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Estimating contact patterns relevant to the spread of infectious diseases in Russia

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Abstract

Understanding human mixing patterns is the key to provide public health decision makers with model-based evaluation of strategies for the control of infectious diseases. Here we conducted a population-based survey in Tomsk, Russia, asking participants to record all their contacts in physical person during the day. We estimated 9.8 contacts per person per day on average, 15.2 when including additional estimated professional contacts. We found that contacts were highly assortative by age, especially for school-age individuals, and the number of contacts negatively correlated with the age of the participant. The network of contacts was quite clustered, with the majority of contacts (about 72%) occurring between family members, students of the same school/university, and work colleagues. School represents the location where the largest number of contacts was recorded – students contacted about 7 individuals per day at school. Our modeling analysis based on the recorded contact patterns supports the importance of modeling age-mixing patterns – we show that, in the case of an epidemic caused by a novel influenza virus, school-age individuals would be the most affected age group, followed by adults aged 35-44 years. In conclusion, this study reveals an age-mixing pattern in general agreement with that estimated for European countries, although with several quantitative differences. The observed differences can be attributable to sociodemographic and cultural differences between countries. The age- and setting-specific contact matrices provided in this study could be instrumental for the design of control measures for airborne infections, specifically targeted on the characteristics of the Russian population.

Keywords

Contact pattern; Human behavior; Airborne infectious diseases; Age; Mathematical modeling

INTRODUCTION

Mathematical modeling has a long history of successful supporting of public health decision-making and is currently commonly used for the design of intervention plans and vaccination programs (1). In order to fulfill this goal, mathematical modeling requires a well-grounded knowledge of all mechanisms regulating the infection transmission process. In particular, disease natural history and contact patterns in the population are essential ingredients. The former is key for defining the type of contact required for infection transmission and for the timeline of infection progression in infected individuals. The latter determines the way the infection spreads in the population. As a consequence, in the last decade lot of attention has been posed on the estimation of human mixing patterns, i.e. who meets whom, how, where and how often (2). In particular, a variety of approaches has been proposed, including population-based surveys (3–7), time-use data (8,9), generation of synthetic populations (9,10), and use of wearable sensors (11,12).