STATE-LEVEL BRAINSTORMING SESSION

“Accelerating FMD Control under LHDCP”

Bihar Animal Sciences University, Patna · State FMD Collaborating Centre, with ICAR-NIFMD

BASU, Patna · 26 October 2026

Disease Intelligence for Predictive Animal Health Surveillance

Foot and Mouth Disease (FMD) Case Study

Dr. K. P. Suresh

Principal Scientist, Disease Informatics Lab, ICAR-NIVEDI, Bengaluru

Prof. P. C. Mahalanobis National Award (2022)

FORECAST

NADRES early warning

District-level FMD risk across India, two months ahead

MODEL

FMD mathematical model

Vaccination targets and control options, from village to State

ASSESS

SAT-1 risk assessment

An exotic serotype now in West Asia and China — how likely is it to reach India?

Foot-and-mouth disease — the disease and what it costs India

A highly contagious viral disease of all cloven-hoofed livestock — endemic in India and a drag on dairy productivity and trade.

THE DISEASE

What FMD is

Agent
FMD virus (*Aphthovirus, Picornaviridae*); seven serotypes — O, A, C, Asia-1, SAT-1, SAT-2, SAT-3

Hosts
Cattle, buffalo, sheep, goats and pigs — all cloven-hoofed animals; pigs amplify airborne spread

Spread
Direct contact, aerosols, fomites (feed, water, vehicles, people) and animal products

In India
O, A and Asia-1 circulate; O causes most outbreaks; no Asia-1 outbreak in the last three years

Signs: *fever and blisters on mouth, feet and teats; low adult mortality, but young calves die of heart damage*

THE COST

What FMD costs India

₹20,897 crore a year

Annual loss in cattle and buffalo, 2013–14 (Govindaraj et al., ICAR-NIVEDI, 2020)

- Milk yield loss
- Lost draught power
- Distress sales
- Treatment costs
- Animal deaths
- Labour time

Beyond the outbreak: abortion, infertility and chronic heat intolerance cut lifetime output; endemic status closes export markets.

Globally: US$ 6.5–21 billion a year in endemic regions.

NATIONAL RESPONSE · NADCP (2019), NOW UNDER LHDCP — BIANNUAL VACCINATION OF ALL CLOVEN-HOOFED LIVESTOCK

147 crore	132 → 40	20.8% → 8.1%	2030
FMD vaccine doses · 8.04 crore farmers	reported FMD outbreaks, 2019 → 2025	NSP antibody prevalence, 2019 → 2025	national goal: FMD-Mukt Bharat

Sources: Govindaraj et al., Indian J. Anim. Sci. 90(7), 2020; Knight-Jones & Rushton, Prev. Vet. Med. 112, 2013; PIB / DAHD, August 2026.

Early warning — acting before the outbreak, not after

An early warning system turns surveillance, climate and ecological data into timely alerts, so animals are protected before disease arrives.

WHAT IT IS

A system that continuously watches the conditions in which diseases spread, **forecasts where and when risk will rise**, and **alerts those who can act** — officials, veterinarians and farmers — while there is still time to prevent losses.

FOUR BUILDING BLOCKS

Risk knowledge	Outbreak history, livestock population, climate and ecology
Monitoring & forecasting	Models estimate risk for every district, months ahead
Warning & communication	Bulletins, SMS and portals reach every level in time
Preparedness & response	Vaccination, biosecurity and surveillance before the season

HOW IT BENEFITS THE LIVESTOCK POPULATION

Vaccinate in time

Herd immunity is built before the risk season, not after cases appear

Fewer outbreaks and deaths

Less illness, mortality and loss of milk, draught power and fertility

Protects farmer income

Avoided losses and lower treatment costs for smallholder households

Targets scarce resources

Vaccine, diagnostics and manpower go to high-risk districts first

Farmers act early

Alerts prompt biosecurity, care with animal movement and timely reporting

One Health and trade

Lower risk of spill-over of zoonoses; supports disease-free zones and trade

FLOW OF THE TALK

From early warning to evidence-based response

Three parts: the NADRES system, why a risk forecast needs mechanistic modelling, and FMD control on the ground — SAT-1 and sampling.

PART A

The NADRES system

01 What is NADRES

02 Disease & climate data

03 The NADRES Data Engine

04 Modelling

05 Output — risk grades & maps

06 Communication of results

PART B

From prediction to mechanism

07 What a risk forecast cannot tell us

08 Limits of AI/ML — and the mathematical remedy

*NADRES tells **where** and **when** risk rises.*

*Mechanistic models tell **how much** and **what works**.*

PART C

FMD control in action

09 FMD mathematical model — concept & method

10 Simulation: Ramanagara district, Karnataka

11 Village, block & farm — a Patna scenario

12 SAT-1 — risk assessment & incursion model

13 FMD sampling plan

14 Preparedness — from forecast to field

NADRES — from reporting outbreaks to forecasting them

A GIS and remote-sensing enabled early-warning system that forecasts livestock disease risk for every district in India, up to two months ahead.

15 diseases modelled

750 district units

36 States / UTs

2 months lead time

6 risk grades

40 + 1 base models + stacking meta-learner

Diseases forecast every month

Viral (7)	Foot-and-mouth disease · Lumpy skin disease · PPR · Bluetongue · Sheep & goat pox · ASF · CSF
Bacterial (4)	Haemorrhagic septicaemia · Black quarter · Anthrax · Enterotoxaemia
Parasitic (4)	Theileriosis · Babesiosis · Trypanosomiasis · Fascioliasis

Without forecasting — reactive

Outbreak → Report → Confirm → Respond

Action begins after animals are already sick — the losses are locked in.

With NADRES — anticipatory

Forecast → Awareness → Biosecurity → Vaccinate & watch → Prevent

Farmers are alerted, biosecurity is tightened and vaccine is positioned before the risk season.



Gold Award

National Awards for e-Governance 2024–25

Conferred on NADRES · DARPG, Government of India

Disease data — three live channels, four being integrated

NADEN reporting, active surveillance and sentinel data feed NADRES today; four further channels are planned to join them.

LIVE TODAY *feeding the NADRES database every month*

NADEN centre reporting

Monthly livestock disease outbreak reports from 36 NADEN centres

Active surveillance

Field and outbreak investigations · quarantine & movement monitoring

Sentinel data

Sentinel villages, farms and animals · event-based sampling

PLANNED *channels being brought into NADRES next*

Community & field inputs

Toll-free helpline · Pashu Sakhi & Sakha · para-vets · veterinarians · farmer chatbot

CADDES & PADDES apps

App interactions captured as structured disease data

Laboratory & genomic data

NGS sequencing → genomic data for molecular epidemiology

News & reports

Media reports and official bulletins

Standardised NADRES database

Per district, per month:

- Outbreaks
- Susceptible animals
- Animals attacked & deaths
- Vaccinations

The raw material every NADRES AI/ML model is trained on.

Climate, ecology and livestock — the drivers of disease risk

Four categories of raw variables, at up to 1 km resolution, describe the conditions in which each disease spreads.

Livestock population

Cattle, buffalo, sheep, goat and pig counts from 6,64,369 villages and 5,564 blocks, aggregated to district density

Source: 20th Livestock Census, DAHD, GoI

Remote sensing

Land surface temperature (1 km) · NDVI & EVI vegetation indices · potential evapotranspiration · leaf area index (500 m)

Source: NASA LAADS DAAC / Earthdata

Meteorological

Air temperature, rainfall, humidity, wind speed, surface & vapour pressure, cloud cover, specific humidity, wet-day frequency

Source: GLDAS (NASA, 0.25°) · CRU (UEA, 0.5°)

Climatic events & ecology

Rainfall > 100 mm · temperature > 35 °C or < 15 °C · forest fires · soil pH & elevation · carbon emission & water bodies

Source: Derived from meteorological & remote-sensing feeds

IMD forecast

8 forecast variables pulled daily from IMD through an API

ENSO features

34 ocean–atmosphere features capture El Niño / La Niña influence

Long archive

Monthly data from 2000 to 2026 for all 750 district units

Feature engineering — turning weather into disease signals

The same rainfall means standing water for Fascioliasis, midge habitat for Bluetongue and spore mobilisation for Anthrax.

