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Modified WLS - Path Analysis Controlling Cattle Skin Defects

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ABSTRACT

The cattle industry has an important role in the economy, especially in providing high-quality cattle skin for various industries. However, fly infestation from the Chloropidae and Muscidae families, causes many defects in cattle skins that negatively affect their economic value. This study aims to identify factors that influence the extent of defects in cattle skins, focusing on the role of temperature, humidity, and fly infestation. The data used in this study were 30 cattles in 3 locations with different heights. The study was conducted in a Malang cattle farming center by measuring temperature and humidity, catching flies, and calculating the defect area on cattle skin. Data were analyzed using path analysis using modified weighting with R Studio software. The weights used were modified by including correlation in the weight matrix. The results showed that temperature had a significant effect on increasing the defect area in the cheek area of cattle, while humidity had no significant effect. In the abdominal area, neither temperature nor humidity affected the defect area. Infestations of Chloropidae and Muscidae flies were also shown to contribute to increased defect area in the cheek area, but not in the abdomen. Preventive strategies for fly control and protection of cattle skin from temperature extremes are recomended, especially in the cheek area.

Keywords: Cattle skin defect; Chloropidae; Fly infestation; Muscidae; Path analysis

INTRODUCTION

The cattle sector is becoming increasingly important due to the rising demand for agricultural products and its contribution to community welfare. One of these is the provision of cattle leather raw materials for a variety of businesses, such as the production of clothing, footwear, and other items made from cattle leather. Since cattle leather is of excellent quality and can be utilized in a variety of ways to boost the economy, it is recognized as one of the most significant industries. Leather that has few or no flaws is considered high grade. As a result, the leather industry strongly discourages the occurrence of flaws in all varieties of leather. Numerous causes, including biological, chemical, and physical ones, can cause leather to develop defects [1]. Parasitic infections

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and skin diseases such as pox can also cause defects in leather, resulting in leather rejection in the leather processing industry[2]. The economic value of cattle leather is affected by defects. Defective leather will cost less than whole, high-quality leather[3].

Infestation by flies can jeopardize the health of cattle and lower the standard of productivity on cattle farms. A fly infestation occurs when the number of flies in a given area, such a farm, rises noticeably. In addition to spreading several parasites and dangerous bacteria, high fly populations can make cattle uncomfortable. Intestinal bacteria (Salmonella), protozoa (Entamoeba hystolica), Oxyrus vermicularis worm eggs, bovine anaplasmosis, and other pathogens can be carried by Musca domestica flies [4]. This is due to the fact that flies breed in areas that are contaminated with bacteria and other harmful organisms, such as trash, animal excrement, and rotting carcasses. Numerous aspects of the cattle's body, such as body hair, limb hair, vomit, and feces, might attract flies [5]. Both direct and indirect impacts may result from a fly infestation. Skin irritation, alopecia, itching, and hair loss are examples of indirect consequences. In the meantime, anemia, stunted growth, and even abrupt death in cattle are direct consequences [4], [6]. Flies need an optimum temperature to reproduce. The optimum temperature for hatching fly eggs is 29°C, while larvae survive to pupate at 27°C, then develop into adult flies at a temperature range of 16°C - 39°C. The fly population is influenced not just by temperature but also by air humidity. The ideal humidity level to reduce the likelihood of fly breeding is 2.2 times higher[7], [8].

Each type of fly has different adaptability. Therefore, it's important to identify the type of fly in order to implement effective control measures in order to address the fly problem on farms [9]. In controlling the fly population, it can be done by using insect nets, regulating temperature, and regulating the number of cattle, cleaning cages, using fly sticker paper, and reducing humidity[10]. Cattle defects are mostly found on the back and scalp, this is due to the large number of flies that often reside on these two parts[11]. There are various efficient ways to overcome flaws in cattle skin. These include chemical preservation, polishing, painting, and tanning (to create tanned leather that is impervious to microbiological and weather damage)[12].

