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Simulation of leaf curl disease dynamics in chili for strategic management options

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Leaf curl, a whitefly-borne begomovirus disease, is the cause of frequent epidemic in chili. In the present study, transmission parameters involved in tripartite interaction are estimated to simulate disease dynamics in a population dynamics model framework. Epidemic is characterized by a rapid conversion rate of healthy host population into infectious type. Infection rate as basic reproduction number, R_0 = 13.54, has indicated a high rate of virus transmission. Equilibrium population of infectious host and viruliferous vector are observed to be sensitive to the immigration parameter. A small increase in immigration rate of viruliferous vector increased the population of both infectious host and viruliferous vector. Migrant viruliferous vectors, acquisition, and transmission rates as major parameters in the model indicate leaf curl epidemic is predominantly a vector -mediated process. Based on underlying principles of temperature influence on vector population abundance and transmission parameters, spatio-temporal pattern of disease risk predicted is noted to correspond with leaf curl distribution pattern in India. Temperature in the range of 15–35 °C plays an important role in epidemic as both vector population and virus transmission are influenced by temperature. Assessment of leaf curl dynamics would be a useful guide to crop planning and evolution of efficient management strategies.

Begomoviruses (family *Geminiviridae*) are the most destructive plant viruses that cause diseases like leaf curl, mosaic, yellow mosaic and yellow vein mosaic in numerous crop plants in the tropical and subtropical world. Leaf curl disease in chili is known to cause by several begomoviruses of which Chili leaf curl virus (ChiLCV) is the most predominant in India[1–3]. ChiLCV is efficiently spread by whitefly (*Bemisia tabaci*) which is abundant year-round in tropical and subtropical climates where wide variety of hosts serves as reservoirs[3–7]. Leaf curl in chili (ChiLCD) is a common disease but recent frequent epidemic outbreaks witnessed repeatedly in the chili growing areas of Central and Southern India is now a growing concern[3,8–10]. ChiLCD is the most damaging in terms of yield loss across the cropping regions[11]. In severe cases, even up to 100% losses of marketable fruit have been reported[12]. In absence of epidemiological information so far no definite management strategy has been evolved. Interaction or contact rate between viruliferous vector and the growing host at initial stages is crucial in epidemic development and thus the period of high contact rate appears critical point of interventions[13,14]. Simulation of epidemics resulted from complex host–vector interaction is of great interest for on-farm management and assessment of agricultural policies and practices[15–17]. Time of whitefly population abundance, especially the growth of viruliferous flies and its effect on host associated leaf curl risk at regional and global scales is of great interest for precise interventions. Type of intervention that ensures low contact rates and keeps the proportion of infectious host at minimum level, are useful in designing precise management strategies[18]. Chili being cultivated in a wide variety of agro-ecosystems in India, disease dynamics in relation to tripartite interaction and transmission behavior are useful for evolving management strategies universally applicable to all climates. Understanding the complex host–vector interactions is also necessary to assess emerging disease risk under rapidly changing cropping patterns as well as global temperature rise scenario[6,19,20].

Leaf curl epidemic is resulted from a complex tripartite interaction between host, vector, and virus where virus transmission plays a central role[15]. Population dynamics models have been used to characterize epidemics resulted from tripartite interaction especially for whitefly transmitted begomovirus in cassava[21–24] and tomato[25]. Environmental factor particularly temperature plays important role in transmission and vector movements[17,22,26]. Virus transmission, latent period, infectious period, replication, titer, movements and symptoms expression etc. are directly linked to temperature[27–29]. For prediction of whitefly population abundance, temperature-dependent

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