Coupling an Agent-Based Model with a Mathematical Model of Rift Valley Fever for Studying the Impact of Animal Migrations on the Rift Valley Fever Transmission

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Abstract. Rift valley fever (RVF) is a disease killing principally animals. In this article, we coupled a mathematical model of animal-mosquito interactions with an agent-based model describing the migrations of hosts between cities. The mathematical model describes animal-mosquito interactions in each city and the agent based-model describes the migrations of animals between cities. The coupled model allows to compute at each time the number of infected animals in all cities and to study the impact of host migrations on the dynamics of infections. The obtained results showed that quarantining certain cities can reduce the number of infected hosts. It is also observed that when the density of animal migrations increases, the number of infection cases increases. The developed model brings solutions to both models (mathematical model and agent-based model) limits. This model could help to study and forecasting the Rift Valley Fever transmission and its outbreak in the short and long term.

Keywords: Mathematical modeling · Agent-based modeling · Rift valley fever · Coupling model · Migration · Infectious disease · Artificial intelligence

1 Introduction

Rift Valley fever is an example of emerging arbovirosis [30]. It is widely distributed in Sahelian Africa [1,2]. At present, RVF (Rift Valley Fever) virus is a

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veterinary health problem in West Africa. During the epidemics period, animal migrations cause new cases of infected animals. Conditions of emergence and re-emergence of RVF motivated the Scientist community to study the impact of animal migrations and animal-mosquito interactions in the spread of RFV. Mathematical models using patches have described the impact of movements of animals and humans on vector-borne disease transmissions [3,7,13] B. Adams et al. [4] have studied the impact of human movements on vector-borne disease transmission. M. Alvim et al. [5] have studied the impact of the human mobility on the transmission of vector-borne diseases between cities. Researchers belonging to different disciplines (mathematics, biology, computer science) have worked on the mechanisms of RVF transmission. Holly et al. [6] have proposed a mathematical model describing interactions between two populations of vectors (Aedes and Culex) and one livestock population. Results of their study have shown that in the area where the contact rate between vectors and livestock is near to 1, the number of infected animals tends to multiply. Mpheshet et al. [8] have developed a mathematical model using a nonlinear differential equations to describe RFV infection in the global scale taking into account mosquitoes, livestock and human hosts. Models using vaccination have been used in order to reduce infection rates during epidemics. Ling Xue et al. [10] have developed a mathematical model based on the hierarchcal network taking into account Aedes vexans mosquitoes, Culex poicilipes mosquitoes and the livestock. It is shown that livestock movements, mosquito populations and climate factors play an important role in the spatial propagation of Rift Valley fever viruses. Xue et al. [9] have proposed a new compartmental model for describing RFV transmission microscopic scale and macroscopic scale. Tianchan et al. [11] have developed a mathematical model of RVF integrating a spatial approach [7] in the study of viruses propagation taking into account livestock movements, vertical transmission between mosquitoes and eggs. Gao et al. [7] have shown that the propagation of RFV depends on contacts between livestock and vectors (mosquitoes). Several studies on vector-borne diseases have been carried out using a microscopic scale. Agent-based models have been developed for studying the transmission of vector-borne diseases [12]. Generally, researchers using agent-based models take into account vector behaviors, host behaviors, vector-host interactions in the environment, climate factors impacts in the environment [16]. Hybrid models integrating mathematical [14] and agent-based models have been developed in order to solve limits of each model [15]. For mathematical models using patches in the modeling of infectious diseases, it's not possible to know the dynamics of RVF transmission in all cities at the same time. Mathematical models use the sequential programming that has a great complexity in term of computations. The mathematical model of Rift valley fever transmission doesn't take into account partial migrations of hosts in cities. In this article, we will develop a hybrid model by coupling a mathematical model with an agent-based model in order to show the impact of animal migrations on the growth of the number of infected animals. This model could help to study the dynamics of infected animals at each time in all cities when putting one or several cities in quarantine.