1. **Anomalies** — against each district's own long-term normal
2. **Lags** — drivers lagged 1, 2 and 3 months
3. **Delta weather** — static 2001–2021 trends; dynamic 2018–2023 change
4. **Seasonality** — cyclic month encoding (sine / cosine)

#	Interaction	Engineered as	Diseases
1	**Heat stress**	THI, THI max, days with THI ≥ 72	FMD, LSD, PPR
2	**Saturation deficit**	VPD, VPD lag 1–3	Theileriosis, Babesiosis
3	**Tick degree-days**	DD tick (degree-days)	Theileriosis, Babesiosis
4	**Midge suitability**	DD BTV; (13–35 °C) × NDVI	Bluetongue, LSD
5	**Waterlog / snail**	DD Fasciola × soil moisture	Fascioliasis
6	**Antecedent rainfall**	SPI-3, API, rainfall lag 1–3	HS, BQ, Anthrax
7	**Drought-then-rain**	Drought-break indicator	Anthrax, BQ
8	**Soil spore window**	Soil pH × moisture × temperature	Anthrax, BQ
9	**Density–heat stress**	Bovine density × THI	HS, FMD
10	**Drought congregation**	Water deficit × density × (1 − NDVI anomaly)	FMD, HS, PPR

#	Interaction	Engineered as	Diseases
11	**Cold–wet stress**	Night LST × wind speed	PPR, Enterotoxaemia
12	**Diurnal thermal stress**	LST diurnal temperature range	FMD, PPR
13	**Pasture flush**	NDVI anomaly; LAI × rainfall lag 1	Enterotoxaemia
14	**Virus survival**	Humidity × cloud cover × (1 − solar rad.)	FMD, Sheep & goat pox
15	**Biting-fly abundance**	Air temp × humidity × NDVI	Trypanosomiasis, LSD
16	**Flood / spore wash-out**	Runoff × rainfall	HS, Anthrax
17	**Wet-day frequency**	Wet days, rainfall events	Fascioliasis, Bluetongue
18	**Wild-boar habitat**	NDVI × elevation std. dev.	ASF, CSF
19	**Seasonality**	Month sin/cos; variable × month sin/cos	All 15 diseases

19 disease-specific climatic interactions, including seasonality

The NADRES Data Engine — climate data for India, every month

An automated pipeline that builds district-level climate data from global satellite and reanalysis sources, month by month from 2000 to the present.

26 yrs	11	~125	~80	16	1,72,752	1.99 crore
2000 – present	satellite & reanalysis sources	raw variables	derived features	disease-risk indices	district-month records	individual values

Five-layer architecture

Presentation	Web portal — browse · select · preview · download
Application	Parameter catalogue · validation · file builder · documentation
Data	Raw climate · derived features · interactions
Processing	Task scheduler · feature derivation · data-health monitor
Source	Google Earth Engine · Google Cloud Storage

Monthly workflow

1. **Select month** — current and any missing months, never just the newest
2. **Source check** — has every satellite finished covering that month?
3. **Export & retrieve** — district averages computed on Earth Engine servers
4. **Validate** — all districts present · values in range · no gaps
5. **Commit raw, then derive** — anomalies · lags · rainfall scores · risk indices
6. **Live** — database · portal · forecasting model

Technology stack

Source	Earth Engine (Python API)
Processing	Python
Computation	pandas · NumPy · PyArrow
Database	SQLite (write-ahead log)
Storage	CSV · Parquet
Portal	Streamlit
Testing	unittest · AppTest

Data and methodology, in one view

From satellite and station data to a single calibrated risk grade per district.

1 Inputs

- **Outbreak history** — outbreaks, susceptible animals, attacks, deaths, vaccinations (NADEN, laboratories, State reports)
- **Climate & weather** — temperature, rainfall, humidity, vapour pressure, wind, cloud cover, drought indices
- **Ecological** — vegetation indices, land surface temperature, soil moisture and chemistry, elevation, fire
- **Livestock population** — cattle, buffalo, sheep, goat and pig counts and densities
- **IMD forecast** — 8 forecast variables pulled daily via API

2 Processing

- Monthly archive, 2000–2026, for 750 district units at up to 1 km resolution
- 93 environmental variables plus 34 ENSO ocean–atmosphere features
- Anomalies against each district's own long-term normal; drivers lagged 1, 2 and 3 months
- Disease-specific climatic interactions — heat stress, waterlogging, drought break, tick and midge suitability, spore survival
- Cyclic month encoding, so the model learns each disease's own seasonality

3 Model & output

- 40 base models across 7 families — regression, tree/boosting, deep and transformer, probabilistic, SVM, AutoML
- Hyper-parameter tuning with Optuna, cross-checked with FLAML
- District-grouped out-of-fold validation with isotonic calibration
- Four ensembles combine the 40 predictions, plus a stacking meta-learner
- One calibrated risk value per district per disease, graded NR to VHR

*The complete monthly cycle — ingest, engineer, train, validate, ensemble, grade, publish — runs in about **10 hours on GPU**, and is repeated afresh every month.*

Modelling — 40 models, one calibrated risk grade per district

Eight stages, repeated afresh every month; the full cycle runs in about 10 hours on GPU.

1 — Input
Outbreaks + climate, ecology, livestock + IMD forecast

2 — Features
Climatic interactions + cyclic seasonality

3 — Tuning
Optuna in three phases, cross-checked with FLAML

4 — Training
40 base models learn each disease

5 — Validation
District-grouped, out-of-fold, isotonic calibration

6 — Ensemble
40 predictions combined by a stacking meta-learner

7 — Risk grading
Six levels, NR through VHR

8 — Output
Bulletins, district risk maps, SMS alerts

Seven model families

- Regression
- Tree & boosting
- Deep learning
- Transformer
- Probabilistic
- SVM
- AutoML

Each monthly run

Several million	climate, ecological & outbreak records
15 × 750	diseases × district units
~1.09 billion	GPU operations across 41 models
~10 hours	end to end

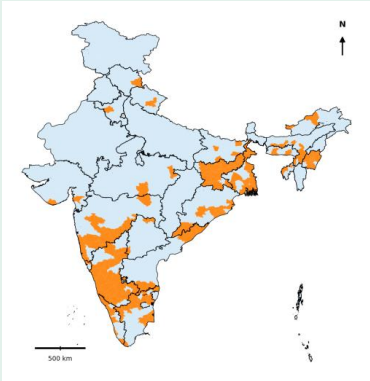
Built to be trusted

- **District-grouped validation** — scored on districts the model has not seen
- **Isotonic calibration** — a predicted risk matches observed frequency
- **Stacked ensemble** — no single model's blind spot decides the grade

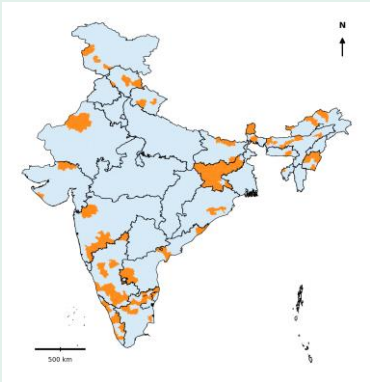
Output — district risk maps in six grades

Grades, not raw probabilities, go to the field: this is the language of every advisory, map and SMS.

Viral diseases

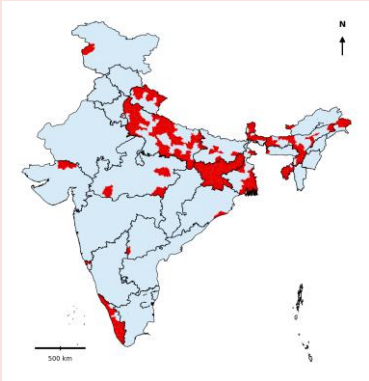


Foot-and-mouth disease

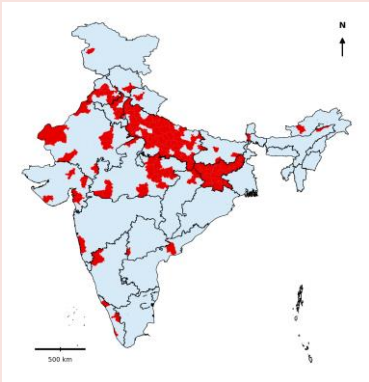


Lumpy skin disease

Parasitic diseases

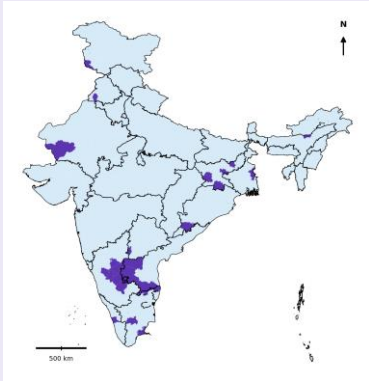


Babesiosis

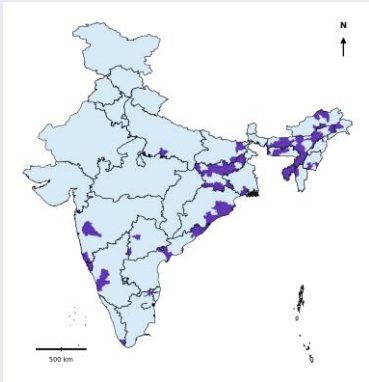


Trypanosomiasis

Bacterial diseases



Anthrax



Enterotoxaemia

VHR	**Very high risk**	Immediate action — vaccination and movement control
HR	**High risk**	Priority surveillance and preparedness
MR	**Medium risk**	Heightened watch
LR	**Low risk**	Routine monitoring
VLR	**Very low risk**	Baseline vigilance
NR	**No risk**	No specific action indicated

HR and VHR districts trigger advisories — keeping the message short and the farmer's attention intact.

