

# Design of a Simulation Model for the Diagnosis of Classical Swine Fever Virus in Ecuadorian Farms

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*Abstract:* - Classical swine fever (CSF) is a disease that slows down animal production and international trade; therefore, its identification is key in pig farms to take the relevant health measures. Therefore, the objective of this research was to design a Susceptible-Exposed-Infected-Recovered (SEIR) simulation model to carry out epidemiological modeling for the identification of outbreaks of classical swine fever in the Sierra Region of Ecuador, using Python software and historical data on incidences of this disease in the provinces of the Ecuadorian highlands, considering the variables pig population, initial number of exposed pigs, initial number of infected, number of pigs removed, contagion rate ( $\alpha$ ), transmission rate ( $\beta$ ), and recovery rate ( $\gamma$ ). The results show that the SEIR model allowed us to determine that the population of susceptible (healthy) pigs decreases over time until reaching zero. This decrease in susceptibility occurred during the first 15 days, which shows that this is the time necessary to infect the entire population with an infected person. Therefore, the exposed population increases during the 15 days that the total infection process lasts and then decreases. It is also identified that throughout these five years of analysis of the past, it has been increasing from 2015 to 2019, which hurt the yields and productivity of pig farms in the Ecuadorian mountains.

*Key-Words:* - Epidemiology, infestation, modeling, prevention, health, classical swine fever.

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## 1 Introduction

Pig farming in Ecuador represents an important economic sector, comprising a mix of small traditional family units, industrial production, and a culture of high pig consumption, [1]. However, the presence of diseases such as classical swine fever (CSF), which hampers animal production and international trade [2], poses a significant challenge. In essence, classical swine fever was first reported in Ecuador in the 1940s and has since caused significant losses to the national swine industry due to its high morbidity and mortality rates, ranging between 40% and 60%, particularly in the Sierra and Coast regions, [3]. The causative agent is the classical swine fever virus, a small enveloped RNA virus of the genus Pestivirus.

The consequences of a CSF epidemic would be serious, so it remains crucial to analyze the behavior of the disease [4] as well as simulate different scenarios for the control of classical swine fever outbreaks. The control of classical swine fever represents an essential context for guaranteeing the sustainability of swine production systems. Thus, the implementation of disease management and control plans is an indispensable part of any program aimed at its containment. In addition to being able to understand the progression of the disease in various conditions as crucial data to manage effective management, in this context, simulating the evolution of the disease is advantageous when controlling swine fever, [5]. This, in turn, facilitates better planning and contributes to the macroeconomic indicators of any country, as well as health and disease management.

A very effective technique to study the spread of infectious diseases arises through the use of mathematical modeling, which allows epidemiological factors to be used at the sample level to predict epidemic dynamics at the population level. Currently, mathematical models serve as a fundamental tool for the study of infectious diseases, identifying how control strategies can modify the dynamics and epidemiology of these diseases, [6].

Using modeling as a tool can facilitate the visualization of the different scenarios that may arise and provide the most appropriate solutions for each case and location. [7], have highlighted the laudable work of simulating the spread of the CSF virus on farms in the Ecuadorian Sierra, with the contribution of relevant information to explore specific surveillance and control strategies for this disease.

Among the diversity of models, there are those with a deterministic component, in which it is explained that inputs will invariably produce the same results without considering the existence of chance or the uncertainty principle. In this scenario, it is closely related to the creation of simulated environments to study hypothetical situations. As a result, these models do not take into account the uncertainty of disease spread, [8]. On the other hand, a model considered stochastic tends to assume variable behavior resulting from a phenomenon that guides random data and where the relationships between variables are determined by probabilistic functions. Therefore, these models incorporate the stochastic component, which turns out to be computationally expensive and has a greater degree of difficulty when analyzing the structure and corresponding findings.

Contributing to the implementation of an approach to the situational phenomenon that occurs in the Sierra region of Ecuador is following the relevance of other similar studies. An example is the one developed by [9], which reflected the success of the use of stochastic SEIR models due to their ability to simulate the evolution of infectious diseases within a farm. This study was carried out in 2018 and focused on "Assessment of the risk of livestock epidemics through a mathematical simulation" coupled with the use of a Be-FAST model, which represents a computer program built on a mathematical model of spatiotemporal stochastic propagation to investigate the transmission of infectious livestock diseases within and between farms. The study concludes by quantitatively describing the possible spread of

diseases that can have serious consequences in the respective countries.

