Modelling Disease Extinction: the Case of African Swine Fever Virus in Wildlife Areas

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In Mathematical Epidemiology disease free states are typically represented as equilibria of dynamical systems which model the respective epidemiological processes. In this setting, the asymptotic stability of a disease free equilibrium is interpreted as disease extinction. However, in the mathematical model extinction never occurs. Indeed, in a complete dynamical system, due to the uniqueness property, solutions may converge to an equilibrium but never reach it. While under constant conditions this is not really a problem, the stated property may result in significant modelling error in situations of varying epidemiological factors. More specifically, one may expect that under favorable conditions persisting for sufficiently long time the host population(s) will be disease free and will remain so even if the conditions change.

This seems to be the case with the African Swine Fever Virus (ASFV). The primary natural host of ASFV is the warthog (*Phacochoerus africanus*), while the primary vector is the soft tick (*Ornithodoros porcinus porcinus*). The disease is monitored by veterinary stations as it infects and is deadly to domestic pigs. ASFV is endemic in the African Savannah. However, there are reports indicating that local extinction may occur in a game reserve. The aim of this research is to study the mechanism of such extinction.

We consider mathematical modelling via positive (only) dynamical systems which allow for an equilibrium to be attained in finite time. The uniqueness of solutions in positive time follows from a one-sided Lipschitz condition. The virus persists mainly in the tick population. Its prevalence decays with time, but it is amplified by interaction with warthogs, e.g. a warthog family inhabiting a tick infested burrow. In the considered model the disease may get extinct provided the rather random event of interaction with warthogs does not occur for sufficiently long time.