Agri Articles
(e-Magazine for Agricultural Articles)
Volume: 06, Issue: 03 (MAY-JUNE, 2026)
Available online at http://www.agriarticles.com
©Agri Articles, ISSN: 2582-9882

Extended SIR Models in Agriculture: Modelling Crop Disease Dynamics

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The classical Susceptible-Infected-Recovered (SIR) epidemiological model, originally developed for human infectious diseases, has found powerful applications in agricultural contexts for modelling the spread of crop pathogens, fungal blights, viral infections, and pest invasions across field and landscape scales. This article provides a comprehensive overview of extended SIR frameworks adapted for agricultural systems, incorporating compartments for exposed hosts, vectors, environmental reservoirs, and chemical treatment interventions. Key mathematical formulations, parameter estimation strategies, and real-world applications including wheat rust, rice blast, citrus greening, and locust outbreak modelling are discussed. The integration of remote sensing, GIS, and climate data to parameterize spatially explicit SIR models is also addressed. Extended SIR models offer a rigorous quantitative basis for designing integrated pest and disease management strategies, optimizing pesticide application timing, and supporting early warning systems.

Keywords: SIR model, crop disease modelling, plant pathology, pest dynamics, SEIR model, integrated pest management, spatiotemporal spread

Introduction

Mathematical epidemiology, particularly the family of compartmental models originated by Kermack and McKendrick [1] in 1927, provides a robust theoretical framework for understanding how infectious diseases propagate through populations. The classical SIR model partitions a host population into three compartments: Susceptible (S), Infected (I), and Recovered (R) individuals, with transitions governed by transmission rate (β) and recovery rate (γ). While originally designed for human and animal diseases, this framework is directly translatable to plant host–pathogen systems [2 - 5], where the 'individuals' are plants or field units and infection occurs through spore dispersal, vector feeding, or physical contact.

Crop diseases and pest infestations represent one of the most significant and persistent threats to global food security. Collectively, biotic stresses caused by fungal, bacterial, and viral pathogens, alongside insect pests and invasive species, are responsible for pre-harvest yield losses estimated at 20–40% of global agricultural production annually, according to the Food and Agriculture Organization (FAO) [6-7]. As climate change alters temperature and precipitation regimes, the geographic range and seasonal dynamics of many plant pathogens are shifting, increasing the urgency for quantitative modelling tools that can predict outbreak trajectories and guide management interventions [8].

Agricultural epidemiology, however, presents challenges that demand significant extensions of the basic SIR framework. Unlike human populations, plant populations cannot move, are grown in structured spatial arrangements (rows, fields, landscapes), experience seasonal environmental forcing, may be treated with fungicides or pesticides that alter transition rates, and often host multiple interacting pathogens or vectors. Extended SIR models incorporating Exposed (E), Vector (V), Treatment (T), and spatial diffusion components have been developed to address these complexities. This article systematically reviews the mathematical structure, parameterization, and applied utility of these extended models in agricultural disease and pest management.

The Classical SIR Model: Foundations

The standard SIR model describes population dynamics through a system of ordinary differential equations (ODEs):

$$dS/dt = -\beta SI/N$$
$$dI/dt = \beta SI/N - \gamma I$$
$$dR/dt = \gamma I$$

Here, $N = S + I + R$ is the total population, β is the contact/transmission rate (spores per unit time per susceptible plant), and γ is the recovery or removal rate. The key epidemiological threshold is the Basic Reproduction Number, $R_0 = \beta/\gamma$. When $R_0 > 1$, an epidemic can establish and spread; when $R_0 < 1$, infections die out. For crop diseases, R_0 encapsulates the potential for a pathogen to invade a fully susceptible field.

In agricultural contexts, 'recovery' is often better interpreted as removal through death, harvest, or roguing of infected plants, rather than true immunological recovery. This distinction is important for parameterizing γ correctly and for interpreting model predictions for management purposes. The SIR framework also assumes homogeneous mixing i.e., equal probability of contact between any two individuals an assumption that requires relaxation in spatially structured crop systems.

