$$S^* = \frac{p\pi K_1 + \eta\pi(1-p) + pAR_H^*}{(\beta I^8 + \mu)K_1}$$

$$E^* = \frac{\beta S^* I^*}{K_2}, I^* = \frac{\varepsilon E^*}{K_3} \rightarrow \qquad (11)$$

$$R_{ES}^* = \frac{\sigma I^*}{K_4}, \quad R_H^* = \frac{\gamma I^* + \delta R_{ES}^*}{R_5}$$

Where $K_1 = (\mu + \eta), R_2 = \mu + \varepsilon, K_3 = \mu + d + \gamma + \sigma, K_4 = \mu + \alpha_1 + \delta, K_5 = \mu + \rho.$

From (11) $E^* = \frac{I^* K_3}{\varepsilon}$.

$$\Longrightarrow \frac{I^* K_3}{\varepsilon} = \frac{\beta S^* I^*}{K_2} \Longrightarrow S^* = \frac{K_2 K_3}{\beta\epsilon}$$

$$\frac{K_2 K_3}{\beta\epsilon} = \frac{\frac{p\pi k_1 + \eta\pi(1-p)}{K_1} + \frac{pK_1(\gamma K_4 + \delta\sigma)I^*}{K_1 K_4 K_5}}{(\beta I^* + \mu)K_1}$$

$$\Longrightarrow I^* = \frac{p\pi\beta\epsilon K_1 K_4 K_5 + \beta\epsilon\eta\pi(1-p)K_4 K_5 - K_1 K_2 K_3 K_4 K_5 \mu}{K_1 K_2 K_3 K_4 K_5 \beta - pK_1\beta\varepsilon(\gamma K_4 - \delta\sigma)}$$

$K^* = K_3 \frac{K_6}{K_7}$ where $K_6 = \rho\pi\beta K_1 K_4 K_5 + \beta\varepsilon\pi\eta(1-p)K_4 K_5 - K_1 K_2 K_3 K_4 \mu.$

$$K_7 = K_1 K_2 K_3 K_4 K_5 \beta - pK_1\beta\varepsilon(\gamma K_4 - \delta\sigma)$$

$$R_{ES}^* = \frac{\sigma K_3 K_6}{K_4 K_7}$$

$$R_H^* = \frac{(\gamma K_4 + \delta\sigma)K_6}{K_4 K_5 K_7} = \frac{K_6(\gamma K_4 + \delta\sigma)}{K_4 K_5 K_7}$$

$$S^* = \frac{K_2 K_3}{\beta\varepsilon}$$

$$M^* = \frac{(1-p)\pi}{K_1}$$

$$E^* = \frac{K_2 K_3 K_6}{\varepsilon K_7}, I^* = \frac{K_6}{K_7}$$

From $I^* = \frac{K_6}{K_7}$

Since the force of infection $\lambda^* = \beta I^* S^*$ then

$$\lambda^* = \beta I^* S^* = \left\{\frac{K_1 K_2 K_3 K_4 K_5 \mu(R_0 - 1)}{K_1 K_2 K_3 K_4 K_5 \beta - pK_1\beta(\gamma K_4 + \delta\sigma)}\right\}$$

Lemma 3:

The endemic Equilibrium point (EEP) exist and is unique and is locally asymptotically stable if and only if $R_0 > 1$. (By Descartes Rule of signs).

RESULT AND DISCUSSION

Numerical Simulation

The numerical simulation of the model was carried out using MATLAB. The estimated parameter values used in the simulation of this model are presented in table 2.1. Since the parameter values are known, then we can solve our system of differential equations (5 - 9), since the model uses six separate differential equations one must use a numerical solver to plot the solution.

This is easier with MATLAB. We used the parameter values (Table 2.1) in MATLAB and plot the graph. The numerical simulation result is displayed in figure 1.1.

