Global Foot-and-Mouth Disease
Research Alliance

A Simulation Model of Foot-and-Mouth Disease in Bangladesh to Support Response and Control Actions

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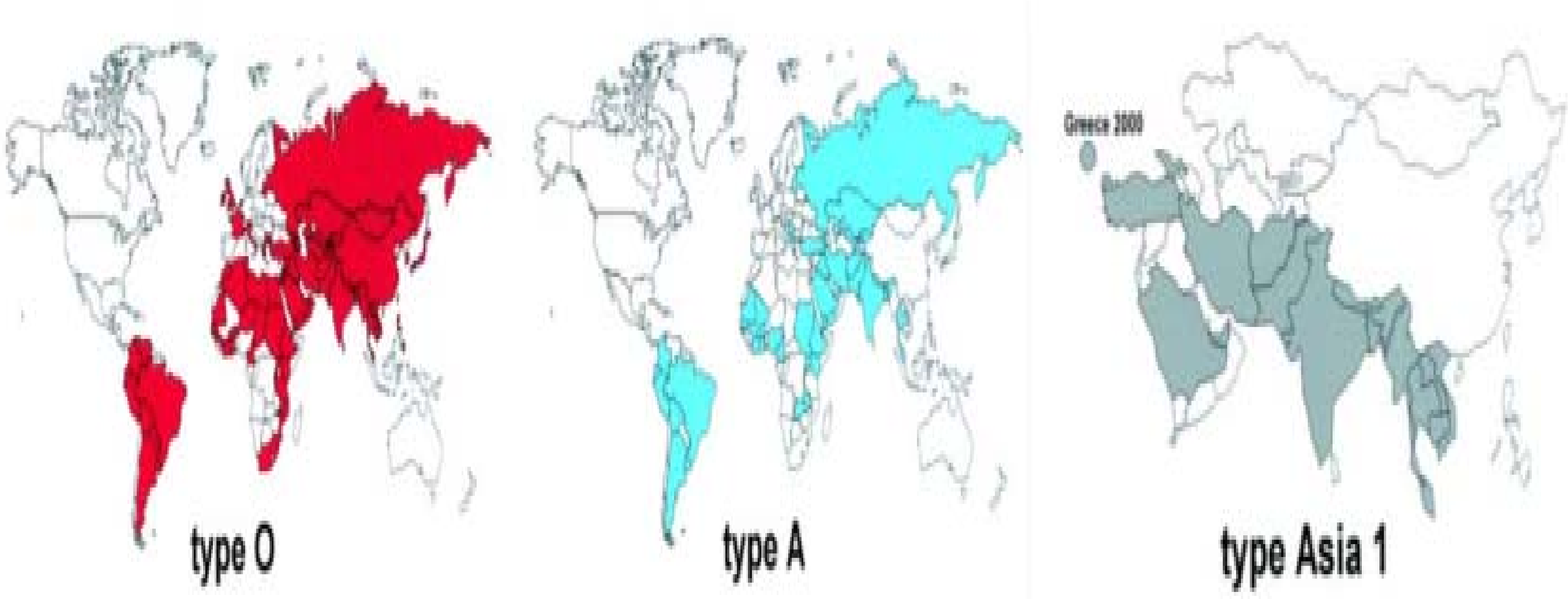
Introduction

Foot and mouth disease endemic in Bangladesh. Three serotypes O, A and Asia 1 are distributed in Bangladesh along with other parts of the world.



FMD modelling in Bangladesh

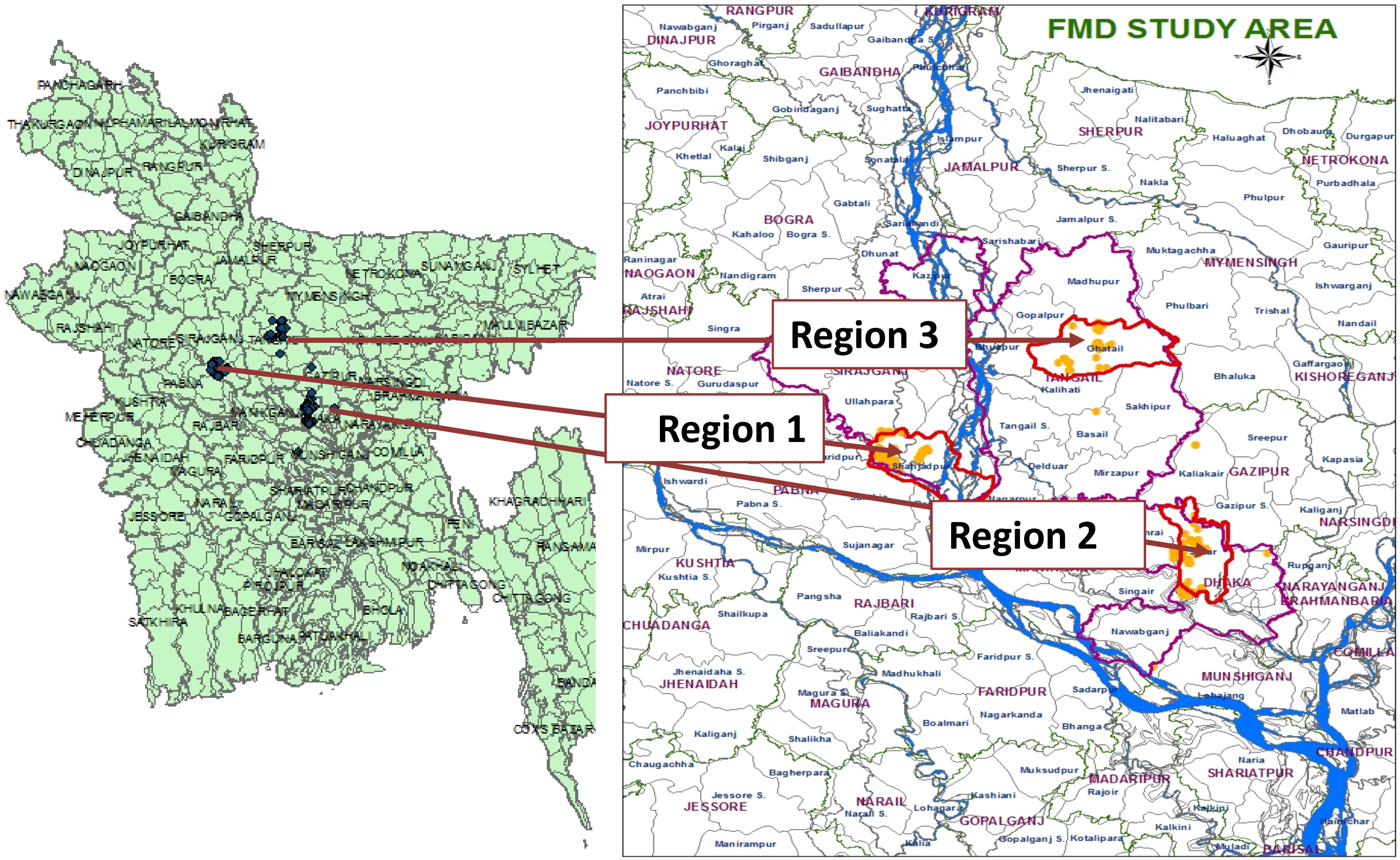
There has been no work on FMD modelling in Bangladesh prior to this study.

