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Logistic Regression Analysis Of Risk Factors Associated With The Emergence And Spread Of Highly Pathogenic Avian Influenza (Ah5n1) In Poultry Farms In Latacunga Canton, Cotopaxi Province – Agrocalidad

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Abstract: *Highly Pathogenic Avian Influenza (HPAI) A(H5N1) clade 2.3.4.4b has become one of the most significant threats to global poultry health. This study identifies risk factors associated with its presence in commercial poultry farms in the Latacunga canton, Ecuador, through the evaluation of 55 variables grouped into four key categories: Sanitary Management, Environmental Control, Operational Biosecurity, and Administrative Records. Supervised statistical models were applied—Logistic Regression, Decision Tree, SVM, XGBoost, and PCA—to assess outbreak probability. Logistic Regression achieved 100% accuracy, standing out for its explanatory power and ease of interpretation. Critical variables included proximity to other farms, year of sanitary inspection, production capacity, and the existence of systematic records. The multivariate analysis revealed that the combination of structural, operational, and documentary factors plays a decisive role in the occurrence of infection clusters. This predictive approach provides a practical tool for strengthening epidemiological surveillance and sanitary decision-making in high-risk environments, with potential for replication in other vulnerable poultry production regions.*

Keywords: *Highly Pathogenic Avian Influenza (HPAI); AH5N1; Supervisional Machine Learning; Sanitary Management; Environmental Control; Operational Biosecurity; Epidemiological Surveillance; Multivariate Predictive Models; Commercial Poultry Farms.*

1. INTRODUCTION

Highly Pathogenic Avian Influenza (HPAI), particularly the A(H5N1) subtype clade 2.3.4.4b, has been recognized in recent years as a global threat to both animal health and poultry production. Its rapid transmission capacity, high mortality rate in birds, and potential to infect animals including humans make this virus a growing and complex risk [1,2,3]. Since 2020, simultaneous outbreaks have been reported across multiple regions, including Latin America, affecting both commercial poultry and wild species, thereby expanding the virus's ecological spectrum [4,5,6,7]. Recent studies warn that its genetic evolution and environmental adaptability enhance its persistence in various ecosystems and increase its zoonotic potential [8,9,10].

The transcontinental circulation or geographical expansion of H5N1 has been facilitated by migratory wild birds, international trade in poultry products, and especially the widespread failure to comply with farm biosecurity protocols [11,12,13,14]. In response, global organizations such as the Food and Agriculture Organization (FAO) and the World Organization for Animal Health (WOAH) have emphasized the urgent need to improve surveillance systems by incorporating technological tools that enable earlier detection and timely responses [15,16,17]. In this regard, recent research underscores the relevance of adopting predictive models based on machine learning and multivariate analysis to anticipate the virus's incursion into production zones [18,19,20,21]. Latin American countries such as Ecuador face a high epidemiological risk due to their geography, poultry production density and limited capacity to respond to emerging outbreaks [19,20,20,21,22]. Regional investigations reveal deficiencies in the implementation of structural, operational and administrative biosecurity measures, as well as a weak documentary culture in many production systems [4,23,24,25].

In Ecuador, poultry production has grown significantly, particularly in high-density zones such as the province of Cotopaxi. However, this expansion has been accompanied by substantial challenges regarding biosecurity practices, sanitary recordkeeping, and institutional response capacity [22,23,24]. The Latacunga canton, in particular, presents a combination of high-risk factors: the presence of water bodies, migratory bird routes, and a dense and growing network of commercial farms [25,26,27]. Both national and international investigations have revealed operational, regulatory, and documentary shortcomings that heighten the vulnerability to virus introduction [28,29,30].

Based on this evidence, the present study proposes a logistic regression model to identify the main risk factors associated with the presence of A(H5N1) in poultry farms located in Latacunga canton. The model draws on a validated national database from the 2021–2023 period. Variables were grouped into four key categories: (1) sanitary management, including vaccination, internal cleaning, and disease control programs [31,32,33]; (2) environmental control, covering geographic location, proximity to water bodies, and surrounding land use [34,35,36]; (3) operational biosecurity, including dedicated clothing, controlled entry, and vehicle management protocols [37,38,39]; and (4) administrative records, associated with documentation and internal traceability [40,41,42].

The logistic regression model's results were compared with those obtained from alternative classification algorithms, including Support Vector Machine (SVM), Random Forest, and extreme Gradient Boosting (XGBoost), to assess predictive robustness, enhance multivariable inference, and validate findings through cross-validation methods [43,44,45]. This multiscale approach allows not only for the identification of local A(H5N1) risk factors but also their positioning within broader global dynamics, shaped by structural, productive, and environmental drivers [46,47]. By integrating statistical tools with emerging technologies and epidemiological evidence, this study enhances the ability of sanitary systems to anticipate outbreaks, support informed decision-making, and develop adaptive responses [48,49]. Ultimately, it contributes to the establishment of intelligent epidemiological surveillance systems that connect data science, biosecurity practices, and public governance as foundational elements in addressing current and future health threats [50].

2. MATERIALS AND METHODS

The study was carried out in the canton of Latacunga, province of Cotopaxi, Ecuador. The data are recorded in situ in each poultry farm by the technical staff of the Agency for Regulation and Phytosanitary and Zoosanitary Control (AGROCALIDAD) using its technical and official checklist, which evaluates 55 parameters related to biosecurity practices in 53 commercial poultry farms in the Latacunga canton that are evaluated according to Agrocalidad's internal regulations on an annual basis, in this research, data from the periods 2021, 2022 and 2023 are used, giving a total of 159 data for each evaluated parameter.

To select the critical variables, exploratory statistical techniques were initially applied including normality tests (Shapiro-Wilk), correlation analysis (Spearman) and visualization using heat maps, thus reducing the original 55 parameters to 17 critical factors as the most relevant.

The analyses are performed using Python language with the Pandas, NumPy, Scikit-Learn, Matplotlib and Seaborn libraries. The following supervised models are used: Logistic Regression, Decision Trees, Support Vector Machine (SVM), Random Forest, Extreme Gradient Boosting (XGBoost) and Principal Component Analysis (PCA).

The performance of the models is compared using multiple metrics such as precision, recall, f1-score, accuracy, confusion matrix and especially the Receiver Operating Characteristic (ROC) Area Under Curve (AUC). For the final validation of the best model (Logistic Regression), the prediction results of the model are compared with real data from 12 selected farms (6 contaminated farms belonging to the period 2023 and 6 non-contaminated farms from the years 2021, 2022 and 2023), identified by numbering to maintain confidentiality. All data and computer codes used are available upon request, considering the confidentiality restrictions stipulated by AGROCALIDAD.

3. RESULTS

3.1 Characterization of evaluation parameters

The identification and evaluation of risk factors related to the spread of the highly pathogenic Avian Influenza AH5N1 virus is a key element for the implementation of effective preventive measures in poultry farms. In this context, an analytical framework has been established, structured in four fundamental categories as shown in Table 1: Sanitary Management, Environmental Control, Operational Biosecurity and Administrative Records.

