpha Y - t_2 - d_4\right| < \infty,$$

$$\left|\frac{\partial f_4}{\partial H}\right| = 0 < \infty.$$

For f_5:

$$\left|\frac{\partial f_5}{\partial X}\right| = 0 < \infty,$$

$$\left|\frac{\partial f_5}{\partial W}\right| = t_1 < \infty,$$

$$\left|\frac{\partial f_5}{\partial Y}\right| = 0 < \infty,$$

$$\left|\frac{\partial f_5}{\partial Z}\right| = |t_2| < \infty,$$

$$\left|\frac{\partial f_5}{\partial H}\right| = |-d_1 - r_1 - r_2| < \infty.$$

Table 2: Notations and description of variables.

Variables	Descriptions
$X(t)$	Population size of susceptible prey
$W(t)$	Population size of infected prey
$Y(t)$	Population size of susceptible predator
$Z(t)$	Population size of infected predator
$H(t)$	Population size of infected population under treatment

(v) *Positivity of* $H(t)$: from infected prey and infected predator population under treatment model in (8) $dH/dt = t_1 W + t_2 Z - d_1 H - r_1 H - r_2 H$, without loss of generality, after removing all positive terms, we have $dH/dt \geq -(d_1 + r_1 + r_2)H$ if and only if $dH/H \geq -(d_1 + r_1 + r_2)dt$ integrating results, $\ln|H| \geq -(d_1 + r_1 + r_2)t + Q$. Then, solving the variable H yields $|H| \geq e^{-(d_1+r_1+r_2)t+Q}$ which is an exponential function which is positive at all times. Therefore, $H(t) > 0$, and hence, $H(t)$ is positive. Thus, variables $X(t)$, $W(t)$, $Y(t)$, $Z(t)$, and $H(t)$ are all positive quantities and remain in $\mathbb{R}_+^5$ for all t.

Theorem 3 (existence). *All solutions of model (8) together with the initial conditions* $X(0) > 0$, $W(0) \geq 0$, $Y(0) \geq 0$, $Z(0) \geq 0$, *and* $H(0) \geq 0$ *exist in* $\mathbb{R}_+^5$, *i.e., the model variables* $X(t)$, $W(t)$, $Y(t)$, $Z(t)$, *and* $H(t)$ *exist for all* t *and remain in* $\mathbb{R}_+^5$.

Proof. Let the system of differential equation (8) be given as

$$f_1 = rX\left(1 - \frac{X+W}{k}\right) + r_1 H - \beta XW - \frac{p_1 XY}{s+X} - \frac{p_3 XZ}{s+X},$$

$$f_2 = \beta XW - t_1 W - d_2 W - \frac{p_2 WY}{s+W} - \frac{p_4 WZ}{s+W},$$

$$f_3 = q\frac{p_1 XY}{s+X} + q\frac{p_2 WY}{s+W} + r_2 H - \alpha YZ - d_3 Y,$$

$$f_4 = q\frac{p_3 XZ}{s+X} + q\frac{p_4 WZ}{s+W} + \alpha YZ - t_2 Z - d_4 Z,$$

$$f_5 = t_1 W + t_2 Z - d_1 H - r_1 H - r_2 H. \tag{13}$$

According to the Derrick and Groosman theorem, let Ω denote the region $\Omega = \{(X, W, Y, Z, H) \in \mathbb{R}_+^5 ; N \leq (\mu/\lambda)\}$. Then, model (8) have a unique solution if $(\partial f_i)/(\partial x_j)$, $i, j = 1, 2, 3, 4, 5$ are continuous and bounded in Ω. Here, $x_1 = X$, $x_2 = W$, $x_3 = Y$, $x_4 = Z$, and $x_5 = H$. The continuity and the boundedness can be shown as follows.

Thus, all the partial derivatives in Table 1, $(\partial f_i)/(\partial x_j)$, $i, j = 1, 2, 3, 4, 5$ exist, continuous, and bounded in a region Ω for all positive values of model variables in Table 2 and

Table 3: Notations and description of parameters.

Parameters	Description of parameters
r, k	Intrinsic growth rate and carrying capacity of susceptible prey
α, β	Disease transmission rates of prey and predator
t_1, t_2	Treatment rate of infected prey and infected predator
r_1, r_2	Recovery rate of infected prey and infected predator
$p_i, i = 1, 2, 3, 4$	Predation coefficients
$f_i, i = 1, 2, 3, 4$	Functional response
$d_i, i = 1, 2, 3, 4$	Death rates
q, s	Efficiency of predation and half-saturation constant

model parameters in Table 3. Hence, by the Derrick and Groosman theorem, a solution for the model (6)–(8) exists and is unique.

4. Stability Analysis

Stability analysis in the absence of predators in the model, that is, when $y(t)$ and $Z(t)$ are zero, model (8) can be written as

$$\frac{dX}{dt} = rX\left(1 - \frac{X+W}{k}\right) + r_1 H - \beta XW = f(X, W, H),$$

$$\frac{dW}{dt} = \beta XW - t_1 W - d_2 W = g(X, W, H),$$

$$\frac{dH}{dt} = t_1 W - d_1 H - r_1 H = h(X, W, H). \tag{14}$$

This system has trivial $E_o(0, 0, 0)$, axial $E_A(k, 0, 0)$, and positive $E_o(X, W, H)$ equilibrium points where

$$X = k - \frac{k\beta}{r} - \frac{\beta}{d_2 + t_1} + \frac{k\beta r_1 t_1}{r(d_1 + r_1)(d_2 + t_1)},$$

$$W = \frac{\beta}{d_2 + t_1},$$

$$H = \frac{\beta}{(d_1 + r_1)(d_2 + t_1)}, \tag{15}$$

with Jacobian matrix

$$J(X, W, H) = \begin{pmatrix} r - \frac{2rX}{k} - \frac{rW}{k} - \beta W & -\frac{rX}{k} - \beta X & r_1 \\ \beta W & \beta X - t_1 - d_2 & 0 \\ 0 & t_1 & -d_1 - r_1 \end{pmatrix}. \tag{16}$$

Theorem 4. *The trivial equilibrium E_o is a saddle point with unstable manifold in X-direction and stable manifold in the WY-plane.*

Proof. The Jacobian matrix at E_o is given by

$$J(E_o) = \begin{pmatrix} r & 0 & r_1 \\ 0 & -t_1 - d_2 & 0 \\ 0 & t_1 & -d_1 - r_1 \end{pmatrix}, \tag{17}$$

to compute eigenvalues compute the det $(J(E_o) - \lambda I_3) = 0$,

$$\begin{vmatrix} r - \lambda & 0 & r_1 \\ 0 & -t_1 - d_2 - \lambda & 0 \\ 0 & t_1 & -d_1 - r_1 - \lambda \end{vmatrix} = 0. \tag{18}$$

Then, $(r - \lambda)(-t_1 - d_2 - \lambda)(-d_1 - r_1 - \lambda) = 0$ is the characteristic polynomial.

Thus, eigenvalues are $\lambda_1 = r > 0, \lambda_2 = -t_1 - d_2 < 0, \lambda_3 = -d_1 - r_1 < 0$ which is a saddle point with unstable manifold in the X-direction and stable manifold in the WY-plane.

Theorem 5. *The axial equilibrium E_A is a saddle point if $\beta k - t_1 - d_2 > 0$ and unstable manifold in X-direction if $\beta k - t_1 - d_2 < 0$, then E_A is stable.*

Proof. The Jacobian matrix at E_A is given by

$$J(E_A) = \begin{pmatrix} -r & -r - \beta k & r_1 \\ 0 & \beta k - t_1 - d_2 & 0 \\ 0 & t_1 & -d_1 - r_1 \end{pmatrix}, \tag{19}$$

to compute eigenvalues compute the det $(J(E_o) - \lambda I_3) = 0$,

$$\begin{vmatrix} -r - \lambda & -r - \beta k & r_1 \\ 0 & \beta k - t_1 - d_2 - \lambda & 0 \\ 0 & t_1 & -d_1 - r_1 - \lambda \end{vmatrix} = 0. \tag{20}$$

Then, $(-r - \lambda)(\beta k - t_1 - d_2 - \lambda)(-d_1 - r_1 - \lambda) = 0$ is characteristic polynomial.

Table 4: Parameter value used in simulation.