Big data approach was used to assess the various factors affecting cattle skin defects, with a focus on how environmental factors such as humidity and temperature affect the abundance of flies (Chlorophidae and Muscidae), which in turn affects the extent of skin defects [13], [14]. Path analysis was chosen as the main method as it allows identification of the cause-and-effect relationship between the factors. According to [15] path analysis is a statistical method used to test relationships between variables that are causal. Path analysis is one of the most widely used methods to evaluate direct, indirect, and total relationships between variables in complex systems [16]. However, conventional estimation approaches such as Ordinary Least Squares (OLS) have limitations, especially in handling data containing heteroscedasticity or correlation between residual variables [17]. OLS applications on similar data models have been carried out and have not been able to accommodate maximum results compared to PLS[18].

These problems can be overcome with the Weighted Least Squares (WLS) approach being a more appropriate solution. WLS allows weighting observations based on residual variance, resulting in more accurate estimates, especially in data that does not meet the assumption of uniformity of variance (homoskedasticity) [19]. The use of WLS is important because it corrects bias due to correlation between latent and observed variables [20]. This is achieved by assigning weights calculated based on the inverse of the residual variance, which ensures that observations with small variances have a greater influence on the estimates [21]. This approach is particularly relevant for data with correlated variables, as it can minimize estimation error and improve the accuracy of the results [22]. The weighted least square used in [23] is not optimal when used in this study because of the correlation between endogenous variables. this is an analysis gap that encourages modification of wls in this study.

This study aims to identify significant variables that influence cattle skin defects, particularly those caused by fly infestation. Using path analysis that considers the correlation between fly arrival and skin defects, this study is expected to find more effective solutions for skin defect control through mapping the direct and indirect effects of environmental factors and fly abundance. The implications are expected to not only help in improving the quality of cattle skins, but also make a positive contribution to productivity and efficiency in the cattle industry as a whole.

METHODS

Data Research

The study was conducted in a cattle housing center Malang in 2024 by measuring temperature and humidity, catching flies, and calculating the area of defects on cattle skin. Fly catching was carried out in the morning using an insect swatter. Flies attached to the cattle's body parts will be captured to identify the type of fly family. Each fly was caught for 15 minutes for 2 weeks on 30 cattle. Details of the variables used in this study are listed in Table 1.

Table 1. Research Variables

No	Variable	Type
1	Humidity (X_1)	Exogenous
2	Temperature (X_2)	Exogenous
3	Chloropidae (Y_1)	Intervening Endogenous
4	Muscidae (Y_2)	Intervening Endogenous
5	Cheek Defect (Z_1)	Pure Endogenous
6	Abdomen Defect (Z_2)	Pure Endogenous

Data Analysis with Modified WLS-Path Analysis

After data on the abundance and extent of cattle defects were obtained, data were analyzed using path analysis. Path analysis is one of the statistical modeling that estimates and tests the cause and effect between complex variables. Unlike regression analysis, path analysis has three types of variables, namely Exogenous Variables, Intervening Endogenous Variables, and Pure Endogenous Variables, where exogenous variables are equivalent to predictor variables, pure endogenous variables are equivalent to response variables, on the other hand, intervening endogenous variables can be predictor variables and are also response variables [22]. Given this complexity, path analysis has three types of influence, namely direct influence (between exogenous variables to intervening/pure endogenous, between intervening endogenous variables to pure endogenous), indirect influence (between exogenous variables to pure endogenous variables, through mediation of intervening endogenous variables), and total influence (the sum of direct influence and indirect influence). The data analysis process was carried out using R Studio software.

The analysis steps applied in this study are as follows.

1. Determine the research variables.
2. Creating a research path diagram.
3. Conduct the research experiment.
4. Estimating the path coefficient using the Weighted Least Squares Method
5. Conduct hypothesis testing on the path coefficient.
6. Checking the validity of the model using the coefficient of determination.
7. Interpreting the magnitude of the path analysis coefficient and the influence in the model formed.