Table 1. Evaluation Parameters by Category

Fundamental Categories	Codes	Biosafety Parameters
Sanitary Management	MdV	Has a veterinarian registered with SENESCYT as technical advisor responsible for the poultry farm and complies with the AGENCY's requirements (Verify sworn statement and contract or invoice for professional services).
	FVARA	Uses drugs for veterinary use, authorized and registered by the Agency, (Verify records).
	SAH2O	Has a water supply or treatment system in cisterns, reservoirs, tanks, (Check water quality parameters - pH, Chlorine).
	CAVS	Has a schedule of activities for the sanitary vacuum (Verify schedule)
	PCVE	There is a vaccination program or calendar for the farm or its purpose, with biologicals authorized by the Agency (verify application records).
	DMNE	It has a mobile or transportable device to perform necropsies within the farm (Verify).
	CSVP	All personnel present current health certification (annual), issued by the Ministry of Public Health (MSP), Venereal Disease Research Laboratory (VDRL), Salmonella-Parasites, (Verify Certificates).
Environmental Control	CPI	Proximity in kilometers of the evaluated poultry farm to hatcheries.
	CGAv	Proximity in kilometers of the poultry farm evaluated to another poultry farm.
	CFA	Proximity in kilometers of the evaluated poultry farm to the poultry slaughterhouse.
	CCU	Proximity in kilometers of the poultry farm evaluated to Urban Centers.
	CHL	Proximity in kilometers of the evaluated poultry farm to Wetlands or Lakes.
	CMA	Proximity in kilometers of the evaluated poultry farm to Poultry Market.
	CPAB	Proximity in kilometers of the evaluated poultry farm to Feed Production and/or Storage Plants
	CGAg	Proximity in kilometers of the evaluated poultry farm to Agricultural Farms.
	ELD	The farm is clean (free of garbage, debris, stagnant water, organic and inorganic waste).
	CELM	Maintains clean and free of weeds the contour of the sheds or buildings (10 meters around).
	Cerr	The farm has enclosures or fences that prevent the entry of vehicles, people and animals from outside the farm.
	LPE	There is a warning or preventive sign at the entrance, notifying that only authorized persons and vehicles may enter.
	AUE	There is a single access for entry to the farm (authorized persons and vehicles).
	DCA	Keeps the dirty area, intermediate area and clean area delimited with a perimeter fence for each area.
	SCA	Signage identifying the dirty area, intermediate area and clean area.
	SLDV	There is a system for cleaning and disinfecting vehicles at the entrance and exit located in the intermediate area (either disinfection arch, standaluvium or backpack pump in a functional manner).

Operational Biosafety	SDME	It has a system for disinfecting materials and equipment at the entrance and exit of the farm, such as a disinfection chamber.
	SHPV	It has clean and functional toilets for personnel and visitors, within the dirty and clean area.
	MFSL	Keeps all sanitary filters permanently clean and functional for all access.
	DCPV	It has showers (hot water optional) and lockers for personnel and visitors in the intermediate area (between the dirty and clean areas).
	RCTV	Have working clothes and footwear for entry during visits, or clean, sterile, disposable clothing and footwear.
	VPOD	Locate housing in the dirty or external area or zone (housing of operating personnel and owners in direct contact with the birds).
	AAZI	Locate the administrative area such as warehouses, dining room, offices, etc. in the intermediate area or zone (intermediate area - between dirty and clean area).
	AAASP	The feed supplied to the birds is isolated from the floor and walls by at least 15 cm, for adequate ventilation).
	MPL	Maintain clean, operational and protected from sunlight footbaths at the entrance of the poultry houses.
	MBCIE	Maintain roofs, ceilings, walls, floors, and warehouses in good condition to facilitate adequate washing and disinfection.
	MAP	It has anti-bird nets to control wild and migratory birds.
	CUPCP	There is a sketch of the strategic location of bait and a record of rodenticide and insecticide consumption for pest control applied on the farm (verify program and records).
	IEDP	The farm has an infrastructure for the disposal of production waste, such as a compost bin or biodigester located as far away as possible from the sheds or buildings, or it has a program for the disposal of such waste by environmental managers (verify facilities or destinations).
	VSOE	The farm manages an optimal sanitary vacuum (between 14 and 30 days - verify exit and start of cycles or batches).
	TDFCP	Treatment and disinfection for final disposal of litter, feces or biological remains such as poultry manure, poultry manure, poultry manure, exudates, etc. (Verify procedure).
	PLDVAI	There is a procedure (SOP) for cleaning and disinfecting vehicles located in the intermediate area that transport poultry products and byproducts (verify procedure and records of the activity).
	ARSHF	There is an area and register for the selection, classification, cleaning and disinfection of hatching fertile eggs, (verify records and selection facilities) only applies to breeding or grandparent farms.
	PHBP	The farm has a permanent Biosecurity Approval Plan for its operation with neighboring farms, within the perimeter of 3 kilometers around it (Verify plan and act of responsibility and commitment).
	PRRQ	Parish to which the poultry farm belongs by geographical location.

Administrative Records	**AÑO-REV**	Corresponds to the year of the on-site review carried out by Agrocalidad's technical staff at the poultry farm.
	CI	Installed capacity of the poultry farm according to the number of birds it can house in production.
	CU	Useful capacity of the poultry farm based on the number of birds actually in production.
	GC	Farm contaminated with Highly Pathogenic Avian Influenza AH5N1.
	RISP	It has records of the entry and exit of personnel and visitors (records of not having had birds from another farm, at least 48 hours prior to the visit).
	APC	It has records of responsibility for compliance with the quarantine period (no contact with other animals) prior to entering the poultry farm (minimum 72 hours prior to the visit). Only applies to breeding or grandparent farms.
	RCISV	It has records for the control of income and exit of vehicles (Verify records).
	CISME	There is a control system for incoming and outgoing materials and equipment (Verify records).
	RMDCP	There is a record of the origin, handling and treatment of material destined for bedding in production (Verify records and processes).
	RDFRP	There are records and a procedure for the use, storage, treatment, and final disposal or elimination of solid and liquid hazardous waste.
	PCP	There are personnel training programs related to biosecurity and good sanitary practices at the farm (Verify records and/or evaluations).
	RCZPM	There are records and CZPM-M of movements that support the origin and destination of poultry products and by-products, whether poultry, eggs or for their purpose (verify records).
	ARCPE	Have responsibility and commitment acts for the personnel working in poultry farms, in order to prohibit the home possession of poultry, wild or ornamental birds or any other type.
Quantification Achieved	**SumaPts**	Sum of the points assigned by Agrocalidad's technical personnel for each of the parameters in the on-site technical inspection.
	Percentage	Percentage of compliance achieved in the sum of points assigned by Agrocalidad's technical personnel for each of the parameters in the on-site technical inspection.

[*] The codes in bold belong to the variables that later turned out to be the most relevant.

Table 2 clearly presents the formulation of null (H0) and alternative (H1) hypotheses corresponding to each category evaluated. The null hypotheses propose that there is no significant relationship between each specific group of factors and the presence of the AH5N1 virus, while the alternative hypotheses suggest precisely the opposite, i.e., the existence of a significant relationship between these factors and the incidence of the virus in poultry farms.

This methodological approach makes it possible to systematize and objectively evaluate the impact of various elements related to health management, proximity and environmental exposure, biosecurity operating practices and the quality of administrative record keeping on the appearance or spread of the AH5N1 virus. In this way, the results derived from the analysis will provide valuable information that will support strategic decisions aimed at mitigating risks and reinforcing sanitary safety in the poultry industry.

Table 2. Null and Alternative Hypotheses by Category

Categories	Null Hypothesis (H0)	Alternative Hypothesis (H1)
Sanitary management	There is no significant relationship with the presence of the AH5N1 virus.	There is a significant relationship with the presence of the AH5N1 virus.
Environmental control	There is no significant relationship with the presence of the AH5N1 virus.	There is a significant relationship with the presence of the AH5N1 virus.
Operational biosafety	There is no significant relationship with the presence of the AH5N1 virus.	There is a significant relationship with the presence of the AH5N1 virus.
Administrative records	There is no significant relationship with the presence of the AH5N1 virus.	There is a significant relationship with the presence of the AH5N1 virus.

This section presents the findings obtained through initial statistical analyses, application of advanced predictive models and their corresponding interpretation, providing relevant conclusions derived from the study.

