

Log-linear association models applied to interpretation of inheritance of hoof conformation and health

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Abstract

Twelve 5 by 5 hoof trait contingency tables with 619 to 724 daughter-dam pairs were analyzed by ten different association models: independence, main diagonal, uniform association, fixed distance, mover-stayer, minor diagonals (I), minor diagonals (II), pure distance, loyalty-distance and quasi-symmetry. Six hoof growth traits were heel height, hoof texture, sole thickness, subsole, toe growth and weight transfer and characterized hoof conformation. Six discrete hoof traits were corkscrew claw, heel erosion, interdigital dermatitis, laminitis, sole ulcers and white line separation. One contingency table represented each trait. Independence models for eight traits (heel height, hoof texture, sole thickness, toe growth, weight transfer, corkscrew claw, sole ulcers and white line separation) were not rejected ($G^2 < 26.3$, $P > 0.05$), and implied that genetic associations were not very strong. But, improved best association models were found for five of the eight traits. Eleven of twelve traits had positive uniform association parameters estimated from uniform association model and negative off-diagonal distance parameters estimated from fixed distance model which supported genetic association between daughters and dams. Combining higher probabilities for daughter and dam with neighboring worst scores and improved fit through the best models, evidence of association between scores of daughters and dams for hoof conformation and health was supported for most hoof traits (heel height, hoof texture, subsole, toe growth, corkscrew claw, heel erosion, interdigital dermatitis and laminitis).

Key words: Log-linear association models, Daughter-dam pairs, hoof.

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Introduction

Regression of daughter on dam was a classic approach for heritability estimation of quantitative traits (Kempthorne and Tandon, 1953). For binary categorical traits, Thompson *et al.* (1985) demonstrated how to use the offspring-dam regression for heritability estimation. The heritability estimation for categorical traits varied by different approaches (Huang and Shanks, 1995, van der Waaij *et al.*, 2005). For example, estimate of heritability for liability was several times higher than that for incidence (Thompson *et al.*, 1985). The meaning of heritability was ambiguous without providing corresponding response scale and link function. Furthermore, inheritance patterns might be important for some categorical trait responses, but "estimated heritability" might be unstable as the incidence of extreme responses was rare. Therefore, in addition to estimation of heritability, supplementary approaches should be helpful for analysis of categorical traits.

Several studies demonstrated the importance of environment effects on the hoof traits (Huang *et al.*, 1995; Offer *et al.*, 2005; Leach *et al.*, 2005), but not many genetic evidences were presented. Glicken and Kendrick (1977) found a genetic disposition for hooves growth by chi-square tests, but lack models to show the inheritance pattern. Log-linear models analyzed associations among variables without distinguishing response or explanatory variables. The analysis of log-linear models has rapidly become a major tool of statistical practice for deciphering multidimensional contingency tables (Freeman, 1987). A well organized introduction was in the book of Bishop *et al.* (1975). A set of log-linear models developed by Leo Goodman and Shelby Haberman were popular in the social sciences (Agresti, 1990). Rutledge and Gunsett (1982) suggested that log-linear models might be useful for animal sciences, but more than a decade later applications were still very limited. The objectives of these analyses were (1) to introduce a variety of log-linear models for genetic application and (2) to use log-linear models in interpreting genetic importance of hoof traits.

Materials and Methods

Hoof traits were collected from ten years of trimming through 1992 at dairy farm of University of Illinois. Heel height, hoof texture, sole thickness, subsole, toe growth and weight transfer characterized hoof conformation and were identified as six hoof growth traits. Six discrete hoof traits were corkscrew claw, heel erosion, interdigital dermatitis, laminitis, sole ulcers and white line separation. Scores of 1 to 5 represented each trait from perfect to severe. Holsteins with 429 to 523 daughter-dam pairs were the major breed among the 619 to 724 daughter-dam pairs. Other minor breeds were Ayrshire, Brown Swiss, Guernsey and Jersey. Because available data was limited and all five breeds were dairy breeds, differences due to breed were not considered. Twelve 5 by 5 contingency tables pooled across breeds were built, based on worst score of lifetime for 12 hoof traits. Worst score of lifetime was the worst score of each cow, daughter or dam, from all available records. Due to limited available animals, all cows were included, including those that remained in the herd at end of 1992. Cell counts in the contingency tables were sums of daughter-dam pairs for each score combination, (1, 1), (1,2), ... (5,5). After computation of ten log-linear models for the lifetime worst score data, a regenerated data set comprising 358 to 428 pairs of worst scores detected between 30 to 48 months inclusive, were also analyzed and compared. For convenience, hereafter, the worst score of lifetime represented the first data set and the worst score of 30 to 48 months represented the second data set. The purpose of the supplemental analysis for data from 30 to 48 months was to eliminate possible confounding between age and severity of hoof

traits for daughters and dams.

