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USE OF MULTIVARIATE ADAPTIVE REGRESSION SPLINES (MARS) FOR PREDICTING PARAMETERS OF BREAST MEAT IN QUAILS

T. Şengül[*1], Ş. Çelik[1] and Ö. Şengül[2]

[1]Bingöl University, Faculty of Agriculture, Department of Anim. Sci. Bingöl, 12000, Turkey
[2]Uludağ University, Faculty of Agriculture, Department of Anim. Sci. Bursa, 16000, Turkey
[*]Corresponding Author E-mail: tsengul2001@yahoo.com

ABSTRACT

The aim of this study was to determine the effects of variety and sex on the color of the breast meat (brightness: L^*, red color: a^*, yellow color: b^*) in quails. In this study, a total of 144 quails from three different varieties (Wild-type, Dark Brown and Golden) were employed. The color and pH parameters of the breast meat were measured in quails slaughtered in week 10. In order to predict the brightness (L^*), red color (a^*), and yellow color (b^*) values of the breast meat, Multivariate Adaptive Regression Splines (MARS) models were implemented. When determining the best model, attention was paid to minimize the Generalized Cross Validation (GCV), Root Mean Square Error (RMSE), and Mean Absolute Deviation (MAD) statistics and to maximize coefficient of determination (R^2) and adjusted R^2 values. In the MARS models constructed to predict L^*, a^* and b^*, it was found that R^2 values were 0.999, 0.999, and 0.999; adjusted R^2 values were 0.997, 0.992, and 0.996; and RMSE values were 0.068, 0.082, and 0.038, respectively. As a result, it could be suggested that MARS modeling may be a useful tool for the prediction of the color parameters of the breast meat.

Keywords: Quail, breast meat, meat color, MARS model.

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INTRODUCTION

Meat color in poultry is affected by age, sex, genotype, feed, intramuscular fat distribution, water content of meat, pre-slaughter conditions, and processing techniques (Froning, 1995). Meat color is dependent largely on myoglobin concentration and partially on the presence of pigments such as hemoglobin in the medium. The discoloration of meat can be attributed to the amount of such pigments contained in the meat. The chemical structure of pigments, and ultimately, the rate of reflection of light that falls on meat change (Northcutt, 2007). The color of poultry meat varies from bluish white to yellow, depending on race, exercise, age and diet.

It was reported that characteristics associated with the color of meat in quails are usually hereditary to a moderate to high extent, and it may be the case that there is an effect of genes linked to sex (Mir et. al., 2017).An argument has emerged that genetics has a predominant role in the control of meat quality characteristics such as color and pH. Selection studies carried out to improve live weight have influenced the quality of meat. As live weight increases, water and protein levels in the carcass decrease, and the carcass fat, number of muscle fibers, muscle fiber lengths (Skiba *et al*., 2012). Heritability values of certain meat quality characteristics in Japanese quails were estimated for brightness (L^*)=0.23, red color (a^*)=0.45, and yellow color (b^*)=0.22 (Oguz *et al*., 2004). In chickens, sex was reported to be an influential factor on many parameters of meat quality (Mehaffey *et al*., 2006; Jaturasitha *et al*., 2008).

The color of quail meat is darker than that of chicken meat, and lighter than that of goose meat. Quails' breast and thigh muscles have almost no fatty tissue (Riegel *et al*., 2003). Muscle fibers are separated by a thin connective tissue giving the characteristic taste of the meat (Hejnowska *et al*., 1999). López *et al*. (2011) reported that there was a significant relationship between sex and the pH ($P<0.05$) of the breast meat in the 24 hours after chickens are slaughtered. They have indicated that female chickens have a lower pH than male chickens. Tougan *et al*. (2013) reported that the taste of meat diminishes as the slaughter age decreases in poultry, but juiciness and tenderness increase. Bilal and Bostan (1996) informed that in quails, age affects the composition of carcass, and sex affects carcass yield.