Maps: districts at elevated risk highlighted, sample monthly forecast.

Communication — one forecast, delivered to every level

Each monthly forecast reaches officials, agromet field units, farmers and the public through dedicated channels.

Officials	Vet-Alert bulletin (monthly) — DAHD, State AHD officials and State government officials
AMFU network	DLT SMS — IMD agromet field units (AMFUs) and their registered farmers
Farmers (Karnataka)	FRUITS SMS alerts to registered farmers
Public	NADRES web portal risk maps · WhatsApp, YouTube, LinkedIn
Apps	LDF & NERLEF mobile apps · CADDES & PADDES (planned)

10.83 crore
FRUITS SMS — cumulative since Nov 2021

23.01 lakh
FRUITS SMS — September 2026 alone

5.15 lakh
DLT SMS — cumulative since Oct 2024

41,003
DLT SMS — September 2026 alone

27.7 lakh
web portal visitors to date

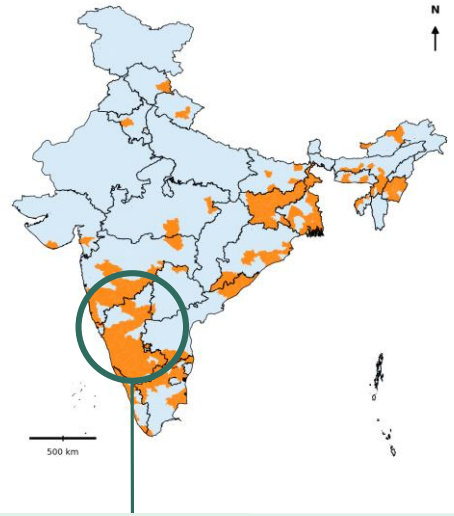
11,546
AMFU alerts — September 2026

Two-way loop: the toll-free helpline **1800-599-4233** lets field officers and veterinarians report back — closing the loop between forecast and ground truth.

From a risk map to real-world answers

AI/ML forecasting flags where risk is high; the questions that follow are answered by mathematical modelling.

1 · AI/ML RISK FORECAST



District X · FMD **VHR** ✓

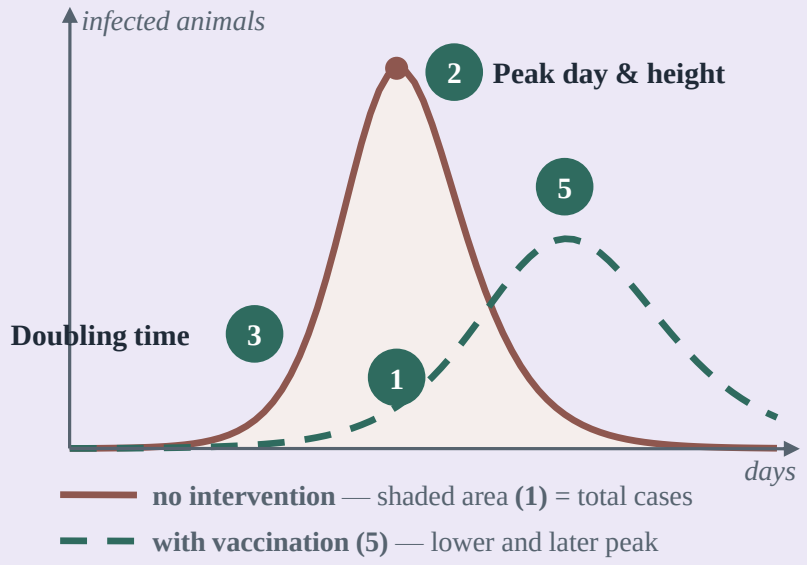
*Tells us **where**, **when** and **how likely***

2 · QUESTIONS IT RAISES

1. How many animals will be infected? ✗
2. When will it peak — and how high? ✗
3. How fast will cases double? ✗
4. How many must be vaccinated? ✗
5. Which intervention works best? ✗

3 · MATHEMATICAL MODEL ANSWERS

4 **HIT = $1 - 1/R_0$**
→ animals to vaccinate



THE MATHEMATICAL MODEL ADDS

- Livestock population
- Movement & contact rates
- Vaccination coverage
- Environmental persistence
- Biology — incubation, R_0

Why AI/ML alone is not enough — and how modelling closes each gap

Data-driven models learn patterns from the past, so they inherit every gap in that past; a mechanistic model encodes how the disease actually spreads.

AI/ML LIMITATION	WHAT THE MECHANISTIC MODEL DOES
Correlation, not causation Learns patterns in past data; cannot explain why transmission happens	**Encodes the mechanism** — contact, incubation, recovery, immunity and environmental survival are explicit parameters.
No history, no prediction A district with zero past cases gets no risk signal, even if it is ecologically primed	**Needs only the population at risk and the biology** — any village or district with susceptible animals can be assessed.
Cannot test the untried Cannot ask "what if we vaccinate?" — it has never seen that scenario	**Simulates what-if scenarios** — vaccination coverage, isolation, movement control, culling — before anything is deployed.
Built on incomplete surveillance Delayed · misreported · non-reported · under-reported data	**Tracks hidden infections** (exposed, asymptomatic) and is validated on outbreak / no-outbreak years, not unreliable raw counts.
Black-box risk scores Hard to defend to policymakers without a mechanism behind the number	**Transparent outputs** — R_0, herd-immunity threshold and a ranking of which control lever matters most.

Hybrid intelligence: NADRES tells *where* and *when* risk rises; the mechanistic model tells *how fast* it spreads, *how much* intervention is needed and *what works*.

A multi-host FMD model: four species, fomites and environment

Cattle, buffalo, pigs and small ruminants are linked through direct contact and shared fomite and environmental transmission.

