Associations Between Egg Production and Clutch Length in Four Selected Lines of Chickens

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Primary Audience: Geneticists, Pedigree Flock Managers, Researchers

SUMMARY

The use of partial records to measure egg production of pedigree breeders has numerous advantages including reduced labor and generation interval. Maintaining egg production in an era where emphasis in breeding programs involves yield and feed conversion presents a challenge to primary breeders. Because breeders obtain individual egg production records, interest in the possibility of using the association of various measures of clutch length with intensity of egg production has been renewed. The correlation of maximum clutch length (prime sequence) throughout lay and during the first 10, 15, and 30 d of lay with percentage hen-day ovulations and normal eggs in four lines (two White Leghorn and two White Plymouth Rock) of chickens during each of 2 yr was measured. Although the rankings of the lines were generally consistent both years for all traits measured, correlations among the sequence lengths with percentage henday ovulations and normal eggs were line specific. Thus, poultry breeders would have to determine which of these measures is most appropriate for inclusion with other measures of egg production for each of their specific lines.

Key words: clutch length, egg production, genetic line

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DESCRIPTION OF PROBLEM

In chickens, egg production of a flock usually increases rapidly during the first 8 to 9 wk from the onset of lay and decreases at a constant rate until the end of the production cycle [1]. On an individual hen basis, egg production increases rapidly during the first 2 wk to a plateau that is maintained for several weeks prior to a gradual decline [2]. Although patterns in egg production are genetically programmed, they may be modified by environmental factors such as nutrition and photoperiod. Robinson et al. [3] characterized age-related changes in egg production according to length of oviposition sequence (clutch) and length of intersequence pauses in broiler breeders to 62 wk of age. They observed that after onset of lay, hens lay short sequences of eggs (6 to 10 d in length) until peak production is reached, after which there is one long clutch of eggs (18 to 32 d in length), which they called the prime sequence. The correlation between the length of the prime sequence and laying rate was 0.40, and they suggested that the length of the prime sequence had potential as a tool to predict the reproductive efficiency of broiler breeders.

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In a subsequent experiment [4] the correlation between length of the prime sequence and rate of lay in broiler breeders was 0.45. Before implementation of this tool in a breeding program, it is necessary to make comparisons among a range of stocks to determine if the criterion to be employed is population specific or general. The experiment reported here was undertaken to determine if the proposed model for the association between the prime sequence and laying rate [3, 4] was consistent among several diverse genetic lines of chickens reared in a common environment.

MATERIALS AND METHODS

Genetic Lines and Husbandry

The chickens used in this experiment were from lines of White Leghorns divergently selected for high (HAS) or low (LAS) antibody response to sheep red blood cells [5, 6] and White Plymouth Rocks divergently selected for high (HWS) or low (LWS) 8-wk body weight [7]. Eggs from age contemporary hens of the four lines were incubated in the same machine. Temperature and relative humidity were set at 37.5°C and 55%, respectively. On Day 18, eggs containing viable embryos were transferred to a hatcher with a temperature of 37°C and relative humidity increasing from 65% to about 75% at time of hatch. At hatch (the first Tuesday in March for each year), chicks were wing-banded, vaccinated for Marek's disease, and placed in floor pens with pine wood shavings as litter. Data were evaluated in 1997 for generations 24 and 40 and in 1999 for generations 26 and 42 of the antibody and weight lines, respectively. A mash diet of 20% CP and 2,685 kcal ME/kg was provided until 56 d of age. From 56 to 126 d of age, the diet fed contained 14% CP and 2,827 kcal ME/kg. Thereafter, the diet fed contained 16% CP and 2,752 kcal ME/kg. To avoid obesity, beginning at 56 d of age, daily feed intake was restricted for HWS pullets. Allocations were 60, 70, 80, and 100 g/pullet to 77, 98, 119, and 140 d of age, respectively. Thereafter, there was an increase of 5 g/wk for the next 8 wk.

Lighting was continuous to Day 7, and from 0500 to 2000 h (15 L:9 D period) to 56 d of age when the chickens were transferred to the grower pens with natural day length. This meant that at our latitude the time from sunrise to sunset ranged

between 14 h 43 min to 14 h 44 min during the 8-d period when the pullets were between 103 and 111 d of age. At 133 d, the chickens were moved to single-bird cages with a 14 L:10 D period.

