26th International Congress on Modelling and Simulation, Adelaide, SA, Australia, 30 Nov–4 Dec 2025
mssanz.org.au/modsim2025

A Systematic Review of Quantitative Models for African Swine Fever: Diversity Across Host and Environmental Drivers

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Abstract: African swine fever (ASF) is a severe viral disease for swine with major economic and food security impact. Transmission occurs through direct pig-wild boar contact and environmental persistence, underscoring the need to model host and environmental drivers. This study aimed to systematically review quantitative modelling approaches for ASF, providing guidance on method selection and ultimately strengthening the evidence base for transmission dynamics and intervention planning. We conducted a PRISMA-guided systematic review of mechanistic, statistical and machine-learning models investigating ASF through 2024. Of 5,690 records, 151 studies met inclusion criteria. Mechanistic (54%) and statistical (40%) approaches dominated, whereas machine learning was infrequently used (9%). Most common objectives were identifying risk factors and evaluating control strategies, with publications concentrated in Europe and Asia and from 2020 onwards. Predictors considered were mainly environment and geography (e.g. climate, landscape) and animal and farm demographics (e.g. pig density, number of farms). Hierarchical Clustering on Principal Components of study features revealed three method-objective-geography clusters. A key gap is the narrowly scoped use of machine learning, limiting its applications in forecasting and intervention evaluation. This review highlights the need to expand innovative approaches, particularly machine learning, to strengthen ASF forecasting, prevention, and control.

Keywords: *African swine fever, infectious disease modelling, mechanistic, statistical, machine learning*

1. INTRODUCTION

African swine fever (ASF) is a highly contagious, often fatal disease of domestic pigs and wild boar, causing severe socio-economic and food-security impacts worldwide (Dixon et al., 2019). Transmission occurs through direct contact between domestic pigs and wild boar and persistence in the environment, including carcasses and fomites (Blome et al., 2020). Modelling has been widely used to investigate transmission dynamics and inform control strategies, yet no comprehensive synthesis of the modelling approaches and its predictors exists. This study aimed to systematically review applications of mechanistic, statistical, and machine learning approaches to ASF, characterising their objectives and predictors to strengthen the evidence base for host–environment transmission dynamics and intervention planning. By mapping the methodological landscape and linking approaches to questions, the review highlights current practice, identifies gaps, and provides guidance for method selection in future epidemiological studies and control strategies.

2. METHODOLOGY AND RESULTS

We conducted a PRISMA-guided systematic review to investigate mechanistic, statistical, and machine-learning approaches used to model ASF, addressing two key questions: First, how have patterns of use of the modelling techniques changed over time and across geographic regions? And second, what modelling objectives and predictors have been examined across different techniques?

We searched PubMed, Embase, Web of Science and Scopus for all peer-reviewed journal articles written in English and published up to 2024. Of 5,690 records found, 151 papers were retained after removing duplications and screening for inclusion and exclusion criteria.

Most studies used mechanistic (82/151, 54.3%) or statistical (61/151, 40.4%) methods, while relatively few applied machine learning (14/151, 9.3%). The majority examined ASF spread in Europe (70/151, 46.4%) and Asia (41/151, 27.2%). All but one were published from 2011, with a notable increase from 2020 onward as the disease spread from Europe to Asia.

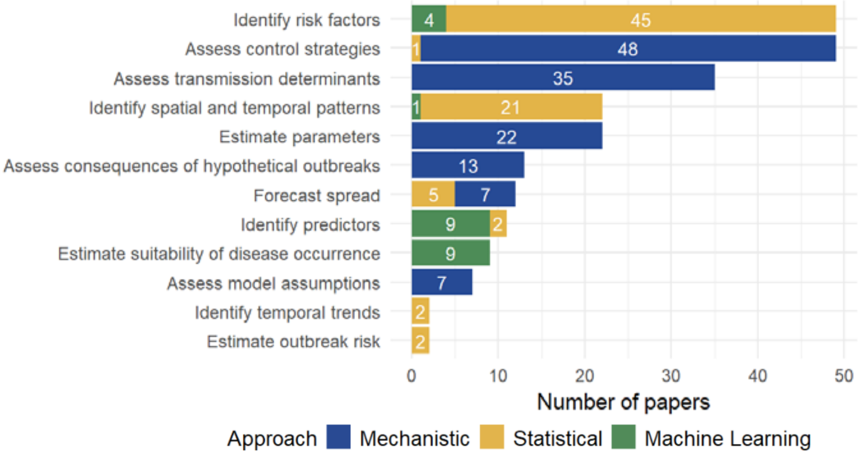

Figure 1. Number of studies addressing each modelling objective by approach.

The models addressed 12 distinct objectives, each preferentially analysed by specific approaches (Figure 1). Mechanistic models most often assessed control strategies (48/82, 58.5%) and transmission determinants (35/82, 42.7%) via simulation, enabling exploration of dynamic interactions of hosts, environments, and interventions across time and space. Statistical models primarily identified risk factors (45/61, 73.8%) and spatiotemporal patterns (21/61, 34.4%) using historical data, providing evidence of host- and environment-related drivers of spread across different settings. Machine-learning studies commonly estimated suitability of disease occurrence (9/14, 64.3%) and identified associated predictors (9/14, 64.3%), highlighting key host and environmental features linked to ASF presence. The variables considered as modelling predictors can be grouped into six categories, with environmental and geographic data (e.g., climate, landscape) and animal and farm demographics (e.g., pig density, number of farms) most commonly used.

To identify method-objective-geography-year clusters across studies, we applied hierarchical clustering on principal components (HCPC) using factor analysis of mixed data (FAMD) to accommodate mixed variable types. Three main clusters were identified:

- Cluster 1 – Mechanistic studies assessing control strategies and transmission determinants in simulated or non-specific settings.
- Cluster 2 – Statistical studies identifying risk factors and spatiotemporal patterns in Europe and Africa.
- Cluster 3 – Machine learning papers estimating suitability of disease occurrence and identifying predictors in Asia and the world.

Mean publication year was similar across clusters (Cluster 1: 2021; Cluster 2: 2020; Cluster 3: 2021; Kruskal-Wallis K = 1.38, p = 0.5022).

3. CONCLUSIONS

This review demonstrates that robust modelling is critical for understanding host and environmental drivers of ASF spread, and for designing control strategies to mitigate its economic and food-security impacts. Method choice depended on the modelling objective, with approaches and predictors applied to specific questions. Publication timing and geography coincide with ASF temporal and spatial spread. Barriers include limited data in vulnerable regions and uneven geographic representation. Machine learning remains underutilised and narrowly applied, limiting its role in forecasting and evaluating intervention. Given the continuing burden of ASF, sustained interest in modelling is expected to refine inference on transmission drivers and guide control design. This review underscores the need to expand innovative approaches, particularly machine learning, to strengthen ASF prevention and control.

ACKNOWLEDGEMENTS

Kim Dianne Ligue-Sabio is a recipient of the John Allwright Fellowship funded by the Australian Government through the Australian Centre for International Agriculture Research and the Philippine Government through the Department of Science and Technology Science Education Institute and Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development.

REFERENCES

Blome, S., Franzke, K., Beer, M., 2020. African swine fever - a review of current knowledge. Virus Res. 287, 198099. https://doi.org/10.1016/j. virusres.2020.198099.

Dixon, L.K., Sun, H., Roberts, H., 2019. African swine fever. Antivir. Res. 165, 34–41. https://doi.org/10.1016/j.antiviral.2019.02.018.