Journal of Nonlinear Modeling and Analysis
Volume 1, Number 4, December 2019, 425–442
http://jnma.ca; http://jnma.ijournal.cn
DOI:10.12150/jnma.2019.425

Modeling of Lone Star Ticks with Deer Migration to Canada*

Jemisa Sadiku[1], Zilong Song[1,†] and Jianhong Wu[1]

Abstract Due to climate change and an increase of favourable habitat, ticks and tick-borne diseases are reported to expand to northern areas in north America. One main factor for lone star ticks to be established in Canada is due to the migration of white-tailed deers from US. In this work, we formulate a compartmental model to study the dynamics of lone star ticks and white-tailed deers, with a focus on migration effect of white-tailed deers. The tick-host interaction and the effect of deer migration are explored analytically and numerically. The positivity of the populations in the model is proved, and the unique positive equilibrium is proved to be asymptotically stable. We conduct sensitivity analysis on a set of parameters, revealing the correlation between the parameters and equilibrium populations. Numerical results show that migration rate of white-tailed deer is one crucial parameter that increases the populations of (infected) ticks and (infected) hosts.

Keywords Lone star tick, deer migration, disease modeling, asymptotic stability, sensitivity analysis.

MSC(2010) 37N25, 92D25, 92D30, 93D20.

1. Introduction

Lone star tick (Amblyomma americanum) is recognized for the first time by Linnaeus in 1758 [19]. It prefers damp forests and humid soil environment [30, 36]. Similar to other ticks, it has four life stages: egg, larvae, nymph and adult, and the transition from one stage to the next is done through questing, feeding and molting [3, 28, 33].

The associated tick-borne diseases and the allergic reaction have aroused increasing attention on lone star tick in recent years. Lone star tick is a vector that can carry pathogens and transmit tick-borne diseases such as STARI (Southern tick-associated rash illness) [10, 13] and Human Monocytic Ehrlichiosis (HME) [1, 19, 28] (CDC website). The preferred host (here white-tailed deer) also plays an important role in disease transmission, as they serve as reservoir for the pathogens. Unlike other species of ticks, lone star tick exhibits *aggressive* and indiscriminate questing behavior [13, 36], which makes bites to humans more likely. In addition, lone star tick causes red meat allergy (delayed-onset allergy) [22, 37], first discovered in

†the corresponding author.
Email address:jemisa.sadiku@gmail.com(J. Sadiku), buctsongzilong@163.com (Z. Song), wujhhida@gmail.com (J. Wu)
[1]Department of Mathematics and Statistics, York University, Toronto, Ontario, Canada
*The authors were supported by Natural Science and Engineering Research Council Canada.

2009 [8]. The allergic reaction could be fatal [7,21,28], and is due to immunoglobulin E (IgE) antibody which is specific for galactose-α-1,3-galactose (alpha-gal). It is claimed that the cause of IgE antibodies is primary from bites of lone star tick [7].

The lone star tick is mostly found in the eastern, southeastern and south-central states of US [32]. However, its distribution and abundance have increased over the past decades, and according to CDC map it expands to more northern and western areas in North America where it was absent in previous years [32]. In particular, it has migrated from endemic areas in the US to new regions in Southern Canada, such as British Columbia, Ontario, south-eastern Manitoba [6,28,29].

Two main factors responsible for the range expansion of lone star ticks are the climate change and the migration of white-tailed deer [32]. Due to climate change, more regions become inhabitable for lone star ticks. Since ticks are small species, they will spread to new regions mainly by migration of their host mammals. White-tailed deer is the main host for lone star tick of all life stages to get the majority of their blood meals, and their populations are positively correlated [3,6,18,28]. The deer migration depends on the deer habitat suitability of the region, which is influenced by two factors: the need for food, shelter and water, and the disturbances from human activities (such as hunting) [6]. In order to better understand or predict the outbreaks of tick-borne diseases, there is need to include the migration effect into the tick-host dynamics.

Various models have been proposed to investigate tick-host dynamics and to address a variety of issues on the tick-borne diseases [25,38]. Specifically for Lone star ticks, there have been computer simulations based on age-structured difference equations [15,27], agent-based models [34], predicative statistical models [20]. Recently, a metapopulation model with migration effect among patches and logistic-type birth term is adopted in [11,12] to study the HME transmission and investigate various tick-control strategies. For another tick-borne disease (Lyme disease) [25], the range expansion of ticks and pathogens has been widely studied by various migration effects including movements of rodents and deer [5] as well as bird migration [16]. The migration of white-tailed deer has also been included in a single patch model with distributed delay (integral) term [2], which models that the deer travels out and then back in the patch. Since the logistic-type birth term may cause negative birth rate at high population density (which could occur with migration effect), other positive density-dependent birth rates have been adopted in modeling of ticks [33,39].

In this paper, we formulate a compartment model, where the hosts and ticks have been divided into susceptible and infected compartments. Our model adopts the Ricker function as the birth term to ensure positivity, which was used in a stage-structured model [39]. It also includes a simple migration term in the dynamics of hosts, with a focus to study the migration effects of white-tailed deer from US to Canada. The positivity of the populations in the model is proved with natural biologically meaningful parameters. With migration effect as a source term, there exists a unique positive equilibrium, which is asymptotically stable. Our numerical results confirms these features and sensitivity analysis is carried out to reveal the effects of parameters. Migration rate is found to be a crucial parameter that increases the populations of (infected) ticks and (infected) hosts.

The rest of the manuscript is arranged as follows. The mathematical model is proposed in Section 2. After non-dimensionalization, Section 3 proves the positivity of the solutions and the stability of the unique positive equilibrium. In Section 4,