Objective:

To develop a SIR model and study the feasibility of using simulation models for evaluating FMD control actions

Methodology

Study areas:



Methodology

- An active surveillance: From September 2013 to August 2015
- Index cases followed by secondary cases were identified within 3 kM radius of the index cases and IPs (Infected Premises)
- Epidemiological data were collected using a prescribed form and GPS machine
- Samples were collected from affected animals for virus detection, characterization and antibody detection

SIR

The model fitted to predicts changes in SIR dynamics over time step

Basic Reproduction Number (R_0)

$$R_o = \frac{\beta}{\gamma}$$

β = transmission rate

$1/\gamma$ = Infectious period

The exponential transmission rate (β) was calculated using Generalized Lineal Model (GLM) (McCullagh and Nelder, 1989)

Simulation model:

A herd-level simulation model described by Keeling et al. (2001) and Tildesley et al. (2008) was applied

$$\lambda_i = N_i . S \sum_{j \in \mathcal{I}(t)} T . N_j . K(d_{i,j}),$$

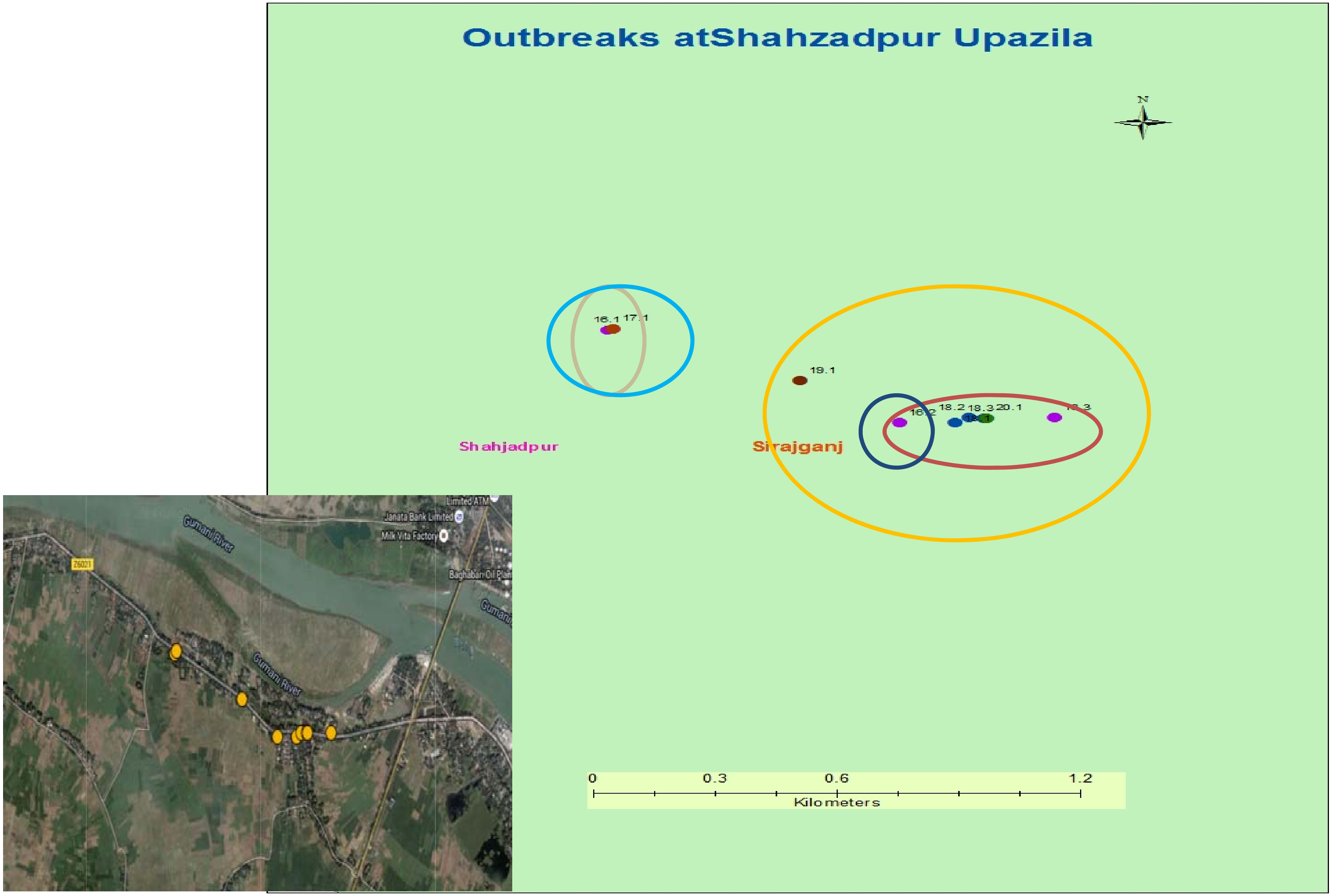
λ_i = Probability of transmission between farm *i* and *j*
N_i = Number of cattle in farm *i*
S = Susceptibility (10.5 for FMD)
T = Transmissibility (7.7×10^{-7} for FMD)
N_j = Number of cattle in farm *j*
$K(d_{i \cdot j})$ = Transmission kernel
$d_{i \cdot J}$ = Eucledian distance between farm *i* and *j*