2 Mathematical Model Formulation

Model Description

We propose a mathematical model of RVF transmission between animal hosts and vectors (Aedes vexans mosquitoes and Culex poicilipes mosquitoes). We take into account vertical and horizontal transmission. For reducing the complexity of the model, there exists a recruitment of new species of mosquitoes and animals at each unit of time. The model of RVF transmission for animals is divided into four compartments: SEIR. $S_h(t)$ is the compartment of hosts presenting a risk of infection. $E_h(t)$ is a compartment of infected animals having a virus, not presenting a sign of infection and not able to infected mosquitoes. $I_h(t)$ is the compartment of infected animals presenting symptoms of the RVF and able to transmit the disease. $R_h(t)$ is the compartment of hosts having had an immunity after an infection with viruses. The size of host populations is N_h and defines by: $N_h = S_h + E_h + I_h + R_h$.

The model of RVF transmission using Aedes vexans mosquito populations is divided into three compartments: SEI. $S_a(t)$ is the compartment of Aedes vexans presenting a risk of infection. $E_a(t)$ is a compartment of infected Aedes vexans having a virus, not presenting a sign of infection and can not able to infect hosts. $I_a(t)$ is the compartment of infected Aedes vexans presenting symptoms of RVF and able to transmit the disease. when infected by the virus of the RVF, each Aedes vexans Mosquito remains infected during its lifetime. The size of Aedes mosquito populations is N_a and defines by: $N_a = S_a + E_a + I_a + R_a$.

Q_a is the compartment of infected eggs of Aedes vexans mosquitoes. P_a is the compartment of Aedes vexans eggs. P_c is the compartment of Culex poicilipes eggs. The model of RVF transmission using Culex poicilipes mosquito populations is divided into three compartments: SEI. $S_c(t)$ is the compartment of Culex poicilipes presenting a risk of infection. $E_c(t)$ is a compartment of infected Culex poicilipes having a virus, not presenting a sign of infection or can not able to infect hosts. $I_c(t)$ is the compartment of infected Culex poicilipes presenting symptoms of RVF and able to transmit the disease. Each Culex poicilipes Mosquito remains infected during its lifetime. The size of Culex poicilipes populations is N_c and defines by: $N_c = S_c + E_c + I_c$.

Mathematical Model of the Transmission

Parameters of the model (Table 1) are defined as follows:

λ_a is the number of eggs laid by each Aedes vexans mosquito, λ_h is the birth rate of hosts (animals), λ_c is the number of eggs laid by each Culex mosquito, α_a is the transovarial infection rate of Aedes vexans $1/\gamma_a$ is the development time of Aedes vexans, $1/\gamma_c$ is the development time of Culex, β_{ha} is the contact rate:host to Aedes vexans, β_{ah} is the ontact rate: Aedes vexans to host, β_{ch} is the contact rate: Culex poicilipes to host, β_{hc} is the contact rate: host to Culex, K_h is the carrying capacity of hosts $\frac{1}{d_c}$ is the Lifespan of Culex, $\frac{1}{d_h}$ is the Lifespan of hosts, $\frac{1}{d_a}$ is lifespan of Aedes vexans, $\frac{1}{i_a}$ is the incubation period in Aedes,

$\frac{1}{i_c}$ is incubation period in Culex poicilipes, $\frac{1}{i_h}$ is the incubation period in hosts. The mathematical model is described with the following ordinary differential equations:

$$\begin{cases} \frac{dP_a}{dt} = \lambda_a N_a - \lambda_a \alpha_a I_a - \gamma_a P_a \\ \frac{dQ_a}{dt} = \lambda_a \alpha_a I_a - \gamma_a Q_a \\ \frac{dS_a}{dt} = \gamma_a P_a - (d_a + \frac{\beta_{ha}.I_h}{N_h})S_a \\ \frac{dE_a}{dt} = \frac{\beta_{ha}.I_h}{N_h} S_a - (d_a + i_a)E_a \\ \frac{dI_a}{dt} = \gamma_a Q_a + i_a E_a - d_a I_a \\ \frac{dN_a}{dt} = \gamma_a (Q_a + P_a) - d_a N_a \end{cases} \tag{1}$$