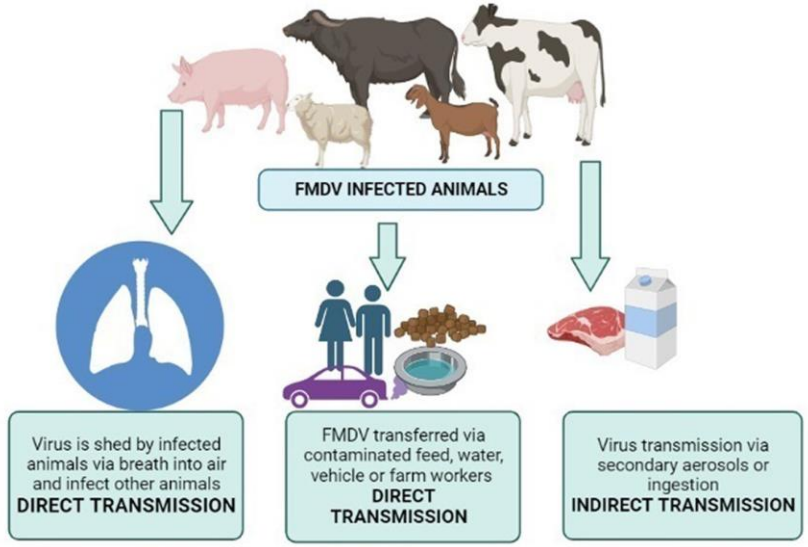
4 host species

24 compartments — 24 coupled ODEs

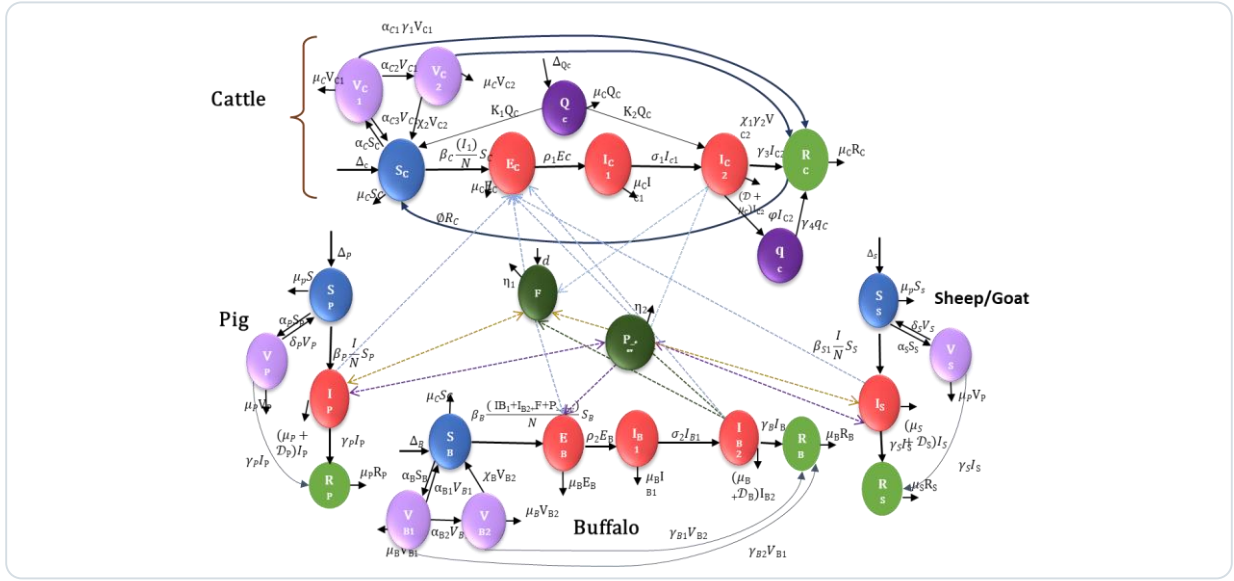
2 fomites (F), environment (P_{env})

44 parameters

How FMD spreads



How the model represents it



Cattle · SEIRVQq (9)
silent & clinical · 2 vaccine levels · quarantine · isolation

Buffalo · SEIRV (7)
two infection stages · two vaccine levels

Pig · SVIR (4)
amplifier — sheds airborne virus

Sheep & goat · SVIR (4)
often mild, so spread goes unnoticed

F · fomites
feed, water, vehicles, farm workers

P_{env} · environment
virus persists < 20 °C, > 55% humidity, pH 7–7.5

How the model is built, tested and used

Six steps take the model from biology to a decision a district can act on.

1 Structure

Cattle ($SV_1V_2EI_1I_2RQq$) act as the central susceptible host, acquiring infection through environmental transmission (f_{ENV}), carrier fomites (F) and direct contact with infected cattle; buffalo contribute via direct and indirect transmission ($SV_1V_2EI_1I_2R$), pigs function as amplifiers (SVIR), while sheep and goats act as silent carriers (SVIR).

2 Parameterise

Biology from literature (incubation 3.6 days, infectious phase 10.8 days); population from the 20th Livestock Census; infection and vaccination from NADRES surveillance; **Genomic Virulence Index (GVI) via genomic data**.

$$\beta_{genomic}(t) = \beta_0 \times [1 + GVI(t) \times \text{scale factor}]$$

3 Prove it is well-posed

Non-negativity: no negative animals.
Boundedness: the population stays finite.
Stability: behaviour around the disease-free and endemic equilibria.

4 Find the threshold

R_0 from the next-generation matrix (spectral radius of FV^{-1}). Below 1 the outbreak dies out; above 1 it persists. Faster doubling means a higher R_0 and a higher herd-immunity threshold (HIT): $1 - 1/R_0$ and Doubling time:

$$T_d = T_g \cdot \frac{\ln(2)}{\ln(R_e)}$$

Where Tg is Generation time

5 Rank the levers

Sensitivity (PRCC): cattle-to-cattle transmission β_C dominates (+0.880). Optimal control (Pontryagin's maximum principle) finds the least-cost mix of vaccination and isolation.

6 Simulate & validate

Fourth-order Runge–Kutta, $\Delta t = 0.1$ day, 50-day horizon; R_e recomputed at every step; validated against district surveillance, 2019–2024.

Ramanagara: set-up and validation against six years of data

Initial conditions from the 20th Livestock Census (2019) and NADRES v2 surveillance — 5,92,366 animals in the model.

Initial conditions

Variable	Description	Value
N_C	Total cattle population	2,87,502
S_C	Susceptible cattle	2,58,003
E_C	Exposed cattle	98
I_{C1}	Asymptomatic infected cattle	49
I_{C2}	Symptomatic infected cattle	476
V_{C1}	Vaccinated, < 3 rounds	28,132
V_{C2}	Vaccinated, ≥ 3 rounds	372
N_B / I_{B2}	Buffalo — total / infected	19,644 / 22
N_P / I_P	Pigs — total / infected	7,102 / 0
N_S / I_S	Sheep & goats — total / infected	2,78,118 / 40
Total	**All livestock in the model**	**5,92,366**

Validation against district surveillance, 2019–2024

Year	Reported cases	Observed	Predicted	Result
2019	62	Yes	Yes	**True positive**
2020	60	Yes	Yes	**True positive**
2021	915	Yes	Yes (897)	**True positive**
2022	0	No	No	**True negative**
2023	49	Yes	Yes	**True positive**
2024	16	Yes	Yes	**True positive**

100%
sensitivity — every outbreak year detected

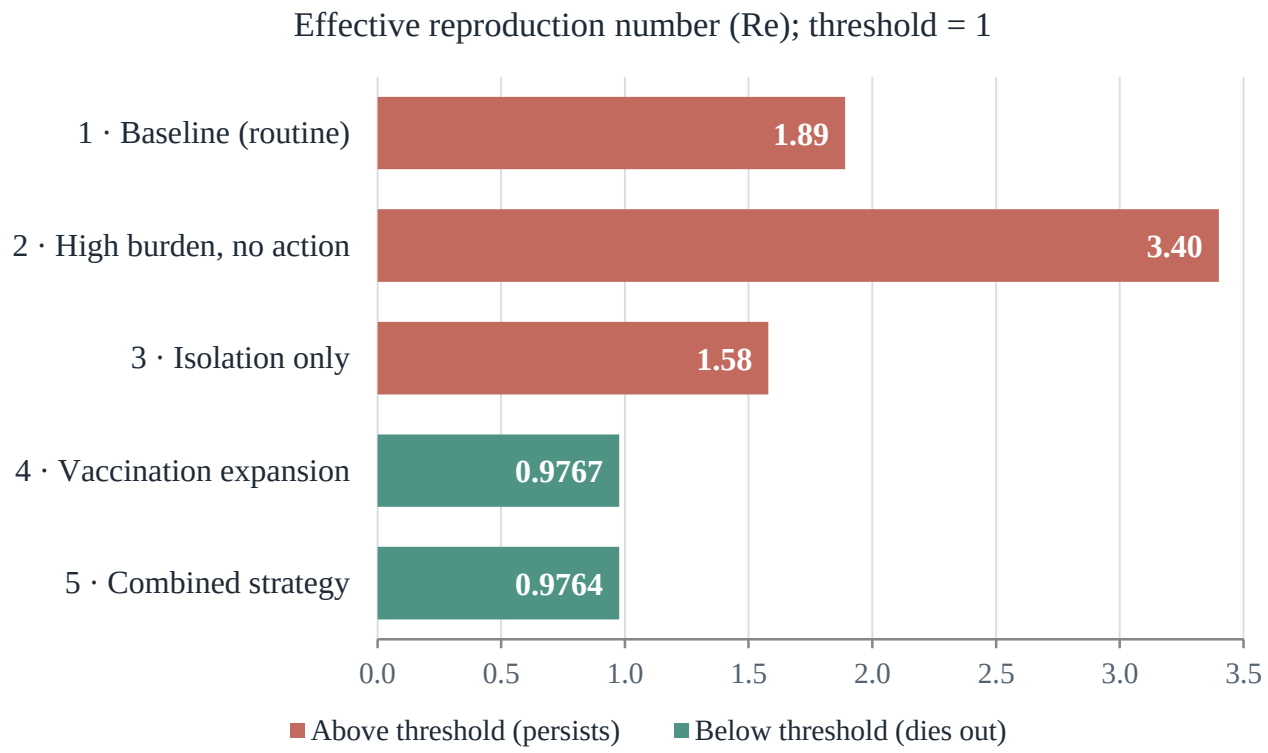
1.95%
error on the 2021 case count (897 vs 915)

6 of 6
years correctly classified, 2022 included

Outbreak years were classified yes / no rather than by case counts, because under-reporting makes absolute counts unreliable — the more robust test, and the one with clearer public-health meaning.