Result:

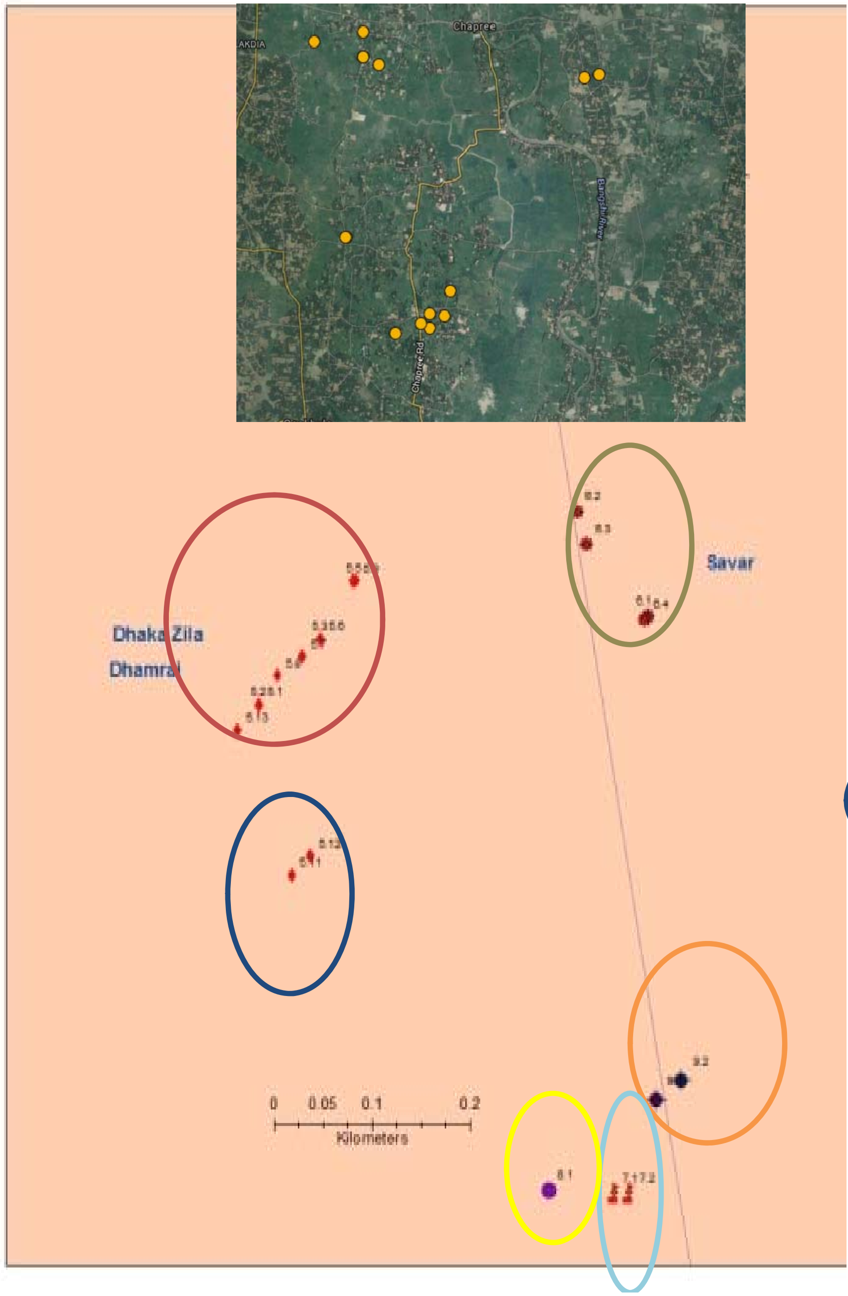
- ✓ Total 21 outbreaks were investigated in 3 regions comprising 64 IPs and with overall morbidity of 52%
- ✓ Among 21 outbreaks, samples for virus isolation were collected from 15 outbreaks and virus could be detected from 12 outbreaks; which included -
    - Type O: 5
    - Type A: 5
    - Type O +A: 1
    - Type Asia 1: 1