$$\begin{cases} \frac{dP_c}{dt} = \lambda_c N_c - \gamma_c P_c \\ \frac{dS_c}{dt} = \gamma_c P_c - (d_c + \frac{\beta_{hc}.I_h}{N_h})S_c \\ \frac{dE_c}{dt} = \frac{\beta_{hc}.I_h}{N_h} S_c - (d_c + i_c)E_c \\ \frac{dI_c}{dt} = i_c E_c - d_c I_c \\ \frac{dN_c}{dt} = \gamma_c (Q_c + P_c) - d_c N_c \end{cases} \tag{2}$$

$$\begin{cases} \frac{dS_h}{dt} = \lambda_h.N_h - (\frac{d_h N_h}{K_h} + \frac{\beta_{ah}.I_a}{N_a} + \frac{\beta_{ch}.I_c}{N_c})S_h \\ \frac{dE_h}{dt} = (\frac{\beta_{ah}.I_a}{N_a} + \frac{\beta_{ch}.I_c}{N_c})S_h - (\frac{d_h N_h}{K_h} + i_h)E_h \\ \frac{dI_h}{dt} = i_h E_h - (\gamma_h + \mu_h + \frac{d_h N_h}{K_h})I_h \\ \frac{dR_h}{dt} = \gamma_h I_h - \frac{d_h N_h}{K_h} R_h \\ \frac{dN_h}{dt} = \lambda_h N_h - \frac{d_h N_h}{K_h} N_h - \mu_h I_h \end{cases} \tag{3}$$

3 Disease Free Equilibrium (DFE), P_0

The disease free equilibrium of the models (1), (2), (3) is obtained by setting the right hand side of (1), (2), (3) equals zero and $E_a = I_a = E_c = I_c = E_h = I_h = 0$. If we transform our system in term of proportions in each compartment by posing $x_i = \frac{X_i}{N_i}$, $i \in \{a, c, h\}$, where X_i is a population of compartment i.

Further computation gives: $p_a = \frac{\lambda_a}{\gamma_a}$, $p_c = \frac{\lambda_c}{\gamma_c}$, $s_a = \frac{\lambda_a}{d_a}$, $s_c = \frac{\lambda_c}{d_c}$, $s_h = \frac{\lambda_h K_h}{d_h}$. $P_0 = (p_a, 0, s_a, 0, p_c, s_c, 0, 0, S_h, 0, 0, 0)$, P_0 is a free equilibrium point in term of proportions.

3.1 The Basic Reproduction Number, R_0

The basic reproduction number R_0 is defined as the average number of secondary infection cases generated by an infected animal during its period of infection when it is introduced into a susceptible animal population [26,27,29]. There are many methods for computing the basic reproduction number. In this work, we have used the theorem of Van den Driessche et al. [17]. The DFE (disease free equilibrium) point is P_0. Variables used when occurs an infection are: Q_a, E_a, I_a for the vertical transmission route and E_a, I_a, E_h, I_h, E_c, I_c for the horizontal transmission route. To compute $R_{0,V}$ and $R_{0,H}$, representing respectively the basic reproduction number when there exists a vertical transmission and the basic reproduction number when there exists a horizontal transmission, we used the next generation matrix approach, as described by Diekmann et al. [29] and van den Driessche and Watmough [17]. For the computation of $R_{0,V}$, we expressed the model equations of system (1) concerning the vertical transmission [28] in vector form as the difference between the rate of new infection in compartment i, called $\mathcal{F}_i$ and the rate of transfert between compartment i and all other compartment due to other processes called $\mathcal{V}_i$. For this case, the compartments involved are infected eggs, exposed Aedes vexans female adults and incectious adults of Aedes poicilipes population. The basic reproduction number is calculated as the spectral radius of the next generation matrix, $\mathrm{M} = F_v.V_v^{-1}$. Using the same approach, we computed $R_{0,H}$. Finally, we have found the following results.