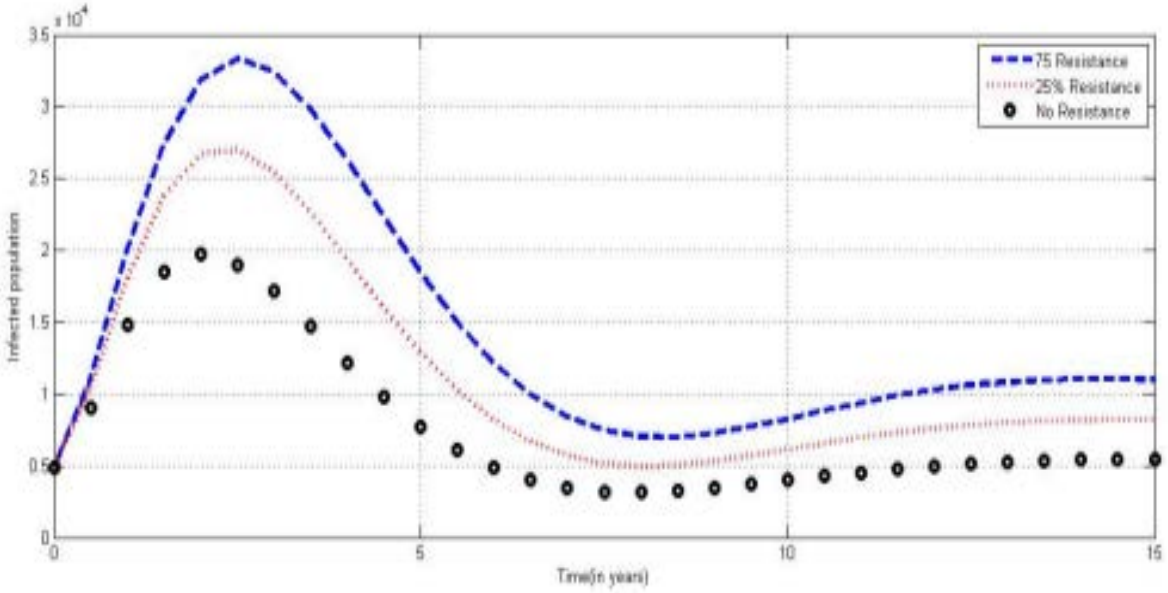

Figure 1.1: Numerical Simulation of Infected Individual against time.

Parameters	**Value**
N	1000
Π	5000
μ	0.9
P	0.04
B	0.05
E	0.06
Γ	0.65
A	0.6
Δ	0.3
α_1	0.04
H	0.088
Σ	0, 0.25, 0.75

Table 2.1: Estimation of Parameter and Constant

The graph of figure (1.1) represent three cases from table (2.1), the first case when $\sigma = 0$ that is the initial state, second case when $\sigma = 0.25$ and the third case when $\sigma = 0.75$. We can see that there was less number of infected population when there is no resistance and infection is increased as we increases the resistance from 25% to 75% with respect to time.

DISCUSSION

From the numerical simulation of the condition in figure (4.1) above, it shows that there was less number of infected population when there is no resistance and infection is

increased as we increases the resistance from 25% to 75%. This was achieved by first choosing $\sigma = 0$ simulation gives $R_0 = 0.865116 < 1$, secondly when $\sigma = 0.25$ simulation gives $R_0 = 0.907885 < 1$ and lastly when $\sigma = 0.75 < 1$ simulation gives $R_0 = 0.751353 < 1$ showing that the disease free equilibrium point (Eq^0) of the model is locally stable in all the three (3) different values of σ. Since the basic reproduction number $R_0 < 1$, it implies that the disease will gradually die out in the population when there are no resistance and the disease will increase when there is resistance to first line of treatment.

SUMMARY

This research was designed to model, analyzed and to study the effect of immunity and drug resistance on the transmission dynamics of tuberculosis using MSEIR model. The disease free equilibrium was obtained Eq^0, the basic reproduction number was obtained (R_0), stability analysis of the model was obtained, the existence of the endemic point and also numerical simulation of the model was done using MATLAB software with estimate values from table (2.1) using different values of sigma (σ) as in figure 1.1 above which shows that there was less number of infected population when there is no resistance and infection is increased as we increase the resistance from 25% to 75% which was also achieved by changing the value of sigma from 0 to 0.25 and then to 0.75. The result shows that there is less number of infected population when there is no resistance to first line of treatment in the population.

CONCLUSION

Mathematical model is a useful technique for solving real life situations; a deterministic model to study the effect of immunity and drug resistance on the transmission dynamics of tuberculosis was modeled and analyzed in order to see the effect of resistance to first line of treatment in a population. The analysis and numerical simulation of the model reveal that the disease free equilibrium (Eq^0) is locally stable since $R_0 < 1$, which implies that TB disease will be gradually eliminated from the population. The numerical simulation of the model was carried out using MATLAB.