Name	Value	Description
r	22.4000	Growth rate of susceptible prey
k	1.0000E03	Carrying capacity of susceptible prey
$r^{-}1$	1.0000	Recovery rate of
Beta	2.4000	Disease transmission rate in prey
$P^{-}1$	1.0000	Predation coefficient of susceptible prey due to susceptible predator
s	1.0000	Half-saturated rate
$P^{-}3$	1.0000	Predation coefficient of susceptible prey due to infected predator
$t^{-}1$	1.0000	Treatment rate of infected prey
$d^{-}2$	1.0000	Death rate of infected prey
$P^{-}2$	1.0000	Predation coefficient of infected prey due to predators
$P^{-}4$	1.0000	Predation rate of infected prey due to infected predator
q	1.0000	Efficiency of predation
$r^{-}2$	1.0000	Recovery rate of susceptible predator
Alpha	2.6000	Disease transmission rate in predator
$d^{-}3$	1.0000	Death rate of susceptible predator
$t^{-}2$	1.0000	Treatment rate of infected predator
$d^{-}4$	1.0000	Death rate of infected predator
$d^{-}1$	1.0000	Death rate of both infected and infected predator under treatment

Thus, $\lambda_1 = -r < 0, \lambda_2 = \beta k - t_1 - d_2, \lambda_3 = -d_1 - r_1 < 0$; hence, the axial equilibrium point is the saddle point if $\beta k - t_1 - d_2 > 0$ and stable if $\beta k - t_1 - d_2 < 0$.

Stability analysis in the absence of infectious disease in system (8), that is, when there is no disease, $W(t), Z(t)$, and $H(t)$ are all zero and model (8) becomes

$$\frac{dX}{dt} = rX\left(1 - \frac{X+W}{k}\right) - \frac{p_1 XY}{s+X} = f(X,Y),$$

$$\frac{dY}{dt} = q\frac{p_1 XY}{s+X} - d_3 Y = g(X,Y). \tag{21}$$

This system contains trivial $E_o(0, \quad 0)$, axial $E_A(k, \quad 0)$, and positive $E_o(X, \quad Y)$ equilibrium points, where

$$X = \frac{r(k-s) + \sqrt{r}\sqrt{k^2 r + 2krs + rXs^2 - 4kp_1}}{2r},$$

$$Y = \frac{qp_1}{d_3\left(s + \left(r(k-s) + \sqrt{r}\sqrt{k^2 r + 2krs + rs^2 - 4kp_1}\right)/2r\right)}, \tag{22}$$

Table 5: Initial conditions used for model variables.

Name	Value	Description
$X[t0]$	1.2000E04	Initial # susceptible prey
$W[t0]$	200.0000	Initial # infected prey
$H[t0]$	1.0000	Initial # under treated prey predator
$Y[t0]$	160.0000	Initial # susceptible predator
$Z[t0]$	180.0000	Initial # of infected predator

and Jacobian matrix is given by

$$J(X,Y) = \begin{pmatrix} r - \dfrac{2rX}{k} - \dfrac{p_1 YS}{(s+X)^2} & \dfrac{qp_1 X}{s+k} \\ \dfrac{qp_1 YS}{(s+X)^2} & \dfrac{qp_1 X}{s+X} - d_3 \end{pmatrix}. \tag{23}$$

Theorem 6. *The trivial equilibrium E_o is a saddle point with unstable manifold in the X-direction and stable manifold in the Y-direction.*

Proof. The Jacobian matrix at E_o is given by

$$J(E_o) = \begin{pmatrix} r & 0 \\ 0 & -d_3 \end{pmatrix}, \tag{24}$$

hence, eigenvalues are $\lambda_1 = r > 0, \lambda_2 = -d_3 < 0$ which is a saddle point.

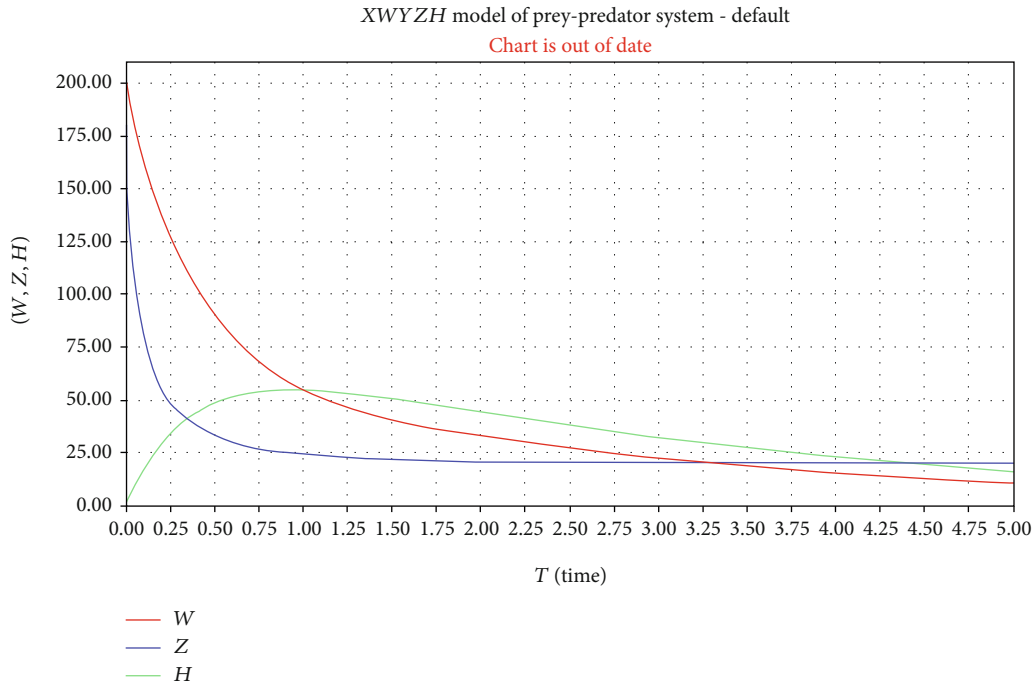

Figure 2: Infected prey-predator with treatment.