$$R_{0,V} = \frac{\lambda_a \alpha_a}{d_a}, R_{0,H} = \sqrt{\frac{\lambda_h i_h K_h}{d_h(\lambda_h + i_h)(\gamma_h + \mu_h + \lambda_h)} \left(\frac{\beta_{hc} \lambda_c i_c \beta_{ch}}{d_c^2(d_c + i_c)} + \frac{\beta_{ha} \lambda_a i_c \beta_{ah}}{d_a^2(d_a + i_a)} \right)}$$

Description of the Results Concerning the Basic Reproduction Number

Since the model incorporates both vertical and horizontal transmission, R_0 for the systems (1), (2), (3) is the sum of $R_{0,V}$ and $R_{0,H}$ [28], thus, $R_0 = R_{0,V} + R_{0,H}$. We have used the following probability: $\frac{i_a}{d_a + i_a}$ is a survival probability of an Aedes vexans mosquito during its incubation period. $\frac{i_c}{d_c + i_c}$ is a survival probability of a Culex poicilipes mosquito during its incubation period. $\frac{i_h}{d_h + i_h}$ is a survival probability of an animal host during its incubation period.

Thus $R_0 = \frac{\lambda_a \alpha_a}{d_a} + R_{0,H}$. It should be noted that a program to fight against RVF will consist to reduce the value of R_0. The following result comes from the

theorem of Van der Driessche et al. [17]. The disease free equilibrium is locally asymptotically stable whenever $R_0 < 1$ and unstable if $R_0 > 1$.

if $R_0 < 1$, In this case, we can expect that the infection could disappear into the host population.

if $R_0 > 1$, each infected host could lead on average more than one new infection. In this case, the disease could persist in each region.

4 The Agent-Based Model of Animal Migrations

In this section, we build an agent-based model describing animal migrations between cities. This agent-based model, coupled with a mathematical model of Rift valley fever help for understanding the impact of migrations on Rift valley fever transmission. We firstly describe the relationships between cities and trucks helping for migrations between cities. Using UML (Fig. 1), we have identified two types of agent: a CityAgent representing a city where exist RVF or not, a TruckAgent representing a truck that allows a certain number of hosts to leave one city to another city.

4.1 Description of the Relationship with the UML Formalism

We suppose that the area of study is divided in cities numbered by $c_1, c_2, .., c_n$. Each city has a local transmission of RVF and uses a mathematical model to describe the propagation of the disease. During the simulation of the mathematical model, the city entity stocks in mathematical variables the number of infected animals at every step. The truck entity help to transport host animals from one city to another city.

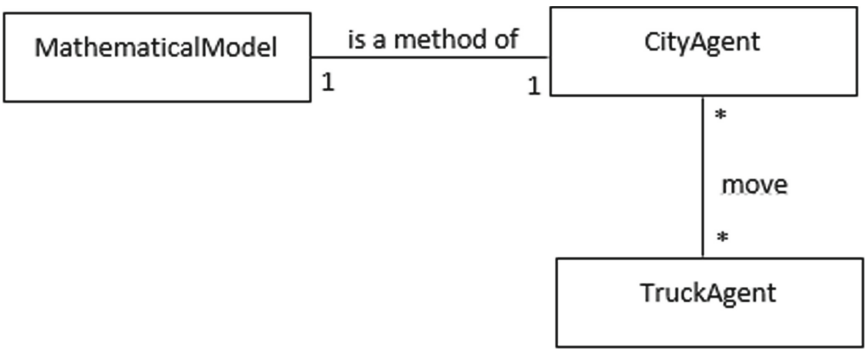

Fig. 1. Architecture of the coupling showing relationships between agent-based model and mathematical model of Rift valley fever in each city.

4.2 Description of Agents

The UML model that we have built allows us to identify two species of agents: The Truck Agent and the City Agent.