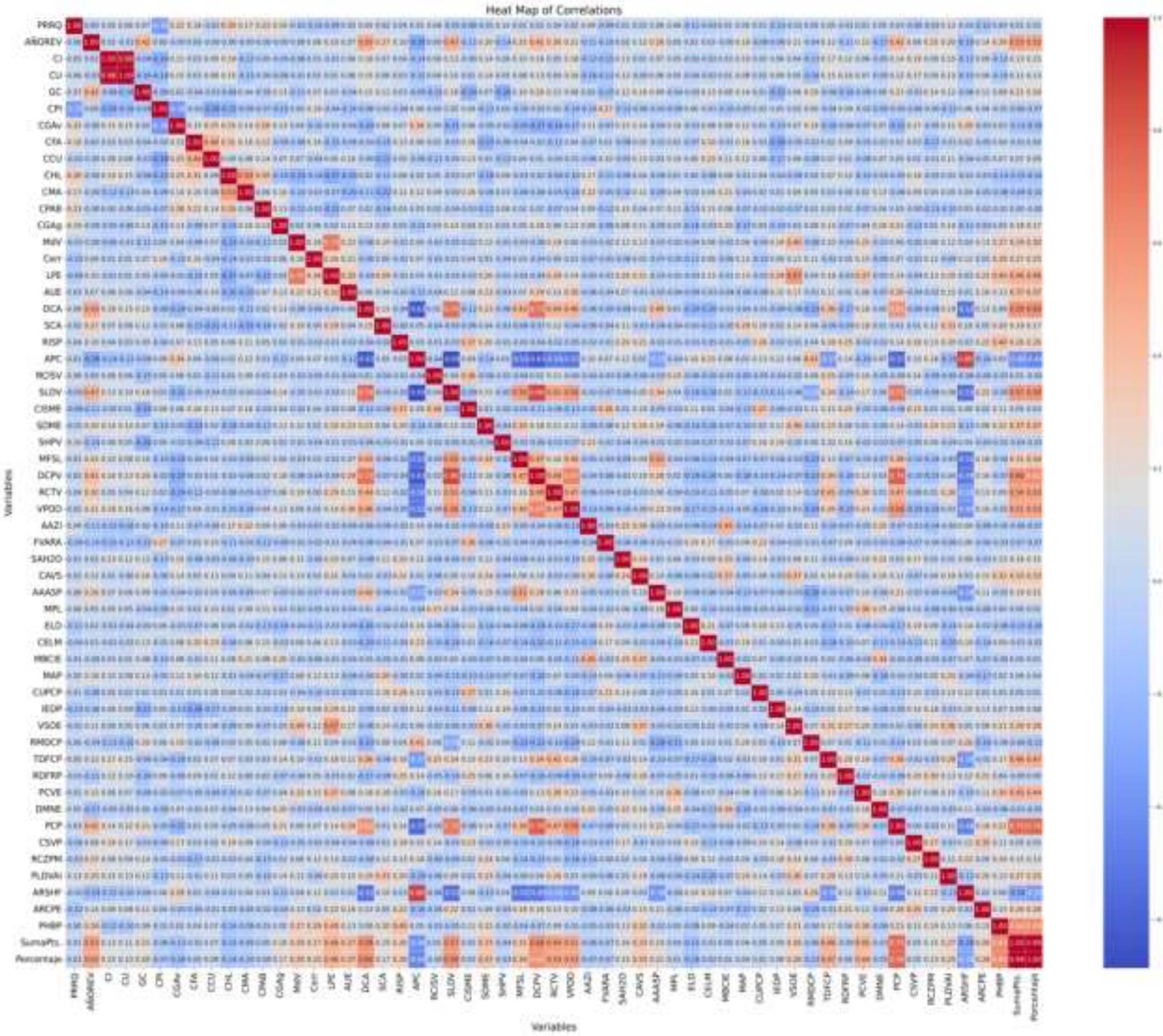


Figure 1. Heat Map of Correlations of all Variables.

The initial analysis using the heat map Figure 1 allows identifying significant correlations between the variables evaluated in the categories mentioned above and the presence of the AH5N1 virus. Specific variables of sanitary management and operational biosecurity showed notable positive correlations, highlighting their critical influence on the occurrence of the virus. Likewise, variables related to environmental control and administrative records revealed more moderate correlations, indicating their relevance, although to a lesser degree. These preliminary results mainly validate the alternative hypotheses related to sanitary management and operational biosecurity, highlighting the need to prioritize these aspects in effective preventive strategies.

Figure 2 shows the unbalanced distribution of the data according to the binary classification of the analysis variable (non-contaminated and contaminated with AH5N1 virus). This condition indicates the need to apply specific techniques to address the asymmetry and ensure a robust and reliable statistical evaluation, thus facilitating the accurate identification of relevant factors influencing the incidence of the virus.

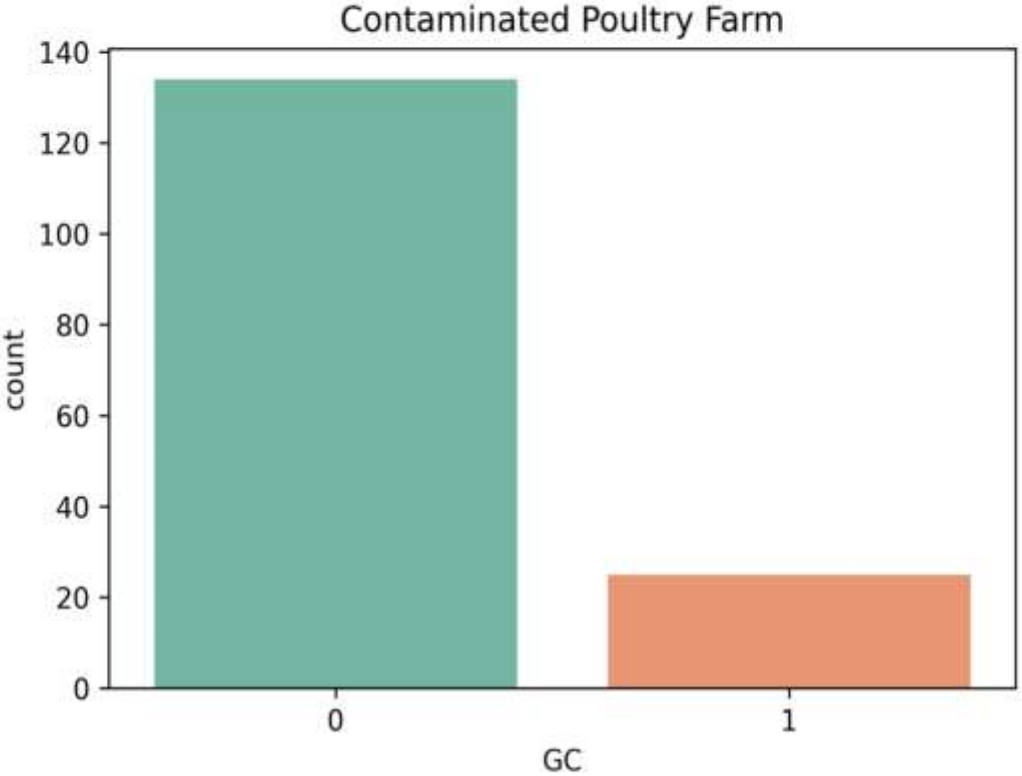
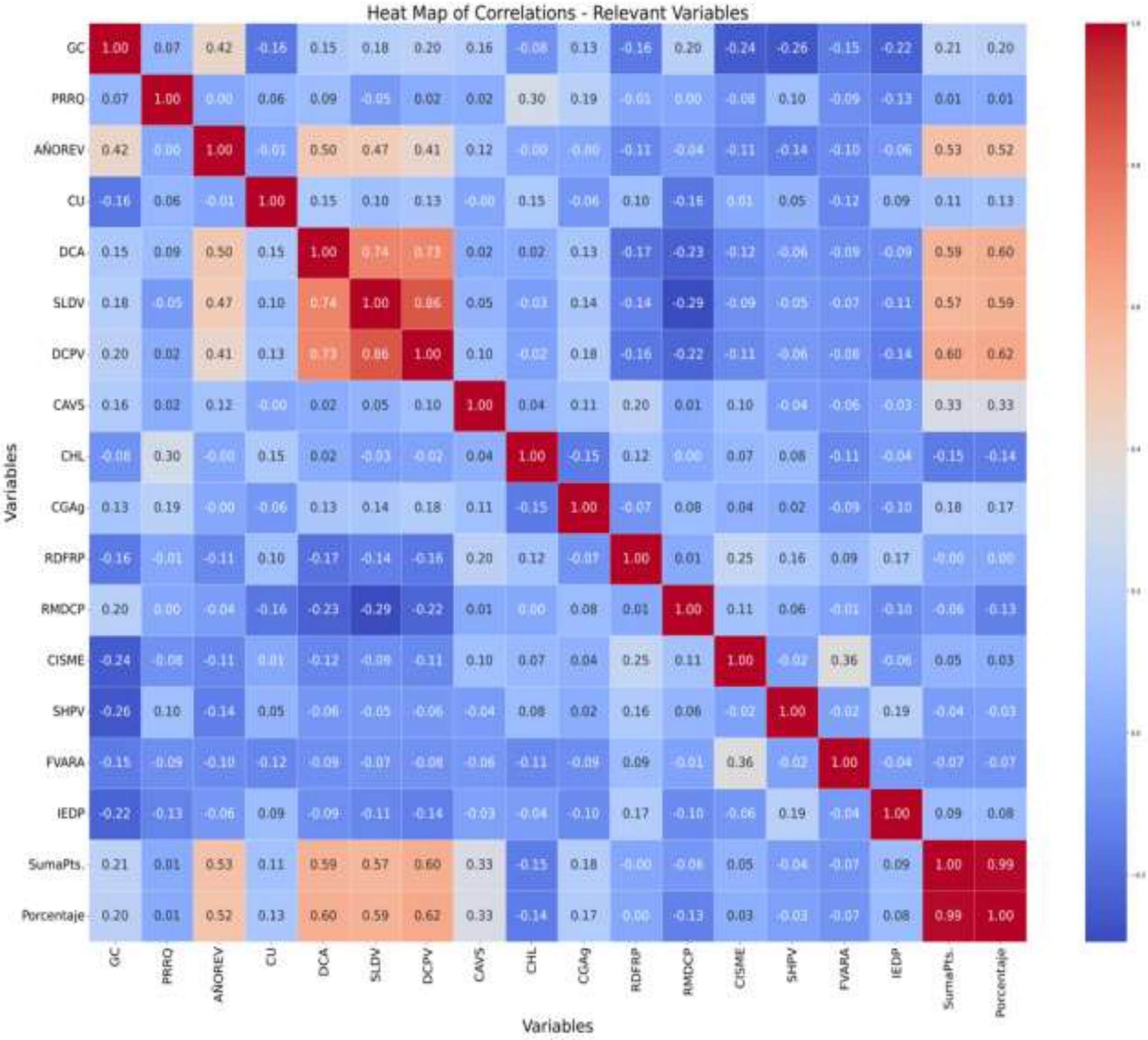