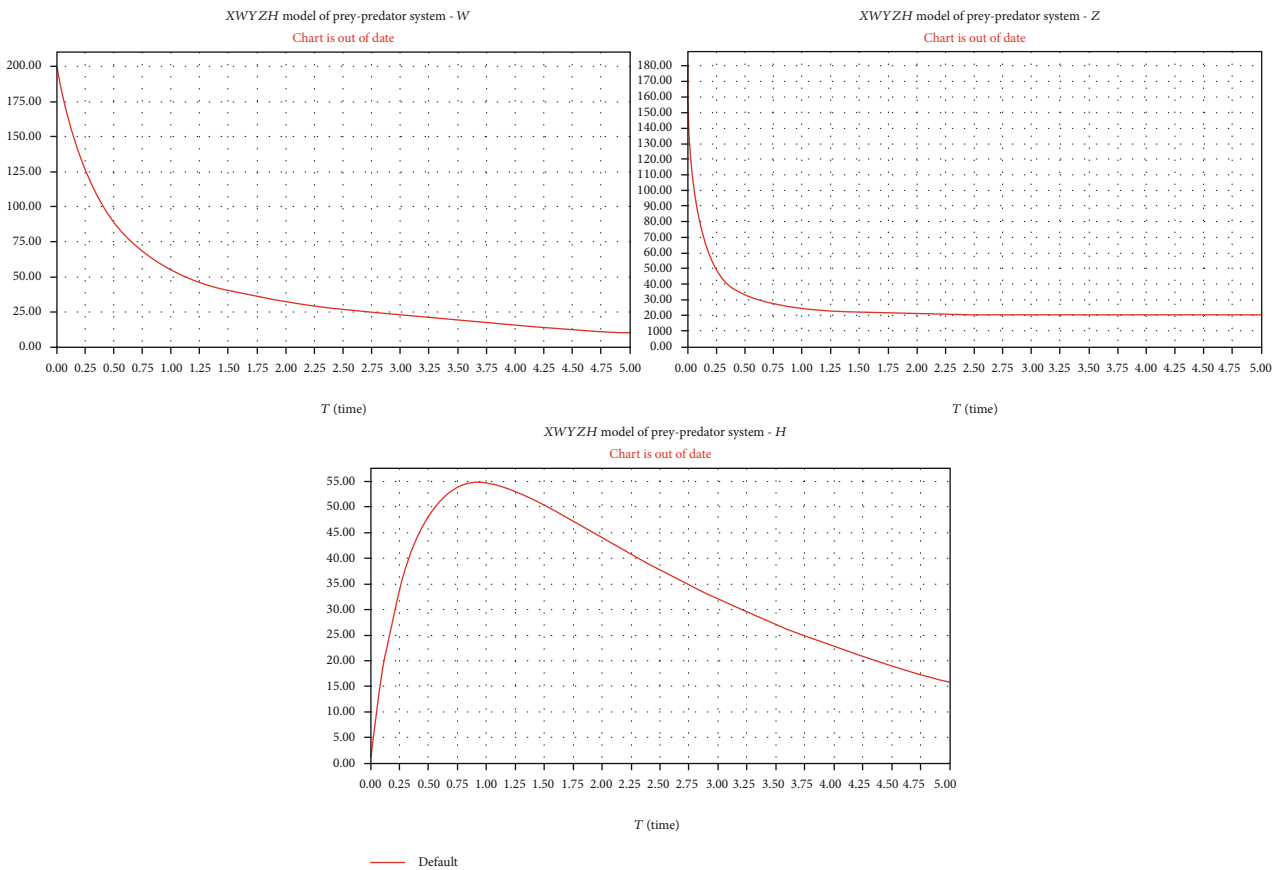

Figure 3: Plots for W, Z, and H.

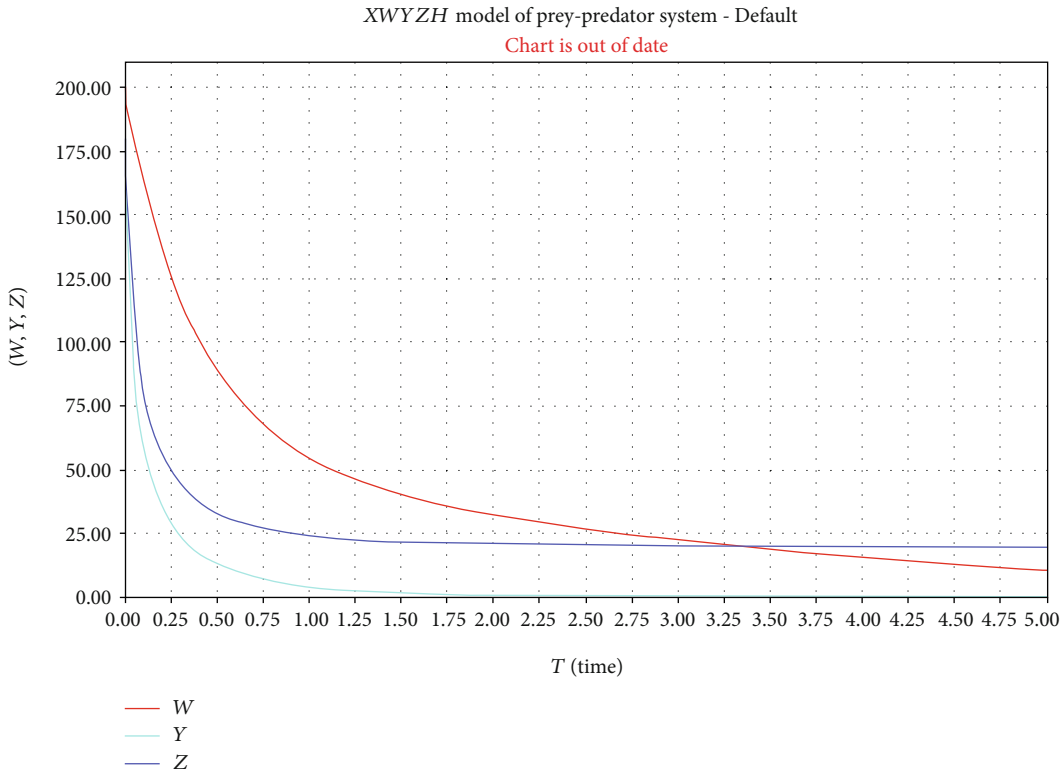

Figure 4: High infection and predation.

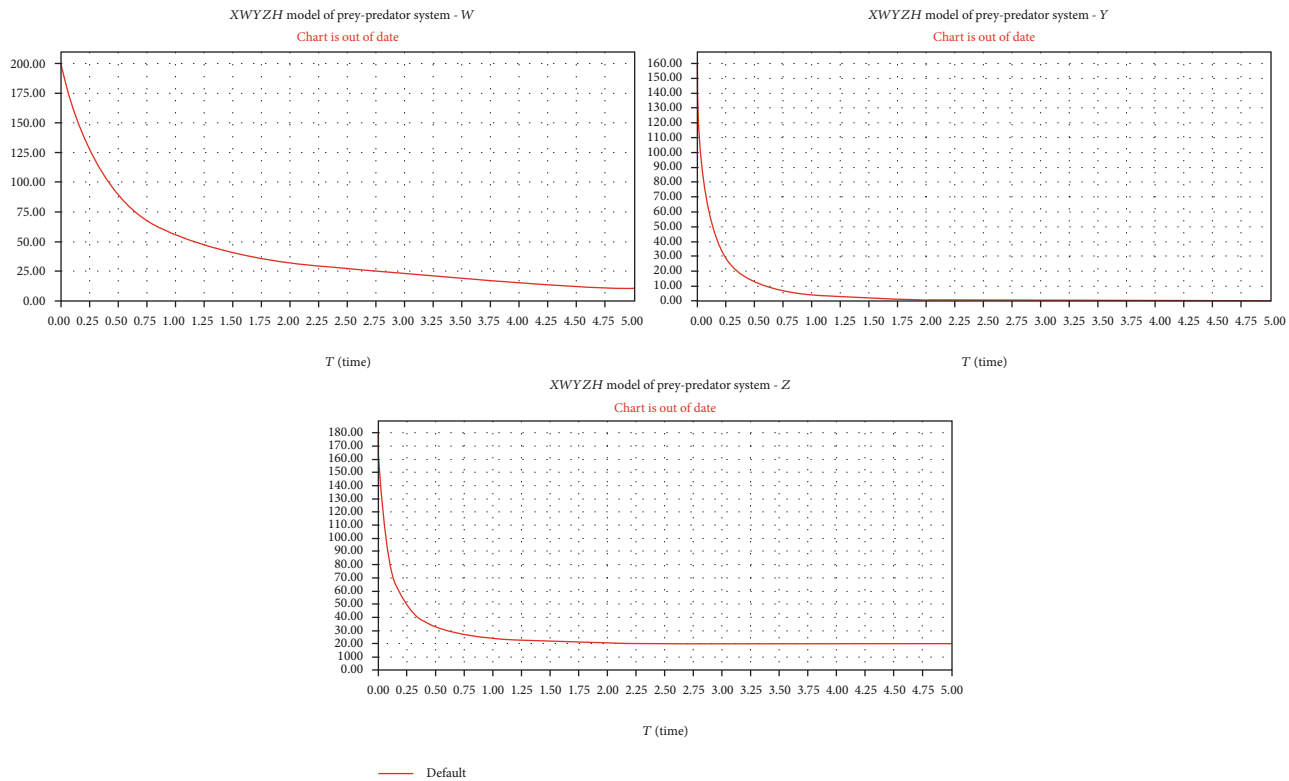

Figure 5: Individual plot for W, Y, and Z.

Theorem 7. *The axial equilibriumE_A is stable if $qp_1k/(s+k) - d_3 < 0$, otherwise unstable.*

Proof. The Jacobian matrix at E_A is given by

$$J(E_A) = \begin{pmatrix} -r & -\dfrac{p_1 k}{s+k} \\ 0 & -\dfrac{p_1 k}{s+k} - d_3 \end{pmatrix}. \tag{25}$$

To find eigenvalues, compute $\det(J(E_A) - \lambda I_3) = 0$,

$$\begin{vmatrix} -r-\lambda & -\dfrac{p_1 k}{s+k} \\ 0 & \dfrac{qp_1 k}{s+k} - d_3 - \lambda \end{vmatrix} = 0. \tag{26}$$

Eigen values are $\lambda_1 = -r < 0, \lambda_2 = qp_1k/(s+k) - d_3$.

