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Global dynamics of a compartmental model for the spread of Nipah virus

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Nipah virus, originated in South-East Asia is a bat-borne virus causing Nipah virus infection in humans. This emerging infectious disease has become one of the most alarming threats to public health due to its periodic outbreaks and extremely high mortality rate. We establish and study a novel SIRS model to describe the dynamics of Nipah virus transmission, considering human-to-human as well as zoonotic transmission from bats and pigs. We determine the basic reproduction number which can be obtained as the maximum of three threshold parameters corresponding to various ways of disease transmission and determining in which of the three species the disease becomes endemic. By constructing appropriate Lyapunov functions, we completely describe the global dynamics of our model depending on these threshold parameters. Numerical simulations are shown to support our theoretical results and assess the effect of various intervention measures. Joint work with Attila Dénes.