City Agent
Each city agent called **CityAgent** uses the mathematical model to compute the number of infected animals at each step of the simulation. The data used by a city agent comes from the mathematical model. Each truck agent is controled by a agent within its environment. One can note that a city agent can refuse or allow to a truck agent the possibility to leave or to enter into a city. Each city agent has the following attributes: each variable of the mathematical model, the total number of animal hosts, the total number of mosquitoes, the total number of truck agent in each city, the number of truck agent that has the authorization to enter in a city, a list of informations about the city border. Every city agent can execute the following methods:controlTruckAgent() allows to control every truck, ComputMathModel() allows for computing the number of infected animals at each step of simulation. detectRfv() allows knowing if there exist RVF infections in the other cities.

Truck Agent
A truck agent allows the transportation of animal hosts from one city to another city. Each truck agent has the following attributes: the number of susceptible animals, the number of susceptible animals, the number of infected animals. Each truck agent has the following methods: MoveCity() allows moving from one city to another city, VerifyMigration() allows verifying if it has the grant to enter into one city, updatData() allows for updating the different values contained within its database.

5 Coupling of EBM Model and ABM Model

The mathematical model describes the dynamics of interactions between animal hosts and mosquitoes causing infections in the city scale. For describing host infections we have used the SEIR model for animal infections and SEI model for mosquito infections. The mathematical model is controled by The agent-based model (ABM) in each city in order to allow the migration of host populations between cities. The main objective of the migration is to study the impact of animal migrations on the prevalence of Rift valley fever in all cities. We have two processes of the transmission RVF, the local transmission and the transmission between cities.

Description of the Coupling
Due to the fact that the simulations will be carried out within the central memory of the computer, we have thought that it's a good thing to model RVF transmission by a mathematical model and the migration of animals between cities by an agent-based model. This collaboration between the two models will help to minimize the storage capacity of the central memory of the computer. At each

time t, using the mathematical model, the city agent computes and stocks the following list values: L = { $P_a(t)$, $Q_a(t)$, $S_a(t)$, $E_a(t)$, $I_a(t)$, $P_c(t)$, $S_c(t)$, $E_c(t)$, $I_c(t)$, $S_h(t)$, $E_h(t)$, $I_h(t)$, $R_h(t)$}. At every arrival in each agent city, each truck agent stocks a certain percentage of the values computed by each city agent and transport them from city to city. Meanwhile, there are a decrease and an increase in each population number due to the arrival and departure of a truck agent. The coupling that exists between the two models is the strong coupling because there exists a transfer of the information (infected populations) from a mathematical model to the agent-based model and from the agent-based model to mathematical model.

6 Numerical Simulation and Results

Experimental Descriptiont
In the platform of the modelling called CORMAS [18] (Fig. 2), each simulation is done in 200 steps corresponding to 200 days of the year. The simulation is organized as follows:

a) in the first part we initialize the virtual learning environment, the parameters that help for creating the different agents.
b) in the second part we use the original data coming from the litterature review.
c) in the last part we analyze the impact of the animal migrations between cities.

Results
To perform the simulation, we have used a grid of 10 square kilometers corresponding to the study of the spread of Rift Valley fever. We also suppose that the area of study is divided into ($n \geq 2$) cities where each city represents a subpopulation including Aedes vexans mosquitoes, livestock (hosts) [31] and Culex poicilipes mosquitoes. For exploring migrations of livestock on the space in all cities, we have done the following assumptions:

– every city has epidemiological parameter values.
– initial values of infected populations in cities 2, 3, 4, 5 are initialize to zero.
– Only one city (city number 1) has infected hosts at the beginning of every simulation.

