Evaluation of Linear Models and Linear Mixed Models to Predict the Effects of Antimicrobial Peptides on Broiler Performance

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Abstract. This study aims to evaluate linear models and linear mixed models that were built based on the database of effect Antimicrobial Peptide (AMP) on broiler performance. The method of this research consists of compiling a database, making models, and evaluating models. The database compiled from a comparative study related to the effect of AMP on body weight, average daily gain, daily feed intake, and the feed conversion ratio from broilers reared at 1-21 days. The model consists of five Linear Models (LM) and five Linear Mixed Models (LMM). The best model determined by Bayesian Information Criteria (BIC) and then the correlation value calculated according to actual vs. predicted value. Based on the lowest BIC value, the representative model for body weight, average body weight gain, and average feed consumption are model 9. Besides that, the feed conversion ratio relates to model 2. Model 9 is a linear mixed model with levels as fixed effects and random effects consisting of studies, broiler breeds, type of peptides, and treatment methods. In conclusion, LMM is better than LM in predicting complex problems such as comparative studies of the effects AMP on broiler performance.

1. Introduction

Recently, the study of big data analysis becomes increasing. One of them is a meta-analysis. A meta-analysis is a sophisticated tool. The meta-analysis used to find out the general conclusions from a case. In nutrition and feed science, meta-analysis used to quantify the dose or level of addition of feed additive. Meta-analysis has much variety based on fundamental methods, one of which is a Linear Mixed Model (LMM). LMM developed from Linear Model (LM). LMM consists of fixed effects and random effects. The fixed effect is the level or dose. Reversely, the random effect is the other factor such as experimental design, type or breed of livestock, ingredient, and study variation. As stated by Sauvant *et al*., LMM is one of the foundations for construct meta-analysis [1].

2. Material and methods

2.1. Data collection

Data obtained from various literature and the main topic of literature was "Effect of AMP on broiler performance". The database consisting of body weight (bw) (grams), average daily gain (adg) (grams/head /day), daily feed intake (dfi) (grams/head/day), and feed conversion ratio (fcr). The database tabulated in Table 1.

Table 1. Database of effect antimicrobial peptide on broiler performance (reared at 1-21 days)

study	broiler	peptide	level	bw	adg	dfi	fcr	Reference
1	AA	free	0	700.00	28.32	41.23	1.46	[2]
1	AA	PAMP	150	843.33	35.30	41.11	1.16	
1	AA	PAMP	200	868.32	36.48	41.29	1.13	
2	ROSS 308	free	0	696.00	31.05	50.19	1.62	[3]
2	ROSS 308	agp	10	763.00	34.24	53.14	1.55	
2	ROSS 308	PP	2500	690.00	30.76	49.29	1.60	
2	ROSS 308	PP	5000	747.00	33.48	53.29	1.59	
2	ROSS 308	PP	7500	752.00	33.71	52.81	1.57	
3	ROSS 308	free	0	737.00	33.00	53.05	1.61	[4]
3	ROSS 308	agp	15	776.00	34.86	54.43	1.56	
3	ROSS 308	AMP-A3	60	747.92	33.52	53.48	1.60	
3	ROSS 308	AMP-A3	90	765.98	34.38	54.10	1.57	
4	ROSS 308	free	0	803.99	36.19	55.95	1.55	[5]
4	ROSS 308	agp	15	857.00	38.71	56.95	1.47	
4	ROSS 308	AMP-P5	40	821.00	37.00	56.52	1.53	
4	ROSS 308	AMP-P5	60	836.96	37.76	56.71	1.50	
5	ROSS 308	free	0	774.33	34.91	48.73	1.41	[6]
5	ROSS 308	lysozyme	70	818.50	37.04	48.78	1.33	
5	ROSS 308	lysozyme	90	813.66	36.75	48.42	1.33	
5	ROSS 308	lysozyme	120	814.50	36.83	49.12	1.35	
6	ROSS 308	free	0	1,016.00	46.29	60.14	1.30	[7]
6	ROSS 308	SBP	1000	1,034.00	47.14	60.67	1.29	
6	ROSS 308	SBP	2000	1,037.00	47.29	60.43	1.28	
6	ROSS 308	SBP	3000	1,026.00	46.76	60.52	1.30	
6	ROSS 308	SBP	4000	1,011.00	46.05	59.10	1.28	
6	ROSS 308	SBP	5000	1,041.00	47.48	59.86	1.26	
6	ROSS 308	SBP	6000	1,031.00	47.00	58.57	1.25	
7	AA	free	0	704.95	31.46	51.38	1.63	[8]
7	AA	agp	10	753.88	33.79	48.70	1.44	
7	AA	plectasin	100	717.97	32.08	46.70	1.44	
7	AA	plectasin	200	709.99	31.70	45.64	1.44	
8	Cobb 500	free	0	874.40	39.67	58.90	1.48	[9]