RECOMMENDATION

In line with this research findings the following recommendations are made;

1. Encourage the use of mathematical models to model real life problems, which simplifies problems in the society.
2. The government should integrate TB programmes into other existing health services such as outreach, maternal and child welfare programmes among others in order to increase its awareness.
3. The government should intensify the education on TB in schools, community gathering, worship centers etc., to sensitize the individuals in the communities of its existence, free access to medical care and treatment duration.
4. TB patients who migrate must be given referral to the clinics in such areas for continuation of treatment.
5. Further research work is also recommended in order to help develop other suitable models to help public health professionals to adopt other strategies to control and eradicate the disease.

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APPENDIX

```
function vprime = tbmodel(t,y)

vprime = zeros(6,1);

p_i = 5000;

rho = 0.56;

beta = 0.05

varepsilon = 0.06;

gamma = 0.65;

alpha = 0.6;

delta = 0.3;

alpha1 = 0.04;

% immunity and resistance parameters
```

eta = 0.088;

sigma = 0; % Variables y(1) = M; y(2) = S; y(3) = E; y(4) = I; y(5) = R_{ES} ; y(6) = R_H ;

yprime(1) = (1-p)*pi-(mu+eta)*y(1);

yprime(2) = p*pi+eta*y(1)-beta*y(2)*y(4)-rho*y(6)-mu*y(1);

yprime(3) = beta*y(2)*y(4)-(mu+varepsilon)*y(3);

yprime(4) = varepsilon*y(3)-(mu+alpha+gamma+sigma)*y(4);

yprime(5) = sigma*y(4)-(mu+alpha1+delta)*y(5);

yprime(6) = gamma*y(4)-(mu+rho)*y(6)+delta*y(5);

function vprime = tbmodel(t,y)
vprime = zeros(6,1);
p_i = 5000; rho = 0.56;
beta = 0.05
varepsilon = 0.06;
gamma = 0.65;
alpha = 0.6;
delta = 0.3;
alpha1 = 0.04;
% immunity and resistance parameters
eta = 0.088;
sigma = 0.25;
% Variables y(1) = M; y(2) = S; y(3) = E; y(4) = I; y(5) = R_{ES} ; y(6) = R_H;
yprime(1) = (1-p)*pi-(mu+eta)*y(1);
yprime(2) = p*pi+eta*y(1)-beta*y(2)*y(4)-rho*y(6) mu*y(1);
yprime(3) = beta*y(2)*y(4)-(mu+varepsilon)*y(3);
yprime(4) = varepsilon*y(3)-(mu+alpha+gamma+sigma)*y(4);
yprime(5) = sigma*y(4)-(mu+alpha1+delta)*y(5);
yprime(6) = gamma*y(4)-(mu+rho)*y(6)+delta*y(5);
function vprime = tbmodel(t,y)
vprime = zeros(6,1);
p_i = 5000; rho = 0.56;
beta = 0.05
varepsilon = 0.06;
gamma = 0.65;
alpha = 0.6;
delta = 0.3;
alpha1 = 0.04;
% immunity and resistance parameters
eta = 0.088;
sigma = 0.75;
% Variables y(1) = M; y(2) = S; y(3) = E; y(4) = I; y(5) = R_{ES} ; y(6) = R_H ;
yprime(1) = (1-p)*pi-(mu+eta)*y(1);
yprime(2) = p*pi+eta*y(1)-beta*y(2)*y(4)-rho*y(6) mu*y(1);
yprime(3) = beta*y(2)*y(4)-(mu+varepsilon)*y(3);
yprime(4) = varepsilon*y(3)-(mu+alpha+gamma+sigma)*y(4);
yprime(5) = sigma*y(4)-(mu+alpha1+delta)*y(5);
yprime(6) = gamma*y(4)-(mu+rho)*y(6)+delta*y(5);

```
y0 = [102520, 12126, 2122, 4844, 1928, 6298];
tspan = [0:0.5:15];
[T, Y ] = ode45('tbmodel', tspan, y0);
[P, Q] = ode45('tbmodel25imm', tspan, y0);
[R, S] = ode45('tbmodel75imm', tspan, y0);
plot(T,Y(:,4),'-')
hold on
plot(P,Q(:,4),'k')
hold on
plot(R,S(:,4),'o')
xlabel('Time(in years)')
ylabel('Infected population')
legend('No Resistance', '25% Resistance', 75% Resistance')
```