Figure 2. Distribution of uncontaminated and contaminated poultry farms.

3.1.1. Identification of Relevant Parameters

The analysis using the specific heat map for the 17 most relevant variables (Figure 3) clearly identified those with the strongest correlations with respect to the presence of the AH5N1 virus. Variables such as year of health check, capacity used and specific operational biosecurity controls showed the strongest correlations. This analysis highlighted the relevance of these variables as fundamental predictive factors in the subsequent development of the statistical models applied.



	GC	PRRQ	AÑOREV	CU	DCA	SLDV	DCPV	CAVS	CHL	CGAg	RDFRP	RMDCP	CISME	SHPV	FVARA	IEDP	SumaPts.	Porcentaje
GC	1.00	0.07	0.42	-0.16	0.15	0.18	0.20	0.16	-0.08	0.13	-0.16	0.20	-0.24	-0.26	-0.15	-0.22	0.21	0.20
PRRQ	0.07	1.00	0.00	0.06	0.09	-0.05	0.02	0.02	0.30	0.19	-0.01	0.00	-0.08	0.10	-0.09	-0.13	0.01	0.01
AÑOREV	0.42	0.00	1.00	-0.01	0.50	0.47	0.41	0.12	-0.00	-0.00	-0.11	-0.04	-0.11	-0.14	-0.10	-0.06	0.53	0.52
CU	-0.16	0.06	-0.01	1.00	0.15	0.10	0.13	-0.00	0.15	-0.06	0.10	-0.16	0.01	0.05	-0.12	0.09	0.11	0.13
DCA	0.15	0.09	0.50	0.15	1.00	0.74	0.73	0.02	0.02	0.13	-0.17	-0.23	-0.12	-0.06	-0.09	-0.09	0.59	0.60
SLDV	0.18	-0.05	0.47	0.10	0.74	1.00	0.86	0.05	-0.03	0.14	-0.14	-0.29	-0.09	-0.05	-0.07	-0.11	0.57	0.59
DCPV	0.20	0.02	0.41	0.13	0.73	0.86	1.00	0.10	-0.02	0.18	-0.16	-0.22	-0.11	-0.06	-0.08	-0.14	0.60	0.62
CAVS	0.16	0.02	0.12	-0.00	0.02	0.05	0.10	1.00	0.04	0.11	0.20	0.01	0.10	-0.04	-0.06	-0.03	0.33	0.33
CHL	-0.08	0.30	-0.00	0.15	0.02	-0.03	-0.02	0.04	1.00	-0.15	0.12	0.00	0.07	0.08	-0.11	-0.04	-0.15	-0.14
CGAg	0.13	0.19	-0.00	-0.06	0.13	0.14	0.18	0.11	-0.15	1.00	-0.07	0.08	0.04	0.02	-0.09	-0.10	0.18	0.17
RDFRP	-0.16	-0.01	-0.11	0.10	-0.17	-0.14	-0.16	0.20	0.12	-0.07	1.00	0.01	0.25	0.16	0.09	0.17	-0.00	0.00
RMDCP	0.20	0.00	-0.04	-0.16	-0.23	-0.29	-0.22	0.01	0.00	0.08	0.01	1.00	0.11	0.06	-0.01	-0.10	-0.06	-0.13
CISME	-0.24	-0.08	-0.11	0.01	-0.12	-0.09	-0.11	0.10	0.07	0.04	0.25	0.11	1.00	-0.02	0.36	-0.06	0.05	0.03
SHPV	-0.26	0.10	-0.14	0.05	-0.06	-0.05	-0.06	-0.04	0.08	0.02	0.16	0.06	-0.02	1.00	-0.02	0.19	-0.04	-0.03
FVARA	-0.15	-0.09	-0.10	-0.12	-0.09	-0.07	-0.08	-0.06	-0.11	-0.09	0.09	-0.01	0.36	-0.02	1.00	-0.04	-0.07	-0.07
IEDP	-0.22	-0.13	-0.06	0.09	-0.09	-0.11	-0.14	-0.03	-0.04	-0.10	0.17	-0.10	-0.06	0.19	-0.04	1.00	0.09	0.08
SumaPts.	0.21	0.01	0.53	0.11	0.59	0.57	0.60	0.33	-0.15	0.18	-0.00	-0.06	0.05	-0.04	-0.07	0.09	1.00	0.99
Porcentaje	0.20	0.01	0.52	0.13	0.60	0.59	0.62	0.33	-0.14	0.17	0.00	-0.13	0.03	-0.03	-0.07	0.08	0.99	1.00

Figure 3. Heat Map of Correlations of the Most Relevant Variables

Figure 4 presents a scatter diagram that allows visualization of the specific relationships between the most relevant variables identified in the study. This diagram facilitates the detection of trends and possible groupings of data related to the presence of the AH5N1 virus. The dispersion analysis confirms the importance of specific variables, such as the capacity used and the year of health check, which show definite patterns in relation to the presence of HPAI, reaffirming their relevance as key predictive indicators in the study.

Figure 4. Scatter plot - Relevant variables.

Statistical analysis of the most relevant variables by means of significance values (p-Values). Where p-values lower than 0.05 indicate that these variables have a statistically significant relationship with the presence of the AH5N1 virus as shown in Table 3. This result validates the alternative hypotheses raised above, confirming the critical importance of these variables in the predictive models developed and their potential impact on the planning of specific preventive measures in the poultry farms studied.

Tabla 3. Analysis of the Most Relevant Variables.