Because the daughter-dam contingency table was a square table and scores had a natural order, some simplified association models reviewed by Agresti (1984), Fingleton (1984) and Goodman (1984) were applicable. Although there were several options to represent a log-linear model, the terminologies and notations of Fingleton (1984) were followed in this analysis. Ten different association models in this analysis were independence, main diagonal, uniform association, fixed distance, mover-stayer, minor diagonals (I), minor diagonals (II), pure distance, loyalty-distance and quasi-symmetry models.

Notation common to more than one model included

P_{ij}	for probability in (i, j) cell,
μ'	for total mean probability,
$\lambda_i^{'A}$	for unknown effect of row i (i=1..5),
$\lambda_j^{'B}$	for unknown effect of column j (j=1..5),
β'	for unknown parameter,
$\{u_i = i\}$	for uniformly increased row effects, $u_1 = 1, u_2 = 2 \dots u_5 = 5$,
$\{v_j = j\}$	for uniformly increased column effects, $v_1 = 1, v_2 = 2 \dots v_5 = 5$,
\bar{u}	for mean of uniformly increased row effects,
\bar{v}	for mean of uniformly increased column effects,
$\lambda^{'M}$	for fixed effect common to main diagonal,
$\lambda_i^{'D}$	for distinct (i, i) cell effect on main diagonal (i=1..5), and
$\lambda_k^{'D}$	for k^{th} distinct off-diagonal effect ($k= i-j , i \neq j$).

Descriptions for each model and constraints follow (alternative constraints existed).

I. Independence models

$$\log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} \quad [1]$$

$$\text{Constraints } \sum \lambda_i^{'A} = \sum \lambda_j^{'B} = 0$$

II. Main diagonal models

$$\log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} + \lambda^{'M} \quad (i = j) \quad [2a]$$

$$\text{or } \log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} \quad (i \neq j) \quad (i \text{ and } j = 1, \dots, 5) \quad [2b]$$

$$\text{Constraints } \sum \lambda_i^{'A} = \sum \lambda_j^{'B} = 0$$

III. Uniform association models

$$\log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} + \beta' * (u_i - \bar{u})(v_j - \bar{v}) \quad [3]$$

$$\{u_i = i\} \text{ and } \{v_j = j\}.$$

$$\text{Constraints } \sum \lambda_i^{'A} = \sum \lambda_j^{'B} = 0$$

IV. Fixed distance models

$$\log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} + \beta^{'*k} \quad (i \neq j, k=|i-j|) \quad [4a]$$

$$\text{or } \log(P_{ij}) = \mu' + \lambda_i^{'A} + \lambda_j^{'B} \quad (i \text{ and } j = 1, \dots, 5) \quad [4b]$$

$$\text{Constraints } \sum \lambda_i^{'A} = \sum \lambda_j^{'B} = 0$$

V. Mover-stayer models

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_{ij}^D \quad (i=j) \quad [5a]$$

$$\text{or } \log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B \quad (i \neq j) \quad (i \text{ and } j = 1, \dots, 5) \quad [5b]$$

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0$$

VI. Minor diagonals models (I):

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_k^D \quad (i \neq j, k=|i-j|) \quad [6a]$$

$$\text{or } \log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B \quad (i=j) \quad [6b]$$

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0$$

VII. Minor diagonals models (II):

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_{ij}^D \quad (i \neq j, k= (j-i) + 5) \quad [7a]$$

$$\text{or } \log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B \quad (i=j) \quad [7b]$$

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0$$

VIII. Pure distance models

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_{ij}^D \quad [8]$$

$$\lambda_{ij}^D = \begin{cases} \sum_{r=i}^{j-1} d_r & (i < j) \\ 0 & (i = j) \\ \sum_{r=j}^{i-1} d_r & (i > j) \end{cases}$$

d_1, d_2, d_3 and d_4 were distances from score 1 to 2, 2 to 3, 3 to 4 and 4 to 5; $\lambda_{12}^D = d_1$, $\lambda_{13}^D = d_1 + d_2$, $\lambda_{14}^D = d_1 + d_2 + d_3$,
 $\lambda_{51}^D = d_1 + d_2 + d_3 + d_4$