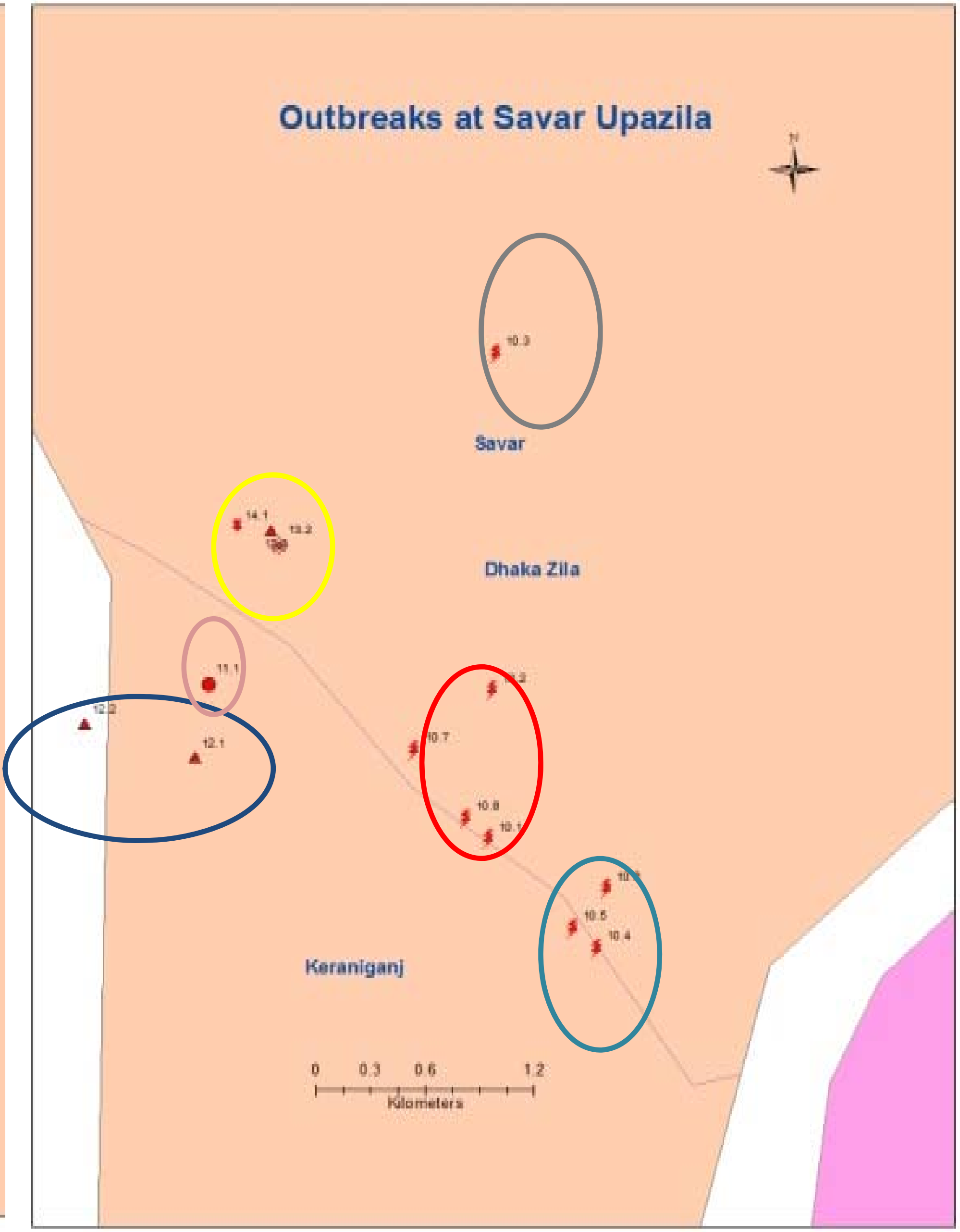
Result

Outbreak distribution in region 1

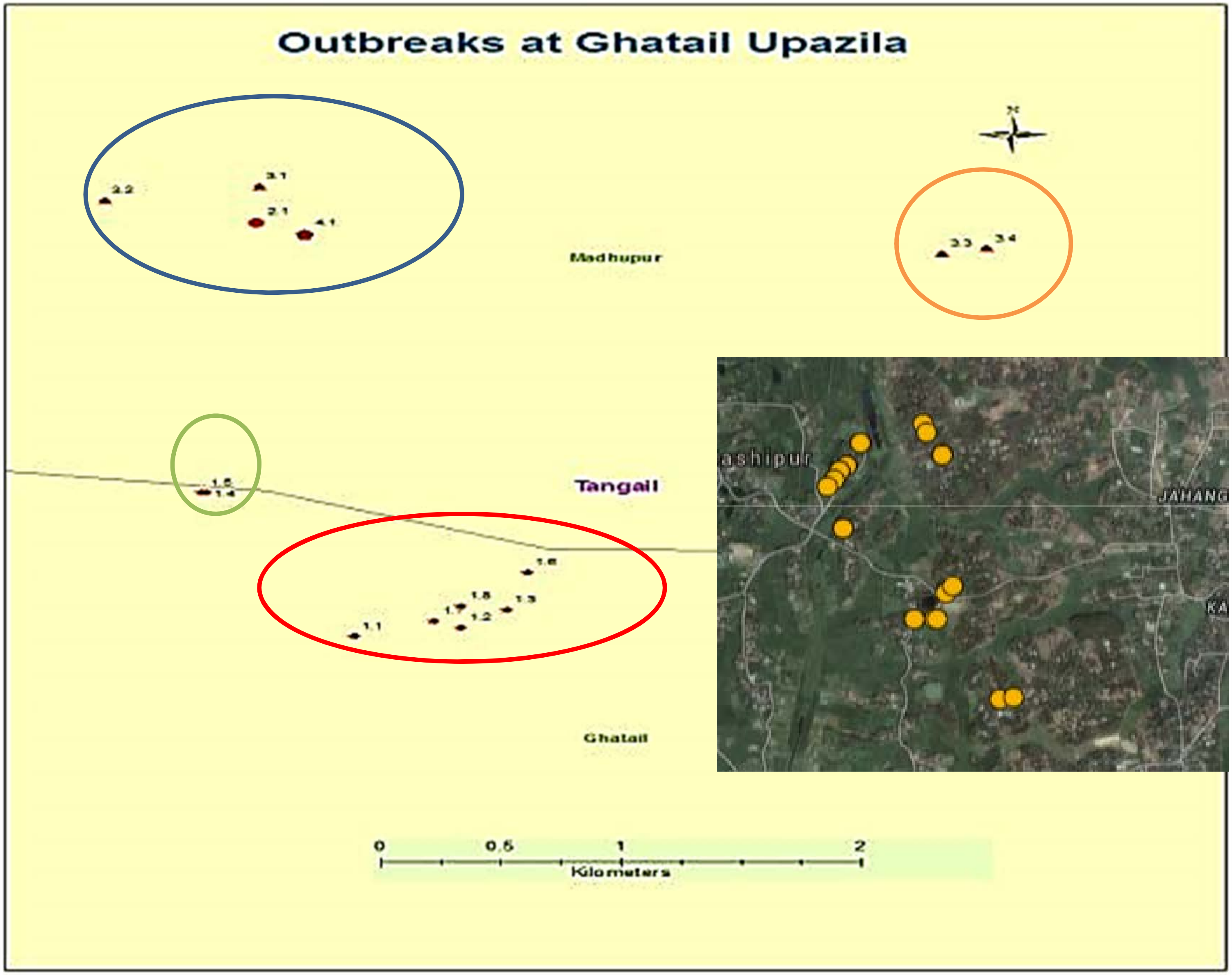


Outbreak distribution in region 2





Outbreak distribution in region 3

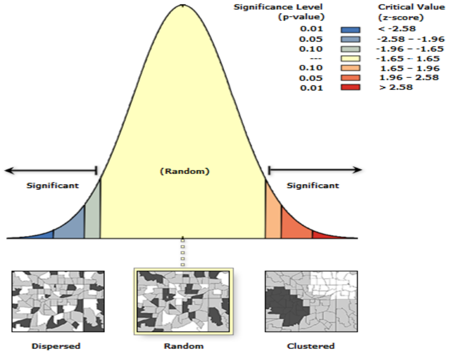


Result

Spatial Autocorrelation (Global Moran's I)