The reality of the context implies heteroskedasticity in the way the phenomenon evolves; in this sense lies the importance of the present study of expanding and evaluating the conditions of outbreaks of classical swine flu in the Sierra region of Ecuador and the usefulness of the model SEIR to adjust scenario simulations that allow a situational diagnosis on farms in Ecuador. In essence, the objective was to design a Susceptible-Exposed-Infectious-Recovered (SEIR) simulation model for the spread of the CSF virus in farms in the Sierra region during the period 2015-2020, whose findings should contribute to farm owners farms and improvements in the population that are economically dependent on pig farming activities, both directly and indirectly. In addition, it can benefit consumers since it seeks to ensure the quality of the meat ready for consumption.

The usefulness of this model lies in its ability to quickly identify outbreaks of classical swine fever. As well as being able to analyze farm data, such as the presence of symptoms in pigs, mortality, and laboratory test results, to detect possible CSF outbreaks early. In addition, the designed SEIR model can simulate different control scenarios for classical swine fever, such as vaccination, sacrifice of infected animals, and movement restrictions, to evaluate effectiveness in reducing the spread of the aforementioned disease.

## 2 Materials and Methods

### 2.1 Type and Design of the Research

The research has an exploratory, descriptive, prospective, and non-experimental scope. It is exploratory because it seeks to understand everything related to CSF and explore historical databases of disease incidence in the provinces of the Sierra region, which will feed information to the SEIR model. The descriptive scope comes into play through the analytical method used to understand and investigate the functioning of the SEIR model. The study is prospective since it predicts the behavior of the disease based on the characterization, description, and operation of the model. Finally, it is non-experimental since it involves investigating and analyzing previously obtained data to feed the mathematical model.

### 2.2 Research Methods

In this research, both deductive and analytical methods were applied. In the deductive method, the

research approach involves studying and analyzing previous work related to the topic, reviewing existing theories about the phenomenon under study, and then testing the hypotheses that arise from those theories. Start with a general statement or hypothesis and examine the possibilities of reaching a specific logical conclusion. This method uses deduction to test hypotheses and theories, which predict specific outcomes if they are correct.

### 2.3 Research Approach

This research applies both qualitative and quantitative approaches, combining them to obtain results on variables and their effects on a specific population. In this way, the best methodology for calculating an SEIR simulation model for the spread of the CSF virus on farms in the Sierra region is analyzed and determined.

### 2.4 Study Population and Sample Selection

For this study, the population of vaccinated pigs from family farms in the Sierra region was used. Non-probabilistic convenience sampling was used because a specific affected population of pigs (from the Sierra region of Ecuador) was selected for the study.

### 2.5 Data Collection Techniques and Instruments

During the data collection process, the data source used for the epidemiological modeling of the SEIR model for CSF outbreaks in the Sierra region of Ecuador came from the database of the Agrocalidad Ecuador system. The data includes records of positive cases corresponding to vaccinated, slaughtered, and quarantined pigs for CSF in the Ecuadorian Sierra.

### 2.6 Data Simulation

The method is based on the construction of a model consisting of the formulation of systems of differential equations that show at a graphic level the behavior and evolution of the epidemiological phenomenon (the spread of the classical swine flu). A SEIR model was used, which is an extension of the SIR (Susceptible, Exposed, Infected, and Recovered) model. It adds a compartment of the population that has been in contact with an infected animal, becomes infected, and enters a period of latency (where it shows no symptoms) before becoming infectious (Figure 1). The states considered for this model are healthy and susceptible to infection (S), exposed (E), infectious (I), and recovered from the disease or eliminated (R). The state transition sequence is as follows:

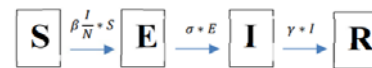


Fig. 1: Diagram of the SEIR model

The interpretation of the dynamics of convergence between states or compartments in the SEIR model is as follows: fraction of the host pig population that is susceptible to infection (S), fraction of pig species infected but not yet transmitting the infection to other animals during the latency period (E), fraction of infected porcine species that can transmit the infection (I), and fraction of recovered porcine species that acquire temporary or permanent immunity (R).