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0 \text{ and } \sum \lambda_{ij}^D = \sum \lambda_{ji}^D$$

IX. Loyalty-distance models

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_{ij}^M + \lambda_{ij}^D \quad [9]$$

λ_{ij}^D was defined the same as for pure distance model

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0 \text{ and } \lambda_{ij}^D = \lambda_{ji}^D$$

X. Quasi-symmetry models

$$\log (P_{ij}) = \mu' + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB} \quad (i \text{ and } j=1, \dots, 5) \quad [10]$$

$$\text{Constraints } \sum \lambda_i^A = \sum \lambda_j^B = 0 \text{ and } \lambda_{ij}^{AB} = \lambda_{ji}^{AB}$$

The criteria of a best model was significant improvement from independence model ($P < 0.05$) and smallest AIC (an information criterion) statistic (Kennedy, 1992). The model likelihood was computed by SAS CATMOD procedure (SAS, 1999) after basic preparation of the design matrices. Ten models were fit to both lifetime worst score and worst score between 30 to 48 months.

Results and Discussion

Due to the consistency of results and agreement between worst score of lifetime and worst score of 30 to 48 months, most discussion will focus on worst score of lifetime. If genetic components were major controlling factors for hoof traits, strong associations between daughters and dams should be expected. Examples of genetic influence were that the diagonal had higher probabilities, reduced probabilities occurred along off-diagonals, or high odds ratios were found for adjacent 2 x 2 sub-tables. Therefore, the parameters of each model were examined in order to search for a meaningful genetic explanation.

Worst score of lifetime data: For five of the six hoof growth traits (heel height, hoof texture, sole thickness, toe growth and weight transfer) independence models were not rejected ($G^2 < 26.3$, $P > 0.05$, Tables 1 and 2). Similar results were found for three of the six discrete hoof traits. P value of the likelihood ratio statistic of the independence model was higher than 0.05 for corkscrew claw, sole ulcers and white line separation (Tables 3 and 4). Totally, independence models of eight of twelve hoof traits were not rejected. P value greater than 5% for independence model implied that genetic associations between daughters and dams were not very strong, but improved best association models were found for five of the eight traits and supported daughter-dam associations. For the other four traits which did not fit independence model well, three of them had an improved best fit model.

(A) Six hoof growth traits

Fixed distance model was best for heel height with significant negative coefficient for off-diagonal cells [4a] which indicated that daughters and dams with extremely different scores occurred less frequently than expected (Table 5). For hoof texture, significant positive adjacent odds ratio of 1.16, was estimated by uniform association model [3]. Daughters of dams scoring one unit higher than other dams had risk of scoring higher by factor of 1.16 (Table 5, $e^{0.149} = 1.16$). Although a Loyalty-distance model [9] was selected as the best model for sole thickness (Table 6), a meaningful explanation could not be obtained through examination of parameters. Because two distance parameters were negative (d_1, d_2) and two were positive (d_3, d_4) and loyalty parameter was negative (λ^M), the expected probabilities of diagonals or neighboring cells from Loyalty-distance model were not always higher than other cells. Minor diagonals (I) and minor diagonals (II) models with 4 and 7 more parameters than independence model were selected best for subsole and toe growth, which with the significant negative parameters indicated that probabilities of off-diagonal score pairs from models [6a and 7a] were lower than the diagonal daughter-dam pairs from model [6b and 7b]. Daughters and dams with dissimilar toe growth scores had a lower probability of occurrence than daughters and dams with the same scores. However, a high p value, 0.43, was found for independence model of weight transfer and all other nine models were not significant improvements, which suggested that no association was found for daughter-dam lifetime contingency table of weight transfer.

