Table S1. Model parameters and variables used for leaf curl epidemic analysis in chili.

Symbol	Name	Estimated range/adjusted
a	Transmission rate	0.057 - 0.10 plant vector^{-1} day^{-1}
K_x	Michaelis-Menten for rate of change in healthy vector (X)	2.8 healthy vector week^{-1}
b	Acquisition rate	0.1115 vector plant^{-1} h^{-1}
i_v	Immigration rate for viruliferous vector	0.34 vector week^{-1}
e_v	Emigration rate for viruliferous vector	0.005 vector week^{-1}
i_x	Immigration rate for healthy vector	0.05 vector week^{-1}
e_x		0.005 vector week^{-1}
u	Death rate for healthy as well as viruliferous vector	0.34 vector week^{-1}
c	Birth rate for healthy as well as viruliferous vector	0.05 vector week^{-1}
S	Healthy plant (1-I)	0-1.0
I	Infectious plant (PCR- positive)	0-0.99
V	Viruliferous vector (PCR-positive)	0.65-0.97
S^*	Healthy plant (1-I^*) at equilibrium	0-1.0
X^*	Healthy vector (1-V)	0-1.0
V^*	Viruliferous vector population at equilibrium	0-1.0
I^*	Infectious population at equilibrium	0-1.0

Table S2. Sampling procedure for estimation of proportion of infection in leaf and whitefly population through PCR detection of ChiLCV.

Step	Composite sampling and PCR detection for ChiLCV	
	Leaf	Whitefly (Wf)
1	200 leaves collected from the individual plant	100 Wf collected from the individual plant
2	Divided into two groups of 125 and 75 leaves. • First, 125 leaves again divided into 5 groups consists of 25 leaves. • Remaining 75 leaves divided into 3 groups consists of 25 leaves in each group.	Divided into two group of 70 and 30 Wf. • First, 70 Wf divided into 7 groups consists of 10 Wf. • Remaining 30 Wf divided into 3 groups consists of 10 flies in each group.
	PCR detection using degenerate primers pairs	
	If not all PCR-positive (in first 5 groups) then follow PCR detection for the remaining 3 group	
	Calculate $P^* = 1-((n-X)/n)^{1/m}$; $n=$ number of groups; $m=$ number of leaves or whiteflies in each group; $X=$ number of groups tested PCR- positive.	
	n=(5+3)=8 m=25	n=7+3=10 m=10
3	If all 5 groups PCR-positive in step 2 then remaining 75 leaves divided in to two groups of 50 and 25 leaves and PCR detection.	If all 5 groups PCR-positive in step 3 then remaining 30 WF divided in to two groups of 20 and 10 WF and PCR detection.
	Group of 50 divided into 10 groups each group having 5 samples	Group of 20 divided into 5 groups each group having 4 samples
	PCR detection using degenerate primers pairs	
	If not all PCR-positive (in 10 groups) then calculate P* with n=10 and m=5	If not all PCR-positive (in 5 groups) then calculate P* with n=5 and m=4
4	If all 10 groups PCR-positive in step 3 then for the remaining 25 leaves PCR detection for each leaf.	If all 5 groups PCR-positive in step 3 then for remaining 10 WF, PCR detection with single fly.
	Calculate P* as simple proportion out of 25 leaves	Calculate P* as simple proportion out of 10 flies
PCR METHOD: For ChiLCV detection, genomic DNA was isolated from the leaf and whitefly samples (CTAB method). PCR was performed in 25 µl reaction mixture containing 20-30 ng genomic DNA, 2.5µl of 10X PCR buffer (Thermo Scientific), 1 µl of each forward (GEM-F) and reverse (GEM-R) primers (Eurofins), 260 µM of dNTP (Thermo Scientific) and 2U of DreamTaq polymerase (Thermo Scientific). Degenerate pair primers (GEM-F: 5'-ATRRTHTGGATGGAYGARAACAT-3';GEM-R:5'AAATCCCCTNTATTTCAAARAT-3') was used to amplify approximately 760 bp sequence partially overlapping the putative AV1, AC3 and AC2 genes (Roy *et al.,* 2015) following amplification steps: 94°C for 2 m, 35 cycles of 94°C for 30 s, 48°C for 45 s and 72°C for 30s; 72°C for 10 m (Thermocycler, Hi-Media). PCR-positive of a sample was confirmed by the presence of specific (760 bp) band in agarose gel (2%).		