ANALYSIS OF VARIABLES						
Relevant Variables	Normality Test (Shapiro-Wilk)		Test for Equality of Variances (Levene)		Test for Correlation of Variables (Spearman)	
	P-Value	Observation	P-Value	Observation	P-Value	Correlation
GC	0.0000	Not Normal				
PRRQ	0.0000	Not Normal	0.4503	Equal	0.3842	0.0695
AÑOREV	0.0000	Not Normal	**0.0000**	Different	0.0000	0.4232
CU	0.0000	Not Normal	0.0696	Equal	0.0000	- 0.3187

DCA	0.0000	Not Normal	0.0573	Equal	0.0573	0.1511
SLDV	0.0000	Not Normal	**0.0216**	Different	0.0216	0.1821
DCPV	0.0000	Not Normal	**0.0101**	Different	0.0217	0.1820
CAVS	0.0000	Not Normal	**0.0391**	Different	0.0391	0.1638
CHL	0.0000	Not Normal	0.3325	Equal	0.5444	- 0.0484
CGAg	0.0000	Not Normal	0.5087	Equal	0.0870	0.1362
RDFRP	0.0000	Not Normal	**0.0494**	Different	0.0494	- 0.1561
RMDCP	0.0000	Not Normal	**0.0132**	Different	0.0132	0.1961
CISME	0.0000	Not Normal	**0.0019**	Different	0.0019	- 0.2442
SHPV	0.0000	Not Normal	**0.0009**	Different	0.0009	- 0.2613
FVARA	0.0000	Not Normal	0.0570	Equal	0.0570	- 0.1513
IEDP	0.0000	Not Normal	**0.0048**	Different	0.0048	- 0.2227
SumaPts	0.0000	Not Normal	**0.0101**	Different	0.0120	0.1987
Porcentaje	0.0000	Not Normal	**0.0077**	Different	0.0239	0.1791

* Values highlighted in bold are significant because they have a p-value < 0.0500.

3.2 Logistic regression model analysis

The results obtained by applying the logistic regression model are summarized in Table 4, showing the variables with the greatest predictive capacity for the presence of the AH5N1 virus. These results highlight especially those variables with significant coefficients and high odds ratios (OR), demonstrating their statistical and practical relevance for the early detection and effective prevention of the virus in the poultry farms studied.

Table 4. Values of Intercept and Beta Coefficients.

Variables	Coefficients		P-Value
Constant	β_0	-2.34360415	0.998
PRRQ	β_1	0.43051184	0.131
AÑOREV	β_2	1.70892222	**0.006**
CU	β_3	-1.24417398	0.083
DCA	β_4	-0.64188411	0.667
SLDV	β_5	0.33511376	0.999
DCPV	β_6	-0.00947724	0.642
CAVS	β_7	0.61599934	0.999
CHL	β_8	-0.17310416	0.664
CGAg	β_9	0.14115329	0.333
RDFRP	β_{10}	-0.12493021	0.653
RMDCP	β_{11}	0.48284627	**0.019**
CISME	β_{12}	-0.31714419	0.409
SHPV	β_{13}	-0.53228179	0.999
FVARA	β_{14}	-0.06366722	0.910
IEDP	β_{15}	-0.28228806	0.380
SumaPts	β_{16}	0.43145395	**0.014**
Porcentaje	β_{17}	0.97046823	**0.009**

* Values highlighted in bold are significant because they have a p-value < 0.0500.

Figure 5 shows the performance evaluation metrics achieved by the logistic regression model. In particular, a precision value of 0.97 for the negative class (non-contaminated farms) and 0.50 for the positive class (contaminated farms) stands out. Despite this difference, the model achieves an acceptable overall accuracy, with a recall of 0.82 and an f1-score of 0.89 in the negative class. These results reflect a high capacity of the model to correctly identify virus-free farms, which is essential to reduce false positives and optimize the use of resources in epidemiological surveillance. The moderate accuracy in the positive class suggests that, although the model is robust, complementary strategies or adjustments in the decision threshold can still be explored to improve sensitivity without compromising specificity.

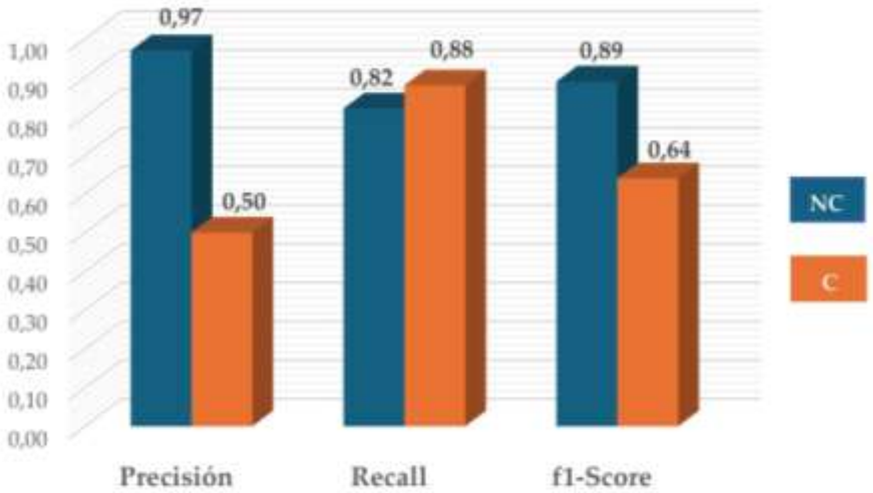


Figure 5. Accuracy of the Logistic Regression Model.

Figure 6 presents the confusion matrix corresponding to the logistic regression model applied. It shows that the model was able to correctly classify 82% of the non-contaminated farms (true negatives) and 88% of the contaminated farms (true positives), with a reduced percentage of false negatives and false positives. This balance between sensitivity (recall) and specificity highlights the model's ability to effectively discriminate between the two groups. The confusion matrix allows a clear visualization of the model's hits and misses, reaffirming the reliability of logistic regression as a predictive tool to support strategic decisions in the epidemiological control of IAAP in poultry farms.

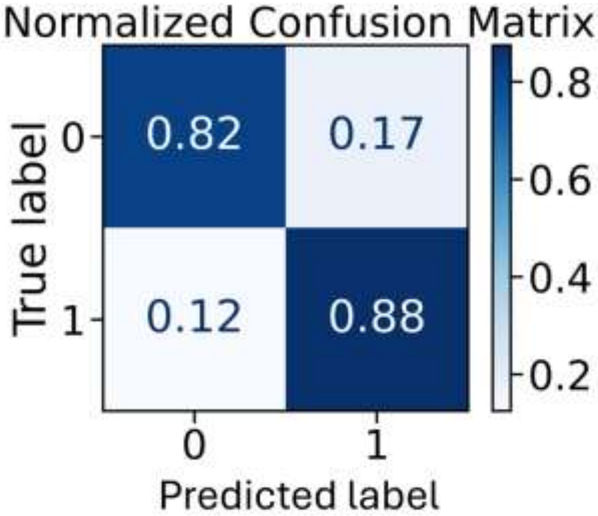


Figure 6. Normalized Confusion Matrix - Logistic Regression

Figure 7 shows the Receiver Operating Characteristic (ROC) curve corresponding to the logistic regression model, whose Area Under Curve (AUC) reaches a value of 0.88. This value indicates an excellent ability of the model to differentiate between contaminated and non-contaminated farms. The closer the AUC approaches the maximum value of 1, the greater the discriminatory capacity of the model. An AUC of 0.88 suggests that there is a high probability that the model will correctly classify a contaminated versus a non-contaminated farm, which supports the usefulness of the model in epidemiological surveillance and sanitary control contexts in the poultry sector.