Which intervention pushes FMD below the threshold?

Effective reproduction number R_e under six scenarios in Ramanagara — below 1, the outbreak dies out.



1 · Baseline — R_e 1.89 · HIT 47%
Routine coverage — only 372 cattle with ≥ 3 rounds
Endemic persistence

2 · High burden — R_e 3.4 · HIT 71%
27,025 symptomatic cattle (9.4% prevalence), no intervention
Peak within days

3 · Isolation only — R_e 1.58 · HIT 37%
Every symptomatic animal isolated (φ 0.01 → 1.0)
Still above 1

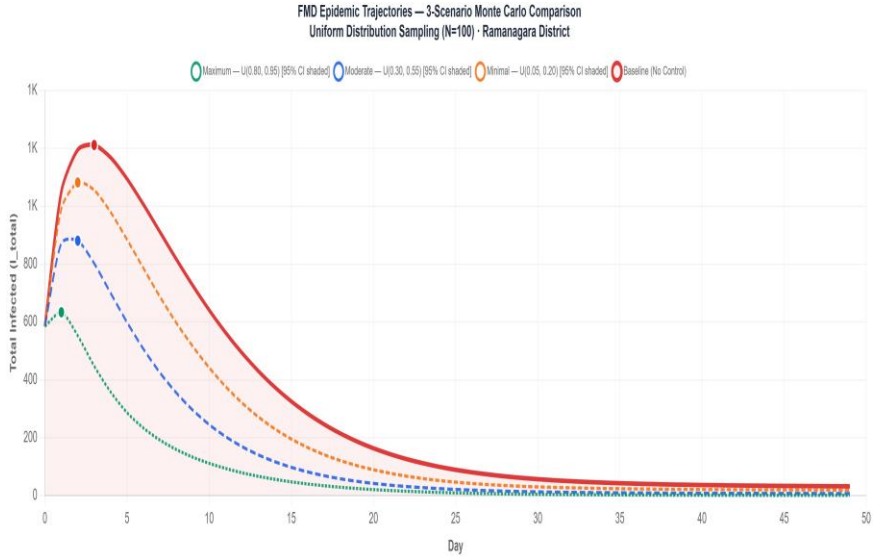
4 · Vaccination — R_e 0.9767
≥ 3-round coverage 372 → 1,60,000 cattle (48.7%)
VC1 28,132 → 30,000; VC2 372 → 1,60,000 (48.7%)
Below threshold

5 · Combined — R_e 0.9764
Scenario 4 + full isolation of symptomatic cattle
Isolation + VC2 372 → 1,60,000
Recommended

Programme implication: coverage, not case removal, is the binding constraint — and the August seasonal peak (R_e 4.26, HIT 77%) is when pre-emptive vaccination guided by NADRES's two-month lead time matters most.

Integrated control — what each level of effort buys

Eight control levers, 100 Monte Carlo runs per intensity level, 50-day horizon.



8 Control measures used in the mathematical modelling simulation

1.Included movement restrictions and quarantine (m_restrict),
2.Biosecurity measures (b_biosecurity),
3.Surveillance and early detection (λ_surv),
4.Outbreak response (θ_outbreak),

5. Culling of infected animals (cull_rate),
6. Quarantine screening efficacy (s_eff),
7. Vaccination effectiveness (ε_vac), and
8. Quarantine-associated mortality (φ_quar).

Peak reduction vs no control

−10.7%	−27.3%	−47.9%
Minimal control	Moderate control	Maximum control

What matters most — leave-one-out ranking

1. **Movement restriction** — acts on the whole force of infection — its removal causes the largest rebound
2. **Surveillance** — drives detection and isolation — without it, infectious animals go unseen
3. **Vaccine effectiveness** — stops waning-immunity animals returning to the susceptible pool
4. **Screening & outbreak response** — smaller alone — they mainly amplify the three above

Conclusion: moderate integrated control is the minimum viable package; maximum intensity nearly halves the epidemic peak and brings it forward to day 1.

Any scale, any place — if FMD were reported in Patna

The same equations run for a farm, village, block or district; only local inputs change. Illustrative application for Patna district, Bihar.

Farm vaccination schedule → **Village** ring vaccination → **Block** deploy vaccinators → **District** control portfolio → **State** vaccine allocation

Only local inputs change: population at risk · starting infections · vaccination immunity · local climate from the NADRES Data Engine

IF FMD IS REPORTED IN A PATNA VILLAGE

Hour 0 — Report & confirm
Helpline 1800-599-4233, NADEN or app; samples for serotyping

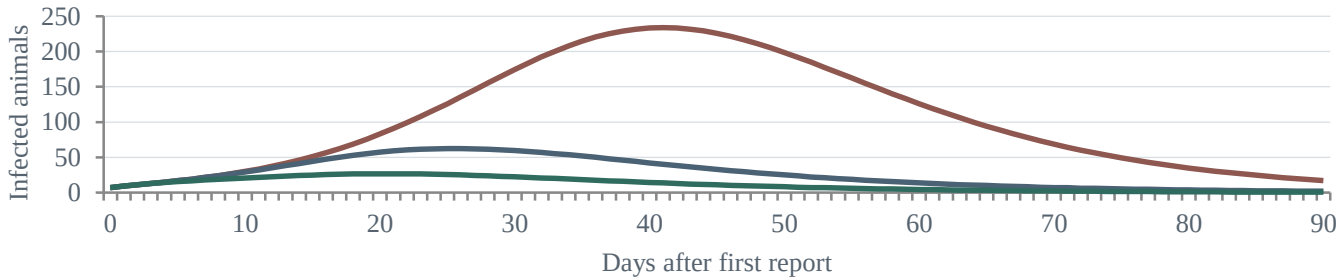
Day 0 — Load village inputs
Cattle, buffalo, sheep and goat counts; vaccination cover; sick animals; weather

Day 0–1 — Simulate
R_e, herd-immunity target, peak size and timing, spill-over between cattle and buffalo

Day 1 — Compare options
Ring vaccination, movement restriction, isolation, biosecurity

Day 2 + — Act & update
Village action sheet; re-run daily with field reports

Illustrative simulation — hypothetical diara village, Patna district



Hypothetical diara village: 800 cattle + 400 buffalo, 20% already immune. Real runs use Patna's own data.

No action
Peak ≈ 230 on day 41
≈ 910 animals infected

Ring vaccination
Peak ≈ 60 on day 25
≈ 230 animals infected

+ movement control
Peak ≈ 27 on day 21
≈ 100 animals infected

Gangetic-plain context the model captures: dense cattle–buffalo smallholder herds · shared diara grazing and flood-time crowding · cattle fairs such as Sonepur and movement across the Nepal border

SAT-1 — an African serotype on the move towards India

A meta-analysis of 122 studies and an evolutionary analysis of 212 sequences both point to SAT-1 as the priority exotic hazard.

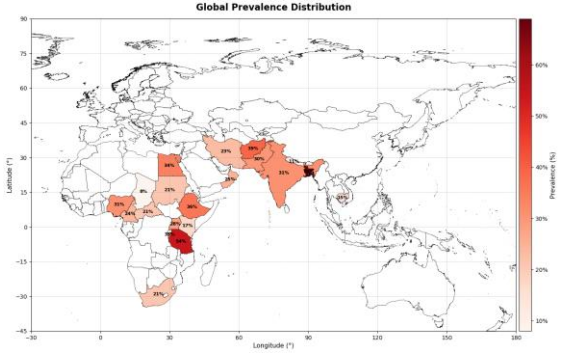
ABOUT SAT-1

SAT-1 (Southern African Territories type 1) is one of the seven FMD serotypes and normally circulates only in sub-Saharan Africa; earlier escapes reached the Middle East in 1962 and 1969–70. **Since January 2025**, East African-origin SAT-1 viruses have caused outbreaks in Iraq, Bahrain and Kuwait, then Türkiye, and in March 2026 SAT-1 reached China (Xinjiang, Gansu). **Immunity is serotype-specific and India's FMD vaccines contain no SAT-1** — Indian cattle and buffalo have no protection against it.

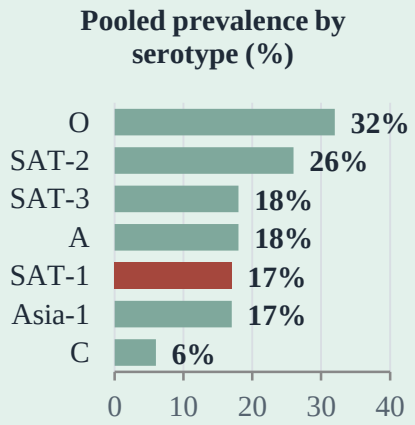
META-ANALYSIS

How common is each serotype in Africa and Asia?