study	broiler	peptide	level	bw	adg	dfi	fcr	Reference
8	Cobb 500	SBP	1000	905.40	41.14	58.00	1.41	
8	Cobb 500	SBP	2000	912.40	41.48	58.33	1.41	
8	Cobb 500	SBP	3000	925.40	42.10	58.38	1.39	
8	Cobb 500	SBP	4000	943.40	42.95	58.90	1.37	
8	Cobb 500	SBP	5000	1,013.40	46.29	58.62	1.27	

level, (mg/kg); bw, body weight (g/h/d); adg, average daily gain (g/h/d); dfi, daily feed intake (g/h/d); fcr, feed conversion ratio; AA, Arbor Acres; PAMP, pig antimikrobial peptida; agp, antibiotic growth promoter; PP, potato protein; SBP, soybean bioactive peptide.

2.2. Build and evaluate the model
The model was built using R programming language version 3.6.0, library("nlme"), and library("lme4").[10, 11, 12] The model was five linear models and five linear mixed models with the formula syntax in Table 2.

Table 2. Syntax formula of the linear model and linear mixed model

Model i	Syntax formula	Type	Fixed effect	Random effect
1	y <- lm(y ~ level, data=data)	LM	level	
2	y <- lm(y ~ level + peptide, data=data)	LM	level, peptide	
3	y <- lm(y ~ level + peptide + treatment, data=data)	LM	level, peptide, treatment	
4	y <- lm(y ~ level + peptide + treatment + broiler, data=data)	LM	level, peptide, treatment, broiler	
5	y <- lm(y ~ level + peptide + treatment + broiler + study, data=data)	LM	level, peptide, treatment, broiler, study	
6	y <- lmer(y ~ level + (1|peptide), data=data)	LMM	level	peptide
7	y <- lmer(y ~ level + (1|peptide) + (1|treatment), data=data)	LMM	level	peptide, treatment
8	y <- lmer(y ~ level + (1|peptide) + (1|treatment) + (1|broiler), data=data)	LMM	level	peptide, treatment, broiler
9	y <- lmer(y ~ level + (1|peptide) + (1|treatment) + (1|broiler) + (1|study), data=data)	LMM	level	peptide, treatment, broiler, study
10	y <- lmer(y ~ level + (1|peptide) + (1|treatment) + (1|broiler) + (1|study) + (1|broiler:treatment:study), data=data)	LMM	level	peptide, treatment, broiler, study, interaction

LM, linear model; LMM, linear mixed model.

The best model was chosen based on the smallest Bayesian Information Criterion (BIC) value and then measured its Person correlation value using actual data vs. predictive data [13, 14].

3. Results and discussion

According to Schwarz, BIC used to select the best model from a limited set of models.[13] Model 9 preferred for body weight, average daily gain, and daily feed intake. Meanwhile, model 2 is more intended for the feed conversion ratio. Model 9 is LMM with a level as a fixed effect and random effect consisting of the peptide, treatment, broiler, and research. Model 2 is LM with level and peptide as fixed effects. Model 2 preferred for the fcr parameter. It assumed if fcr is ratio value, so the random effects from broiler and peptide will disappear. The Bayesian information criteria are in Table 3.

Table 3. Bayesian information criterion values

Model i	BIC			
	bw	adg	dfi	fcr
1	458.71	234.87	237.66	-33.79
2	443.53	222.21	223.90	-62.59
3	443.53	222.21	223.90	-62.59
4	441.45	218.03	211.98	-58.79
5	429.58	197.24	189.76	-60.82
6	426.76	216.33	222.18	-43.93
7	430.37	219.94	225.79	-40.32
8	432.33	220.51	216.12	-36.72
9	392.71	180.93	174.36	-62.47
10	396.20	184.38	176.28	-62.35

BIC, Bayesian Information Criterion; bw, body weight (g/h/d); adg, average daily gain (g/h/d); afi, average feed intake (g/h/d); fcr, feed conversion ratio.

Pearson correlation value for the model built using bodyweight, average daily gain, and daily feed intake were 0.98, 0.99, and 0.98, respectively. Pearson correlation >0.90 this means that the actual value strongly correlated with the predicted value (model 9).[14] Besides that, the feed conversion ratio was 0.89, which means it is moderately correlated.

Table 4. Selected model and Person correlation value (actual vs. predictive)

	bw	sdg	dfi	fcr
Model i	9	9	9	2
Correlation	0.9896	0.9901	0.9876	0.8936

bw, body weight (g/h/d); adg, average daily gain (g/h/d); dfi, daily feed intake (g/h/d); fcr, feed conversion ratio.

4. Conclusion

It can be concluded, based on the BIC, the database of effect antimicrobial peptide on broiler performance can be described well using a linear mixed model (model 9) dan linear model (model 2). The random effect consists of studies, broiler breeds, type of peptides, and treatment that can be estimated by LMM.

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