In terms of this dynamic, the flow in the spread of the CSF virus is defined using a system of ordinary differential equations to adjust the modeling of the phenomenon of interest for a fixed population (10,000 swine species):

$$N=S+E+I+R \quad (1)$$

$$ds / dt = \mu *(NS) - \beta *((SI))/N - vS \quad (2)$$

$$dE / dt = \beta *((SI))/N - (\mu + \sigma)*E \quad (3)$$

$$dI / dt = \sigma E - (\gamma + \mu)YO \quad (4)$$

$$dR / dt = \gamma I - \mu R + vS \quad (5)$$

Where  $\mu$  is the mortality rate in the population (not related to the disease),  $\beta$  is the effective contact rate a parameter that controls the frequency with which contact of the susceptible swine species results in a new exposure, resulting in infected at a  $v$ , which represents the vaccination rate, if there is a supply of a vaccine (in this case assumed to be zero),  $\sigma$  is the rate at which an exposed individual becomes infectious, and  $\gamma$  is the rate at which that an infected individual recovers and becomes resistant. This model considers a priori that it tends to handle a constant value (10,000 porcine species) for the population under study as an initial condition, based on the information obtained from the Con case records. With this information, parameters such as the fatality rate are determined, which is low for this phenomenon in the evaluation of the CSF virus for the highland region of Ecuador. This indicator of the fatality rate is considered low due to the control strategies that have been implemented, compared to the limitations in the control of other diseases that occur in other affected animal species within the Sierra region. In essence, it has been determined that all infected pig hosts have a high probability of acquiring immunity.

### 2.7 Design of the SEIR Model in Python

To develop the SEIR model, the parameters to be used and their respective formulas are first determined. It is necessary to use the infection data registered in the Ecuadorian Sierra region to determine the required rates by using the following formulas:

$$\text{Tasa de infección } (\beta) = \frac{\text{Total de positivos}}{\text{Población total} \times \text{T tiempo de observación}} \quad (6)$$

$$\text{Tasa de incidencia } (\sigma) = \frac{\text{Total positivos}}{\text{Población total}} \quad (7)$$

$$\text{Tasa de recuperación } (\gamma) = \frac{\text{Total en cuarentena} - \text{Total sacrificados}}{\text{Población total}} \quad (8)$$

After defining the system of differential equations and the formulas that determine the required rates, the Euler algorithm is formulated in Python to solve the differential equations in the model. To do this, initial population data, time, and rates of infection, incidence, and recovery entered by the user are used. The Python programming language is used, using Visual Studio Code version 1.72, and the necessary libraries for the development and compilation of the programming were downloaded, including in this case the "matplotlib" library.

Once the code to solve the differential equations using the Euler method is completed, the graphical user interface (GUI) of the program is designed for user interaction to obtain a friendly environment for handling the present study. The "tkinter" tool was used to create spaces and buttons for the program interface.

## 3 Results

### 3.1 Analysis of CSF Infection Data to Determine Its Feasibility of Use in the Susceptible-Exposed-Infectious-Recovered (SEIR) Model

Based on data from the Animal Health Surveillance Office (SIZSE) [10], Table 1 shows the number of pigs in the Sierra region that tested positive for CSF infection, the number of those slaughtered, and the population registered for each year.

In Table 1, it can be seen that positive cases of CFP have been increasing from 2015 to 2018. However, from that year onwards, there has been a decrease in positive cases until 2020 (Figure 2). Which coincides with a lower pork production rate as a result of the COVID-19 pandemic.