RESULTS AND DISCUSSION

Modified Weighted Least Squares

The parameter estimation used for path analysis that will be developed in this study is Weighted Least Square (WLS). This is because the errors are not identical resulting in unequal error variances. For each *i*, denoted $var(\varepsilon_i) = \sigma_i{}^2$ so the OLS method cannot be done because the OLS method has the assumption that the errors are identical (homogeneity in the error variance). In order to ε_i fulfill the identical assumption, then the transformation is carried out by multiplying ε_i with **W**. The diagonal matrix whose elements consist of the component vectors **W** is called the weighting matrix where **W** is equal to $\hat{\mathbf{\Sigma}}^{-1}$. The WLS method estimates the parameters by minimizing the following equation.

$$\begin{aligned}\varepsilon^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\varepsilon &= (\underset{\sim}{YZ}-\mathbf{X}\underset{\sim}{\beta})^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}(\underset{\sim}{YZ}-\mathbf{X}\underset{\sim}{\beta}) \qquad (1)\\ &= (\underset{\sim}{YZ}-\mathbf{X}\underset{\sim}{\beta})^{\mathrm{T}}(\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}-\hat{\mathbf{\Sigma}}^{-1}\mathbf{X}\underset{\sim}{\beta})\\ &= \underset{\sim}{YZ}^{\mathrm{T}}\,\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}-\underset{\sim}{YZ}^{\mathrm{T}}\,\hat{\mathbf{\Sigma}}^{-1}\mathbf{X}\underset{\sim}{\beta}-\underset{\sim}{\beta}^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}+\underset{\sim}{\beta}^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\mathbf{X}\underset{\sim}{\beta}\end{aligned}$$

In accordance with the properties of the rotate matrix where $\underset{\sim}{\beta}^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}=\underset{\sim}{YZ}^{\mathrm{T}}\,\hat{\mathbf{\Sigma}}^{-1}\mathbf{X}\underset{\sim}{\beta}$

$$\varepsilon^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\varepsilon=\underset{\sim}{YZ}^{\mathrm{T}}\,\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}-2\underset{\sim}{\beta}^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ}+\underset{\sim}{\beta}^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\mathbf{X}\underset{\sim}{\beta}$$

Minimum value $\varepsilon^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\varepsilon$ obtained when $\dfrac{\partial(\underset{\sim}{\varepsilon}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{\varepsilon})}{\partial\underset{\sim}{\beta}}=\underset{\sim}{0}$ thus obtaining the following estimates:

$$\hat{\underset{\sim}{\beta}}=(\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\mathbf{X})^{-1}\mathbf{X}^{\mathrm{T}}\hat{\mathbf{\Sigma}}^{-1}\underset{\sim}{YZ} \qquad (2)$$

The form of the $\hat{\mathbf{\Sigma}}_{mm}$ matrix used will follow the following matrix.

$$\hat{\mathbf{\Sigma}}=\begin{bmatrix}\hat{\mathbf{\Sigma}}_1 & \hat{\mathbf{\Sigma}}_{12} & \cdots & \hat{\mathbf{\Sigma}}_{1m}\\ \hat{\mathbf{\Sigma}}_{12} & \hat{\mathbf{\Sigma}}_2 & \cdots & \hat{\mathbf{\Sigma}}_{2m}\\ \vdots & \vdots & \ddots & \vdots\\ \hat{\mathbf{\Sigma}}_{1m} & \hat{\mathbf{\Sigma}}_{2m} & \cdots & \hat{\mathbf{\Sigma}}_m\end{bmatrix}_{m\times m} \qquad (3)$$

Assuming the correlation between the residuals of each pure endogenous variable relationship, the correlation calculation of the errors in each response has the form of correlation and weighted variance matrix of size $mn \times mn$ where $m =$ the number of pure endogenous variables plus intervening endogenous variables as shown in equation below.