Narinc *et al*. (2013) reported that the final pH, L^*, a^* and b^* color values of breast meat quality characteristics of 5-week-old broilers were found 5.94, 43.09, 19.24 and 7.74, respectively. The authors have reported that there was a high and negative correlation between pH and body weight, and a lower and positive correlation between the L^* value and these characteristics ($P<0.05$). Remignon *et al*. (1998) reported that long-term stress increases the pH of breast meat in quails, but does not affect the L^*, a^* and b^* color values. Genchev *et al*. (2008) have determined that the L^*, a^* and b^* values of the breast meat 30 minutes, 24 hours and 7 days after the slaughter of 5-week-old quails were 43.22, 8.02, 11.04;

40.81, 10.16, 9.55; and 45.67, 11.68, 14.48, respectively. In the earlier study reported that color parameters (L^*, a^* and b^*) in the meat of young and old quails were determined to be 58.93, 12.86, 20.86 and 61.54, 6.84, 19.81, respectively (Boni *et al.*, 2010). Nasirifar *et al.* (2016) found that the L^*, a^* and b^* color values were 37.8, 37.9; 11.9, 13.1; and 12.8, 14.5, respectively for male and female quails aged 2 weeks.

With the scope of buying preference of consumers, the meat color characteristics were determinative factors. To make an accurate decision in determining factors affecting the characteristics, use of sophistical statistical methods is recommendable. In this concept, more emphasis on powerful statistical approaches i.e. Artificial Neural Networks (ANNs) and MARS is still required in literature. There were a few of animal science studies on MARS modeling. (Aytekin *et al.*, 2018; Celik and Yilmaz, 2018; Celik *et al.*, 2018; Erturk, 2018; Erturk *et al.*, 2018; Aksoy *et al.*, 2018a; Aksoy *et al.*, 2018b, Sahin *et al.*, 2018; Aksoy *et al.*, 2019; Celik, 2019). However, to our best knowledge, the published information on predicting color parameters of the quail breast meat through MARS data mining algorithm has not yet been documented. To fill this gap in poultry literature, an attempt was made in the present investigation to find factors affecting brightness (L^*), red color (a^*) and yellow color (b^*) characteristics in the breast meat of 10-week-old male and female quails through MARS modeling.

MATERIALS AND METHODS

Material: The animal materials of the research consisted of a total of 144 Japanese quails from 3 different varieties, which were raised in the research coop of the Department of Animal Sciences at Bingol University, Faculty of Agriculture, Bingol province located in Eastern Anatolia Region of Turkey. The Wild-type, Dark Brown and Golden quails were used as the quail varieties. The quails were placed into space compartments as 3 replicates where there were 48 male and female quails from each variety in each compartment. Throughout the entire trial period, the animals were housed in the same compartments. The study was carried out for 10 weeks. The trial was designed as to have 6 groups and 8 quails in each replication. The quails were fed with feed containing 23% raw protein and 3100 kcal/kg ME in the first week, and with feed containing 20% raw protein and 3250 kcal/kg ME in the consequent weeks. At the end of the fattening period (week 10), 4 animals were slaughtered from each group, and brightness (L^*), red color (a^*), yellow color (b^*) and pH were measured in their breast meat (skinless). A Lovibond (RT SERIES for MODEL SP60) was used to determine the color of the meat, and a Testo 205 device was used to measure the pH level.

Method: Three different MARS models were implemented separately for different dependent variables (L, a^* and b^*) to identify whether meat color in quails was affected by variety (Wild-type, Dark Brown and Golden) and sex (male and female). These models were as follows:

Model 1: The dependent variable was L^*, and the independent variables were a^*, b^*, pH, sex, and variety.

Model 2: The dependent variable was a^*, and the independent variables were L^*, b^*, pH, sex, and variety.

Model 3: The dependent variable was b^*, and the independent variables were L^*, a^*, pH, sex, and variety.

In these models, variety and sex were factors, whereas L^*, a^*, b^*, and pH were treated as continuous variables.

The MARS model is one of the methods used to reveal the effects of independent variables on a dependent variable when analyzing data. This method is a multivariate non-parametric regression technique developed by Friedman (1991) that uses complex algorithms that can evaluate many variables together.

The MARS algorithm can be rewritten as follows (Eyduran *et al*, 2019):

$$f(x) = \beta_0 + \sum_{m=1}^{M} \beta_m \prod_{k=1}^{K_m} h_m(X_{v(k,m)})$$

Where

f(x) is the predicted value of the dependent variable, β_0 is an intercept, $h_m(X_{v(k,m)})$ is the basis function, where $v(k,m)$ is an index of the predictor for the m_{th} component of the k_{th} product, K_m is the parameter controlling the order of interaction.