Thus, E_A is stable if $qp_1k/(s+k) - d_3 < 0$ and otherwise unstable.

Theorem 8. *The positive equilibrium E is stable if $[r - 2rX/k - p_1YS/(s+X)^2] + [qp_1k/(s+k) - d_3] > 0$ and $[r - 2rX/k - p_1YS/(s+X)^2][qp_1k/(s+k) - d_3] + qp_1{}^2XYS/(s+X)^3 > 0$.*

Proof. The Jacobian matrix at E is given by

$$J(X, Y) = \begin{pmatrix} r - \dfrac{2rX}{k} - \dfrac{p_1 YS}{(s+X)^2} & \dfrac{qp_1 X}{s+k} \\ \dfrac{qp_1 YS}{(s+X)^2} & \dfrac{qp_1 X}{s+X} - d_3 \end{pmatrix}. \tag{27}$$

Then, compute $\det(J(E) - \lambda I_3) = 0$,

$$\begin{vmatrix} r - \dfrac{2rX}{k} - \dfrac{p_1 YS}{(s+X)^2} - \lambda & \dfrac{qp_1 X}{s+k} \\ \dfrac{qp_1 YS}{(s+X)^2} & \dfrac{qp_1 X}{s+X} - d_3 - \lambda \end{vmatrix} = 0. \tag{28}$$

Then,

$$\underbrace{\left(r - \frac{2rX}{k} - \frac{p_1 YS}{(s+X)^2} - \lambda\right)}_{a}\underbrace{\left(\frac{qp_1 X}{s+X} - d_3 - \lambda\right)}_{b} + \underbrace{\frac{sqp_1{}^2 XY}{(s+X)^3}}_{c} = 0, \tag{29}$$

is a characteristic polynomial.

Using the Routh-Hurwitz criterion, the quadratic polynomial is stable if $a + b > 0, ab + c > 0$, otherwise unstable.

Equilibrium points in model (8) are steady state points of the form (X, W, Y, Z, H) of model ((8)) that satisfies $dX/dt = dW/dt = dY/dt = dZ/dt = dH/dt = 0$, provided that each variable is nonnegative. In model ((8)), five steady state points are identified and listed here: trivial steady state $E_o(0, 0, 0, 0, 0)$, axial steady state E_A $(k, 0, 0, 0, 0)$, disease-free steady state $\bar{E}$ $(\bar{X}, 0, \bar{Y}, 0, 0)$, and endemic steady state $E^*(X^*, W^*, Y^*, Z^*, H^*)$. Computation of disease free and endemic equilibrium points is presented as follows.

Disease-free equilibrium points (DFEP) of model (8) are steady state solutions when there is no infectious disease in the population. In the absence of infectious disease in the prey-predator system, the variables $W(t) = Z(t) = H(t) = 0$ and $dX/dt = dW/dt = dY/dt = dZ/dt = dH/dt = 0$. Then, model (8) become

$$\begin{cases} r\bar{X}\left(1 - \dfrac{\bar{X}}{k}\right) - \dfrac{p_1 \bar{X}\bar{Y}}{s+X} = 0, \\ \dfrac{qp_1 \bar{X}\bar{Y}}{s+\bar{X}} - d_3\bar{Y} = 0. \end{cases} \tag{30}$$

Thus, solving $\bar{X}$ and $\bar{Y}$, it is found that $\bar{X} = d_3 s/(qp_1 - d_3)$ and $\bar{Y} = rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2 k$, and hence, disease-free equilibrium point (DFEP) of model (8) is given by

$$\begin{aligned} \bar{E} &= \{\bar{X}, \quad 0, \quad \bar{Y}, \quad 0, \quad 0\} \\ &= \left\{\frac{d_3 s}{qp_1 - d_3}, \quad 0, \quad \frac{rsq(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 k}, \quad 0, \quad 0\right\}. \end{aligned} \tag{31}$$

The endemic equilibrium point (EEP) is positive equilibrium point $E^*(X^*, W^*, Y^*, Z^*, H^*)$ obtained by solving model equation (8) as $dX/dt = dW/dt = dY/dt = dZ/dt = dH/dt = 0$ for which all variables are nonzero

$$\begin{cases} rX^*\left(1 - \dfrac{X^* + W^*}{k}\right) + r_1 H^* - \beta X^* W^* - \dfrac{p_1 X^* Y^* + p_3 X^* Z^*}{s+X^*} = 0, \\ \beta X^* W^* - t_1 W^* - d_2 W^* - \dfrac{p_2 W^* Y^* + p_4 W^* Z^*}{s+W^*} = 0, \\ q\dfrac{p_1 X^* Y^*}{s+X^*} + q\dfrac{p_2 W^* Y^*}{s+W^*} + r_2 H^* - \alpha Y^* Z^* - d_3 Y^* = 0, \\ q\dfrac{p_3 X^* Z^*}{s+X^*} + q\dfrac{p_4 W^* Z^*}{s+W^*} + \alpha Y^* Z^* - (t_2 + d_4)Z^* = 0, \\ t_1 W^* + t_2 Z^* - (d_1 + r_1 + r_2)H^* = 0. \end{cases} \tag{32}$$

Then, solving for the variables X^*, W^*, Y^*, Z^*, and H^*, the endemic equilibrium points of the model exists and a simplified result is obtained

$$X^* = (-r\beta d_1 + [2kr - rs - 2k\beta]d_1 d_2 - r\beta r_1 + 2krd_2 r_1),$$

$$W^* = \frac{\beta - s(d_2 + t_1) - \sqrt{4(s\beta - p_2 - p_4)(t_1 + d_2) + (s[t_1 + d_2] - \beta)^2}}{2(t_1 + d_2)},$$

$$Y^* = \frac{1}{d_3}\left(-\alpha - \frac{rr_2}{r_1} + \frac{r\beta r_2}{r_1} + \frac{r\beta r_2}{2kr_1(t_1 + d_2)} - \frac{rsd_2 r_2}{2kr_1(t_1 + d_2)} - \frac{rsr_2 t_1}{2kr_1(t_1 + d_2)}\right),$$

$$Z^* = \frac{1}{t_2 + d_4}\left(\alpha + \frac{qp_4}{s + \left(\beta - (t_1 + d_2) + \sqrt{4(s\beta - p_2 - p_4)(t_1 + d_2) + (s[t_1 + d_2] - \beta)^2}\right)/2(t_1 + d_2)}\right),$$

$$H^* = \frac{1}{r_1}\left(\beta - r + \frac{r\beta - rsd_2 - rst_1}{2k(t_1 + d_2)}\right). \tag{33}$$

To study the stability analysis of equilibrium points of model (8), it is better to linearize model (8) using variation matrix. Let us represent the model (8) as system of parametrical equations as follows:

$$\frac{dX}{dt} = f(X, W, Y, Z, H) = rX\left(1 - \frac{X + W}{k}\right) + r_1 H - \beta XW - \frac{p_1 XY}{s + X} - \frac{p_3 XZ}{s + X}, \tag{34}$$

$$\frac{dW}{dt} = g(X, W, Y, Z, H) = \beta XW - t_1 W - d_2 W - \frac{p_2 WY}{s + W} - \frac{p_4 WZ}{s + W}, \tag{35}$$

$$\frac{dY}{dt} = h(X, W, Y, Z, H) = q\frac{p_1 XY}{s + X} + q\frac{p_2 WY}{s + W} + r_2 H - \alpha YZ - d_3 Y, \tag{36}$$

$$\frac{dZ}{dt} = i(X, W, Y, Z, H) = q\frac{p_3 XZ}{s + X} + q\frac{p_4 WZ}{s + W} + \alpha YZ - t_2 Z - d_4 Z, \tag{37}$$

$$\frac{dH}{dt} = j(X, W, Y, Z, H) = t_1 W + t_2 Z - d_1 H - r_1 H - r_2 H. \tag{38}$$