37,791	→	628	→	122
records screened		full texts assessed		studies included



Pooled FMD prevalence by country, 2004–2024



EVOLUTIONARY ANALYSIS

How fast is each serotype changing?

Root-to-tip regression confirmed temporal signal; Bayesian molecular-clock and demographic models then estimated rates and divergence times.

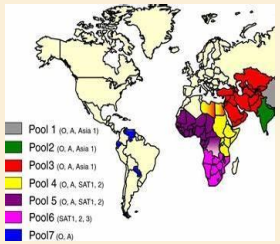
Serotype	Sequences	Substitution rate, $\times 10^{-3}$ subs/site/yr (95% HPD)	tMRCA, year (95% HPD)
SAT-1	**23**	**73.1 (16.8–159)**	**1875 (1779–1954)**
C	11	28.9 (3.99–59.0)	1926 (1891–1952)
Asia-1	22	4.20 (0.76–7.37)	1943 (1909–1957)
O	82	2.70 (2.01–3.56)	1944 (1925–1958)
A	43	1.80 (1.16–2.65)	1921 (1890–1949)
SAT-3	12	1.48 (1.25–1.71)	1753 (1716–1786)
SAT-2	19	1.26 (0.27–2.42)	1702 (1369–1917)

SAT-1 evolves ≈ **27× faster** than serotype O, the serotype behind most outbreaks in India — a sign of rapid diversification and active expansion.

How likely is SAT-1 to reach India?

Hazard identification, a scenario tree for the live-animal import pathway, and Monte Carlo simulation for two source countries — China and Kuwait.

1. HAZARD IDENTIFICATION



Historic pools



SAT-1, 2025–26 · WOAH, FAO

3. OUTPUT

CHINA → INDIA

1.91×10^{-5} per animal moved | **0.88** PQ | **≈ 1.1 yr** to incursion (414 days)

95% CI per animal: $7.1 \times 10^{-7} – 5.3 \times 10^{-5}$

KUWAIT → INDIA

5.41×10^{-5} per animal moved | **0.59** PQ | **≈ 1.7 yr** to incursion (615 days)

95% CI per animal: $2.0 \times 10^{-6} – 1.5 \times 10^{-4}$

2. SCENARIO TREE · ONE INFECTED ANIMAL, SOURCE HERD → INDIAN HERD

Notation	Definition	China → India	Kuwait → India	Source
P1	Probability of a SAT-1 FMD outbreak in the source country	$1 - e^{-t\lambda}$, t = 1, λ = 1/6	$1 - e^{-t\lambda}$, t = 1, λ = 32/12	WAHIS
P2	Probability of FMD infection in livestock	β(370, 1100)	β(712, 5391)	China: Aslam J et al., 2025; Kuwait: Aslam & Alkheraije, 2023
P3	False-negative clinical examination of infected livestock at source	1 − P3a	1 − P3a	–
P3a	Sensitivity of cELISA	Uniform(95.5%, 100%)	Uniform(95.5%, 100%)	Wong et al., 2020
P4	Probability that infected livestock survive transport	1 − P4a	1 − P4a	–
P4a	Mortality of livestock in long-distance transport	β(193, 276037)	β(193, 276037)	Simova et al., 2017
P5	False-negative clinical examination at India	1 − P3a	1 − P3a	–
P6	Contact of infected livestock with susceptible animals in India	1 − (P6a × P6b)	1 − (P6a × P6b)	–
P6a	Possibility of quarantine for infected livestock	β(0.23, 11.07)	β(0.23, 11.07)	Martinez-Lopez et al., 2008
P6b	Positive clinical examination of infected livestock during isolation	β(4.21, 0.07)	β(4.21, 0.07)	Martinez-Lopez et al., 2008
Q	Export volume of live cattle from the source country	Triang(0, 0, 3,056,828)	Triang(0, 0, 125,417)	FAO STAT
P	Probability of SAT-1 FMD in a live animal exported to India	P1 × P2 × P3 × P4 × P5 × P6	P1 × P2 × P3 × P4 × P5 × P6	–
PQ	Probability that at least one exported animal is infected	$1 - (1 - P)^Q$	$1 - (1 - P)^Q$	–
N_y	Expected number of years until at least one SAT-1 incursion	1 / PQ	1 / PQ	–

$P = P1 \times P2 \times P3 \times P4 \times P5 \times P6 \rightarrow PQ = 1 - (1 - P)^Q \rightarrow$ years to first incursion = 1 / PQ

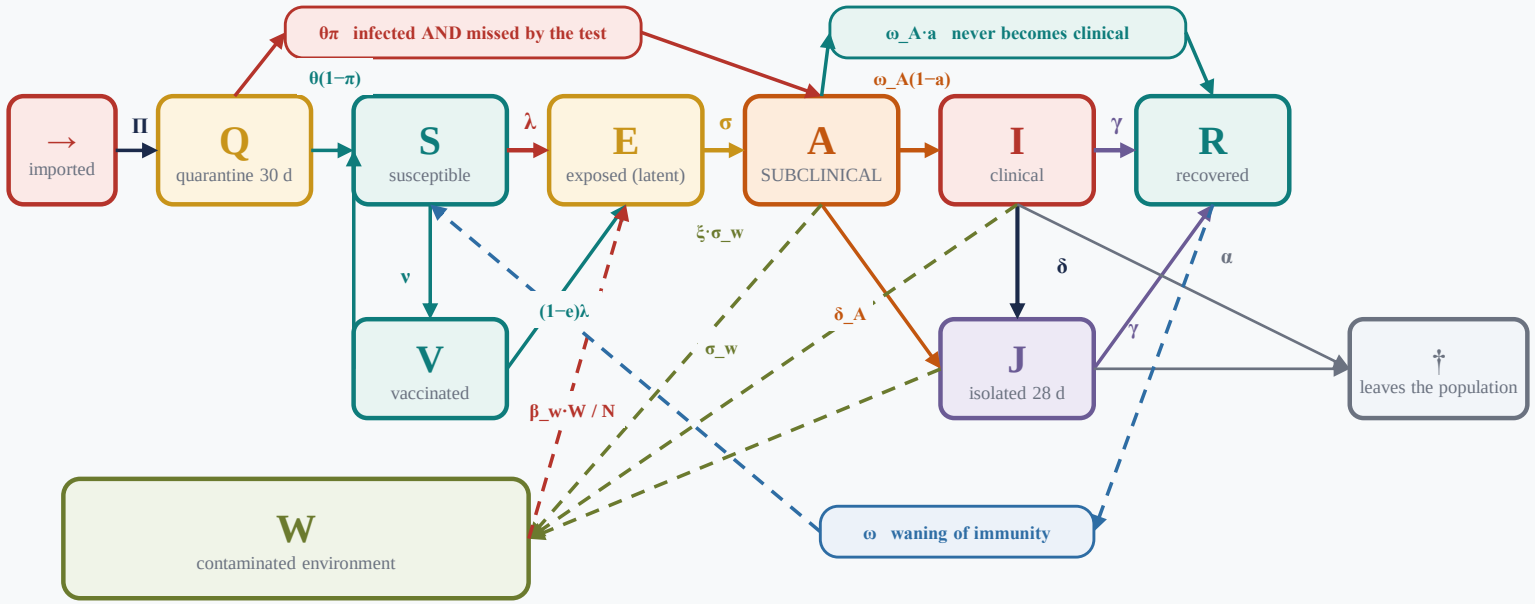
What drives the risk: missed detection at export (P3) and at India's border (P5), Spearman ρ 0.68 and 0.67. *Gold rows differ by pathway; merged cells are shared.*

Low risk per animal, high risk overall: Kuwait is riskier per animal (frequent outbreaks, P1), China overall (far larger exports, Q). Strengthen border screening, surveillance and targeted sampling now.

SAT-1 incursion model for India

What follows if SAT-1 enters India: one bovine host class (cattle + buffalo pooled), controls as parameters.

Solid *= animals move between compartments.* ***Dashed*** *= contamination or environmental influence; no animals move.*



Why model it: the risk assessment puts the first SAT-1 incursion 1–2 years away, and Indian cattle and buffalo have no SAT-1 immunity.

What it captures: cattle + buffalo pooled as one host; every infection passes through a subclinical stage **A** that clinical inspection cannot see; detected animals go to one isolation compartment **J**; virus shed into the environment **W** persists by temperature, humidity and soil pH.