Traits and Statistical Analyses

A pullet was considered sexually mature when at least two eggs were laid within a 10-day period with the age that the first egg was laid being considered the age at sexual maturity [8]. Data for ovipositions were obtained daily for each pullet from the date of first egg until the last trap day, which was the second Friday in December (283 d of age). Each oviposition was classified as normal or defective with defective eggs including double yolk, membrane, soft shell, extra calcified, and compressed or slab sided [9].

Data were summarized as sequence 1-10, 1-15, and 1-30 and defined as the maximum number of consecutive days in which there were ovipositions (clutch length) during the first 10, 15, and 30 d of egg production, respectively. Maximum sequence was the longest number of consecutive days of lay from the onset of lay until the last trap day. Percentage hen-day and percentage henday normal egg production were calculated for each individual by dividing the number of ovulations and normal eggs by days from first egg to the last trap day. Data were analyzed within years by analysis of variance with line as the main effect. Prior to analysis, percentages were transformed to arc sine square roots. When line effects were significant, multiple means were compared using Duncan's multiple range test. Within each year and line, phenotypic correlations were calculated between total hen-day production with sequences 1-10, 1-15, 1-30, and maximum sequence. Significance for all tests was considered as $P \le 0.05$.

RESULTS AND DISCUSSION

There were considerable differences among lines for percentage hen-day ovulations and percentage hen-day normal egg production with means consistently greater for the White Leghorn than the White Rock lines (Table 1). Within breeds, the incidence of defective eggs was greater for line HAS than LAS and for line HWS than LWS; these results were consistent with those

			% Hen-day		Sequence ^B					
Year ^A	Line ^A	n	Ovulations	Normal eggs	1-10	1–15	1–30	Maximum		
1997	HWS	82	66.0 ± 1.6^{b}	$54.6 \pm 1.4^{\circ}$	2.5 ± 0.1^{b}	3.3 ± 0.2^{b}	4.2 ± 0.2^{b}	$6.0 \pm 0.3^{\circ}$		
	LWS	53	$54.5 \pm 1.7^{\circ}$	$54.4 \pm 1.7^{\circ}$	2.1 ± 0.2^{b}	2.5 ± 0.2^{b}	3.3 ± 0.3^{b}	3.3 ± 0.3^{d}		
	HAS	39	69.6 ± 1.9^{b}	64.8 ± 2.3^{b}	2.3 ± 0.2^{b}	2.8 ± 0.3^{b}	4.8 ± 0.6^{b}	8.7 ± 0.6^{b}		
	LAS	39	78.5 ± 1.5^{a}	77.4 ± 1.4^{a}	4.7 ± 0.4^{a}	$7.0~\pm~0.7^a$	12.3 ± 1.3^{a}	17.0 ± 1.7^{a}		
1999	HWS	79	60.4 ± 1.6^{b}	$53.0 \pm 1.4^{\circ}$	3.0 ± 0.2^{b}	3.7 ± 0.2^{b}	$5.3 \pm 0.3^{\circ}$	6.9 ± 0.3^{b}		
	LWS	78	61.1 ± 1.7^{b}	60.5 ± 1.7^{b}	2.9 ± 0.2^{b}	3.6 ± 0.2^{b}	$4.1 \pm 0.3^{\circ}$	$4.9 \pm 0.3^{\circ}$		
	HAS	44	76.6 ± 1.6^{a}	74.7 ± 1.7^{a}	2.9 ± 0.2^{b}	4.0 ± 0.4^{b}	7.1 ± 0.7^{b}	14.4 ± 1.3^{a}		
	LAS	45	79.7 ± 1.0^{a}	79.3 ± 1.0^{a}	4.3 ± 0.3^{a}	$6.5~\pm~0.5^a$	11.3 ± 1.0^{a}	15.7 ± 1.7^{a}		

TABLE 1. Means and SEM for percentage hen-day ovulations, percentage hen-day normal eggs, and 1–10, 1–20, 1–30 and maximum sequence lengths by year and line

^{a-c}Means within a column for a year with different superscripts are significantly different ($P \le 0.05$).