Then, the variation matrix of these functions (36) is given by

$$V(X, W, Y, Z, H) = \begin{pmatrix} f_X & f_W & f_Y & f_Z & f_H \\ g_X & g_W & g_Y & g_Z & g_H \\ h_X & h_W & h_Y & h_Z & h_H \\ i_X & i_W & i_Y & i_Z & i_H \\ j_X & j_W & j_Y & j_Z & j_H \end{pmatrix}, \tag{39}$$

where each element of the matrix represents partial derivatives of functions (36) with respect to model variables and computations of each element of the variation matrix are given as

$$V(X, W, Y, Z, H) = \begin{pmatrix} f_X & -\frac{rX}{k} - \beta X & -\frac{p_1 X}{s + X} & -\frac{p_3 X}{s + X} & r_1 \\ \beta W & g_W & -\frac{p_2 W}{s + W} & -\frac{p_4 W}{s + w} & 0 \\ \frac{sqp_1 Y}{(s + X)^2} & \frac{sqp_2 Y}{(s + X)^2} & h_Y & -\alpha y - d_3 & r_2 \\ \frac{sqp_3 Z}{(s + X)^2} & \frac{sqp_4 Z}{(s + W)^2} & \alpha Z & i_z & 0 \\ 0 & t_1 & 0 & t_2 & -d_1 - r_1 - r_2 \end{pmatrix}, \tag{40}$$

where, $f_X = r - 2rx/k - rW/k - \beta W - s(p_1 Y + p_3 Z)/(s + X)^2$, $g_W = \beta X - t_1 - d_2 - s(p_2 Y + p_4 Z)/(s + W)^2$, $h_Y = qp_1 X/(s + X) + qp_2 W/(s + W) - \alpha Z - d_3$, $i_z = qp_3 X/(s + X) + qp_4 W/(s + W) - \alpha Y - t_2 - d_4$.

Theorem 9 (TEP). *Trivial equilibrium point* E_o $(0, 0, 0, 0, 0)$ *exists and always locally asymptotically unstable.*

Proof. Consider the variation matrix (40) at E_o.

$$V(E_o) = \begin{pmatrix} r & 0 & 0 & 0 & r_1 \\ 0 & -t_1 - d_2 & 0 & 0 & 0 \\ 0 & 0 & -d_3 & 0 & r_2 \\ 0 & 0 & 0 & -t_2 - d_4 & 0 \\ 0 & t_1 & 0 & t_2 & -d_1 - r_1 - r_2 \end{pmatrix}. \tag{41}$$

Eigenvalue of variation matrix can be computed from the characteristic polynomial $\det(V(E_o) - \lambda I_5) = 0$

$$\begin{vmatrix} r-\lambda & 0 & 0 & 0 & r_1 \\ 0 & -t_1-d_2-\lambda & 0 & 0 & 0 \\ 0 & 0 & -d_3-\lambda & 0 & r_2 \\ 0 & 0 & 0 & -t_2-d_4-\lambda & 0 \\ 0 & a_1 & 0 & a_2 & -d_1-r_1-r_2-\lambda \end{vmatrix} = 0, \tag{42}$$

$\Longrightarrow (r-\lambda)(-t_1-d_2-\lambda)(-d_3-\lambda)(-t_2-d_4-\lambda)(-d_1-r_1-r_2-\lambda)=0$ is the characteristic polynomial. The eigen values are $\lambda_1 = r, \lambda_2 = -t_1-d_2, \lambda_3 = -d_3, \lambda_4 = -t_2-d_4, \lambda_5 = -d_1-r_1-r_2$. Thus, the trivial equilibrium point is locally asymptotically unstable due to the parameter r is nonnegative.

Theorem 10 (AEP). *Axial equilibrium point $E_A(k,0,0,0,0)$ exists and always locally asymptotically stable in model (8) if and only if model parameters satisfy the conditions: $\beta k - t_1 - d_2 < 0$, $qp_1k/(s+k) - d_3 < 0$, and $qp_3k/(s+k) - t_2 - d_4 < 0$. Otherwise, E_A is locally asymptotically unstable.*

Proof. Consider the variation matrix (40) at $J(E_A)$

$$V(E_A) = \begin{pmatrix} -r & -r-\beta k & -\frac{p_1k}{s+k} & -\frac{p_3k}{s+k} & r_1 \\ 0 & \beta k - t_1 - d_2 & 0 & 0 & 0 \\ 0 & 0 & \frac{qp_1k}{s+k} - d_3 & d_3 & r_2 \\ 0 & 0 & 0 & \frac{qp_3k}{s+k} - t_2 - d_4 & 0 \\ 0 & t_1 & 0 & t_2 & -d_1-r_1-r_2 \end{pmatrix}. \tag{43}$$

Then, it is possible to find eigenvalue of this variation matrix as $\det(V(E_A - \lambda I_5) = 0$,

$$\begin{vmatrix} -r-\lambda & -r-\beta k & -\frac{p_1k}{s+k} & -\frac{p_3k}{s+k} & r_1 \\ 0 & \beta k - t_1 - d_2 - \lambda & 0 & 0 & 0 \\ 0 & 0 & \frac{qp_1k}{s+k} - d_3 - \lambda & d_3 & r_2 \\ 0 & 0 & 0 & \frac{qp_3k}{s+k} - t_2 - d_4 - \lambda & 0 \\ 0 & t_1 & 0 & t_2 & -d_1-r_1-r_2-\lambda \end{vmatrix} = 0. \tag{44}$$

Use first column to find the determinant,

$$\Longrightarrow (-r-\lambda)\begin{vmatrix} \beta k - t_1 - d_2 - \lambda & 0 & 0 & 0 \\ 0 & \frac{qp_1k}{s+k} - d_3 - \lambda & d_3 & r_2 \\ 0 & 0 & \frac{qp_3k}{s+k} - t_2 - d_4 - \lambda & 0 \\ t_1 & 0 & t_2 & -d_1-r_1-r_2-\lambda \end{vmatrix} = 0. \tag{45}$$

Use first row to compute the remaining determinant,

$$\Longrightarrow(-r-\lambda)(\beta k-t_1-d_2-\lambda)\begin{vmatrix}\frac{qp_1k}{s+k}-d_3-\lambda & d_3 & r_2\\ 0 & \frac{qp_3k}{s+k}-t_2-d_4-\lambda & 0\\ 0 & t_2 & -d_1-r_1-r_2-\lambda\end{vmatrix}=0. \tag{46}$$

Use first column to get the characteristic polynomial,

$$\Longrightarrow(-r-\lambda)(\beta k-t_1-d_2-\lambda)\left(\frac{qp_1k}{s+k}-d_3-\lambda\right)\cdot\begin{vmatrix}\frac{qp_3k}{s+k}-t_2-d_4-\lambda & 0\\ t_2 & -d_1-r_1-r_2-\lambda\end{vmatrix}=0,$$

$$\Longrightarrow(-r-\lambda)(\beta k-t_1-d_2-\lambda)\left(\frac{qp_1k}{s+k}-d_3-\lambda\right)\cdot\left(\frac{qp_3k}{s+k}-t_2-d_4-\lambda\right)(-d_1-r_1-r_2-\lambda)=0, \tag{47}$$

is characteristic polynomial. Then, eigenvalues are

$$\lambda_1=-r,\lambda_2=-d_1-r_1-r_2,\lambda_3=\beta k-t_1-d_2,\lambda_4=\frac{qp_1k}{s+k}-d_3,\lambda_5=\frac{qp_3k}{s+k}-t_2-d_4. \tag{48}$$

The axial equilibrium point E_A is locally asymptotically stable, if

$$\beta k-t_1-d_2<0,\ \frac{qp_1k}{s+k}-d_3<0,\ \frac{qp_3k}{s+k}-t_2-d_4<0. \tag{49}$$

Otherwise, E_A is locally asymptotically unstable.

Theorem 11 (DFEP). *The disease-free equilibrium point* $\bar{E}(\bar{X},\ 0,\ \bar{Y},\ 0,\ 0)=\{d_3s/(qp_1-d_3),\ 0,\ rsq(kqp_1-kd_3-d_3s)/(qp_1-d_3)^2k,0,0\}$ *exists and is always locally asymptotically stable if and only if the model parameter satisfy conditions (i)* $\beta\bar{X}-t_1-d_2-sp_2\bar{Y}/s^2\le 0$, *(ii)* $qp_3\bar{X}/(s+X)-\alpha\bar{Y}-t_2-d_4\le 0$, *(iii)* $\{r-2r\bar{X}/k-sp_1\bar{Y}/(s+\bar{X})^2\}+\{qp_1\bar{X}/(s+\bar{X})-d_3\}>0$, *and (iv)* $\{r-2r\bar{X}/k-sp_1\bar{Y}/(s+\bar{X})^2\}\{qp_1\bar{X}/(s+\bar{X})-d_3\}+sqp_1{}^2\bar{X}^2/(s+\bar{X})^3>0$.