Table 1. Historical Data on the Spread of Classical Swine Fever in the Sierra Region, Ecuador. Period 2015-2020

Years	Positives		sacrificed		Population	
2015	79	18.54%	48	11.27%	426	100.00%
2016	76	15.87%	180	37.58%	479	100.00%
2017	30	25.64%	8	6.84%	117	100.00%
2018	54	21.43%	17	6.75%	252	100.00%
2019	28	13.33%	7	3.33%	210	100.00%
2020	21	23.86%	6	6.82%	88	100.00%

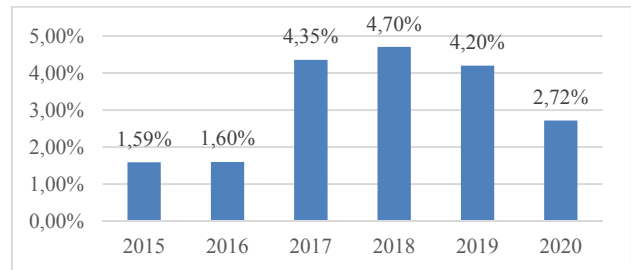


Fig. 2: Positive cases of classical swine fever in pig farms in the Ecuadorian Sierra. Period 2015-2020

Classical swine fever cases more than doubled between 2017 and 2019 compared to previous years (Figure 1). Furthermore, the data show that the percentage of pigs slaughtered in 2016 increased significantly (Figure 3). This could be due to poor disease control during that period. Starting in 2017, the percentage decreased, and there was a slight increase in cases in 2018. Finally, a decrease in sacrifices is evident until 2020.

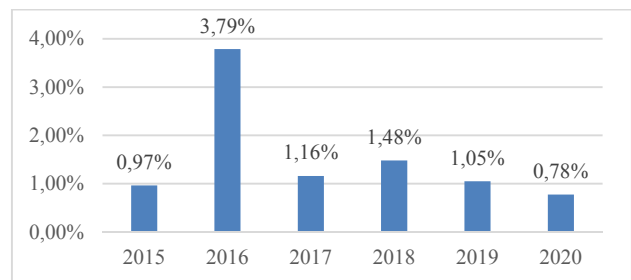


Fig. 3: Cases of pigs slaughtered due to classical swine fever in pig farms in the Ecuadorian Sierra. Period 2015-2020

The number of pigs in quarantine increased from 2015 to 2019, indicating better control of the disease (Figure 4). However, in 2020, the number of pigs in quarantine decreased, in parallel with a decrease in yields, due to the health restrictions imposed by COVID-19, which affected pig production.

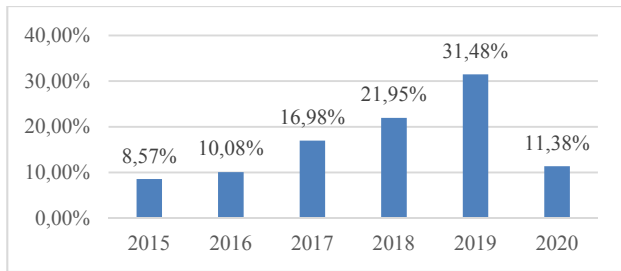


Fig. 4: Cases of pigs in quarantine due to classical swine fever in pig farms in the Ecuadorian Sierra. Period 2015-2020

### 3.2 Estimation of Population Parameters of the Susceptible-Exposed-Infectious-Recovered Epidemiological Model

Table 2 shows the dynamics of growth and decline in transmission rates throughout the study period. It indicates that in 2019, the transmission rate was the lowest compared to other years, while in 2018, the highest transmission rate was observed.

Table 2. Annual transmission rate of classical swine fever (CSF) in pig farms in the Ecuadorian Sierra. Period 2015–2020

Year	Transmission Speed	Population
2015	0.569	426
2016	0.454	479
2017	0.572	117
2018	0.613	252
2019	0.383	210
2020	0.581	88

Table 3. Maximum peak for developing classical swine fever (CSF) infection in pig farms in the Ecuadorian Sierra. Period 2015-2023

Year	Maximum Peak Day
2015	fifty
2016	59
2017	41
2018	44
2019	59
2020	40
2021	41
2022	48
2023	fifty
Maximum value	59
Minimum value	40
Average	48

During the period 2015–2023, it was shown that in pig farms in the Ecuadorian highlands, the CSF virus takes a minimum of 40 days to reach its peak of contagion, an average of 48 days, and a maximum of 59 days (Table 3). Therefore, when an initial sign of CSF infection is determined in a pig,

there is a period of less than 40 days to implement infection containment strategies in other pigs.