(B) Six discrete hoof traits

Although corkscrew had genetic predisposition for abnormal horn formation (Edwards, 1987), the contingency tables were not supportive of strong daughter-dam relationships. Fixed distance model (Table 7) was best for corkscrew claw with significant negative coefficients for off-diagonal cells which indicated that daughters and dams with extremely different scores occurred less frequently than expected (Table 5). Only

two dams with worst score 5 for lifetime had daughters with worst score 5, the easiestly distinguished abnormal claw shape. From sire point of view, the 62 cases of corkscrew claw, cows with score 5, were daughters of 49 different sires from total of 256 sires with lifetime data on daughters (Fig. 1). Five of seven sires with at least 20 daughters had severely affected daughters (score 5) for which independence model could not be rejected by sire analysis ($P=0.42$). Based on limited information and involuntary culling practices, the inheritance patterns were not clear. Management should be at least as important as genetics for control of corkscrew claw. Peterse (1985) discussed the puzzlement about the origin of corkscrew claw and concluded that housing conditions might play an important role. Huang and Shanks (1995) suggested improper trimming might be important, also. Because heel erosion had higher probabilities of occurrence on (1,1) and (5,5) cells, and laminitis had higher probabilities in (1,1), (2,2), (4,4) and (5,5) cells, a mover-stayer model was best and supported the inheritance of the same scores (excellent or severe) between two generations. Hoyer (1991) reported a single small pedigree study of laminitis in Jerseys and suggested that laminitis was caused by a recessive autosomal gene. Greenough (1991) reviewed other genetic evidence for laminitis and suggested a hypothesis favoring a multifactorial etiology. Logue *et al.* (1993) reviewed several studies and suggested that overemphasis on nutrition alone, also, was ill-advised. The results of this analysis (Table 7) supported that genetics was involved but that genetics might not necessarily be the major controlling factor for laminitis. No simple model, with only one additional parameter than independence model, was best for interdigital dermatitis (Table 7). Minor diagonals (II) model with seven negative parameters was best and suggested that diagonals from model [7b] had higher probabilities than off-diagonals from model [7a]. Alternatively, applying an option of contrast parameterization, for the minor diagonals (II), the estimated parameters for symmetrical response of 1st to 4th off-diagonals were -0.39, -0.61, -0.71 and -0.45, and the parameters for contrast between upper and lower 1st to 3rd off-diagonals were 0.11, 0.41 and 0.44. Four negative parameters for the off-diagonals supported that diagonals (dam's scores = daughters' scores) had higher probabilities of occurrence than probabilities of unequal scores between daughter and dam. Three positive contrast parameters implied that worse daughters from better dams ($i > j$) had higher probabilities of occurrence than better daughters from worse dams ($i < j$) after adjusting for independence and four common diagonal distances. The unequal probabilities

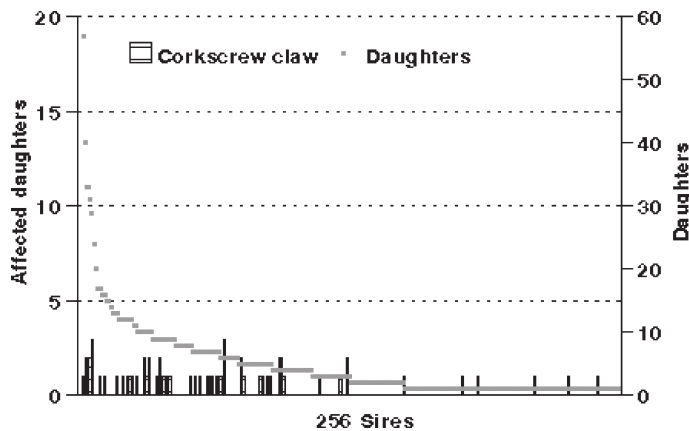


Fig. 1. Affected daughters (score 5) from 49 to 256 sires for corkscrew claw. A total of 62 from 1232 daughters were affected over the 10 years of trimmings.

of daughters from dams demonstrated the importance of environmental effects beyond genetic effects. Even though dams had better scores, daughters remained at risk of being severely affected with interdigital dermatitis. For sole ulcers and white line separation, no better model was found than independence model which was considered best for both traits. Usually sole ulcers were hypothesized to have a high correlation with laminitis (Weaver, 1986), but low incidence of sole ulcers and other environmental factors dimmed the potential genetic component for sole ulcers. From perspective of sire families, a total of 213 affected daughters (score 5) came from 103 different sires and seven sires, with at least 20 daughters, all had affected daughters (exact test $P=0.26$) which implied the weakness of sire-daughter associations (Fig. 2).