Proof. Consider the variation matrix (40) at disease-free equilibrium point $\bar{E}(\bar{X},0,\overline{Y},0,0)$ such that

$$V(\bar{E})=\begin{pmatrix}r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{(s+\bar{X})^2} & -\frac{r\bar{X}}{k}-\beta\bar{X} & -\frac{p_1\bar{X}}{s+\bar{X}} & -\frac{p_3\bar{X}}{s+\bar{X}} & r_1\\ 0 & \beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2} & 0 & 0 & 0\\ \frac{sqp_1\bar{X}}{(s+\bar{X})^2} & \frac{sqp_2\bar{Y}}{(s+\bar{X})^2} & \frac{qp_1\bar{X}}{s+\bar{X}}-d_3 & -\alpha\bar{Y}-d_3 & r_2\\ 0 & 0 & 0 & \frac{qp_3\bar{X}}{s+\bar{X}}-\alpha\bar{Y}-t_2-d_4 & 0\\ 0 & t_1 & 0 & t_2 & -d_1-r_1-r_2\end{pmatrix}. \tag{50}$$

Then, it is possible to find the determinant of the variation matrix as $\det\left(V(\bar{E})-\lambda I_5\right)$

$$\begin{vmatrix} r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{\left(s+\bar{X}\right)^2}-\lambda & -\frac{r\bar{X}}{k}-\beta\bar{X} & -\frac{p_1\bar{X}}{s+\bar{X}} & -\frac{p_3\bar{X}}{s+\bar{X}} & r_1 \\ 0 & \beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}-\lambda & 0 & 0 & 0 \\ \frac{sqp_1\bar{X}}{\left(s+\bar{X}\right)^2} & \frac{sqp_2\bar{Y}}{\left(s+\bar{X}\right)^2} & \frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda & -\alpha\bar{Y}-d_3 & r_2 \\ 0 & 0 & 0 & \frac{qp_3\bar{X}}{s+\bar{X}}-\alpha\bar{Y}-t_2-d_4-\lambda & 0 \\ 0 & t_1 & 0 & t_2 & -d_1-r_1-r_2-\lambda \end{vmatrix}. \tag{51}$$

To find eigenvalues, compute the determinant using second row

$$\left(\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}-\lambda\right)*\begin{vmatrix} r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{\left(s+\bar{X}\right)^2}-\lambda & -\frac{p_1\bar{X}}{s+\bar{X}} & -\frac{p_3\bar{X}}{s+\bar{X}} & r_1 \\ \frac{sqp_1\bar{X}}{\left(s+\bar{X}\right)^2} & \frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda & -\alpha Y-d_3 & r_2 \\ 0 & 0 & \frac{qp_3\bar{X}}{s+\bar{X}}-\alpha Y-t_2-d_4-\lambda & 0 \\ 0 & 0 & 0 & -d_1-r_1-r_2-\lambda \end{vmatrix}. \tag{52}$$

Now again use third row to find determinant:

$$\left(\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}-\lambda\right)\left(\frac{qp_3\bar{X}}{s+\bar{X}}-\alpha\bar{Y}-t_2-d_4-\lambda\right)*\begin{vmatrix} r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{\left(s+\bar{X}\right)^2}-\lambda & -\frac{p_1\bar{X}}{s+\bar{X}} & r_1 \\ \frac{sqp_1\bar{X}}{\left(s+\bar{X}\right)^2} & \frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda & r_2 \\ 0 & 0 & -d_1-r_1-r_2-\lambda \end{vmatrix}. \tag{53}$$

Then, use third row to find characteristic polynomial

$$\left(\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}-\lambda\right)\cdot\left(\frac{qp_3\bar{X}}{s+\bar{X}}-\alpha\bar{Y}-t_2-d_4-\lambda\right)(-d_1-r_1-r_2-\lambda)*\begin{vmatrix} r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{\left(s+\bar{X}\right)^2}-\lambda & -\frac{p_1\bar{X}}{s+X} \\ \frac{sqp_1\bar{X}}{\left(s+\bar{X}\right)^2} & \frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda \end{vmatrix}$$

$$\cdot\left(\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}-\lambda\right)\left(\frac{qp_3\bar{X}}{s+X}-\alpha\bar{Y}-t_2-d_4-\lambda\right)\cdot(-d_1-r_1-r_2-\lambda)*\left\{\left(r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{(s+\bar{X})^2}-\lambda\right)\cdot\left(\frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda\right)+\frac{sqp_1{}^2\bar{X}^2}{(s+\bar{X})^3}\right\}=0. \tag{54}$$

Eigenvalues are

$$\lambda_1=\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2},\lambda_2=\frac{qp_3\bar{X}}{s+\bar{X}}-\alpha\bar{Y}-t_2-d_4,\lambda_3=-d_1-r_1-r_2, \tag{55}$$

and the remaining eigenvalues can be obtained from the roots of quadratic equation:

$$\underbrace{\left(r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{(s+\bar{X})^2}-\lambda\right)}_{a}\underbrace{\left(\frac{qp_1\bar{X}}{s+\bar{X}}-d_3-\lambda\right)}_{b}+\underbrace{\frac{sqp_1{}^2\bar{X}^2}{(s+\bar{X})^3}}_{c}=0. \tag{56}$$

It is known that a quadratic equation $(a-\lambda)(b-\lambda)+c=0$ is locally asymptotically stable if and only if $a+b>0$ and $ab+c>0$, using such *Routh-Hurwitz criterion*, the disease-free equilibrium point $\bar{E}(\bar{X},0,\overline{Y},0,0)$ is locally asymptotically stable if

$$\left\{r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{(s+\bar{X})^2}\right\}+\left\{\frac{qp_1\bar{X}}{s+\bar{X}}-d_3\right\}>0,\left\{r-\frac{2r\bar{X}}{k}-\frac{sp_1\bar{Y}}{(s+\bar{X})^2}\right\}\left\{\frac{qp_1\bar{X}}{s+\bar{X}}-d_3\right\}+\frac{sqp_1{}^2\bar{X}^2}{(s+\bar{X})^3}>0,$$

$$\lambda_1=\beta\bar{X}-t_1-d_2-\frac{sp_2\bar{Y}}{s^2}\le 0,\ \lambda_2=\frac{qp_3\bar{X}}{s+X}-\alpha\bar{Y}-t_2-d_4\le 0, \tag{57}$$

where $\bar{X}=d_3s/(qp_1-d_3)$ and $\bar{Y}=rsq(kqp_1-kd_3-d_3s)/(qp_1-d_3)^2k$. Otherwise, the disease-free equilibrium point is asymptotically unstable.

Now let us see again the global stability analysis of model (8) around the endemic equilibrium point or positive equilibrium point $E^*(X^*,W^*,Y^*,Z^*,H^*)$ which shows coexistence. For that, let us state the following theorem and prove by taking appropriate Lyapunov function L.