After building the most suitable MARS model, the basis functions that did not contribute much to the model fitting performance were eliminated in the pruning process based on the following generalized cross-validation error (GCV) (Koronacki and Ćwik 2005):

$$GCV(\lambda) = \frac{\sum_{i=1}^{n}\left(y_i - y_{ip}\right)^2}{\left(1 - \frac{M(\lambda)}{n}\right)^2}$$

Where:

n is the number of training cases, y_i is the observed value of a response variable, y_{ip} is the predicted value of a response variable, $M(\lambda)$ is a penalty function for the complexity of the model with λ terms.

To measure the predictive performance of MARS, the following goodness of fit criteria were calculated (Willmott and Matsuura, 2005; Takma *et al.*, 2012; Ali *et al.*, 2015);

1. Coefficient of Determination

$$R^2 = 1 - \frac{\sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2}{\sum_{i=1}^{n}(Y_i - \bar{Y})^2}$$

2. Adjusted Coefficient of Determination

$$Adj.R^2 = 1 - \frac{\frac{1}{n-k-1}\sum_{i=1}^{n}\left(Y_i - \hat{Y}_i\right)^2}{\frac{1}{n-1}\sum_{i=1}^{n}(Y_i - \bar{Y})^2}$$

3. Root-mean-square error (RMSE) presented by the following formula;

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2}$$

4. Standard deviation ratio (SD_{ratio});

$$SD_{ratio} = \sqrt{\frac{\frac{1}{n-1}\sum_{i=1}^{n}(\varepsilon_i - \bar{\varepsilon})^2}{\frac{1}{n-1}\sum_{i=1}^{n}(Y_i - \bar{Y})^2}}$$

SD ratio estimates should be less than 0.40 for a good fit explained by some authors (Grzesiak *et al.*, 2003; Grzesiak and Zaborski, 2012).

5. Mean absolute deviation (MAD):

$$MAD = \frac{1}{n}\sum_{i=1}^{n}\left|Y_i - Y_{ip}\right|$$

where: n is the number of cases in a set, k is the number of model parameters, Y_i is the actual (observed) value of an output variable, Y_{ip} is the predicted value of an output variable, s_m is the standard deviation of model errors, s_d is the standard deviation of an output variable.

Statistical evaluations on MARS algorithm was specified using STATISTICA program (12.5 version). See the book of Eyduran *et al.* (2019) to obtain more detailed information about MARS algorithm.

RESULTS

L^* (brightness) value: A MARS model was constructed by selecting variety, sex, a^*, b^* and pH as independent variables to predict the L^* value of the breast meat. Model fit statistics for the L^* are presented in Table 1.

Table 1. Model 1 goodness of fit criteria and GCV values according to order of interactions.

Order of int.	Maximum number of BF	Number of BF	Number of terms	GCV	R^2	Adj. R^2	SD_{ratio}	RMSE	MAD
1	80	16	11	1.778	0.961	0.925	0.445	0.738	0.485
1	90	16	11	1.778	0.961	0.925	0.445	0.738	0.485
1	100	16	11	1.778	0.961	0.925	0.445	0.738	0.485
2	80	38	20	0.160	0.999	0.997	0.135	0.068	0.044
2	90	38	20	0.160	0.999	0.997	0.135	0.068	0.044
2	100	38	20	0.160	0.999	0.997	0.135	0.068	0.044

BF: Basis functions, int: interactions

According to the goodness of fit results shown in Table 1, the best model was found to be the MARS model with 20 terms and the second degree interactions. For this model, the parameters were predicted as follows: GCV=0.160, R^2=0.999, Adj. R^2=0.997, SD_{ratio}=0.135, RMSE=0.068 and MAD=0.044. Basis functions and coefficients are given in Table 2 according to the aforementioned model.

Table 2. Results of the Model 1 MARS algorithm (for L^*).