Worst score of 30 to 48 Months: Highly consistent results supporting genetic association between daughter and dam, were found for worst score of lifetime and worst score of 30 to 48 months. Although some best models were different (Tables 6 and 7), identical best models were found for hoof texture, interdigital dermatitis, sole ulcers and white line separation. Uniform association model and fixed distance model had the same sign for 11 of 12 traits (Table 5). The only sign changes of the estimated parameters were for white line separation, but the estimated two β' parameters, for uniform association model and fixed distance model (Table 5), were nearly zero and highly nonsignificant ($P=0.82$ and $P=0.94$). Because the nine models were similar, sometimes a different best model was selected under different data edits, although a genetic interpretation through meaningful parameters remained. Laminitis had mover-stayer model as best model for worst score of lifetime, but had fixed distance model as best model for worst score of 30 to 48 months. Genetic explanation was evidenced by higher probabilities on diagonal cells (1, 1), (2, 2), (4, 4) and (5, 5) and decreasing probabilities along the off-diagonals of the daughter-dam contingency table. Because observed frequencies of some score pairs were very small (or zero) in this on farm study, random error could cause mathematically selected best models to vary. In addition, worst scores defined from the same symptoms by different age periods, lifetime or 30 to 48 months, had different biological meaning. Because, not all the same best models were found for each pair of worst scores further approaches should be stimulated to investigate submerged facts among disagreements. Interpretations of genetic components were similar for both data sets although slightly different best models were selected for some traits.

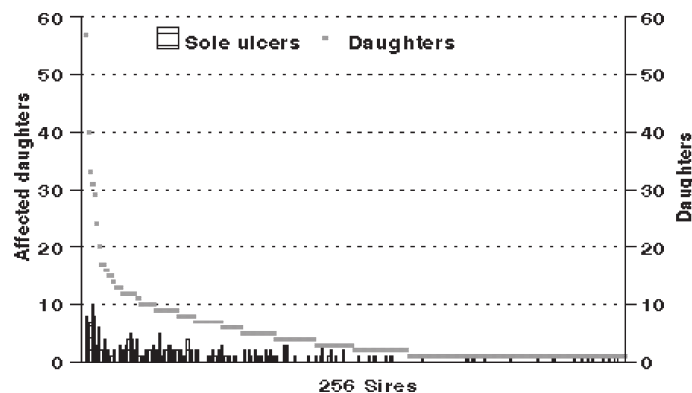


Fig. 2. Affected daughters (score 5) from 103 of 256 sires for sole ulcers. A total of 213 from 1232 daughters were affected over the 10 years of trimmings.

Table 1. Likelihood ratio statistics of different models for heel height, hoof texture and sole thickness

Model	df ¹	Heel height			Hoof texture			Sole thickness					
		G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²
Independence	16	24.3	0.08	40.3	—	24.2	0.09	40.2	—	23.6	0.10	39.6	—
Main diagonal	15	19.5	0.19	37.5		22.5	0.10	40.5		23.5	0.07	41.5	
Uniform association	15	13.9	0.53	31.9		17.7	0.28	35.7	6.5*	20.7	0.15	38.7	
Fixed-distance	15	13.0	0.60	31.0	11.3**	19.0	0.22	37.0		21.8	0.11	39.8	
Minor diagonals(I)	12	9.8	0.64	33.8		17.2	0.14	41.2		19.4	0.08	43.4	
Pure distance	12	10.8	0.63	34.8		18.4	0.19	42.4		15.0	0.38	39.0	
Mover-stayer	11	14.6	0.20	40.6		17.4	0.14	43.4		18.5	0.10	44.5	
Loyalty-distance	11	10.6	0.56	36.6		17.0	0.15	43.0		12.4	0.50	38.4	11.2*
Minor diagonals(II)	9	3.6	0.98	33.6		15.8	0.11	45.8		17.3	0.07	47.3	
Quasi-symmetry	6	6.4	0.70	42.4		8.7	0.36	44.7		6.2	0.72	42.2	

¹ df: degrees of freedom of residuals.
AIC (an information criteria) = G² + 2* number of parameters estimated.
ΔG²: reduction in likelihood ratio statistics between selected and independence models.
*, **: selected models: * P < 0.05 or ** P < 0.01 for ΔG² considering corresponding degrees of freedom.