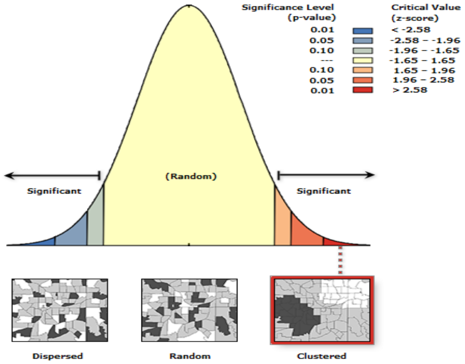
Region-1 (Shahjadpur)

Z score: -1.14
P value: 0.25



Random pattern

Region-2 (Savar, Gazipur, Keraniganj)

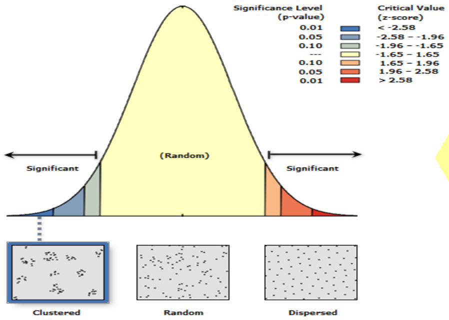


Z score: 13.57
P value: 0.00

Clustered pattern

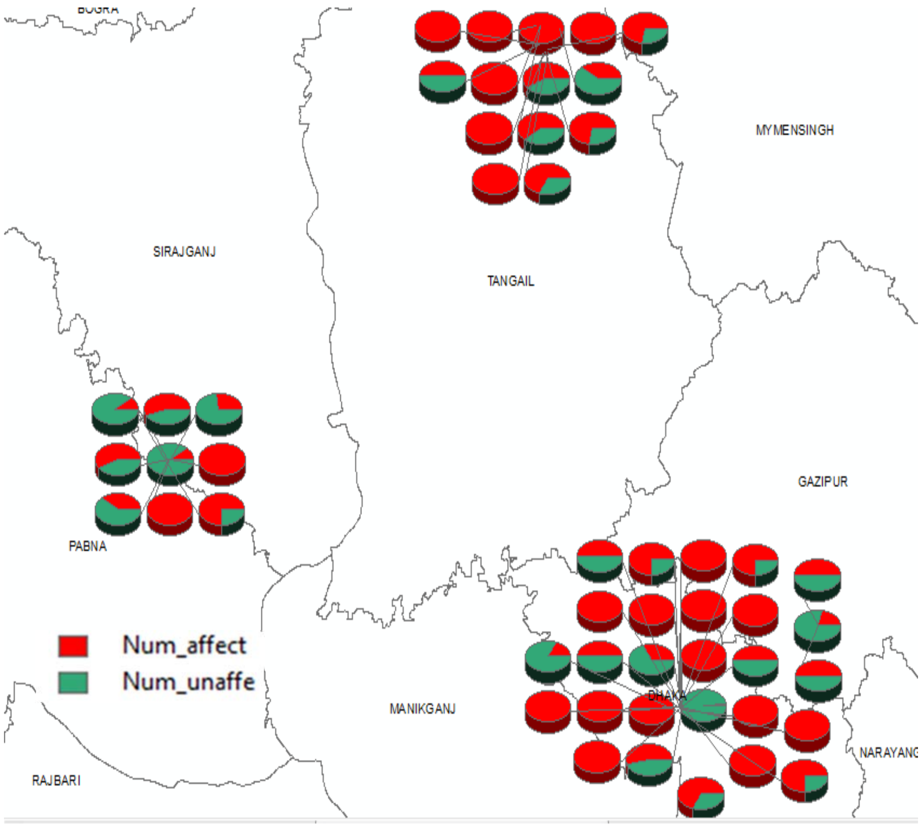
Region-3 (Tangail, Ghatail)