Theorem 12 (global stability). *Endemic equilibrium point* $E^*(X^*,W^*,Y^*,Z^*,H^*)$ *exists and globally asymptotically stable.*

Proof. Define appropriate Lyapunov function $L(X,W,Y,Z,H)=(1/2)(X-X^*)^2+(\alpha_1/2)(W-W^*)^2+(\alpha_2/2)(Y-Y^*)^2+(\alpha_3/2)(Z-Z^*)^2+(\alpha_4/2)(H-H^*)^2$, where $\alpha_1,\alpha_2,\alpha_3,\alpha_4>0$ are chosen properly such that $dL/dt=0\forall(X^*,W^*,Y^*,Z^*,H^*)\in\mathbb{R}^5_+$ and $dL/dt\le 0\forall(X,W,Y,Z,H)\in\mathbb{R}^5_+$.This implies E^* of the system is Lyapunov stable and $dL/dt<0$, $\forall(X,W,Y,Z,H)\in\mathbb{R}^5_+$ near E^*. This implies E^* is globally asymptotically stable point. Now differentiate the Lyapunov function L with respect to t

$$\frac{dL}{dt}=(X-X^*)\frac{dX}{dt}+\alpha_1(W-W^*)\frac{dI}{dt}+\alpha_2(Y-Y^*)\frac{dY}{dt}+\alpha_3(Z-Z^*)\frac{dZ}{dt}+\alpha_4(H-H^*)\frac{dH}{dt}. \tag{58}$$

Now substitute the model equation (8) into (58), we have the following equation:

$$\begin{aligned}\frac{dL}{dt}=&(X-X^*)\left[rX\left(1-\frac{X+W}{k}\right)+r_1H-\beta XW-\frac{p_1XY}{s+X}-\frac{p_3XZ}{s+X}\right]+\alpha_1(W-W^*)\\&\cdot\left[\beta XW-t_1W-d_2W-\frac{p_2WY}{s+W}-\frac{p_4WZ}{s+W}\right]+\alpha_2(Y-Y^*)\left[q\frac{p_1XY}{s+X}+q\frac{p_2WY}{s+W}+r_2H-\alpha YZ-d_3Y\right]\\&+\alpha_3(Z-Z^*)\left[q\frac{p_3XZ}{s+X}+q\frac{p_4WZ}{s+W}+\alpha YZ-t_2Z-d_4Z\right]+\alpha_4(H-H^*)[t_1W+t_2Z-d_1H-r_1H-r_2H].\end{aligned} \tag{59}$$

Take out X,W,Y,Z,H from each bracket and write a change as follows

$$\begin{aligned}\frac{dL}{dt}=&(X-X^*)(X-X^*)\left[r\left(1-\frac{X+W}{k}\right)+\frac{r_1H}{X}-\beta W-\frac{p_1Y}{s+X}-\frac{p_3Z}{s+X}\right]+\alpha_1(W-W^*)(W-W^*)\\&\cdot\left[\beta X-t_1-d_2-\frac{p_2Y}{s+W}-\frac{p_4Z}{s+W}\right]+\alpha_2(Y-Y^*)(Y-Y^*)\cdot\left[q\frac{p_1X}{s+X}+q\frac{p_2W}{s+W}+\frac{r_2H}{Y}-\alpha Z-d_3\right]\\&+\alpha_3(Z-Z^*)(Z-Z^*)\left[q\frac{p_3X}{s+X}+q\frac{p_4W}{s+W}+\alpha Y-t_2-d_4\right]+\alpha_4(H-H^*)(H-H^*)\left[\frac{t_1W}{H}+\frac{t_2Z}{H}-d_1-r_1-r_2\right].\end{aligned} \tag{60}$$

By rearranging, it is obtained that

$$\frac{dL}{dt} = -(X - X^*)^2[$$

$$-r\left(1 - \frac{X+W}{k}\right) - \frac{r_1 H}{X} + \beta W + \frac{p_1 Y}{s+X} + \frac{p_3 Z}{s+X}] - \alpha_1 (I - I^*)^2[-\beta X + t_1 + d_2 + \frac{p_2 Y}{s+W} + \frac{p_4 Z}{s+W}] - \alpha_2 (Y - Y^*)^2[-q\frac{p_1 S}{s+X} - q\frac{p_2 W}{s+W} - \frac{r_2 H}{Y} + \alpha Z + d_3] - \alpha_3 (Z - Z^*)^2[-q\frac{p_3 X}{s+X} - q\frac{p_4 W}{s+W} - \alpha Y + t_2 + d_4] - \alpha_4 (H - H^*)^2[-\frac{t_1 W}{H} - \frac{t_2 Z}{H} + d_1 + r_1 + r_2].$$

Thus, it is possible to set $\alpha_1, \alpha_2, \alpha_3, \alpha_4$ such that $dL/dt \le 0$ and endemic equilibrium point E^* is globally stable point.

5. Basic Reproduction Number

The basic reproduction number denoted by R_0 and defined as the expected number of people getting secondary infection among the whole susceptible population. This number shows a potential for spread of disease within a given population. When $R_0 < 1$, each infected individual produces on average less than one new infected individual so that the disease is expected to die out. On the other hand, if $R_0 > 1$, then each individual produces more than one new infected individual so that the disease is expected to continue spreading in the population.

Theorem 13. *The basic reproduction number for infected prey at disease-free equilibrium point (DFEP)* $\bar{E}(\bar{X}, 0, \bar{Y}, 0, 0) = (d_3 s/(qp_1 - d_3), \quad 0, \quad rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2 k, 0, 0)$ *is given by*

$$R_{01} = \frac{(qp_1 - d_3)^2 k\beta d_3 s^2}{(qp_1 - d_3)\{(qp_1 - d_3)^2 ks(t_1 + d_2) + rsqp_2(kqp_1 - kd_3 - d_3 s)\}}. \tag{62}$$

Proof. Consider infected prey equation in (8), we have the following model equation

$$\frac{dW}{dt} = \beta XW - t_1 W - d_2 W - \frac{p_2 WY}{s+W} - \frac{p_2 WZ}{s+W} = \left(\beta X - \left[t_1 + d_2 + \frac{p_2 Y}{s+W} + \frac{p_2 Z}{s+W}\right]\right) W. \tag{63}$$

Now let us define functions F and V, $F = \beta X$, $V = t_1 + d_2 + p_2 Y/(s+W) + p_2 Z/(s+W)$.

Evaluate F and V at DFEP $\bar{E}(\bar{X}, 0, \bar{Y}, 0, 0) = (d_3 s/(qp_1 - d_3), \quad 0, \quad rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2 k, 0, 0)$,

$$F(\bar{E}) = \beta\bar{X} = \frac{\beta d_3 s}{qp_1 - d_3}, \quad V(\bar{E}) = t_1 + d_2 + \frac{p_2 \bar{Y}}{s} = t_1 + d_2 + \frac{rsqp_2(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 ks} = \frac{(qp_1 - d_3)^2 (t_1 + d_2) ks + rsqp_2(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 ks}. \tag{64}$$

Then, the basic reproduction number of infected prey is

$$R_{01} = FV^{-1} = \frac{\beta d_3 s}{qp_1 - d_3} * \frac{(qp_1 - d_3)^2 ks}{(qp_1 - d_3)^2 (t_1 + d_2) ks + rsqp_2(kqp_1 - kd_3 - d_3 s)},$$

$$R_{01} = \frac{(qp_1 - d_3)^2 k\beta d_3 s^2}{(qp_1 - d_3)\{(qp_1 - d_3)^2 (t_1 + d_2) ks + rsqp_2(kqp_1 - kd_3 - d_3 s)\}}. \tag{65}$$

Theorem 14. *The basic reproduction number for infected predators at disease-free equilibrium point (DFEP)* $\bar{E}(\bar{X}, 0, \bar{Y}, 0, 0) = (d_3 s/(qp_1 - d_3), \quad 0, \quad rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2 k, 0, 0)$ *is given by*

$$R_{02} = \frac{(qp_1 - d_3)(qp_3 d_3)k + \alpha rsq(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 (t_2 + d_4)k}. \tag{66}$$

Proof. Consider the infected predator model equation in (8), we have the following equation

$$\frac{dZ}{dt} = q\frac{p_2 WZ}{s+W} + q\frac{p_3 XZ}{s+W} + \alpha YZ - t_2 Z - d_4 Z = \left[q\frac{p_2 W}{s+W} + q\frac{p_3 X}{s+W} + \alpha Y - (t_2 + d_4)\right] Z. \tag{67}$$

Now let us define functions F and V as $F = q(p_2 W/(s+W)) + q(p_3 X/(s+W)) + \alpha Y$, $V = t_2 + d_4$. Then, evaluate F and V at (DFEP) $\bar{E}(\bar{X}, 0, \bar{Y}, 0, 0) = (d_3 s/(qp_1 - d_3), \quad 0, \quad rsq(kqp_1 - kd_3 - d_3 s)/(qp_1 - d_3)^2 k, 0, 0)$,

$$F(\bar{E}) = \frac{qp_3 d_3 s}{s(qp_1 - d_3)} + \frac{\alpha rsq(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 k} = \frac{(qp_1 - d_3)(qp_3 d_3)k + \alpha rsq(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 k},$$

$$V(\bar{E}) = t_2 + d_4. \tag{68}$$

Therefore, the basic reproduction number of infected predator is $R_{02} = FV^{-1}$, and hence,

$$R_{02} = \frac{(qp_1 - d_3)(qp_3 d_3)k + \alpha rsq(kqp_1 - kd_3 - d_3 s)}{(qp_1 - d_3)^2 (t_2 + d_4)k}. \tag{69}$$