Table 2. Likelihood ratio statistics of different models for subsole, toe growth and weight transfer

Model	df ¹	Subsole				Toe growth				Weight transfer			
		G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²
Independence	16	29.8	0.02	45.8	—	16.9	0.30	32.9	—	16.3	0.43	32.3	—
Main diagonal	15	29.7	0.01	47.7		16.9	0.32	34.9		15.7	0.40	33.7	
Uniform association	15	26.2	0.04	44.2		15.7	0.40	33.7		13.8	0.54	31.8	
Fixed-distance	15	28.6	0.02	46.6		16.8	0.33	34.8		13.4	0.57	31.4	
Minor diagonals(I)	12	21.0	0.05	45.0		6.5	0.92	30.5	10.4*	12.2	0.43	36.2	
Pure distance	12	22.3	0.03	46.3		15.6	0.34	39.6		12.9	0.38	36.9	
Mover-stayer	11	27.4	0.00	53.4		15.3	0.23	41.3		13.3	0.27	39.3	
Loyalty-distance	11	21.3	0.03	47.3		15.2	0.23	41.2		12.5	0.33	38.5	
Minor diagonals(II)	9	10.1	0.34	40.1	19.7*	6.1	0.91	36.1		9.8	0.37	39.8	
Quasi-symmetry	6	14.3	0.03	50.3		1.6	0.00	37.6		3.9	0.69	39.9	

¹ df: degrees of freedom of residuals.
AIC (an information criteria) = G² + 2* number of parameters estimated.
ΔG²: reduction in likelihood ratio statistics between selected and independence models.
*, **, selected models: * P <0.05 or ** P <0.01 for ΔG² considering corresponding degrees of freedom.

Table 3. Likelihood ratio statistics of different models for corkscrew claw, heel erosion and interdigital dermatitis

Model	df ¹	Corkscrew claw				Heel erosion				Interdigital dermatitis			
		G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²
Independence	16	18.3	0.31	34.3	—	42.7	0.00	58.7	—	43.2	0.00	59.2	—
Main diagonal	15	17.3	0.30	35.3		30.5	0.01	48.5		24.9	0.00	542.9	
Uniform association	15	12.6	0.63	30.6		17.7	0.28	35.7		31.7	0.00	49.7	
Fixed-distance	15	11.7	0.70	29.7	6.6**	19.6	0.19	37.6		25.9	0.04	43.9	
Minor diagonals(I)	12	6.4	0.90	30.4		17.0	0.15	41.0		20.8	0.05	44.8	
Pure distance	12	9.4	0.66	33.4		11.8	0.46	35.8		20.9	0.05	44.9	
Mover-stayer	11	13.3	0.28	39.3		5.7	0.89	31.7	37.0**	18.1	0.08	44.1	
Loyalty-distance	11	7.2	0.78	33.2		6.2	0.86	32.2		19.9	0.05	45.9	
Minor diagonals(II)	9	4.6	0.87	34.6		13.1	0.16	43.1		12.1	0.21	42.1	31.1**
Quasi-symmetry	6	2.9	0.82	38.9		4.5	0.61	40.5		7.7	0.26	43.7	

¹ df: degrees of freedom of residuals.
AIC (an information criteria) = G² + 2* number of parameters estimated.
ΔG²: reduction in likelihood ratio statistics between selected and independence models.
*, **: selected models: * P < 0.05 or ** P < 0.01 for ΔG² considering corresponding degrees of freedom.

Table 4. Likelihood ratio statistics of different models for laminitis, sole ulcers and white line separation

Model	df ¹	Laminitis				Sole ulcers				White line separation			
		G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²	G ²	P	AIC	ΔG ²
Independence	16	29.2	0.02	45.2	—	6.5	0.98	22.5	—	19.5	0.25	35.5	—
Main diagonal	15	28.0	0.02	46.0		6.3	0.97	24.3		19.4	0.20	37.4	
Uniform association	15	22.8	0.09	40.8		6.4	0.97	24.4		19.3	0.20	37.3	
Fixed-distance	15	23.5	0.07	41.5		6.3	0.97	24.3		19.4	0.19	37.4	
Minor diagonals(I)	12	21.1	0.05	45.1		2.9	0.00	26.9		12.3	0.42	36.3	
Pure distance	12	21.5	0.04	45.5		6.2	0.90	30.2		17.2	0.14	41.2	
Mover-stayer	11	12.9	0.30	38.9	16.3**	5.9	0.88	31.9		17.0	0.11	43.0	
Loyalty-distance	11	20.7	0.04	46.7		6.1	0.87	32.1		16.5	0.12	42.5	
Minor diagonals(II)	9	20.6	0.01	50.6		1.8	0.99	31.8		6.7	0.67	36.7	
Quasi-symmetry	6	8.9	0.18	44.9		2.2	0.90	38.2		5.2	0.52	41.2	