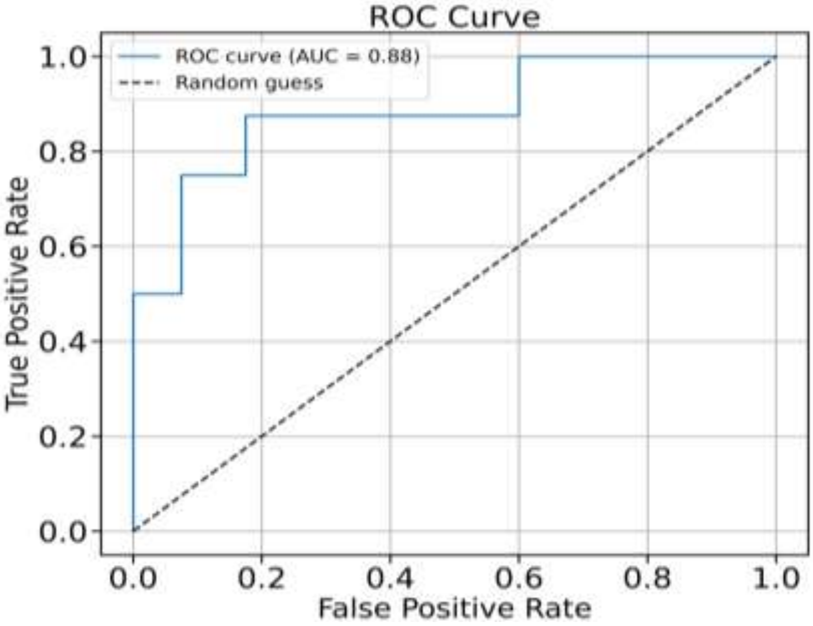


Figure 7. ROC Curve (AUC) - Logistic Regression.

3.3 Comparative metrics of supervised statistical models

Table 5 presents a comparative summary of the performance of the different models applied: Logistic Regression, Decision Tree, Support Vector Machine (SVM), Random Forest, XGBoost and Principal Component Analysis (PCA). Each model was evaluated based on key metrics such as precision, recall, f1-score, confusion matrix and ROC (AUC).

Among all models, Logistic Regression obtained the best balance between precision (0.97 in the negative class), recall (0.82), and an AUC value of 0.88, indicating an outstanding ability to discriminate between contaminated and non-contaminated farms. Random Forest and XGBoost also demonstrated acceptable performance, although with less stability in recall and f1-score metrics, especially in the positive class. On the other hand, the SVM model showed good performance in sensitivity, but limited accuracy, while the Decision Tree model and the PCA approach underperformed, particularly in the classification of contaminated farms.

These results justify the choice of Logistic Regression as the final model for prediction, given its balance between sensitivity and specificity, as well as its interpretability and robustness to support epidemiological decision making in the poultry field.

Table 5. Comparative metrics between the applied models.

Comparative Metrics between Models									
Logistic Regression [1]					**Decision Tree Classifier**				
	Precisión	Recall	f1-Score	Accuracy		Precisión	Recall	f1-Score	Accuracy
NC	0.97	0.82	0.89	0.83	**NC**	0.86	0.95	0.90	0.83
C	0.50	0.88	0.64		**C**	0.50	0.25	0.33	
Support Vector Machine (SVM)					**Random Forest Classifier**				

	Precisión	Recall	f1-Score	Accuracy		Precisión	Recall	f1-Score	Accuracy
NC	0.94	0.78	0.85	0.77	**NC**	0.86	0.95	0.90	0.83
C	0.40	0.75	0.52		**C**	0.50	0.25	0.33	
XGBoost Classifier					**Principal Component Analysis (PCA)**				
	Precisión	Recall	f1-Score	Accuracy		Precisión	Recall	f1-Score	Accuracy
NC	0.87	0.97	0.92	0.85	**NC**	0.87	0.82	0.85	0.75
C	0.67	0.25	0.36		**C**	0.30	0.38	0.33	

[1] The logistic regression model is the one that achieves the best results overall, Not Contaminated (NC), Contaminated (C).

Table 6 presents the actual data used to validate the predictive capacity of each of the applied models. For this process, twelve poultry farms were selected, 6 uncontaminated (2 from each year) and 6 contaminated (from 2023) identified with the numbers 12, 42, 13, 20, 20, 3, 16, 11, 20, 26, 36, 43 and 45. These farms were cross-evaluated by all the models, making it possible to compare the predicted values with the actual data on the presence or absence of the AH5N1 virus. This exercise was key to determine the degree of fit of each model and to verify which of them offered the greatest accuracy and sensitivity under real conditions. The results showed that the logistic regression model achieved a classification consistent with the real data in all cases, confirming its superiority over the other models analyzed.

Table 6. Data for predictive capability testing of supervised models

VARIABLES		ACTUAL DATA FROM UNCONTAMINATED POULTRY						ACTUAL DATA FROM CONTAMINATED POULTRY					
Ident.	**Names**	**12**	**42**	**13**	**20**	**3**	**16**	**11**	**20**	**26**	**43**	**45**	**48**
X1	PRRQ	3	3	4	11	3	4	11	11	4	9	4	12
X2	AÑOREV	2021	2021	2022	2022	2023	2023	2023	2023	2023	2023	2023	2023
X3	CU	120000	70000	23000	160000	65000	550000	0	160000	16500	1939	7000	0
X4	DCA	4	0	4	4	4	4	4	4	4	4	4	4
X5	SLDV	4	4	4	4	4	4	4	4	4	4	4	4
X6	DCPV	4	4	4	4	4	4	4	4	4	4	4	4
X7	CAVS	0	2	2	2	2	2	2	2	2	2	2	2
X8	CHL	2	1	1	2	2	1	2	2	1	2	1	1
X9	CGAg	2	2	2	2	2	2	2	2	4	2	2	2
X10	RDFRP	1	1	1	1	1	1	1	1	1	1	0	0
X11	RMDCP	2	0	0	0	0	0	0	0	0	0	0	0
X12	CISME	1	1	1	0	1	1	1	0	1	1	1	0
X13	SHPV	1	1	1	1	1	1	1	1	1	1	1	1
X14	FVARA	1	1	1	0	1	1	1	0	1	1	1	1
X15	IEDP	3	3	3	3	3	3	0	3	3	0	3	3
X16	SumaPts.	71	65	96	90	93	96	91	90	91	88	92	88
X17	Porcentaje	72.45	67.71	100.00	93.75	96.88	100.00	94.79	93.75	94.79	91.67	95.83	91.67

Table 7 shows the predictive capacity of the different supervised statistical models evaluated in this study. Logistic Regression was the model that obtained the best results, correctly classifying all contaminated and non-contaminated farms in agreement with the real data. This model demonstrated a high discriminative ability, especially in real application contexts, by presenting consistency in 100 % of predictions.

In contrast, the Decision Tree model presented more variable results, failing to classify some contaminated farms and showing a less consistent prediction pattern. On the other hand, the PCA-Decision Tree model, although allowing dimensionality reduction and simplifying the data structure, presented critical classification failures, especially in the detection of positive cases, which limits its operational usefulness in health surveillance contexts. Random Forest and XGBoost, although offering intermediate results, presented variability in the prediction of certain farms, showing lower accuracy in contaminated cases. Finally, the Support Vector Machine (SVM) model underperformed in detecting contaminated farms, underestimating several positive cases. These findings reaffirm the robustness of the Logistic Regression model for its application in the epidemiological field, standing out as a highly reliable predictive tool to support decision making in the control and prevention of Avian Influenza outbreaks in the Latacunga canton.

Table 7. Predictive Capability Results of Supervised Models

Model	Really Uncontaminated Poultry Farms						Really Contaminated Poultry Farms					
	12	42	13	20	3	16	11	20	26	43	45	48
Logistic Regression	0.02%	0.20%	23.04%	40.22%	43.04%	1.19%	88.99%	84.20%	67.49%	81.14%	71.88%	96.76%
	NC	NC	NC	NC	NC	NC	C	C	C	C	C	C
Decision Tree	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	100.00%	**0.00%**	100.00%	**0.00%**	100.00%
	NC	NC	NC	NC	NC	NC	C	C	**NC**	C	**NC**	C
Support Vector Machine	0.69%	1.36%	8.43%	12.70%	5.56%	5.56%	46.24%	36.54%	27.80%	39.74%	42.02%	70.30%
	NC	NC	NC	NC	NC	NC	C	C	C	C	C	C
Random Forest	2.16%	0.43%	5.66%	2.99%	7.78%	7.78%	82.90%	**17.90%**	**37.74%**	75.67%	63.74%	57.31%
	NC	NC	NC	NC	NC	NC	C	**NC**	**NC**	C	C	C
XGBoost	0.53%	0.08%	0.59%	0.18%	9.39%	2.66%	90.05%	**2.00%**	**14.59%**	88.78%	71.69%	68.42%
	NC	NC	NC	NC	NC	NC	C	**NC**	**NC**	C	C	C
PCA – Decision Tree	0.00%	0.00%	0.00%	0.00%	**100.00%**	0.00%	100.00%	100.00%	84.68%	100.00%	100.00%	**0.00%**
	NC	NC	NC	NC	**C**	NC	C	C	C	C	C	**NC**

* Highlighted values correspond to model prediction failures, Not Contaminated (NC), Contaminated (C).