^AIn years 1997 and 1999 were generations 24 and 26 for lines HAS and LAS, which were selected for high and low antibody response to sheep red blood cells, respectively, and generations 40 and 42 for lines HWS and LWS, which were selected for high and low body weight at 8 wk of age, respectively. ^BSequence is defined as consecutive days when there were ovipositions during the first 10, 15, and 30 d of lay as well as

^BSequence is defined as consecutive days when there were ovipositions during the first 10, 15, and 30 d of lay as well as the longest sequence during the laying period.

previously reported for these lines [6, 7]. LAS pullets had consistently longer 1 to 10 d, 1 to 15 d, and 1 to 30 d sequences than pullets from the other lines. Maximum sequence length was greatest for LAS and least for LWS pullets.

Correlations between percentage hen-day ovulations and sequence lengths varied among lines (Table 2). The increase in correlation coefficients for year 1997 from sequence 1–10 to 1– 30 was approximately twofold greater for HWS than for LWS and HAS pullets and was threefold for LAS. The seeming inconsistency across genetic lines was because the correlation of percentage hen-day ovulations with sequence 1–10 in line HWS was very low and followed a pattern also evident (although greater in magnitude) in 1999. Overall maximum sequence was similar or more highly associated with percentage hen-day ovulations than sequence 1–30. Therefore, whether sequence 1–30 would suffice as an association, rather than the extra effort required for maximum sequence would be line specific.

Correlations for percentage hen-day normal eggs with sequence length in terms of year and genetic line (Table 3) follow a similar pattern to that for percentage hen-day ovulations. These results were consistent with those [3, 4] showing a positive correlation between the prime sequence length and the laying rate. Although the values obtained from our data were generally higher than

TABLE 2. Correlations between	percentage hen-day	y ovulations and sequence	lengths by year and line
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		Sequence						
Year ^A	Line ^A	1-10	1–15	1–30	Maximum			
1997	HWS	0.36**	0.47**	0.56**	0.55**			
	LWS	0.59**	0.66**	0.70**	0.74**			
	HAS	0.52**	0.54**	0.62**	0.57**			
	LAS	0.56**	0.62**	0.62**	0.71**			
1999	HWS	0.00	0.19*	0.36**	0.54**			
	LWS	0.40**	0.43**	0.54**	0.56**			
	HAS	0.30*	0.35*	0.50**	0.60**			
	LAS	0.49**	0.54**	0.68**	0.72**			

^AIn years 1997 and 1999 were generations 24 and 26 for lines HAS and LAS, which were selected for high and low antibody response to SRBC, respectively, and generations 40 and 42 for lines HWS and LWS, which were selected for high and low body weight at 8 wk of age, respectively. *P < 0.05.

 $^{**}P \le 0.01$

TABI	_E 3.	Correlations	between	percentage	hen-d	ay normal	l eggs a	and	sequence	lengths	by	year	and	line
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		Sequence						
Year ^A	Line ^A	1–10	1–15	1–30	Maximum			
1997	HWS	0.22*	0.37**	0.56**	0.57**			
	LWS	0.59**	0.66**	0.68**	0.73**			
	HAS	0.48**	0.54**	0.60**	0.58**			
	LAS	0.59**	0.67**	0.67**	0.71**			
1999	HWS	0.04	0.28*	0.39**	0.54**			
	LWS	0.40**	0.44**	0.53**	0.56**			
	HAS	0.29*	0.39**	0.53**	0.56**			
	LAS	0.48**	0.53**	0.66**	0.70**			

^AIn years 1997 and 1999 were generations 24 and 26 for lines HAS and LAS, which were selected for high and low antibody response to SRBC, respectively, and generations 40 and 42 for lines HWS and LWS, which were selected for high and low body weight at 8 weeks of age, respectively.

 $*P \le 0.05.$ $**P \le 0.01.$

those reported previously [3, 4], rarely in either our data or those from others did maximum sequence length account for more than 50% of the total variation in egg production.

CONCLUSIONS AND APPLICATIONS

- 1. Comparisons among lines were made between sequence length during the first 10, 15, and 30 d of lay as well as maximum sequence length with percentage hen-day production in four lines of chickens in each of 2 yr.
- 2. Patterns for associations between sequence length and percentage hen-day production were similar for both years.
- 3. Rankings of stocks for traits measured were consistent across years.
- 4. Associations between sequence length and percentage hen-day production were line specific and thus had varying applicability.
- 5. Sequence length, combined in an index with other measures of egg production, may have application in pedigree breeding programs, particularly for meat stocks.

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