Extended SIR Frameworks for Agriculture

The SEIR Model: Incorporating Incubation Periods

Many plant pathogens [5] exhibit a latency period between initial infection and symptom expression, during which infected tissues are not yet infectious to neighbouring plants. This latent period is captured by introducing an Exposed (E) compartment, yielding the SEIR model:

$$dE/dt = \beta SI/N - \sigma E;\ dI/dt = \sigma E - \gamma I$$

where σ is the rate of progression from exposed to infectious (σ = 1/latent period). The SEIR model has been applied extensively to wheat yellow rust (Puccinia striiformis f. sp. tritici), where the latent period of 7–14 days under moderate temperatures significantly shapes epidemic development curves. Similarly, rice blast (Magnaporthe oryzae) models frequently employ SEIR structures to capture the post-infection incubation before sporulating lesions appear.

The SIRV Model: Incorporating Vaccination/Treatment

Chemical fungicide or pesticide applications act analogously to vaccination in human epidemiology they reduce the susceptible pool or slow the transition to infection. An extended SIRV model adds a Vaccinated or Treated (V) compartment:

$$dS/dt = -\beta SI/N - \nu S;\ dV/dt = \nu S - \rho V$$

where ν is the treatment application rate and ρ is the rate of pesticide efficacy decay (as fungicide protection wanes over time). This formulation allows optimisation of spray timing and dosage to minimise epidemic severity while reducing chemical inputs. Economic threshold modelling integrates the SIRV framework with cost–benefit analysis to determine when treatment application maximizes net returns for farmers.

Key Parameters and Estimation Methods

Accurate parameterization is the cornerstone of any useful predictive model. For agricultural SIR models, the principal parameters transmission rate (β), recovery/removal rate (γ), latent period (1/σ), and vector dynamics parameters must be estimated from experimental or observational data. Table 1 summarizes the primary parameters and their estimation approaches.

Table 1. Key parameters in extended SIR agricultural disease models.

Parameter	Symbol	Typical Range	Estimation Method
Transmission rate	β	0.01–2.0 day^{-1}	Field infection experiments
Recovery/removal rate	γ	0.05–0.5 day^{-1}	Lesion senescence data
Latent period	$1/\sigma$	3–21 days	Controlled inoculation
Basic reproduction number	R_0	>1 for epidemics	Derived: β/γ
Dispersal coefficient	D	0.01–100 m^2/day	Spore trap transects
Vector transmission rate	β_1, β_2	0.001–0.5 day^{-1}	Transmission trials

Modern parameter estimation employs Bayesian inference with Markov Chain Monte Carlo (MCMC) sampling, maximum likelihood estimation from time-series disease progress data, and machine learning-assisted fitting using remote sensing-derived disease maps. Sentinel field plots with regular disease assessment provide ground truth for model calibration. Climate-driven parameter functions (e.g., temperature-dependent β and σ) further improve model realism across seasons and geographies.

Case Studies and Agricultural Applications

Wheat Rust Epidemics

Wheat stem rust (Puccinia graminis f. sp. tritici), stripe rust (P. striiformis), and leaf rust (P. triticina) collectively represent the most economically damaging fungal diseases of wheat globally. SEIR models have been used to simulate rust epidemics under different temperature and humidity scenarios in South Asia and East Africa. Results consistently show that R_0 increases sharply with temperature in the 15–25°C range, and that early-season fungicide application (reducing ν in the SIRV model) can reduce final disease severity by 60–80% when applied during the E to I transition. Remote sensing from Sentinel-2 and Landsat has enabled landscape-scale parameterization of spatial rust spread models across the Indo-Gangetic Plain.

Rice Blast Management in Asia

Rice blast, caused by Magnaporthe oryzae, annually destroys enough rice to feed 60 million people. SEIR models for blast epidemics incorporate humidity-driven infection efficiency and temperature-dependent latent periods. SIR-based economic threshold models have been integrated into decision support systems used by extension services in China, India, and Bangladesh, guiding fungicide spray advisories based on disease progress curve trajectories. Coupling SIR dynamics with spatially distributed weather data from agrometeorological networks allows sub-district level outbreak predictions with 5–7-day lead times.