$$\hat{\Sigma}=\begin{bmatrix}
\hat{\sigma}_1^2 & 0 & \cdots & 0 & \hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & 0 & \cdots & 0 & \cdots & \hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m & 0 & \cdots & 0\\
0 & \hat{\sigma}_1^2 & \cdots & 0 & 0 & \hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & \cdots & 0 & \cdots & 0 & \hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m & \cdots & 0\\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & \cdots & \vdots & \vdots & \ddots & \vdots\\
0 & 0 & \cdots & \hat{\sigma}_1^2 & 0 & 0 & \cdots & \hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & \cdots & 0 & 0 & \cdots & \hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m\\
\hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & 0 & \cdots & 0 & \hat{\sigma}_2^2 & 0 & \cdots & 0 & \cdots & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m & 0 & \cdots & 0\\
0 & \hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & \cdots & 0 & 0 & \hat{\sigma}_2^2 & \cdots & 0 & \cdots & 0 & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m & \cdots & 0\\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & \cdots & \vdots & \vdots & \ddots & \vdots\\
0 & 0 & \cdots & \hat{\rho}_{12}\hat{\sigma}_1\hat{\sigma}_2 & 0 & 0 & \cdots & \hat{\sigma}_2^2 & \cdots & 0 & 0 & \cdots & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m\\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots\\
\hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m & 0 & \cdots & 0 & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m & 0 & \cdots & 0 & \cdots & \hat{\sigma}_m^2 & 0 & \cdots & 0\\
0 & \hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m & \cdots & 0 & 0 & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m & \cdots & 0 & \cdots & 0 & \hat{\sigma}_m^2 & \cdots & 0\\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & \cdots & \vdots & \vdots & \ddots & \vdots\\
0 & 0 & \cdots & \hat{\rho}_{1m}\hat{\sigma}_1\hat{\sigma}_m & 0 & 0 & \cdots & \hat{\rho}_{2m}\hat{\sigma}_2\hat{\sigma}_m & \cdots & 0 & 0 & \cdots & \hat{\sigma}_m^2
\end{bmatrix}_{mn\times mn} \quad (4)$$

Descriptive Statistics of Fly Arrivals And Skin Defect Areas

The research that has been conducted shows that the location of cattle defects is widest in the cheek and belly areas as shown in Figure 1, which presents a frequency graph of cattle defect area by body location. Five areas were observed: cheek, shoulders, body, hips and Abdomen.