¹ df: degrees of freedom of residuals.
AIC (an information criteria) = G² + 2* number of parameters estimated.
ΔG²: reduction in likelihood ratio statistics between selected and independence models.
*, **: selected models: * P <0.05 or ** P <0.01 for ΔG² considering corresponding degrees of freedom.

Table 5. Parameter estimates for uniform association and fixed distance models

Trait	Uniform association		Fixed distance	
	β_U	Standard error	β_F	Standard error
-----Lifetime-----				
Heel height	0.142 **	0.044	-0.204***	0.061
Hoof texture	0.149 *	0.059	-0.143 *	0.062
Sole thickness	0.079 NS	0.047	-0.077 NS	0.057
Subsole	0.042 NS	0.023	-0.042 NS	0.039
Toe growth	0.067 NS	0.061	-0.023 NS	0.064
Weight transfer	0.037 NS	0.023	-0.069 NS	0.040
Corkscrew claw	0.081 *	0.034	-0.128 **	0.049
Heel erosion	0.076 ***	0.016	-0.137 ***	0.029
Interdigital dermatitis	0.075 ***	0.022	-0.164 ***	0.040
Laminitis	0.066 *	0.026	-0.097 *	0.040
Soleulcers	-0.003 NS	0.014	0.010 NS	0.027
White line separation	0.007 NS	0.018	-0.006 NS	0.034
-----30 to 48 Months-----				
Heel height	0.330 ***	0.084	-0.242 **	0.088
Hoof texture	0.186 *	0.074	-0.154 NS	0.081
Sole thickness	0.083 NS	0.068	-0.056 NS	0.072
Subsole	0.002 NS	0.031	-0.007 NS	0.054
Toe growth	0.185 *	0.093	-0.023 *	0.092
Weight transfer	0.056 NS	0.032	-0.077 NS	0.053
Corkscrew claw	0.049 NS	0.046	-0.130 *	0.065
Heel erosion	0.099 ***	0.022	-0.182 ***	0.039
Interdigital dermatitis	0.038 NS	0.033	-0.139 **	0.057
Laminitis	0.075 NS	0.039	-0.132 *	0.058
Sole ulcers	-0.069 NS	0.039	0.117 NS	0.071
White line separation	-0.007 NS	0.029	0.004 NS	0.052

NS $P \geq 0.05$, * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$.

Table 6. Likelihood ratio statistics (G^2) of different models for hoof growth traits on worst score of 30 to 48 months

Model	df ¹	Heel height		Hoof texture		Sole thickness		Subsole		Toe growth		Weight transfer	
		G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2
Independence	16	28.1		18.3		10.6		31.2		13.4		26.5	
Main diagonal	15	27.8		18.1		10.5		31.1		8.2	5.2*	26.4	
Uniform association	15	11.7	16.4**	12.0	6.3* \oplus	9.2		31.2		9.6		23.3	
Fixed-distance	15	20.7	\oplus	14.8		10.1		31.2		7.4		24.4	
Minor diagonals(I)	12	9.7		10.5		6.5		29.4		6.6	\oplus	21.2	
Pure distance	12	19.7		13.0		9.8		15.6		6.5		13.6	12.9*
Mover-stayer	11	23.8		15.2		8.6		18.5		6.3		16.5	
Loyalty-distance	11	12.2		9.7		8.2	\oplus	15.5	15.7**	6.4		13.1	
Minor diagonals(II)	9	9.0		5.6		4.7		26.6	\oplus	6.3		16.8	
Quasi-symmetry	6	5.7		7.1		1.0		11.9		0.5		10.2	

¹ df: degrees of freedom of residuals.
** , * : Selected models, * $P < 0.05$ or ** $P < 0.01$ for ΔG^2 , reduction in likelihood ratio statistics between selected and independent models, considering corresponding degrees of freedom and with smallest AIC, AIC (an information criteria) = $G^2 + 2 \times$ number of parameters estimated.
 \oplus : A reference model, the best model for worst score of lifetime.

