Using Mathematical Modeling to Simulate Chagas Disease Spread by Congenital and Blood Transfusion Routes

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ABSTRACT

Chagas disease is an important health problem in Latin America. Due to the mobility of Latin American population, the disease has spread to other countries. In this work, we used a mathematical model to gain insight into the disease dynamics in a scenario without vector presence as well as to assess the epidemiological effects provided by control strategies.

KEYWORDS

Chagas disease; mathematical modeling; simulation; blood transfusion transmission; congenital transmission

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1 INTRODUCTION

According to the World Health Organization, around 8 million people are infected by Chagas world-wide. Around 30-40% of infected people develop cardiomyopathy, digestive megasyndromes, or both. Demographic data of Spain were used on simulations because it is the European country which hosts more Latin Americans immigrants and possible diseases carriers. As there is no vector presence, the only transmission routes are by congenital transmission or by blood transfusion.

2 MATERIALS AND METHODS

We introduce a deterministic compartmental model for Chagas transmission distinguishing people from countries with and without vector presence, as well as men and women to take into account the vertical transmission. Consequently, population was classified into eight compartments.

3 RESULTS

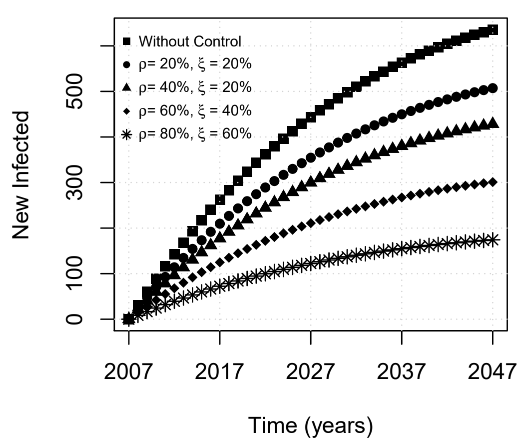

Figure 1: Epidemiological effect of control strategies. ρ: proportion of treatment in infected newborns and, ξ: effective surveillance in blood transfusion.

4 CONCLUSIONS

Mathematical models can be used as valuable tools to explore different scenarios and to justify decision making in public health policies for control and treatment of the disease.

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