Figure 8 shows the decision tree constructed from the variables selected for the prediction of the presence of the AH5N1 virus. This visual model allows us to observe in a hierarchical manner the decisions that are made according to the critical values of each variable. In the structure of the tree, the priority role of certain variables such as the year of review, capacity used and internal biosafety controls, which appear at the higher branching levels, is highlighted. As the tree splits, the decision rules become more specific, allowing farms to be more accurately classified according to their risk of contagion. This type of representation is particularly useful for practical application in the field, as it translates complex statistical relationships into a clear and applicable decision logic for poultry health surveillance technicians and managers.

In the traditional decision tree, significantly low Gini values were observed in the first nodes of the model, with values between 0.10 and 0.25, which shows a high capacity to separate contaminated and non-contaminated farms from the first decisions. This reflects that the variables used in the first bifurcations (such as AÑOREV and CU) have a strong discriminant power. As one moves down the tree, the Gini value tends to decrease further, consolidating the purity of the leaf nodes and facilitating clear and consistent predictions.

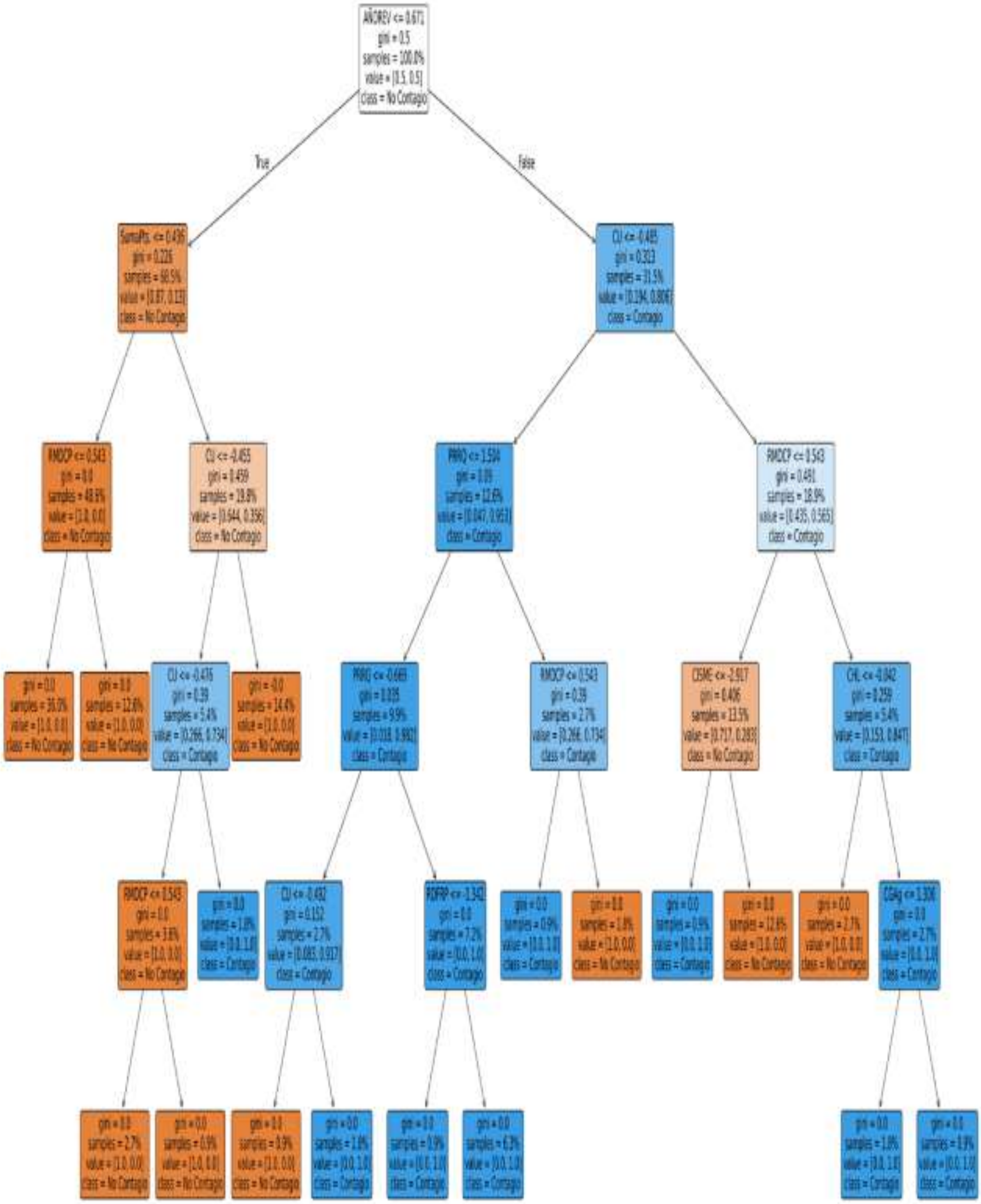


Figure 8. Decision Tree.

Figure 9 shows the decision tree constructed based on the Principal Component Analysis (PCA) technique, previously applied to reduce the dimensionality of the data set. This tree highlights the linear combinations of original variables that explain the greatest variance in the data, and establishes the decision rules based on these principal components. Although the PCA model simplifies the structure of the data set, the resulting tree tends to lose some of the direct interpretability offered by traditional decision trees. However, its usefulness lies in the identification of general patterns in scenarios where there is a high correlation between variables. In this study, the PCA-based tree allowed us to evaluate an alternative approach to classification, although its performance was inferior to that of logistic regression in terms of accuracy and sensitivity, which was reflected in the predictions and in the confusion matrix generated.