We solved the mathematical model of RVF using a fourth-order Runge-Kutter schema with the time step equal to one day. For studying the transmission of Rift valley fever between cities, a number of simulations were carried out in a virtual platform containing five city agents, five truck agents. Each city agent has a computer program used for the implementation of the mathematical model. We used the following initial values for the mathematical model: for city number 1, 5000 eggs of Aedes vexans mosquitoes, 4999 susceptibles Aedes vexans mosquitoes, 1 infected Aedes vexans mosquito, 5 infected animals, 1000 susceptible hosts, 5000 eggs of Culex poicilipes, 5000 susceptibles Culex mosquitoes, others initial values in city 1 are putting to zero. Within city 2, 3, 4, 5 we used 5000 eggs of

Aedes vexans mosquitoes, 5000 susceptibles Aedes vexans mosquitoes, 0 infected Aedes vexans mosquito, 0 infected animal, 1000 susceptible hosts, 5000 eggs of Culex poicilipes, 5000 susceptibles Culex mosquitoes. Several simulations were carried out corresponding to 200 days. For the first simulation, we introduced infected animals only in the city number 1 and not taking into account migrations and obtained results in (Fig. 3) showing the number of infected hosts within all cities. For the second simulation, we take into account truck agent migrations between cities and obtained results in (Fig. 4) showing the number of infected hosts within all cities, in (Fig. 5) and (Fig. 6) showing the number of infected hosts within city number 1 and city number 2. We observed two processes of infected animals. The local evolution of infected animals in each city and the global evolution of infected animals between cities.

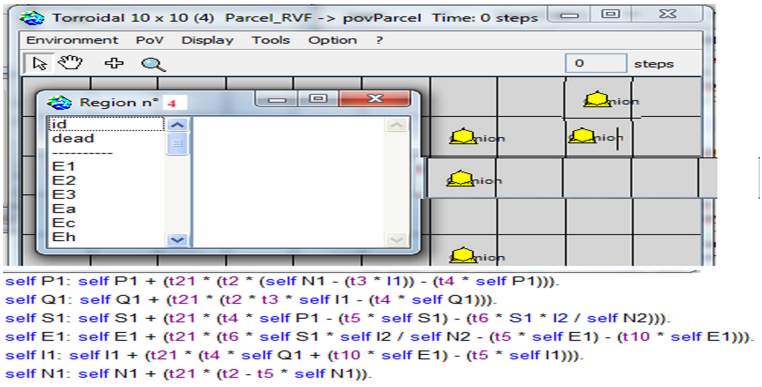

Fig. 2. Screenshot showing the virtual environment, the five vitual cities and the first lines of the source code of the mathematical model managed by city agents.

7 Discussion

Each city agent used a mathematical model for computing the number of infected animals and infected mosquitoes during the spread of Rift valley fever. Due to the fact that, each agent city is autonomous, all city agents carried out their computations at the same time. It's a great advantage because it is possible with this coupled model to know at every time the number of infected cases in all cities at the same time. Several mathematical models used patches for studying migrations between cities, but during the phase of implementation, the sequential programming is used to compute the number of infected animals. Sequential programming has a great cost in term of computations. Comparatively to the mathematical models using patches, the coupled model allows reducing the time of computations because each city agent is in charge of the execution of the mathematical model. The mathematical model using patches

Table 1. Parameters of the mathematical model

Parameter	Value	Units	References
λ_a	0.1	1/day	–
λ_h	0.0027	1/day	–
λ_c	0.1	1/day	–
α_a	0.05	1/day	[25]
$1/\gamma_a$	10	days	[19]
$1/\gamma_c$	10	day	[19]
β_{ah}	0.15	1/day	[32–38]
β_{ha}	0.15	1/day	[32–36]
β_{ch}	0.0176	1/day	[33–36]
β_{hc}	0.15	1/day	[32–36]
K_h	1000	–	–
$\frac{1}{d_c}$	10	day	[19–21]
$\frac{1}{d_h}$	370	day	[22]
$\frac{1}{d_a}$	10	day	[21]
$\frac{1}{i_a}$	6	day	[23]
$\frac{1}{i_c}$	6	day	[23]
$\frac{1}{i_h}$	4	day	[24]