BASIC REPRODUCTION NUMBER, R_0

$$R_0 = (S_0 + V_0(1-\varepsilon))\,[\,D_A\,Q\,(D_I\,D_J\,\delta\,\sigma_2\,(1-\kappa) + D_I\,\sigma_2 + 1) + D_A\,\beta_W\,\sigma_W\,(D_I\,D_J\,\delta\,\eta_J\,\sigma_2 + D_I\,\eta_I\,\sigma_2 + 1)\,/\,(D_W\,N_0)\,]$$

Where:

- $D_A = 1 / (\sigma_2 + \gamma_A)$ (duration in asymptomatic state)
- $D_I = 1 / (\delta + \gamma_I)$ (duration in active infectious state)
- $D_J = 1 / (\gamma_J + \alpha_J)$ (duration in isolated state)
- $D_W = \mu_W(1 + d)$ (environmental clearance rate)
- $Q = \beta(1 - m)(1 - b) / N_0$ (effective direct transmission rate)

PARAMETERS AND THEIR MEANING

Symbol	Meaning	Value
Π	imported animals per day	0
θ	1 / quarantine duration	1/30 d
π	arrivals infected AND missed by the test	0.01
λ	force of infection (direct + environmental)	derived
σ	1 / latent period (E)	1/1.5 d
ω_A	1 / subclinical stage (A)	1/2 d
a	share leaving A that never turns clinical	0.20
ξ	infectiousness of A vs clinical	0.50
γ	recovery rate (γ + α = 1 / infectious period)	1/10 d
α	disease death rate (case-fatality share)	0.02
δ	clinical detection, I → J	0–0.6 /d
δ_A	active testing of A, A → J	0–0.6 /d
κ	isolation effectiveness (leakiness of J)	0–0.95
ν	vaccination rate	0–0.06 /d
e	vaccine efficacy (leaky)	0.75
ω	waning of immunity	1/180 d
σ_w	virus shedding into environment	1.0
β_w	environmental transmission rate	0.0052
μ_w	environmental decay (T, RH, soil pH)	1/14 d at 20 °C
d	disinfection — acts on μ_w only	0–0.95
m, b	movement control, biosecurity	≤ 0.95, ≤ 0.90
N	living animals: S + V + E + A + I + J + R	—

Without a vaccine, SAT-1 needs stronger-than-standard control

Scenario 180-day runs · **0 vaccine doses in every column**
· **Standard control from day 0:** 1 movement: 25%, 2 biosecurity: 30%, 3 isolation: 70%, 4 disinfection: 30%, 5 detection: ×4 · ***Scaled-up control***: 1–5 raised together until Rc < 1 in every month

State (entry route)	R₀ no control	Rc with standard control	Cases at day 0	NO CONTROL (nothing done)		STANDARD CONTROL (1–5, from day 0)		SCALED-UP CONTROL (Rc < 1)		
				Outbreak lasts (days)	Animals infected in 180 days	Outbreak lasts (days)	Animals infected in 180 days	Outbreak lasts (days)	Animals infected in 180 days	Control needed: level of each measure
Rajasthan **Pakistan route** 27.6 M bovines	**3.84**	**1.76**	**5**	> 180	**25.69 M**	> 180	580	**46**	**10**	**1** movement −59% **2** biosecurity −70% **3** isolation 95% **4** disinfection +70% **5** detection ×8.1 (sick found in ~2.5 days) **2.35× the standard package**
			15	> 180	**25.73 M**	> 180	1,740	**68**	**32**	
			50	> 180	**25.77 M**	> 180	5,797	**86**	**108**	
			100	> 180	**25.80 M**	> 180	11,586	**96**	**217**	
Uttar Pradesh **Nepal route** 52.0 M bovines	**3.44**	**1.46**	**5**	> 180	**48.25 M**	> 180	231	**30**	**8**	**1** movement −60% **2** biosecurity −72% **3** isolation 95% **4** disinfection +72% **5** detection ×8.2 (sick found in ~2.4 days) **2.40× the standard package**
			15	> 180	**48.31 M**	> 180	693	**48**	**24**	
			50	> 180	**48.35 M**	> 180	2,308	**64**	**79**	
			100	> 180	**48.37 M**	> 180	4,616	**73**	**159**	
Meghalaya **North-East interface** 0.9 M bovines	**3.24**	**1.30**	**5**	> 180	**860,613**	> 180	449	**80**	**19**	**1** movement −35% **2** biosecurity −42% **3** isolation 95% **4** disinfection +42% **5** detection ×5.2 (sick found in ~3.8 days) **1.40× the standard package**
			15	> 180	**862,404**	> 180	1,343	**107**	**60**	
			50	> 180	**864,480**	> 180	4,426	**130**	**202**	
			100	> 180	**865,718**	> 180	8,712	**143**	**404**	
Maharashtra **Sea route (trade)** 19.6 M bovines	**3.25**	**1.31**	**5**	> 180	**18.29 M**	> 180	268	**40**	**10**	**1** movement −42% **2** biosecurity −51% **3** isolation 95% **4** disinfection +51% **5** detection ×6.1 (sick found in ~3.3 days) **1.70× the standard package**
			15	> 180	**18.30 M**	> 180	804	**61**	**32**	
			50	> 180	**18.31 M**	> 180	2,680	**81**	**107**	
			100	> 180	**18.32 M**	> 180	5,356	**93**	**214**	
Madhya Pradesh **Interior (indirect)** 29.1 M bovines	**3.44**	**1.46**	**5**	> 180	**27.09 M**	> 180	302	**31**	**8**	**1** movement −57% **2** biosecurity −69% **3** isolation 95% **4** disinfection +69% **5** detection ×7.9 (sick found in ~2.5 days) **2.30× the standard package**
			15	> 180	**27.11 M**	> 180	905	**50**	**25**	
			50	> 180	**27.12 M**	> 180	3,017	**67**	**83**	
			100	> 180	**27.13 M**	> 180	6,032	**77**	**166**	

> 180 = still going when the 180-day run ends · Animals infected include the starting cases (M = million) · R = animals one sick animal infects (above 1 the outbreak grows) · SAT-1 never seen in India
5 early detection ×8.1: *$\delta = \delta_0 \times (1 + u)$, $\delta_0 = 0.05$/day (sick animal found in ~20 days) · standard $u = 3 \rightarrow \times 4$ (~5 days) · scaled-up $u = 3 \times 2.35 = 7.05 \rightarrow \times 8.1$, found in $1 \div (0.05 \times 8.05) \approx 2.5$ days (Rajasthan)*

No control
0.86–48.4 M animals infected in 180 days; no outbreak is over by day 180.

Standard control is not enough
Rc stays above 1 in all 5 States; 20 of 20 runs are still active on day 180.

Scaled-up control stops it
1.40–2.40× the standard package: 8–404 cases, over in 30–143 days, 0 vaccine doses.

Evolution of FMD sampling methodology in India

From outbreak-triggered specimens to WOAH-aligned, two-stage stratified random sampling under LHDCP.

Pre-1978 – 2003

Passive surveillance
No formal sampling; outbreak-triggered specimens only. Serotyping by guinea-pig test (1943–64), CFT (1964–65), ELISA (1996), PCR (2005).

2003–04

FMD-CP launched
First sampling SOP, 54 districts: 10 villages per district, 10 cattle + 10 buffalo per village; paired pre- and post-vaccination sera.

2008

Non-random sampling
Parallel DIVA-based surveillance begins, with convenience / purposive sampling.

2018–19

Nationwide FMD-CP
Phased expansion (54 → 221 → 331+ districts) completes; over 1 million sera tested in 2017–18.

2019

NADCP launched
Centrally funded national scheme adds sheep, goat and pig; the old sampling SOP continues short-term.

2020

WOAH-aligned redesign
NIVEDI & NIFMD launch two-stage stratified sampling: PPS villages; species- and age-stratified (5:4:1) animals; in-house Epi-Calc tool.

2026

Round IX (LHDCP)
Current two-stage stratified random design: sampling without replacement, villages as PSUs, animals as SSUs selected by PPS.