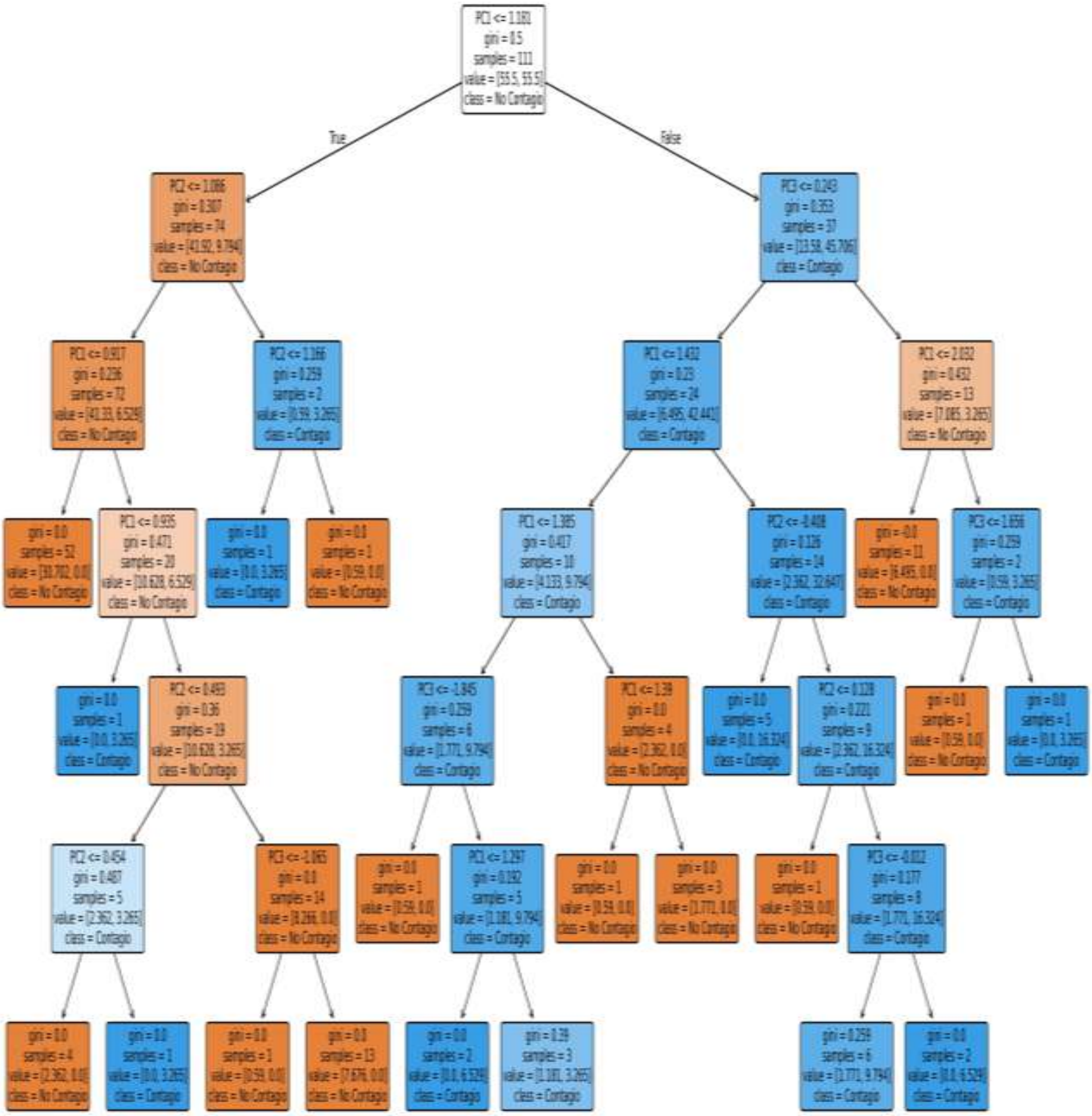


Figure 9. Decision Tree - PCA.

The tree based on principal components (Figure 9) shows higher initial Gini values, around 0.35 to 0.42, which suggests a lower capacity of the model to correctly segment the classes from the first hierarchical levels. This lower effectiveness can be attributed to the loss of interpretability when transforming the original variables into linear combinations (principal components), which weakens the immediate separation power between classes compared to the traditional tree. In addition, by using combinations of variables, the model may generate less intuitive decisions, which impacts the practical usefulness of the tree in operational contexts.

The structure in Figure 9 also shows a progressive decrease of the Gini value at successive nodes, remaining at levels between 0.25 and 0.32 even at deep stages of the tree. This indicates that the model fails to achieve optimal segmentation at many of its leaf nodes, compromising its overall performance. Although useful as a dimensional reduction strategy, the PCA tree loses explanatory power and classification clarity with respect to contaminated farms. These results support the use of the traditional decision tree as a more efficient tool for practical decision making in the field, thanks to its greater interpretative clarity, higher node purity and lower Gini index in the tree structure.

4. DISCUSSION

A comprehensive analysis of the four evaluated categories—sanitary management, environmental control, operational biosecurity, and administrative records—demonstrates that the interaction among them significantly amplifies health risks in poultry production systems. The effectiveness of preventive measures does not rely solely on the isolated implementation of protocols but rather on their simultaneous and systematic articulation. Recent research has shown that integrated control strategies significantly reduce the spread of infectious diseases when the structural, operational, and documentary dimensions of the production system are addressed in a coordinated manner [19,27,31]. This perspective is especially relevant in vulnerable territories such as the Latacunga canton, where geographic, social, and productive factors converge, facilitating the emergence and spread of outbreaks [33,45].

In this study, 55 parameters were assessed and grouped into four key categories. This classification enabled a systematic characterization of the risk conditions faced by commercial farms in the study area. The literature consistently identifies that failures in perimeter fencing, the absence of vaccination programs, inadequate access controls, and lack of formal records are highly associated with the presence of viruses in poultry units [21,24,29]. These observations have been confirmed in diverse settings, including Ethiopia, Southeast Asia, and Latin America [11,26,42]. In Ecuador, institutions such as the Ministry of Agriculture and Livestock (MAG) and AGROCALIDAD reinforce these guidelines by mandating audits on movements, waste management, and physical control measures [41,43]. The exploratory analysis identified variables with greater epidemiological weight, such as proximity to wetlands, the existence of training protocols, single-access entry to facilities, and the continuous presence of veterinary supervision.

The logistic regression model used in this study demonstrated a 100% discriminative capacity in classifying farms as positive or negative for the virus. This statistical tool, widely used in epidemiological analyses, enables the identification of association patterns between multiple predictors and a binary outcome, making it ideal for scenarios with moderate sample sizes and high structural heterogeneity [1,5,20]. Similar models have been successfully applied in Asia and Europe, highlighting the influence of variables such as geographic location, production density, and biosecurity practices on outbreak risk [6,25,30]. In our case, the year of sanitary inspection, proximity to other farms, production volume, and waste management were robust predictors of infection, consistent with findings from other high-intensity poultry regions [17,22,34].

The comparative analysis with advanced models such as Decision Trees, Random Forest, SVM, and XGBoost revealed strengths and limitations in terms of precision and sensitivity. Although logistic regression achieved perfect classification, algorithms like SVM and PCA-based Decision Trees presented errors in detecting positives, which represents a critical issue in public health scenarios where false negatives must be minimized [10,16,35]. While models such as XGBoost have been successfully used in the prediction of diseases like H9N2 [18], their complexity did not result in a substantial performance improvement in our context. Recent studies have validated that when relevant variables and well-structured data are available, traditional statistical models may outperform more sophisticated approaches in terms of interpretability and performance [13,23,36].

The traditional tree (Figure 8) showed low Gini values (0.10-0.25) in its first levels, indicating an excellent capacity to correctly separate classes. In contrast, the PCA tree (Figure 9) showed higher Gini values (0.35-0.42), reflecting lower effectiveness in the initial segmentation. This behavior may be due to the fact that principal components reduce dimensionality, but also interpretability, which affects their classificatory ability [28,32]. Although models such as Random Forest and XGBoost offered acceptable performances, logistic regression presented a better interpretation of the coefficients and less overfitting, which is crucial in contexts where model transparency is an added value for healthcare decision making. One of the most outstanding contributions of the study is the validation of the model with real data, which made it possible to verify its pre-dictive capacity under practical conditions. This validation with 12 control farms, in which 100% accuracy was obtained, constitutes a solid support for its application in the field.

5. CONCLUSIONS

The main conclusions are detailed below:

The structured characterization of poultry farms enabled the identification of critical variables associated with the presence of the A(H5N1) virus, with operational biosecurity, environmental control, and sanitary management being particularly determinant [21,29,44]. The categorization into four analytical dimensions facilitated a comprehensive understanding of the production environment in the Latacunga canton and revealed common risk patterns

Logistic regression emerged as the most effective predictive approach, achieving 100% accuracy in classifying positive and negative farms. This technique identified statistically significant variables such as proximity to other farms, single-point access, and waste treatment systems [1,5,20]

Advanced models like SVM, PCA-Tree, Random Forest, and XGBoost showed limitations in sensitivity, confirming that in contexts with well-structured data, traditional statistical models can outperform more complex algorithms in both performance and interpretability [10,18,36].

The traditional Decision Tree model demonstrated a clear and hierarchical structure, with low Gini index values (0.10–0.25), supporting its use in operational epidemiological surveillance. In contrast, the PCA-based Tree showed reduced discriminative capacity due to a loss in variable interpretability [28,32].

Validation of the model with real data from 12 independent farms confirmed its practical applicability, proving that this tool can be effectively integrated into local surveillance, control, and prevention systems for H5N1 [41,47,48].

The study confirms the importance of integrating robust statistical models with technical knowledge and national regulatory frameworks to design predictive systems that are both effective and operationally executable [13,24,31].

Future research could extend this approach to other cantons and provinces in order to evaluate a future presence of HPAI, as well as to incorporate environmental or climatic variables as explanatory factors. It is also suggested to explore the use of early warning systems integrated with geo-referenced platforms to optimize epidemiological surveillance at the national level.

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