have used the sequential programming and the coupled model used the parallel programming that is known to reduce the time of computations. We note that, if the mathematical model has n patches, if the time of computing in each patch is p, the total time to know the number of infected animals in all patches when executing the mathematical model is p.n comparatively to the coupled model where this number is p. In mathematical models using patches for describing the impact of migrations between cities, authors often used a macroscopic scale comparatively to the coupled model using a microscopic scale between cities. The other advantage of the coupled model is the possibility to take into account environmental factors and behaviors of cities influencing the migration of truck agents. When putting 4 cities agent in quarantine and leave one city with several cases of infected animals (city agent number 1), after the execution of the coupled model in 200 steps of simulation, the total number of infected animals found was approximatively zero (Fig. 3). When allowing migrations of all five truck agents between cities, the total number of infected animals found was 862 (Fig. 4). We can say that animal migrations increase the number of infected animals in each city. Putting some cities in quarantine could help to eradicate RVF disease. On the (Fig. 2) the number of infected animals after 200 steps of simulation in the agent city number 1 is almost zero when there are no migrations, when taking

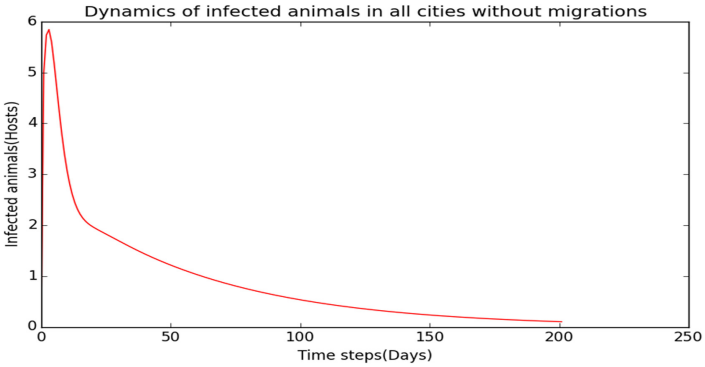

Fig. 3. Dynamics of infected hosts in all cities without migrations. The number of infected hosts is equal to the number of infected hosts within city number 1

account into migrations, on (Fig. 5) the number of infected animals after 200 steps of simulations in agent city number 1 is around 166 and greater than the initial value of infected animals which is 5. We can also say that the number of infected animals in one city that has already been infected could present the new cases of infection (Fig. 5) when migrations were authorized between cities. If the city agent number 2 has zero infected (Fig. 7) and if the migrations of truck agents are allowed, one can observed new infections cases (Fig. 6). The model that we have developed gives the possibilities to control the authorization of animal migrations, to put certain cities in quarantine and observed the dynamics of infections in all cities at the same time whereas the model developed by Buyu et al. [39] have used migrations of animals at each step of simulation and not take into account putting in quarantine certain cities. We can say that avoid migrations of animals in certain cities in the period of epidemics of Rift valley fever could help to eradicate Rift Valley fever. At different geographical locations (in each city), migrations of livestocks (hosts) increase the number of infected animals comparatively to the results obtained by Tianchan et al. [11]. The migration rates from city agent to another city agent have a great impact on the variation in spatial transmission of Rift valley [11], comparatively to our work, we note that the spatial migration of livestock increase the populations of infected and non infected animals (Fig. 4, Fig. 5, Fig. 6).

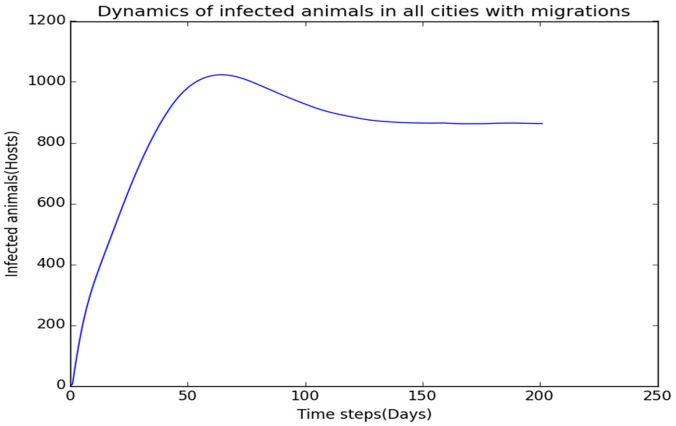

Fig. 4. Dynamics of infected animals with migration in all cities.