### 3.3 Estimation of the Areas Most Affected by the Classical Swine Fever Virus in the Sierra Region during the Period 2015-2023

The analysis of data disaggregated by canton determines that there is a peak in spikes in CFP contagion in Quito (43%) and Zapotillo (21%) of the Sierra in the Republic of Ecuador. In addition, it is necessary to note that the trend in the prevalence of positive cases of CPP decreased during the coverage period of 2020-2022, a prominent situation resulting from quarantine restrictions and a reduction in mobilization dictated by public health policies to mitigate the spread of SARS-CoV-2. The cantons of Quito, Chillanes, Guaranda, and Loja, in the Ecuadorian Sierra region, recorded the highest numbers of CSF cases (Figure 5).

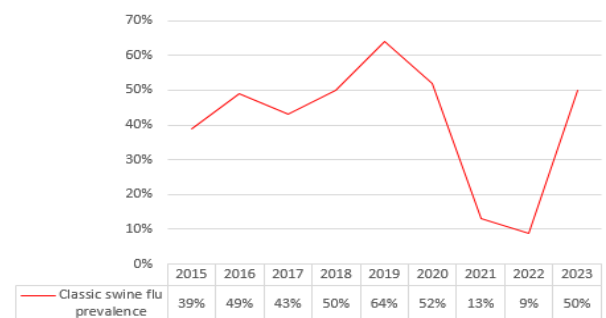


Fig. 5: Trend in annual prevalence of CSF in pig farms in the Ecuadorian Sierra

In 2016, the cantons of Quito and Guaranda reported the highest number of CSF cases, comprising 32% and 17%, respectively. In 2017, the cantons of Quito and Pelileo recorded the highest number of CSF cases, representing 23% and 20%, respectively. When describing the behavior in 2018, the cantons of Cumandá and Guaranda registered the highest number of CSF cases with percentages of 30% and 20%, respectively. In 2019, the cantons of Quito and Zapotillo had the highest number of CSF cases, representing 43% and 21%, respectively. Finally, in 2020, the cantons of Chillanes and Sevilla de Oro registered higher cases of CSF, with percentages of 33% and 19%, respectively. In 2021, the behavior will be reduced to 13 only in the Loja canton. However, as shown in Table 4, for the year 2022, there is only a 9% prevalence in the Echeandia canton and other new records of CFP cases for the Sierra region of Ecuador in the year 2023 within the Cañar cantons (20%), Troncal (23%), and Caluma (7%).

These findings express that the phenomenon that governs the presence of PCC cases represents a fortuitous behavior in the distribution in each of the cantons located in the Sierra region of the Republic of Ecuador. This demonstrates significant variability in the cantons with the highest number of positive CSF cases, ranging between a minimum of 11% and a maximum of 43%. The canton of Quito appeared in most years, leading the statistics. This fact could be related to greater economic activity with geographic interaction that defines the location of a greater number of pig farms in that region, which increases the risk of transmission. Greater economic activity and the greater number of pig farms may contribute to more interactions between pigs in a susceptible state and those moving to an infected state, leading to a higher rate of virus transmission in that area.

Table 4. Percentage prevalence of classical swine fever (CSF) by cantons

Canton	Annual prevalence percentage									
	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Quito	15%	32%	23%		43%					
Loja	13%						13%			
Lacatunga	11%									
Guaranda		17%		20%						
Pelillo			20%							
Cumanda				30%						
Slipper					21%					
Chillanes						33%				
Golden Seville						19%				
Echeandia								9%		
Cañar									20%	
The Trunk									23%	
Caluma									7%	

## 4 Discussion

The results found in this study agree with the data reported in previous studies that show a prevalence of the CSF virus in Ecuador in different demographic regions. For example, in 2010, the prevalence was 0.169%; in 2012, it was 0.14%; in 2013, it was 0.18%; in 2014, it was 0.078%; and finally, in 2015, it was 0.89%. These findings align with what was reported in 2020 by the World Organization for Animal Health (WOAH), establishing that this disease is present in four countries: Colombia, Brazil, Ecuador, and Peru. The presence of classical swine fever in several

countries makes it difficult to achieve its eradication, [11].