Locust Swarm Dynamics

Desert locust (Schistocerca gregaria) outbreaks present a landscape-level pest spread challenge amenable to SIR-analogous modelling. Patch-level models track susceptible vegetation areas, infested patches (I), and defoliated-then-recovering patches (R), with transition rates driven by locust population density, dispersal distance, and wind patterns. FAO's SWARMS locust monitoring system incorporates elements of this framework. Extended SIR models coupling vegetation–locust–wind dynamics have been used to project swarm spread trajectories across the Horn of Africa and Arabian Peninsula, informing aerial spray interventions.

Integration with Remote Sensing and GIS

Remote sensing and GIS technologies have dramatically enhanced the spatial resolution and temporal frequency of inputs available for parameterizing agricultural SIR models. Satellite platforms including Sentinel-2 (10 m multispectral), Landsat-8/9 (30 m), and commercial high-resolution systems (Planet, 3 m) provide regular imagery from which disease-related spectral indices such as the Normalized Difference Vegetation Index (NDVI), the Red Edge Chlorophyll Index (CIre), and thermal anomalies can be extracted to monitor epidemic spread across fields and landscapes.

Vegetation indices sensitive to chlorosis, necrosis, and canopy thinning enable mapping of disease severity zones, which serve as the spatial initialization of SIR model compartments at landscape scale. Time-series analysis of these indices allows derivation of epidemic growth curves (logistic or Gompertz functions) from which β and γ can be estimated without intensive ground sampling. Drone-based hyperspectral imaging enables even finer resolution disease mapping within individual fields, suitable for within-field spatial SIR modelling. GIS-based landscape analysis provides information on crop variety distribution, field connectivity (critical for spatial spread modelling), and proximity to inoculum sources such as infected volunteer plants or alternative hosts.

Limitations and Future Directions

Despite their utility, extended SIR models for agricultural systems face several limitations. First, homogeneous mixing assumptions underlying ODE-based models are violated in structured crop systems where plants occupy fixed positions in rows and fields, limiting pathogen contact to neighbours. Agent-based models and network models that represent individual plant spatial relationships may better capture short-range epidemic dynamics but require substantially greater computational resources and data inputs.

Second, parameter uncertainty particularly in β and σ, which vary with genotype, environment, and pathogen race limits the precision of epidemic forecasts. Ensemble modelling approaches that propagate parameter uncertainty through multiple models runs and report probabilistic forecasts (rather than single deterministic trajectories) are increasingly recommended for operational disease warning systems. Third, most SIR models treat pathogen evolution as static, whereas in reality, pathogen populations evolve rapidly in response to host resistance genes and fungicide exposure. Eco-evolutionary SIR extensions that couple within-season epidemic dynamics with between-season pathogen population genetics are an active research frontier.

Future directions include the integration of machine learning (particularly deep learning applied to satellite time series) with mechanistic SIR models in hybrid architectures that retain physical interpretability while improving predictive accuracy. Climate change scenario modelling using extended SEIR frameworks will be critical for anticipating shifts in disease risk zones and developing climate-resilient crop variety deployment strategies. Finally, real-time integration of ground sensor networks, citizen science disease reporting, and SIR model outputs into decision support platforms accessible via mobile applications represents a high-priority pathway for translating these advances into farmer-level impact.

Conclusion

Extended SIR models — encompassing SEIR, SIRV, vector-host coupled, and spatiotemporal PDE formulations — provide a rigorous, flexible, and increasingly data-rich framework for understanding and managing crop disease and pest outbreaks in agricultural systems. From wheat rust in South Asia to citrus greening in Florida and locust invasions across Africa, these models have demonstrated their capacity to generate actionable insights for disease management timing, pesticide optimization, regulatory policy design, and early warning system development. The convergence of mathematical epidemiology with remote sensing, GIS, climate science, and machine learning is rapidly expanding both the spatial scale and predictive horizon of these tools. As food security pressures mount in the face of climate change and growing global population, investment in agricultural disease modelling infrastructure including long-term epidemiological datasets, model validation programs, and farmer-facing decision support tools will be essential for protecting crop yields and sustaining agricultural livelihoods worldwide.

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