	Basic function	Coefficient
	Constant (intercept)	38.772
BF1	max(0; Female)	18.479
BF2	max(0; b-8,79)*max(0; Female)	3.368
BF3	max(0; a-19.02)*max(0; Female)	30.774
BF4	max(0; 19.02-a)*max(0; Female)	-7.266
BF5	max(0; Wild-type)	-5.468
BF6	max(0; Wild-type)*max(0; Female)	48.052
BF7	max(0; a-15.89)*max(0; b-8.79)*max(0; Female)	-2.810
BF8	max(0; a-15.89)	-3.764
BF9	max(0; a-15.89)*max(0; Dark-Brown)	-1.336
BF10	max(0; a-15.89)*max(0; b-8.79)	0.251
BF11	max(0; a-15.89)*max(0; Wild-type)	-4.478
BF12	max(0; a-15.89)*max(0; Wild-type)*max(0; Female)	-15.370
BF13	max(0; b-8.79)	2.291
BF14	max(0; Dark-Brown)	3.024
BF15	max(0; a-15.89)*max(0; b-8.79)*max(0; Wild-type)	1.680

BF16	max(0; 19.02-a)*max(0; b-12.46)*max(0; Female)	206.121
BF17	max(0; pH-6.38)*max(0; Female)	-10.658
BF18	max(0; 6.38-pH)*max(0; Female)	-19.545
BF19	max(0; b-8.79)*max(0; Golden)*max(0; Female)	-0.633

Explanations for other basis functions and coefficients can be said to be similar to the results given in Table 2. The MARS equation of Model 1 that was obtained according to these results was as follows.

L=38.772+18.479*max(0; Female)+3.368*max(0; b-8.79)*max(0; Female)+30.774*max (0; a-19.02)*max(0; Female)-7.266*max(0;19.02-a)*max(0; Female)-5.468*max(0; Wild-type)+48.052*max(0; Wild-type)*max(0; Female)-2.81*max(0; a-15.89)*max(0; b-8.79)*max(0; Female)-3.764*max(0; a-15.89)-1.336*max(0; a-15.89)*max(0; Dark-Brown)+ 0.251*max(0; a-15.89)*max(0; b-8.79)-4.478*max(0; a-15.89)*max(0; Wild-type)-15.370*max(0; a-15.89)*max(0; Wild-type)*max(0; Female)+2.291*max(0; b-8.79)+3.024*max (0; Dark-Brown)+1.680*max(0; a-15.89)*max(0; b-8.79)*max(0; Wild-type)+206.121*max(0; 19.02-a)*max(0; b-12.46)*max(0; Female)- 10.658*max(0; pH-6.38)*max(0; Female)-19.545*max(0; 6.38-pH)*max(0; Female)-0.633*max(0; b-8.79)*max(0; Golden)*max (0; Female).

Table 3. Predicted L^* values based on the values of independent variables.

a^*	b^*	pH	Variety	Sex	L^*
20	12	6.50	Wild-type	Male	32.262
20	12	6.50	Wild-type	Female	38.235
20	12	6.50	Dark-Brown	Male	31.498
20	12	6.50	Dark-Brown	Female	52.589
20	12	6.50	Golden	Male	33.965
20	12	6.50	Golden	Female	53.023
24	15	6.35	Wild-type	Male	77.945
24	15	6.35	Wild-type	Female	51.868
24	15	6.35	Dark-Brown	Male	27.293
24	15	6.35	Dark-Brown	Female	77.815
24	15	6.35	Golden	Male	35.104
24	15	6.35	Golden	Female	81.692

a^* (red color) value: A MARS algorithm was built by selecting variety, sex, L^*, b^* and pH as independent variables to predict the a^* value of the breast meat. The model fit statistics used to predict a^* using the MARS algorithm are given in Table 4.

Table 4. Model 2 goodness of fit criteria and GCV values according to order of interactions (for a^*).

Order of int.	Maximum number of BF	Number of BF	Number of terms	GCV	R^2	Adj. R^2	SD_{ratio}	RMSE	MAD
2	80	10	7	2.689	0.803	0.718	0.443	1.186	1.025
2	90	10	7	2.689	0.803	0.718	0443	1.186	1.025
2	100	10	7	2.689	0.803	0.718	0.443	1.186	1.025
3	80	12	8	2.619	0.738	0.702	0.540	1.447	1.102
3	80	12	8	2.619	0.738	0.702	0.540	1.447	1.102
3	80	12	8	2.619	0.738	0.702	0.540	1.447	1.102
4	100	40	19	0.242	0.999	0.992	0.031	0.082	0.057

The results of the MARS model including the basis function and the coefficients are presented in Table 5. A MARS model with 23 basis functions and 4-way interactions was selected as the most suitable model. For this model, the parameters were calculated as follows: GCV=3.011, R^2=0.999, Adj. R^2=0.992, SD_{ratio}=0.031, RMSE=0.082 and MAD=0.057.