Following this context, the study by [12] is cited, which, under a descriptive research methodology based on the application of structured surveys, showed, as a result of a prevalence of 7% of the CSF virus during the years 2014 to 2021, a significant reduction in pork production in the Carlos Julio Arosemena Tola canton, Napo province, Ecuador. In contrast, the reality situation in the Ecuadorian Sierra region, which constitutes the approach to the problem in its 12 provinces, is compared with the statistics of recent years, which indicate a moderate prevalence of the CSF virus in its different farms within the region. Sierra region.

In general terms, significant findings from the study are presented that allow us to assume an increase in positive cases of CSF until 2018, followed by a decrease until 2020 due to the increase in the number of pigs in quarantine expected until 2019, coinciding with a decrease in positive cases in 2020. Therefore, the lowest rate of spread of the CSF virus in swine animals occurs due to the conditions of restrictions on movement and quarantine resulting from the COVID-19 pandemic. This refers to the effectiveness in the use of control and quarantine measures. In comparison with the presentation of variable behavior in the annual PPC transmission rates, presenting the lowest rate in 2019 and the highest in 2018, this reality allows us to raise questions about the factors that influence the fluctuation of the spread of the disease in swine animals. The parameters estimated in the SEIR model indicate that the estimated time of at least 40 days for the CSF virus to reach its peak of contagion is crucial for the timely implementation of containment strategies. Furthermore, the results lead to establishing an average of 48 days and a maximum of 59 days for the active evolution of the disease in swine animals.

Between 2017 and 2019, there was a doubling of cases of classical swine fever due to the measures implemented in 2016 related to a high percentage of pigs slaughtered. Cantons most affected by the Classical Swine Fever virus are Quito and Zapatillo, with spikes in contagion in other cantons over the years. This phenomenon is attributed to the greater economic activity and number of pig farms found in Quito; the above is a factor related to the prevalence of CSF cases in that region. It would be appropriate to explain in future research the economic and geographic impact of the disease and the possible reasons behind these disparities. These findings show the importance of control and surveillance of classical swine fever in the Sierra region of Ecuador

to mitigate the spread of the virus and protect swine production.

The contributions of this study on classical swine fever in the Sierra region of Ecuador during the period 2015-2023 compared to previous works present in the literature are mainly related to the management of updated and specific data on the incidence of classical swine fever PPC in the Sierra region of Ecuador for an extended period. Which tends to enrich the existing literature with relevant and recent information. In addition, obtaining detailed analysis of trends in positive cases, transmission rates, and impacts on control measures implemented in a specific context represented by the Sierra region of Ecuador. The construction of the SEIR model, it was focused on the estimation of population parameters in a specific territorial context to enrich the understanding of the dynamics of the disease and cognitive competencies at the level of epidemiological and veterinary literature.

The generalizability of the findings of this study on classical swine fever in the Sierra region of Ecuador to other contexts may vary depending on several factors. In this sense, each territorial context is conditioned at an epidemiological, geographical, and production management level. Therefore, this implies controlling local variables and variables on the virulence of the virus strain, the immune response of the animals, and the effectiveness of the control measures implemented. Ultimately, each model must be built under the criteria inherent to the phenomenon under study in the territorial space that defines it. However, the findings preserve the principle of comparability granted by the methodology in the construction of SEIR models.

The increasing prevalence of classical swine fever in the Sierra region of Ecuador can be attributed to several factors, including the movement of infected pigs, the implementation of inadequate biosecurity measures on pig farms, and a lack of effective control and surveillance measures. This high prevalence translates into the transfer of pig animals that are in a state of infection with the disease within the territory of the Sierra region, added to the uncertainty caused by the limitations in the application of detection tests, which causes a greater level of risk in the event of possible contagion. In addition, it is annexed that it is unlikely to implement strategies for management and control in biosafety and quarantine measures to correct and contain the spread of the virus in the pig population that lives on the different farms in the Sierra region of Ecuador.