Table 7. Likelihood ratio statistics (G^2) of different models for discrete hoof traits on worst score of 30 to 48 months

Model	df ¹	Corkscrew claw		Heel erosion		Interdigital dermatitis		Laminitis		Sole ulcers		White line separation	
		G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2	G^2	ΔG^2
Independence	16	25.3		33.7		40.4		13.4		16.7		14.1	
Main diagonal	15	19.8	5.5*	19.8		26.6		9.8		15.3		14.1	
Uniform association	15	24.1		12.1		39.1		9.6		13.1		14.1	
Fixed-distance	15	21.4	⊕	12.0	21.7**	34.6		8.1	5.3*	13.6		14.1	
Minor diagonals(I)	12	19.4		10.0		17.6		7.4		11.3		13.7	
Pure distance	12	20.6		11.4		32.9		3.8		9.9		8.9	
Mover-stayer	11	18.4		13.4	⊕	23.9		4.0	⊕	8.0		7.4	
Loyalty-distance	11	18.4		11.4		23.4		3.7		8.0		8.0	
Minor diagonals(II)	9	15.5		7.7		10.4	30.0**⊕	7.2		10.4		10.9	
Quasi-symmetry	6	13.5		4.1		13.2		1.3		4.2		4.8	

¹ df: degrees of freedom of residuals.

**, * : Selected models, * $P < 0.05$ or ** $P < 0.01$ for ΔG^2 , reduction in likelihood ratio statistics between selected and independent models, considering corresponding degrees of freedom and with smallest AIC, AIC (an information criteria) = $G^2 + 2 \times$ number of parameters estimated.

⊕ : A reference model, the best model for worst score of lifetime.

Conclusions

Genetic components for hoof traits existed. Daughters of dams scoring one unit higher than other dams had risk of scoring higher with adjacent odds ratio greater than one in eleven of twelve lifetime hoof traits. The more diverse scores of daughters and dams had lower probabilities of occurrence in ten out of twelve hoof traits recorded between 30 and 48 months. Evidence of significant association between scores of daughters and dams for hoof conformation and health was supported for heel height, hoof texture, subsole, toe growth, corkscrew claw, heel erosion, interdigital dermatitis and laminitis. The selected log-linear models with estimated parameters provided a simple and concise presentation of daughter-dam associations.

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以對數線性關聯模式解釋腳蹄健康與遺傳⁽¹⁾

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摘要

使用 10 種不同的關聯模式分析 12 個由 619 至 724 對『母女』配對的 5×5 評分次數分配表（列聯表，Contingency Table），10 種不同的關聯模式分別為：independence, main diagonal, uniform association, fixed distance, mover-stayer, minor diagonals (I), minor diagonals (II), pure distance, loyalty-distance 與 quasi-symmetry。十二個評分次數分配表，包括六個腳蹄性狀：蹄跟高（heel height）、蹄質地（hoof texture）、蹄底厚度（sole thickness）、層偽趾面（subsole）、趾生長（toe growth）與 承重狀況（weight transfer）。另外六個評分次數分配表則分別為螺旋蹄（corkscrew claw）、蹄根壞損（heel erosion）、趾間炎（interdigital dermatitis）、蹄葉炎（laminitis）、蹄底潰瘍（sole ulcers）、白線裂痕（white line separation）等腳蹄性狀。其中八個性狀〔蹄跟高、蹄質地、蹄底厚度、趾生長、承重狀況、螺旋蹄、蹄底潰瘍、白線裂痕〕independence model 未能被棄卻（ $G^2 < 26.3$, $P > 0.05$ ），顯示蹄性狀母女遺傳關聯性不強，然而八個性狀中仍有五個可以找到較佳的解式模式。而在參數估計上 uniform association model 中 12 個性狀中仍有 11 個得到『正值』，而 fixed distance model 則估得『負值』的 off-diagonal distance parameters，顯示母女間的遺傳關聯的存在。由於較差分數臨近的母女對出現機率較高以及較佳模式的選取顯示母女關聯存在於蹄跟高、蹄質地、層偽趾面、趾生長、螺旋蹄、蹄根壞損、指間炎與蹄葉炎等腳蹄性狀。

關鍵詞：對數線性關聯模式、母女對、腳蹄。

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