Table 5. Prediction results of the Model 2 MARS algorithm (for a*).

	Basic function	Coefficient
	Constant (Intercept)	13.621
BF1	max(0; b-12.75)	-3.690
BF2	max(0; 12.75-b)	2.701
BF3	max(0; 38.7-L)	35.313
BF4	max(0; Golden)	1.521
BF5	max(0; b-12.46)* max(0; Golden)	-3.397
BF6	max(0; 12.46-b)* max(0; Golden)	-1.401
BF7	max(0; 38.7-L)* max(0; Golden)	3.353
BF8	max(0; 39.64-L)* max(0; Golden)	-2.055
BF9	max(0; 12.46-b)* max(0; Golden)*	1.357
BF10	max(0; Male)	23.286
BF11	max(0; pH-6.33)	-821.001
BF12	max(0; 6.33-pH)	9.254
BF13	max(0; b-12.24)	-7.872
BF14	max(0; pH-6.38)* max(0; Golden)	-20.650
BF15	max(0; 6.38-pH)* max(0; Golden)	22.809
BF16	L*max(0; 6.33-pH)	-5.826
BF17	max(0; 38.7-L)*pH	-1.675
BF18	max(0; 38.7-L)* max(0; Male) max(0; Male)	1.791

The MARS equation of Model 2 according to these results was as follows.

a= 13.6 + 1.52 * Golden + 1.79 * Male + 35.3 * max(0, 38.7- L) + 9.25 * max(0, b -12.2)+ 2.7 * max(0, 12.8 - b) -3.69 * max(0, b - 12.8) - 821 * max(0, 6.33 - pH)+ 23.3 * max(0, pH - 6.33) + 22.8 * L * max(0, 6.33 -pH) - 5.83 * max(0, 38.7 - L) * pH + 3.35 * max(0, 38.7 - L) * Golden - 2.06 * max(0, 39.6 - L) * Golden +0.318 * max(0, L - 39.6) * Golden - 1.67 * max(0, L - 38.7) * Male -1.4 * max(0, 12.5 - b) * Golden - 3.4 * max(0, b - 12.5) *Golden - 20.7 * max(0, 6.38 - pH) * Golden - 7.87 * max(0, pH - 6.38) * Golden + 1.36 * max(0, b - 12.5) * Golden* Male

b* (yellow color) value: A MARS algorithm was created by selecting variety, sex, L*, a* and pH as independent variables to predict the b* value of the breast meat in quails. The model fit statistics for the MARS algorithm are given in Table 6.

The results of the MARS model including the basis function and the coefficients are presented in Table 7. A MARS model with 21 basis functions and 3-way interactions was obtained as the best model. For this model, the parameters were found as follows: GCV=0.029, R^2=0.999, Adj. R^2=0.996, SD_{ratio}=0.132, RMSE=0.038 and MAD=0.026.

Table 6. Model 3 goodness of fit criteria and GCV values according to order of interactions (for b*).

Order of int.	Maximum number of BF	Number of BF	Number of terms	GCV	R^2	Adj. R^2	SD_{ratio}	RMSE	MAD
2	80	6	5	0.946	0.919	0.897	0.533	0.621	0.480
2	90	6	5	0.946	0.919	0.897	0.533	0.621	0.480
2	100	6	5	0.946	0.919	0.897	0.533	0.621	0.480
3	80	42	21	0.029	0.999	0.996	0.132	0.038	0.026
3	90	42	21	0.029	0.999	0.996	0.132	0.038	0.026
3	100	42	21	0.029	0.999	0.996	0.132	0.038	0.026

Table 7. Prediction results of the Model 3 MARS algorithm (for b*).