To mitigate the implications inherent in the spread of classical swine flu, it is essential to

implement comprehensive control and prevention strategies, including strict biosecurity and quarantine measures at the territorial level within pig farms. Another key factor is detecting the evolution of the virus within the litter of animals in advance and achieving notification of positive cases to official entities. At the same time, achieving the promotion of vaccination programs with collaboration between government authorities, veterinarians, and pig breeders will effectively reduce the impact of this disease on the pork industry in the Ecuadorian Sierra.

The management and control of classical swine flu as an endemic disease represents a fundamental approach due to the considerable impact it causes on the economy of Ecuador, and even more so when the number of positive cases increases within pig farms in the Sierra region. The consequences and impacts of this disease are focused on the increase in the rate of morbidity and deaths in pigs. In this order, the occurrence of strong economic losses is emphasized both for large pig producers and for those where breeding is family or micro-enterprise, with absolute predominance in backyard and family pig breeding, [4]. Consequently, this impacts the consumption and export of pork resources, [13].

In response to this challenge, to control and eradicate this highly contagious viral disease that affects both domestic and wild pigs, Ecuador has implemented a classical swine flu control and eradication project since 2012. However, the current situation describes the non-existence of any experimental design that is decisive in controlling or reducing the spread of the disease. It has been a specific strategy to develop vaccination processes as a preventive mechanism since 2016 for pigs over 45 days old, [14].

Despite these efforts, there is a considerable prevalence and transmission rate of classical swine fever in the territory of the Sierra region of Ecuador. This scenario assumes it is vital to generate constant surveillance mechanisms, implement detection days, and evaluate measures to generate immediate responses to situations of exponential spread and contain the different infection states of classic swine flu. The formulation stage of projects involved in the control and mitigation of classical swine fever in the Sierra region must require a comprehensive and multidisciplinary approach to include the best practices of biosecurity, quarantine, and research on the evolution of the phenomenon. Indeed, a link between government authorities, veterinarians, and pig farmers must be assumed to propose public policies conducive to protecting the pork industry,

and public health, and consolidating the capacity to market pork products in international markets.

It has been evident that within the vaccination process and implementation of sanitary measures as a control mechanism for classical swine flu in the Sierra region of Ecuador, the results indicated that for the year 2019, the notification of 523 cases of classical swine fever was achieved in 13 provinces of Ecuador. In this context, the empirical evidence provided by laboratory tests validated the presence of 100 positive cases of classic swine flu, and the remaining 423 cases showed negative results. At the territorial level, it was the provinces of Morona Santiago and Los Ríos that had the highest number of confirmed cases, followed by the provinces of Pichincha and Zamora Chinchipe. Regarding vaccination, 1,649 establishments (95%) applied some type of vaccine, while the remaining 5% did not apply any. These vaccination data related to classical swine fever are important for consideration in the control and eradication programs of this disease. Countries that have successfully eradicated classical swine fever have often relied on mass vaccination programs, [15].

Despite the positive cases observed in the Ecuadorian Sierra, the results showed that 85% of the 5,000 simulations resulted in the non-spreading of classical swine fever (i.e., 85% of intentionally infected farms did not further spread the disease). Specifically, only 73 of the backyard farm simulations affected other farms. The spread of the disease was mainly local, with an average number of infected districts equal to 4 and an average distance from the source of infection to the infected farm of 4.5 km. In such scenarios, vaccination could be considered a strategy. Regions where the disease remains endemic have used live attenuated vaccines to limit the effects of the disease or as a first step in a comprehensive program for the control and eradication of the virus, [16]. The implementation of targeted vaccination programs in areas with a higher prevalence of classical swine fever could effectively reduce the transmission and impact of the disease.

As mentioned above, the most critical factor for the spread of the epidemic between farms is local infection that occurs in nearby farms. The study also describes control measures that, as demonstrated in this work, effectively stop the spread of the disease. The study concludes that carrying out simulations is of great value for making decisions that improve prevention and control programs since they help determine the most appropriate course of action according to the specific scenario.