Z score: 3.72
P value: 0.00019



Clustered pattern

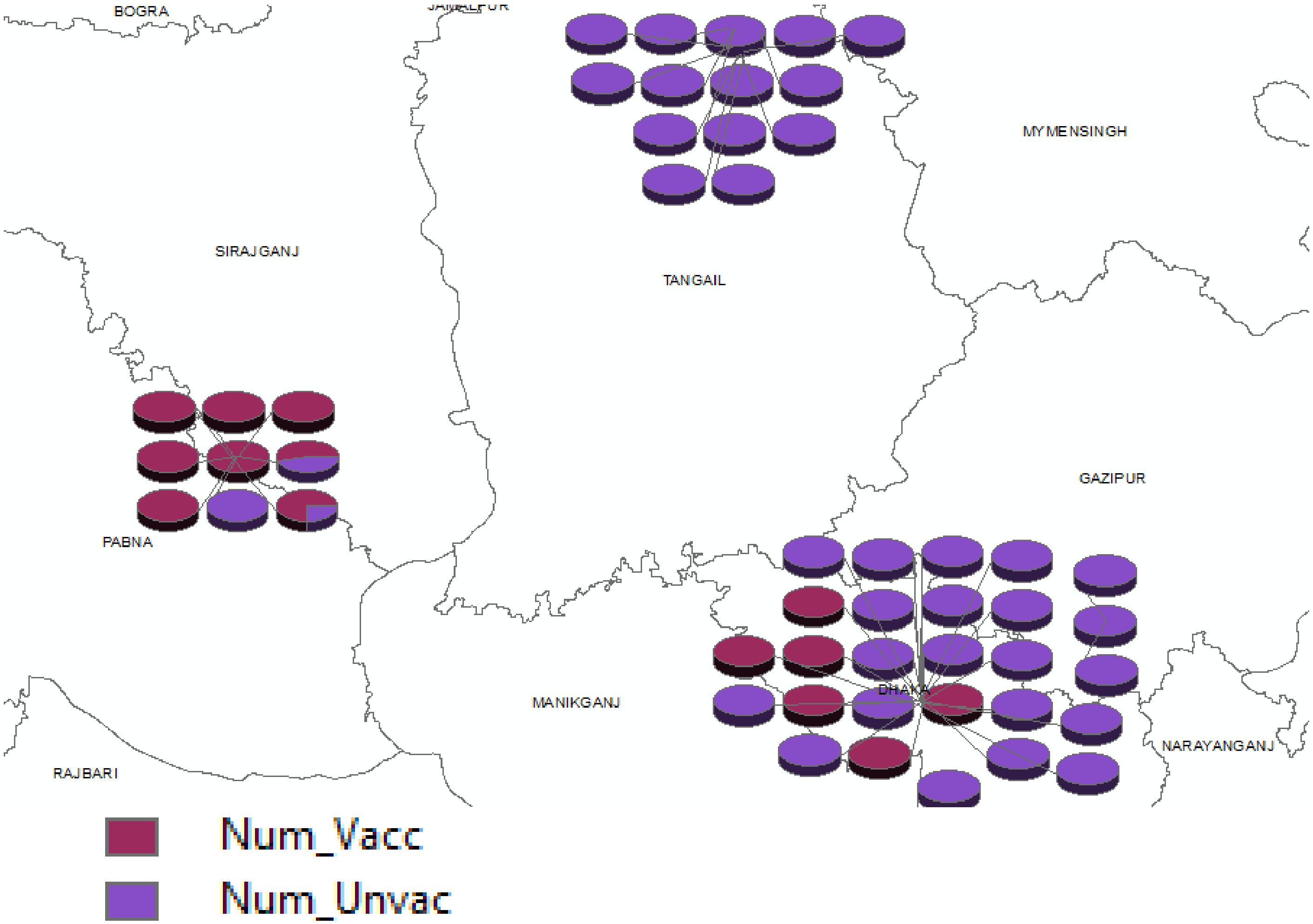
Morbidity pattern



Morbidity	% herd
100%	47%
≥ 50% but <100%	43%
<50%	10%

Result

Outbreak distribution in vaccinated and non-vaccinated herds in different regions



Transmission rate were calculated by GLM and finally Basic reproduction ration (R_0) were estimated:

Outbreak	Transmission rate (β)	Average period of infectiousness (days) ($1/\gamma$)	R_0
1	3.25	2.50	8.12
2	3.70	5.50	20.32
3	1.56	3.00	4.69
4	2.99	4.00	11.97
5	1.15	4.00	4.61
6	1.84	3.38	6.22
7	4.14	4.00	16.57
8	3.19	1.75	5.58
9	3.11	3.25	10.11
10	1.46	3.00	4.37
11	3.27	3.50	11.44
12	3.19	1.00	3.19
13	3.05	3.50	10.68
14	3.28	2.38	7.78
15	3.15	2.00	6.30
16	3.01	3.00	9.03
17	3.16	2.84	8.99
18	3.23	3.67	11.85
19	1.16	3.50	4.07
20	1.20	4.50	5.39
21	1.36	1.60	2.17
Average	**2.70**	**3.21**	**8.26**

R_0 and Critical Vaccination Threshold (q_c)

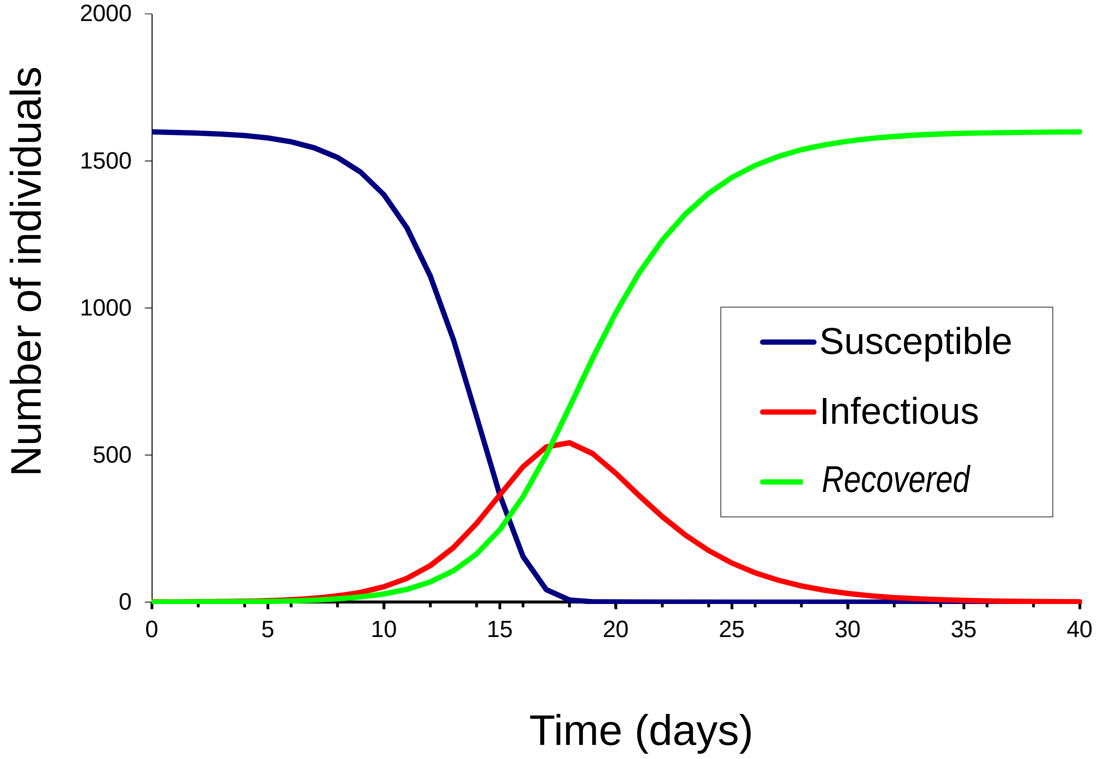
Average R_0: 8.26

$q_c = 1 – 1/R_0$

In the present case q_c = 87.89%

At least 87.89% a cattle need to be vaccinated to stop FMD spread

SIR model



Inputs:

Time step: 1 day

Population size: 2000

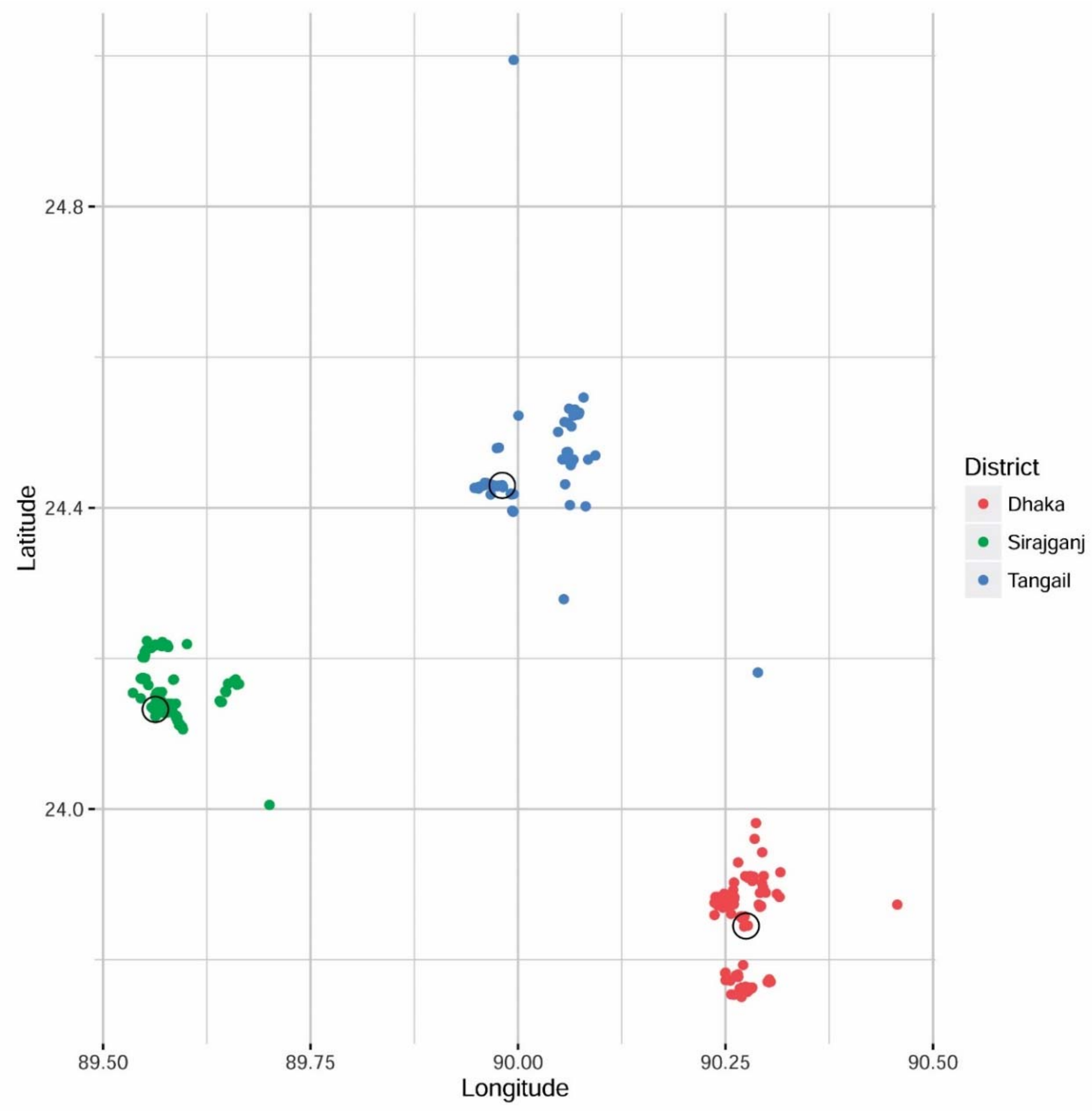
Latency: 3 days

Infectiousness: 3.14 days

R_0: 8.26

Result

Seeding of the index case and simulation of outbreaks in 3 regions



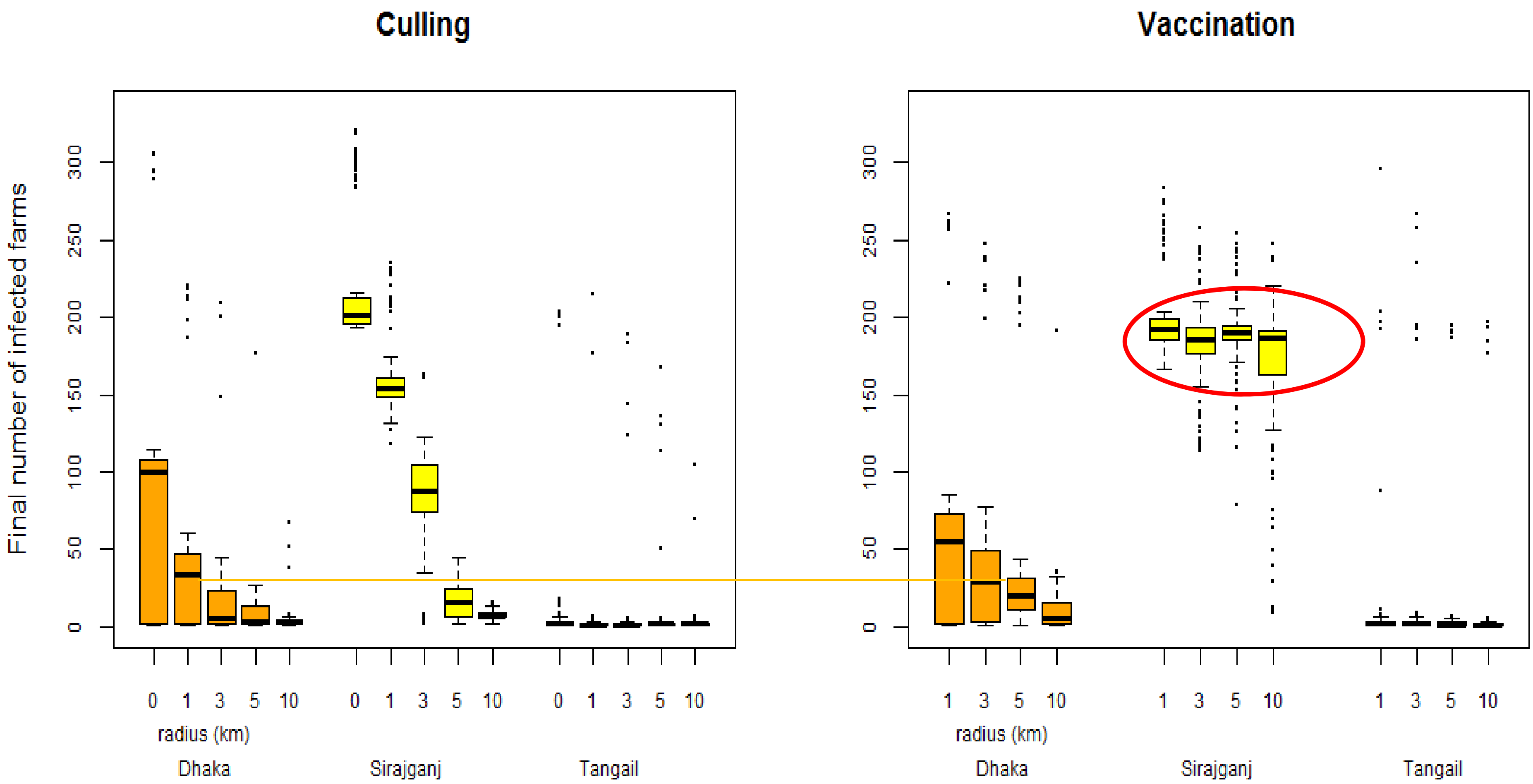
Estimated Transmission kernel ($K(d_{ij})$:

$K(d_{ij}) = ge - {}^{hd}{}_{ij}$

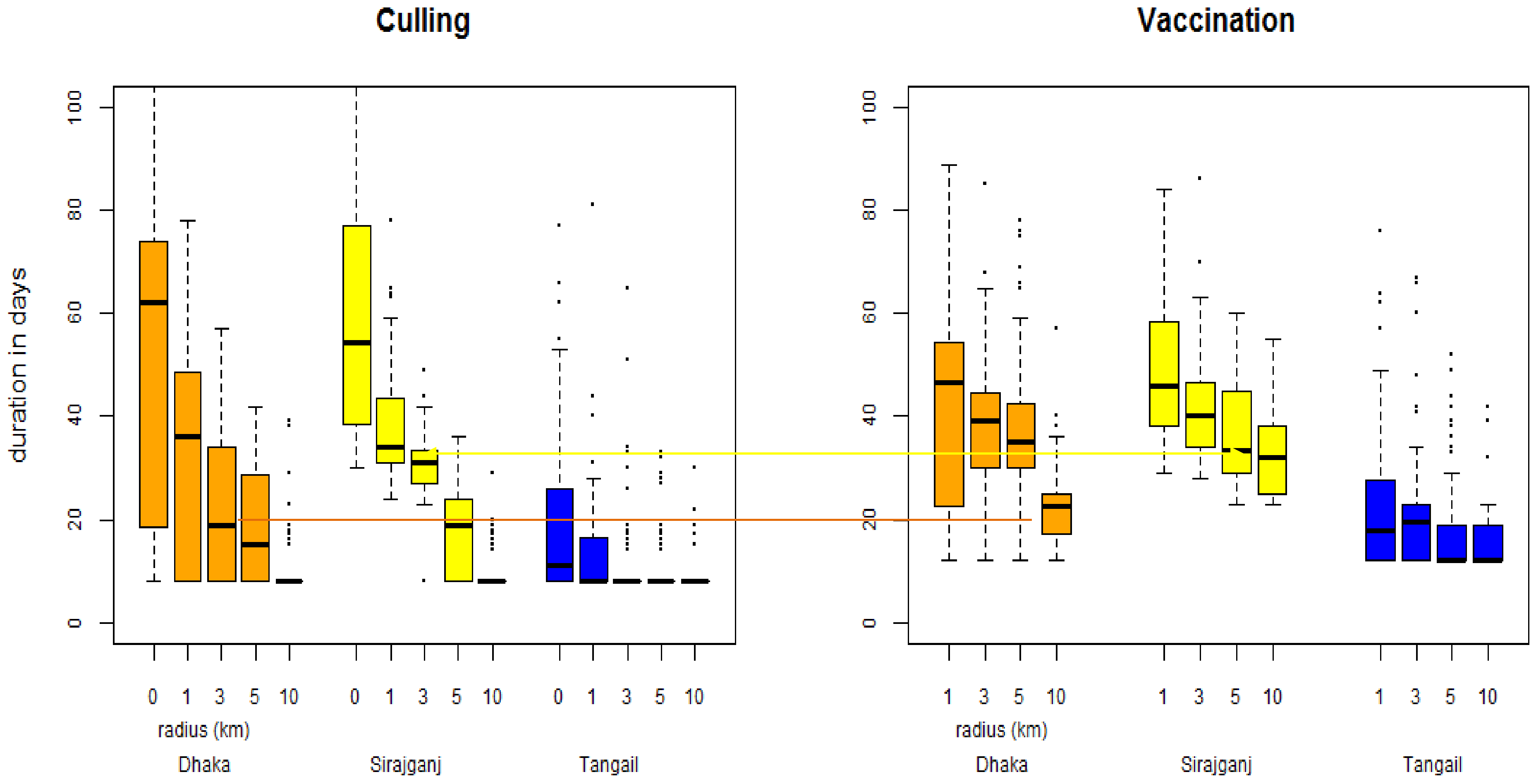
$g = 12.5$
$h = 0.17$

Result

Impact of culling or reactive vaccination on the number of infected farms as predicted in outbreak simulations



Impact of culling or reactive vaccination on the duration of FMD outbreak as predicted in outbreak simulations



Conclusion

- Extensive and intensive farming practices are associated with clustered and dispersed FMD outbreaks respectively
- Outbreaks were also observed in some vaccinated animals which leads the question of antigenic mismatching between vaccine and field strain.
- The average Basic Reproduction Number (R_0) ranged from 2.17 to 20.32 with an average of **8.26**
- SIR model suggests that all the susceptible animals within an epidemiological unit are likely to be affected within 10 to 20 days from the detection of the index case
- Outbreak simulation model appears to be applicable in predicting the impact of FMD control actions

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Thank you

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