	Basic function	Coefficient
	Constant	-10.003
BF1	max(0; a-15.89)	0.763
BF2	max(0; L-31.69)	0.264
BF3	max(0; a-15.89)*max(0; Wild-type)	2.737
BF4	max(0; L-31.69)*max(0; Wild-type)	2.226
BF5	max(0; L-31.69)*max(0; pH-6.16)*max(0; Wild-type)	-2.727
BF6	max(0; a-15.89)*max(0; Dark-Brown)	0.521
BF7	max(0; Dark-Brown)	16.0004
BF8	max(0; L-31.69)*max(0; Dark-Brown)	-0.0009
BF9	max(0; a-15.89)*max(0; pH-6.16)*max(0; Wild-type)	2.653
BF10	max(0; L-31.69)*max(0; pH-6.16)	0.521
BF11	max(0; L-31.69)*max(0; pH-6.16)*max(0; Female)	-0.892
BF12	max(0; Golden)	17.459
BF13	max(0; a-15.89)*max(0; Wild-type)*max(0; Female)	-9.330
BF14	max(0; L-31.69)*max(0; Wild-type)*max(0; Female)	5.656

BF15	max(0; Female)	0.849
BF16	max(0; a-19.02)*max(0; Female)	-0.180
BF17	max(0; 19.02-a)*max(0; Female)	0.029
BF18	max(0; L-31.69)*max(0; Dark-Brown)*max(0; Female)	0.066
BF19	max(0; L-31.69)*max(0; a-15.89)*max(0; Wild-type)	-0.368
BF20	max(0; pH-6.38)*max(0; Female)	2.649

The MARS equation obtained for Model 3 according to these results was as follows.

b*=-10.0031+0,763*max(0; a-15.89)+0.264*max(0; L-31.69)+2.737*max(0; a-15.89)* max(0; Wild-type)+2.226*max(0; L-31.69)*max(0; Wild-type)-2.727*max(0; L-31.69) *max(0; pH-6.16)*max(0; Wild-type)+0.521*max(0; a-15.89)*max(0; Dark-Brown)+16.0004*max(0; Dark-Brown)-0.0009*max(0; L-31.69)*max(0; Dark-Brown)+ 2.653*max(0; a-15.89)*max(0; pH-6.16)*max(0; Wild-type)+0.521*max(0; L-31.69) *max(0; pH-6.16)-0.892*max(0; L-31.69)*max(0; pH-6.16)*max(0; Female)+ 17.459*max (0; Golden)-9.330*max(0; a-15.89)*max(0; Wild-type)*max(0; Female)+ 5.656*max (0; L-31.69)*max(0; Wild-type)*max(0; Female) + 0.849*max(0; Female)- 0.180*max (0; a-19.02)*max(0; Female)+0.029*max(0; 19.02-a)*max(0; Female)+ 0.066*max(0; L-31.69)*max(0; Dark-Brown)*max(0; Female)-0.368*max(0; L-31.69)*max(0; a-15.89) *max(0; Wild-type)+2.649*max(0; pH-6.38)*max(0; Female).

DISCUSSION

The use of the MARS model in the stock farming area is very limited. However, the results obtained in the present study contain much more descriptive findings than commonly used models. The model have been successfully used in the subjects of cattle raising (Aytekin *et al.*, 2018; Ertürk *et al.*, 2018), sheep raising (Karadas *et al.*, 2017; Eyduran *et al.*, 2017) and beekeeping (Aksoy *et al.*, 2018a, Aksoy *et al.*, 2018b).

This study presented detailed information on the definition of the color of the breast meat in quails belonging to different varieties and sexes through the MARS model. $a^*>15.89$, $b^*>8.79$, $pH<6.38$ and female quails had a significant effect on the L* value of the breast meat in quails in general. The factor that affected the L* the most was the basis function with 3-way interactions where $a^*<19.02$, $b^*>12.46$ and the quails were female.

The a* value of the breast meat was positively influenced with interaction $L^*>31.69$ and $b^*>8.79$. However, it was not influenced by sex and the Wild-type variety.

The variables that increased the b* value of breast meat the most were the Golden variety, the Dark-Brown variety, and the $L^*> 31.69$, Wild-type variety and female quail interaction, respectively.

Conclusions: In conclusion, in quails, the L* (Model 1) and b* (Model 3) values were explained better by the MARS model with second degree interactions, while the a* value (Model 2) was defined better by the model with first degree interactions.

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