The choice of models depends on the transmission characteristics of the disease. In this

case, the SEIR model aligns well with the epidemiology of the disease in the Ecuadorian Sierra. Stochastic models, such as the Be-Fast model, are used to simulate the spread of diseases between farms, [9]. However, these models may not be suitable for evaluating the behavior of large populations in response to suggested state changes, where deterministic models based on dynamical systems are more appropriate. These deterministic models evaluate changes in the states of a population and are suitable for evaluating viral diseases, such as those used during the COVID-19 pandemic, [17], [18]. The use of adequate modeling is essential to explain, understand, and manage the processes that establish the dynamics for the spread of diseases in swine animals, as well as to apply the appropriate control strategies in the specific territorial context in which they occur.

## 5 Conclusions

The findings in the present study have been decisive in affirming that the Sierra region of the Republic of Ecuador has shown significant variability in cases of classic swine flu in the last eight years. Quito is the canton that leads the statistics due to the increase in economic activity and the proximity of pig farms, which increase the risk of transmission of the virus. However, during the year 2020, a fortuitous event occurred that reduced the amount of contagion, which translates into travel limitations due to the danger of contagion of COVID-19 in the Ecuadorian population.

By considering the data collection process and constant monitoring of the phenomenon associated with classic swine flu to be relevant to form reliable data and information necessary to define a decision-making process in line with the existing reality, This line of recommendation has been supported by the events that have arisen in the health emergencies of the human race worldwide, where the process of control and management of timely and reliable information on the COVID-19 pandemic managed to successfully contain the spread of the disease.

In addition, it is necessary to consolidate a control process with the establishment of specific measures to guarantee accurate monitoring and records of the cases raised for this type of disease in pigs to formulate appropriate control strategies for the protection of the health of both human beings and animals. In this context, the findings are relevant to channel decision-making processes within disease prevention and management programs in the Republic of Ecuador, consolidating adjusting strategies at the official level to the



circumstances and challenges of the phenomenon of interest. This will translate into greater capacity within the Ecuadorian swine industry to resist and mitigate the impacts of classical swine fever based on continuous monitoring and adaptation of public policies.

In conclusion, the compilation of data recorded on cases of classical swine flu must allow the parameters of the SEIR epidemiological model to be adequately estimated and defined in terms of the rate of infection, transmission, and recovery of pigs. This estimation of parameters has considered the animals in a state of quarantine, those that have been sacrificed, and includes the interrelation between the specific population of pigs and the level of infection within the territory that makes up the mountains of Ecuador. For this model, the values of  $\alpha = 0.01$ ,  $\beta = 0.003$ , and  $\gamma = 0.01$  were used.

The SEIR model shows how diseases spread over time among the pig population. It is demonstrated that the number of susceptible (healthy) pigs will eventually drop to zero. This decline in susceptibility happens within the first fifteen days, which is the amount of time needed for the illness to propagate and infect every susceptible individual, beginning with one diseased pig. The number of exposed pigs grows throughout this time as more of them contract the virus, and it progressively declines as the infection worsens or the animals recover.

The number of infected pigs grows somewhat over time, suggesting that the population is still being spread. As some affected people finally recover from the illness and develop immunity, the number of recovered pigs is also rising. The swine population's infection and recovery patterns, as well as the dynamics of illness, are all well-represented by this SEIR model.

To monitor the process with a minimum level of risk that leads to effectively restricting the spread of the disease, it is vital to implement control techniques and methods to contain the infection dynamics that occur in the swine population of the Sierra region in Ecuador. To do this, it is necessary to manage the knowledge of the inherent characteristics of the aforementioned population through behavior analysis, leading to the prediction of future events assuming the implementation of focused preventive strategies and adequate control aimed at reducing or mitigating the impact of the disease in the industry swine in the Sierra region. Being vaccination program-specific, one of the improvement strategies consists of the use of biosafety procedures with the early identification and isolation of sick animals to stop the spread of

the implications for classical swine virus infection. In definitive terms, SEIR modeling is the basic tool for decision-making and improving disease prevention methods in the context of classical swine flu on farms in the Sierra region of Ecuador.

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