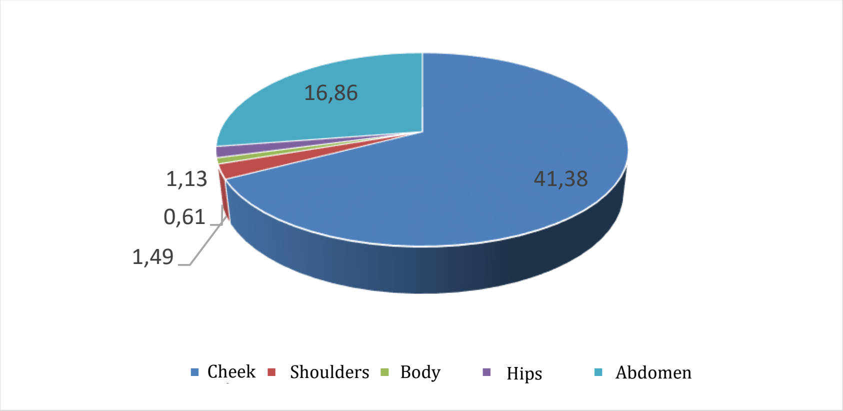

Figure 1. Pie Chart of Cattle Defect Area by Location

Most cattle defects are located on the cheek and belly, so more attention needs to be paid to the prevention of defects on the cheek and belly of cattle. Therefore, this study focuses on the cheek and belly area of cattle. The cheek and belly area of cattle is an area that often interacts directly with the environment and is susceptible to exposure to microorganisms such as bacteria and parasites. In addition, the skin in the cheek and belly area tends to be thinner with less fat layer and connective tissue compared to the torso, hips and shoulders. This thinness is accompanied by less fat and connective tissue, which results in less protection against mechanical stress or impact. As a result, these areas are more prone to damage when exposed to external stresses, such as when cattle lie on hard or rough surfaces. The combination of direct contact with the environment and weaker skin structure makes the cheeks and belly vulnerable points for skin problems. On the other hand, the results of the descriptive analysis also showed that the dominant families of flies coming to cattle body parts were flies from the Chloropidae and Muscidae families. This is shown by the pie chart image in Figure 2.

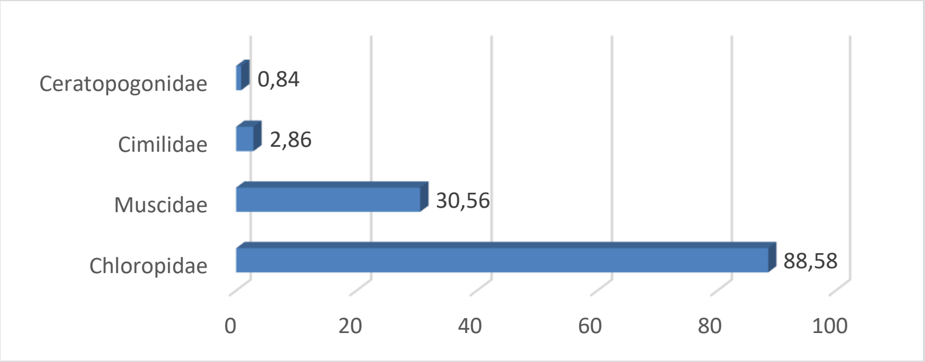

Figure 2. Frequency of Fly Arrival by Family

Flies of the Chloropidae family, often known as grass flies, are attracted to moist and warm areas of the cattle's body, such as the eyes and nose, where they can find a food source in the form of body fluids. In addition, the cattle's body environment, which provides stable warmth and moisture, is an ideal place for these flies to breed. Flies from the Muscidae family, such as houseflies, also frequently land on cattle because they are attracted to organic matter such as sweat, blood and feces found on the skin of cattle. These flies often act as disease vectors, transferring pathogens from one cattle to another, especially through open wounds or moist areas on the skin. The presence of flies from both families is also influenced by environmental factors, such as food availability, temperature and humidity, which are often optimal in areas where cattle are kept. Therefore, this study focused on the infestation of Chloropidae and Muscidae flies while assessing the temperature and humidity of the housing area. The research conceptual model and beta coefficient are shown in Figure 3.

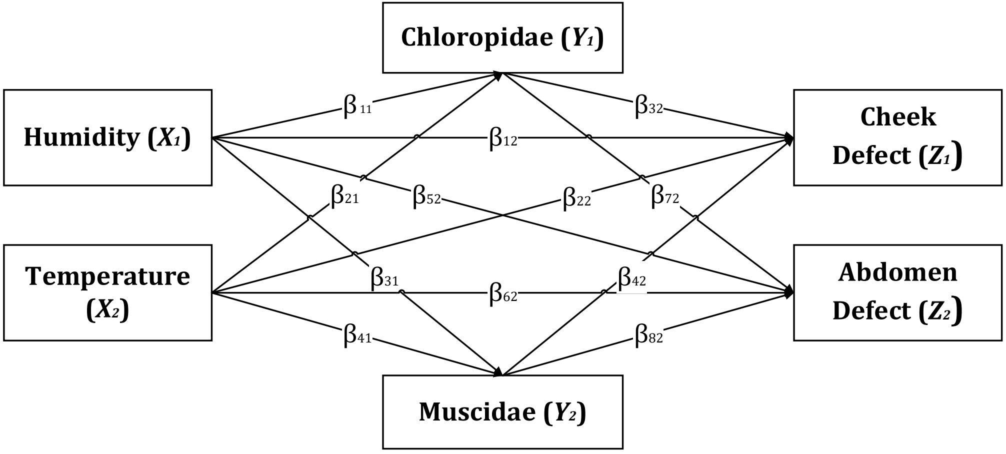

Figure 3. Research Conceptual Model

The results were obtained based on the help of R software with beta parameter values and p-values as shown in the following table.