6. Simulation

In this section, simulation of model (8) is carried out using DEDiscover version: 2.6.4. software. For simulation, a set of meaningful values are assigned to model parameters in Table 4, and initial values for model variables are given in Table 5. The model is arranged in such a way for simulation

purposes.

$$\frac{dX}{dt} = r * X * \left(1 - \frac{X+W}{k}\right) + r^{-}1 * H - \text{beta} * X * W - P^{-}1 * X * \frac{Y}{s+X} - P^{-}3 * X * \frac{Z}{s+X} \text{//susceptible prey,}$$

$$\frac{dW}{dt} = \text{beta} * X * W - t^{-}1 * W - d^{-}2 * W - P^{-}2 * W * \frac{Y}{s+W} - P^{-}4 * W * \frac{Z}{s+W} \text{//infected prey,}$$

$$\frac{dY}{dt} = q * P^{-}1 * X * \frac{Y}{s+X} + q * P^{-}2 * W * \frac{Y}{s+W} + r^{-}2 * H - \text{alpha} * Y * Z - d^{-}3 * Y \text{//susceptible predator,}$$

$$\frac{dZ}{dt} = q * P^{-}3 * X * \frac{Z}{s+X} + q * P^{-}4 * W * \frac{Z}{s+W} - \text{alpha} * Y * Z - t^{-}2 * Z - d^{-}4 * Z \text{//infected predator,}$$

$$\frac{dH}{dt} = t^{-}1 * W + t^{-}2 * Z - d^{-}1 * H - r^{-}1 * H - r^{-}2 * H \text{//both infected populations under treatment.} \quad (70)$$

From simulation in Figures 2 and 3, it can be concluded that treatment is a helpful tool to minimize or eradicate infection. It is shown that as the treatment rate increases on infected prey-predator, then the infected prey-predator population decreases rapidly. This shows due to the fact that the infected prey-predator population is recovering and moves to susceptible classes and that contributes to the susceptible prey-predator population to rise in number.

In the sample simulation in Figures 4 and 5, it is shown that high infection and predation results in the whole prey-predator population declining to a certain level. Therefore, it is better to implement treatment mechanisms to sustain stability of the prey-predator system.

7. Conclusions and Recommendation

In this paper, It can be concluded that the formulated model is mathematically meaningful, valid, and biologically well posed by proving the boundedness, positivity, and existence of the solutions of the model. Trivial, axial, disease-free, and endemic equilibrium points are investigated. Moreover, It is observed that in our model, trivial equilibrium point is always locally asymptotically unstable. Axial equilibrium point is locally asymptotically stable if and only if the variables satisfy the following three conditions: (i) $\beta k - (t_1 + d_2) < 0$, (ii) $qp_1 k - d_3(s+k) < 0$, and (iii) $qp_3 k - (t_2 + d_4)(s+k) < 0$.

Treatment is a helpful tool to minimize or eradicate infection in the prey-predator system. Therefore, providing treatment in an infected prey-predator system creates opportunity to recover from illness and the prey-predator population can be saved and exists in stable situation. Thus, it is recommended to apply treatment on infected prey-predator to make the whole prey-predator population safe and abundant in nature. One can extend this paper by assuming the predator grows logistically or by adding parameter like death rate on the prey or by including other variables like vaccination, immigration, migration on prey-predator system, and these things can be considered as limitation of this paper.

Data Availability

No primary data were used to support this study, and it is all secondary data.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

References

[1] S. Kumar and H. Kharbanda, "Stability analysis of prey-predator model with infection, migration and vaccination in prey," 2017, http://arxiv.org/abs/1709.10319vl [math.DS].

[2] R. K. Naji and K. A. Hasan, "The dynamics of prey-predator model with disease in prey," *Mathematics in Computer Science*, vol. 2, no. 4, pp. 1052–1072, 2012.

[3] J. Chattopadhyay and O. Arino, "A predator-prey model with disease in the prey," *Nonlinear Analysis*, vol. 36, no. 6, pp. 747–766, 1999.

[4] A. F. Bezabih, "Mathematical eco-epidemic model on prey-predator system," *IOSR Journal of Mathematics (IOSR-JM)*, vol. 16, no. 1, pp. 22–34, 2020.

[5] S. Sudipa, O. P. Misra, and J. Dhar, "Modeling a predator–prey system with infected prey in polluted environment," *Applied Mathematical Modelling*, vol. 34, no. 7, pp. 1861–1872, 2008.

[6] A. F. Bezabih, G. K. Edessa, and P. R. Koya, "Mathematical eco-epidemiological model on prey-predator system," *Mathematical Modeling and Applications*, vol. 5, no. 3, pp. 183–190, 2020.

[7] A. F. Bezabih, G. K. Edessa, and P. R. Koya, "Mathematical epidemiology model analysis on the dynamics of COVID-19 pandemic," *American Journal of Applied Mathematics*, vol. 8, no. 5, pp. 247–256, 2020.

[8] S. P. Bera, A. Maiti, and G. Samanta, "A prey-predator model with infection in both prey and predator," *Univerzitet u Nišu*, vol. 29, no. 8, pp. 1753–1767, 2015.

[9] Y. T. Hewindati, F. A. A. Faeldog, and F. A. Abdullah, "Dynamics of disease spread in a predator-prey system," *Advanced Studies in Biology*, vol. 6, no. 4, pp. 169–179, 2014.

[10] C. M. Silva, "Existence of periodic solutions for periodic eco-epidemic models with disease in the prey," *Journal of Mathematical Analysis and Applications*, vol. 453, no. 1, pp. 383–397, 2017.

[11] A. Hugo, E. S. Massawe, and O. D. Makinde, "An eco-epidemiological mathematical model with treatment and disease infection in both prey and predator population," *Journal of Ecology and Natural Environment*, vol. 4, no. 10, pp. 266–273, 2012.

[12] G. K. Edessa, B. Kumsa, and P. R. Koya, "Modeling and simulation study of the population dynamics of commensal-host-

parasite system," *American Journal of Applied Mathematics*, vol. 6, no. 3, pp. 97–108, 2018.

[13] S. Tolcha, B. Kumsa, and P. R. Koya, "Modeling and simulation study of mutuality interactions with type II functional response and harvesting," *American Journal of Applied Mathematics*, vol. 6, no. 3, pp. 109–116, 2018.

[14] S. Saha and G. P. Samanta, "A prey-predator system with disease in prey and cooperative hunting strategy in predator," *Journal of Physics A: Mathematical and Theoretical*, vol. 53, no. 48, article 485601, 2020.

[15] S. Sah, A. Maiti, and G. P. Samanta, "A predator-prey model with strong Allee effect and disease in prey population," *International Journal of Ecological Economics and Statistics*, vol. 40, no. 2, pp. 92–112, 2019.

[16] S. Sah, A. Maiti, and G. P. Samanta, "A Michaelis–Menten predator–prey model with strong Allee effect and disease in prey incorporating prey refuge," *International Journal of Bifurcation and Chaos*, vol. 28, no. 6, article 1850073, 2018.

[17] S. Saha and G. P. Samanta, "Analysis of a predator–prey model with herd behavior and disease in prey incorporating prey refuge," *International Journal of Biomathematics*, vol. 12, no. 1, article 1950007, 2019.

[18] M. Ashok, A. K. Pal, and G. P. Samanta, "On the dynamics of evolutionary Leslie-Gower predator-prey eco-epidemiological model with disease in predator," *Ecological Genetics and Genomics*, vol. 10, article 100034, 2019.

[19] S. Sharma and G. P. Samanta, "Analysis of a two prey one predator system with disease in the first prey population," *International Journal of Dynamics and Control*, vol. 3, no. 3, pp. 210–224, 2015.

[20] S. Sharma and G. P. Samanta, "A Leslie-Gower predator-prey model with disease in prey incorporating a prey refuge," *Chaos, Solutions and Fractals*, vol. 70, no. 1, pp. 69–84, 2015.

[21] M. Haque, "A predator-prey model with disease in the predator species only," *Real World Applications*, vol. 11, no. 4, pp. 2224–2236, 2010.