Relation of the detectability in strains to the endemicity of an infectious disease: A mathematical model

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Numerous studies have provided the evidence of the superinfection/coinfection with multiple strains in various infectious diseases, such as malaria, HBV, HCV, SARS-CoV-2, dengue, particularly common in HIV. Although the characterization of multiple genotypes strains could contribute to identifying the disease infection, it may encounter a difficulty in the detection of novel or mutant strains. On the other hand, the superinfection of a detectable strain could enhance the possibility for infectives to be diagnosed and quarantined, which in turn helps to suppress the disease spread.

In this work, we consider the epidemic dynamics of an infectious disease with n strains, focusing on the detectability depending on the strain. Our model is given by the following system of ordinary differential equations ($i = 1, 2, \ldots, n$):

$$\frac{dS}{dt} = \mu N - \sum_{i=1}^{n} \beta_i I_i S - \mu S;$$

$$\frac{dI_i}{dt} = \beta_i I_i S + \sum_{j=i+1}^{n} \varepsilon_{ij} \beta_i I_i I_j - \sum_{j=1}^{i-1} \varepsilon_{ji} \beta_j I_j I_i - \sigma_i I_i - \rho_i I_i - \mu I_i;$$

$$\frac{dQ_i}{dt} = \sigma_i I_i - \alpha_i Q_i - \mu Q_i;$$

$$\frac{dR}{dt} = \sum_{i=1}^{n} \rho_i I_i + \sum_{i=1}^{n} \alpha_i Q_i - \mu R,$$

where S, I_i, Q_i, and R are the population densities of susceptibles, infectives who hold strain i as the strain with the highest detectability, isolated individuals with strain i, and recovered ones respectively. The total population size is denoted by $N = S + \sum_{i=1}^{n} I_i + \sum_{i=1}^{n} Q_i + R$. Parameter σ_i is the quarantine rate of the infective who holds strain i as the strain with the highest detectability, where we assume that $\sigma_i > \sigma_j$ for $i < j$ according to the strain-dependent detectability for the infective. $\beta_i I_i$ gives the infection force of strain i for the susceptible with the coefficient β_i, and $\varepsilon_{ij} \beta_i I_i$ gives that for the infective who holds strain j as the strain with the highest detectability, where $0 \leq \varepsilon_{ij} \leq 1$. We here assume that the quarantine efficiency reflects the detectability of strain, so that it is determined by the most detectable strain in the infective. α_i and ρ_i are the recovery rates of the infective with strain i respectively under and out of the isolation. μ is the natural death rate in the population. We are trying to discuss the relation of such multi strains with different detectabilities to the endemicity in the disease spread.