Table 2. Table of Parameter Values and p-values

Relationship	Parameters	Beta Value	SE	p-value	Description
$X_1 \rightarrow Y_1$	β_{11}	-2,896	1,014	0,005	Sig
$X_2 \rightarrow Y_1$	β_{21}	-5,483	1,679	0,002	Sig
$X_1 \rightarrow Y_2$	β_{12}	-0,596	1,014	0,558	Not Sig
$X_2 \rightarrow Y_2$	β_{22}	-0,790	1,679	0,639	Not Sig
$X_1 \rightarrow Z_1$	β_{13}	0,904	1,037	0,386	Not Sig
$X_2 \rightarrow Z_1$	β_{23}	-3,969	1,741	0,025	Sig
$Y_1 \rightarrow Z_1$	β_{33}	0,847	0,114	0,000	Sig

Relationship	Parameters	Beta Value	SE	p-value	Description
$Y_2 \rightarrow Z_1$	β_{43}	0,320	0,296	0,023	Sig
$X_1 \rightarrow Z_2$	β_{14}	-0,760	1,037	0,466	Not Sig
$X_2 \rightarrow Z_2$	β_{24}	1,248	1,740	0,475	Not Sig
$Y_1 \rightarrow Z_2$	β_{34}	0,096	0,113	0,397	Not Sig
$Y_2 \rightarrow Z_2$	β_{44}	0,264	0,296	0,374	Not Sig

Based on Table 2, the path analysis equation model is obtained as equation below.

$$Y_{1i} = 411{,}908 - 2{,}896\,X_{1i} - 5{,}483\,X_{2i} + \varepsilon_{1i}$$
$$Y_{2i} = 86{,}995 - 0{,}596\,X_{1i} - 0{,}790\,X_{2i} + \varepsilon_{2i}$$
$$Z_{1i} = 25{,}826 + 0{,}904\,X_{1i} - 3{,}969\,X_{2i} + 0{,}847\,Y_{1i} + 0{,}320\,Y_{2i} + \varepsilon_{3i}$$
$$Z_{2i} = 4{,}504 - 0{,}760\,X_{1i} - 1{,}248\,X_{2i} + 0{,}096\,Y_{1i} + 0{,}264\,Y_{2i} + \varepsilon_{4i}$$

where i is the index for the i^{th} object of n in each variable

The results of the analysis show that there are several variable relationships that have significant and insignificant effects. Humidity and temperature had an effect on the arrival of Chloropidae flies, while humidity and temperature had no effect on the arrival of Muscidae flies. Humidity and temperature play an important role in influencing the arrival of flies from the Chloropidae family. Chloropidae flies are very sensitive to changes in environmental conditions, especially humidity and temperature. High humidity and warm temperatures create an ideal environment for the development and activity of these flies. Under these conditions, Chloropidae flies are more active in searching for hosts, such as cattle, as they need moisture to maintain water balance in their bodies and optimal temperatures for reproduction and metabolic activities. In contrast, flies from the Muscidae family have a higher tolerance to variations in humidity and temperature. These flies are known to be more adaptive and able to survive in a wide range of environmental conditions, including suboptimal environments. Therefore, the arrival of Muscidae flies on cattle is less influenced by humidity and temperature, but more dependent on the availability of food sources and suitable breeding sites. According to [13], this difference is due to the evolutionary adaptation of the two fly families, where Muscidae flies have evolved to survive in more diverse environmental conditions, while Chloropidae flies are more dependent on specific microclimate conditions for fly survival.