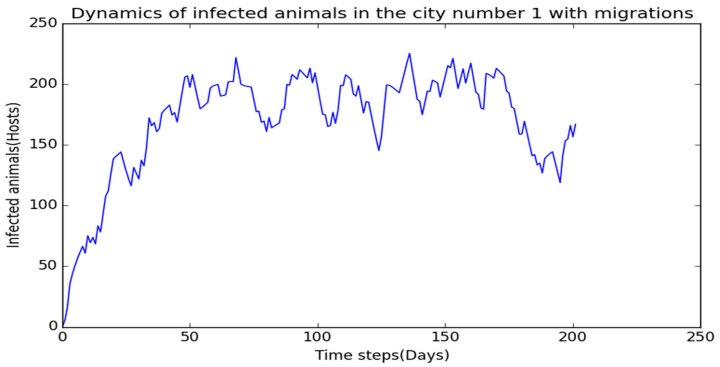

Fig. 5. Dynamics of infected animals with migrations in city number 1

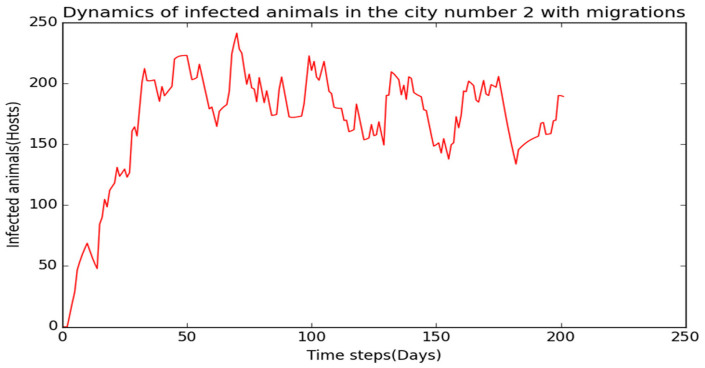

Fig. 6. Dynamics of infected animals with migrations in city number 2

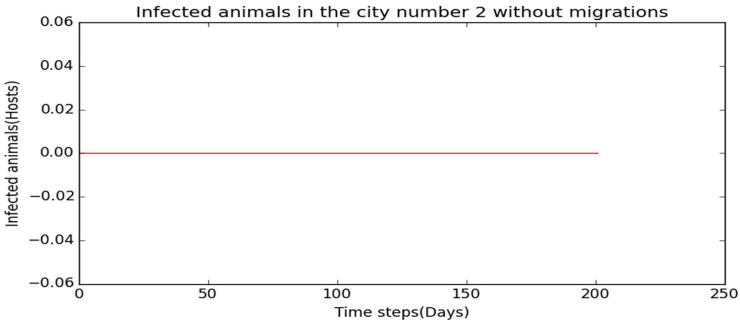

Fig. 7. Dynamics of infected animals without migrations in city number 2

8 Conclusion

In this study, we have built an epidemiological model of the RVF transmission taking into account migrations between cities. Based on previous works, we found that our model confirm the fact that migrations of infected animals increase the total number of infected cases in the environment. This model is a virtual platform helping to simulate the transmission of RVF between cities. This work shows benefices of coupling an agent-based model with a mathematical model in order for studying certain characteristics of the spread of the Rift valley Fever in several cities. The coupled model allows resolving some limits posed by the two models (mathematical model and agent-based model). With the coupled model it is possible to know the average number of infected animal hosts in all cities at every time. We have also shown that the coupled model improves the complexity of the mathematical model using patches in term of the time of computations. We have shown that, when certain cities are in quarantine, it is possible for observing the evolution of the RVF transmission in the other cities. We have shown that, when one city is in quarantine, the new cases of infections could not appear in this city. This coupled model could help in studying the impact of migrations in the transmission of other infectious diseases and their eradication.

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