CURRENT DESIGN AT A GLANCE

Methodology	Two-stage stratified random sampling
Key parameters considered	Design prevalence · cluster-level prevalence · diagnostic sensitivity · specificity · confidence interval
Sampling frame	20th Livestock Census data enable reconstruction of the sampling frame, restoring true random village selection without replacement
Village / cluster selection	Villages selected as primary stage units by probability proportional to size (PPS)
Sample size	Moderate — **13,000–15,000 samples per State**

WHY THE FRAME NEEDS REBUILDING

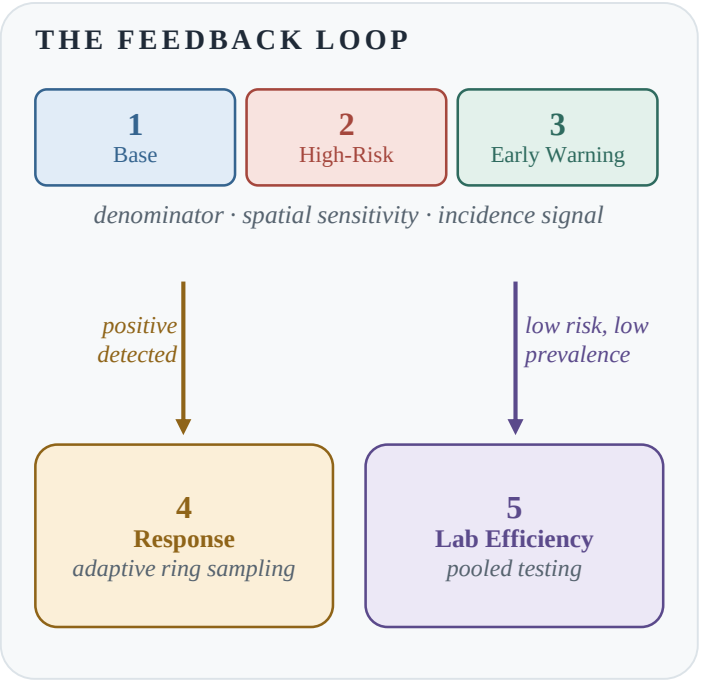
The current sampling frame, based on the 20th Livestock Census, has **diminished after nine monitoring rounds** because previously sampled villages are systematically excluded — constraining random village selection.

Remedy: reconstruct the frame from Livestock Census data, restoring true random village selection without replacement.

Five sampling layers for early warning

Integrated disease surveillance and sampling approaches for early warning under sporadic animal disease.

Layer	Sampling method	Primary parameter estimated	Resource allocation strategy
1 · Base layer	Two-stage stratified PPS + within-cluster SRS	Unbiased population seroprevalence (P) & herd immunity	Moderate, uniform baseline coverage
2 · High-risk layer	Disproportionate risk-stratified sampling	Surveillance system sensitivity (SSe) & early incursion detection	High sample density per cluster / taluk
3 · Early warning layer	Longitudinal cohort / fixed-panel sampling	True incidence (seroconversion) & temporal freedom	Repeated longitudinal follow-up on fixed IDs
4 · Response layer	Thompson's adaptive cluster / spatial ring sampling	Outbreak delimitation, R_e & proof of eradication	Event-triggered surge capacity around positives
5 · Lab efficiency layer	Dorfman hierarchical pooled screening	Sustained freedom in clean zones	Minimal lab cost per animal (70–80% test savings)



How the layers connect: Layers 1–3 continuously generate the population denominator, targeted spatial sensitivity and longitudinal incidence signals. A positive detection escalates a region into adaptive ring sampling (Layer 4); a region confirmed as low-risk and low-prevalence is streamlined into cost-effective pooled testing (Layer 5).

New FMD surveillance framework — seven components

Each component sits in one of the five layers and answers a different surveillance question.

A — BASE LAYER — Naive Calf Cohort

- First vaccination **(6–11 months)**
- Detects recent natural virus circulation
- Clean NSP signal

B — EARLY WARNING LAYER — Longitudinal Dairy Sentinel

- **Fixed enrolled dairy animal**, revisited every round
- SPCE + NSP monitoring
- 24-month evidence accumulation window

C — EARLY WARNING LAYER — Region-Specific Livestock Species

- Covers **sheep, goat, pigs, yak, mithun and any additional species specific to the State's population**
- Monitors amplifying host
- Detects silent circulation

D — BASE LAYER — District NSP Survey

- **District-level NSP baseline; resumes from year 2** as a cross-sectional survey
- Provides the population-level denominator that contextualises Component B's longitudinal signal

E — HIGH-RISK LAYER — Taluk Risk Surveillance

- High-risk taluks
- **Borders, markets & movement**
- Activates in year 2 for priority districts, based on the four components (A–D)

F — RESPONSE LAYER — Outbreak-centric Surveillance

- **3–10 km ring sampling: adaptive sampling**
- Time-series clearance: sample at 30 d, 90 d & 6 m post-outbreak
- Proves eradication of viral pockets and quantifies passive-reporting sensitivity

G — LAB EFFICIENCY LAYER — Low-Risk Surveillance

- Targets consistently **NSP-negative, high-immunity (> 80% SPCE) & low-movement taluks**
- Sustains statistical proof of freedom while optimising lab and field budgets

Parameterisation of surveillance design

Twelve quantities fix how many villages and animals are sampled — and how much confidence a negative result buys.

P^* Design prevalence

10%, 5%, 2%, 1%, 0.5%, 0.2%

Threshold infection level surveillance must rule out with 95% confidence; defines the WOAH phase (Control → Free without vaccination). Lower P* needs more sensitive surveillance.

K Clusters (villages) per round

7 – 25

Number of villages or cluster visits per surveillance round — the primary sample-size lever.

m Animals per cluster

5 – 30

Animals tested per village visit or event (m = 6 bovines or 5 pigs per cluster); directly sets cluster-level sensitivity.

SSe_{sys} System sensitivity

$$SSe_{sys} = 1 - (1 - P_v \cdot Se_C)^K$$

Probability of detecting infection if present at P*. Combining components: $SSe_{sys} = 1 - \prod(1 - SSe_i)$.

Se_T Diagnostic test sensitivity

$$Se_T = P(\text{test} + \mid \text{animal truly infected})$$

Probability that a diagnostic test correctly identifies an infected animal as positive.

Se_C Village-level sensitivity

$$Se_C = 1 - (1 - P \times Se_T)^m$$

Probability of detecting at least one positive animal in a village truly infected at or above the animal-level design prevalence.

DEFF Design effect

$$DEFF = 1 + ICC \times (m - 1)$$

Variance of an estimate under the cluster design relative to its variance under simple random sampling.

ICC Intracluster correlation

$$ICC = (1/\pi_h - 1) \cdot p / (1 - p)$$

How strongly infection status is correlated within a cluster: biological ICC 0.158 (geographic herds), operational ICC 0.053 (assembled groups).

π_h Between-cluster prevalence

$$\pi_h = 1 / [1 + ICC \times (1 - p) / p]$$

Assumed share of villages infected if FMD is present at threshold; in the WOAH FreeCalc framework π_h is set equal to P*.

π_w Within-cluster prevalence

$$\pi_w = p / \pi_h$$

Proportion of animals within an infected cluster that carry detectable NSP antibodies.

P Power

$$Power = 1 - (1 - P)^n$$

Probability of detecting at least one infected or test-positive animal, given disease is present at the assumed prevalence.

r Non-response rate

$$N_{final} = n_{required} / (1 - r)$$

Share of selected villages, farmers or animals that cannot be sampled or give unusable data; sample size is inflated for it.

Preparedness — turning forecast risk into field readiness

A two-month lead time pays off only if something changes on the ground before the risk season.

T − 2 months — Forecast issued — HR / VHR districts flagged → **T − 1 month** — Pre-position vaccine, cold chain, kits and teams → **Risk season** — Detect early, confirm fast, contain locally

CONFIRM
Diagnostics

Is it really the forecast disease — and how fast can we say so?

- Sample kits and cold chain pre-positioned in HR / VHR districts
- Rapid laboratory confirmation; serotyping (O, A, Asia-1 — and SAT-1 watch) guides vaccine choice
- Without confirmation, cases blur into the general sickness baseline

PROTECT
Vaccination

Who do we protect, and where?

- Campaigns timed before the risk season in flagged districts
- Ring vaccination around confirmed foci
- Track multi-round coverage — it decides herd immunity

DETECT
Surveillance

Where is the disease now, and in which host?

- Intensified active surveillance in flagged districts
- Sentinel villages, NADEN reports and helpline calls
- Field findings feed back into NADRES every month

PREDICT
Disease modelling

How much of each — when, and where does it pay?

- Turns surveillance data into transmission parameters
- Estimates R_0 and the herd-immunity threshold — the vaccination target
- Tests interventions virtually before field deployment

Thank you

From forecasting where disease will strike — to modelling what will stop it

Dr. K. P. Suresh
Principal Scientist, ICAR-NIVEDI, Bengaluru
suresh.kp@icar.org.in
Livestock disease helpline: 1800-599-4233