Temperature had an effect on the area of cattle skin defects on the cheek, while humidity had no effect on the area of cattle skin defects on the cheek. Temperature affects the area of cattle skin defects on the cheek because the cheek is an area that is more exposed to the external environment. The cheek has a thinner skin layer and is more sensitive to temperature changes, which can cause skin damage faster than other areas. Rising temperatures can worsen this condition by accelerating skin dehydration and increasing the activity of damaging microorganisms. In contrast, humidity has no significant effect on the extent of skin defects on the cheeks as the skin in this area may be more resistant to fluctuations in humidity, or due to other factors such as better air circulation around the face. On the belly, neither temperature nor humidity had any effect on the extent of the cattle skin defect. This could be due to several factors. Firstly, the skin in the abdominal area is usually thicker and better protected by the subcutaneous fat layer, which provides additional protection against environmental fluctuations. Secondly, the belly is often less directly exposed to the external environment, reducing the impact of temperature and humidity. Thirdly, the skin on the abdomen may have a better circulatory system, which helps in maintaining skin integrity despite changes in temperature or humidity. According to [24] the skin thickness and better natural protection in the bovine abdomen area make it less susceptible to external influences such as temperature and humidity than other areas such as the cheeks.

The arrival of flies from the Chloropidae and Muscidae families can influence the increase in the area of defects on cattle, particularly on the cheeks, but not on the abdomen. These flies are known as disease vectors and can cause irritation on the skin of livestock. Chloropidae and Muscidae flies are often attracted to the face and head area of animals due to appealing secretions, such as tears and other fluids. On the cheek area, which is open and more exposed, these flies can cause wounds due to biting or licking activity, which eventually leads to an increase in the defect area. On the other hand, the cattle’s abdomen is more protected, has thicker skin, and lacks the secretions that attract flies, so these flies do not have a significant impact on that area. Additionally, repeated fly activity in a specific area, such as the cheeks, can cause ongoing irritation that disrupts the wound healing process. This can enlarge the defect area on the cheek. Conversely, the protected abdomen area does not experience as extensive defect enlargement as the cheek area.

CONCLUSIONS

This study shows that the largest defect areas on cattle occur in the cheek and abdomen regions. Environmental factors such as temperature and humidity play different roles in influencing the defect area in these regions. Temperature has been shown to significantly affect the increase in defect area on the cheeks, while humidity has no effect. In the abdomen area, neither temperature nor humidity has a significant impact on the defect area. Additionally, the presence of flies from the Chloropidae and Muscidae families also contributes to the increase in defect area on the cheeks but not on the abdomen. These flies tend to attack the cheek area because it has thinner and more exposed skin, while the abdomen is more protected.

There are several steps that need to be taken to reduce and prevent the increase in defect area on cattle, particularly in the cheek and abdomen regions. First, preventive and control measures should be implemented against flies, especially those from the Chloropidae and Muscidae families, which have been shown to significantly contribute to skin damage in the cheek area. Measures such as using fly traps, safe insecticide sprays, and maintaining the cleanliness of the barn environment should be strengthened. In addition, efforts should be made to protect the cattle’s skin from extreme temperatures, particularly in the more vulnerable cheek area. Using protective covers or coatings on exposed areas can help reduce the risk of skin damage due to high temperatures. Furthermore, managing the cattle's environment, particularly by keeping temperature and humidity at optimal levels, is important. Good ventilation and appropriate temperature regulation can help maintain the health of the cattle’s skin and prevent further damage. Regular monitoring of the cattle’s skin condition, especially on the cheeks and abdomen, should be part of the maintenance procedure. With early detection and proper treatment, skin damage can be prevented before it becomes a more serious problem. Further research is needed to explore other factors that may influence the defect area on cattle, including genetic aspects and specific microclimate conditions that may contribute to the vulnerability of cattle skin to damage.

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