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A comparison of the interaction, with two types of environment, of pure strains or strain crosses of poultry†

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1. INTRODUCTION

When planning a programme to improve some particular trait in a stock of animals to be raised in a variety of environments, it is necessary to know if genotype-environment interaction is important. There have been numerous conflicting reports on the importance of genotype-environment interaction for different traits under defined conditions. There is no general agreement on what criteria should be used in predicting how important a genotype-environment interaction may be in any given set of conditions. It may not be practicable to conduct a full-scale test of the whole range of genotypes encountered in all the environments in which they are to be raised. If breeders could make predictions from facts already known about the genetic control of a particular trait, they would be in a better position to select the most appropriate breeding programme.

An earlier comparison of the performance of half sib groups of poultry in two separate sets of environments (Hull & Gowe, 1962) indicated that important genotype-environment interactions occurred only when (*a*) the environments had a marked effect on performance for a particular trait, and (*b*) there were also large genetic differences among the groups. The second stipulation was obvious only when the interaction of the same sire groups with environments was compared among traits which had a markedly different between-group genetic variance. A more critical test could be made by examining the interaction of two sets of genetic groups, differing in between-group genetic variance, with the same environmental treatments.

In a report concerning the optimum allocation of given test facilities in order to obtain maximum discrimination of genetic worth for yield of corn varieties, Sprague & Federer (1951) present data whose interpretation is relevant to this investigation. The interaction of a set of single crosses (F_1's between two inbred

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lines) with environment was greater than that of other crosses having a smaller between-variety genetic variance and larger within-variety genetic variance. This held both for variety × location interaction and for variety × year interaction.

This report is concerned with the comparison of the interactions of pure strains and strain crosses of poultry with two types of environments. The genetic differences among pure (that is, more or less inbred) strains of poultry would be expected to be greater than those among the strain crosses derived from these pure strains. If the extent of genotype-environmental interaction is related in some degree to the total genetic variance, the interaction of the pure strains with environment might be expected to be greater than that of the strain crosses.

2. EXPERIMENTAL METHODS

The experiment consisted of a test of the performance of birds of the various strains and strain crosses reared on two nutritional levels duplicated at two locations. It was thus possible to estimate the interaction both of the pure strains and of the cross strains either with location (farm) or with nutritional treatment.

The tests were carried out at two Branch Farms of the Research Branch, Canada Department of Agriculture, located at Lethbridge, Alberta, and Charlottetown, Prince Edward Island (referred to hereafter as Farms 1 and 2, respectively). The tests were repeated in four consecutive years; 1956, 1957, 1958 and 1959, referred to as years 1 to 4 respectively. Each performance test lasted 500 days from date of hatch so there was an overlap of test populations at each location. The pure strains used in these studies were commercial single comb White Leghorn strains, originating in North America, which had been maintained under selection for high egg production as closed flocks for a considerable period of time (varying from about 15 to 30 years as far as can be determined). Since most commercial breeders usually used from 10 to 20 sires per generation, the inbreeding coefficient (Wright's F) for the pure strains might vary from about a low of 10% to a high of 40% (based on $1/8M$, where M is the number of males used per generation). In the first year pure strains and strain cross progeny were obtained from crossing six pure stocks but in each of the succeeding three years pure-bred and crossbred progeny were obtained by crossing only five stocks.

The eleven pure strains used in the first two years were all different. In the third year five of the eleven strains which combined best were used again. In the fourth year four different strains and one of the original eleven strains were used, so that over the four years a total of fifteen different Leghorn pure strains was used in these experiments.

Chicks to be used in the tests were produced in the following manner. In each year, except for the first, five pens were provided, each pen containing a random sample of about forty pullets of each of the five parent strains. Males of one pure strain were mated to each pen so that one pure strain group and five strain cross groups were obtained by trap-nesting the females and identifying the eggs by dam. In the first year, the same procedure was followed, using six pens. From thirty to

forty males were used in each pen by rotating two groups of males through the pens every two days. Eggs were saved for a period varying from seven days to fourteen days and they were incubated at a different location from the test farms (Central Experimental Farm, Ottawa). This mating procedure gave thirty strain crosses (fifteen crosses and their reciprocals) the first year and twenty each of the three succeeding years. (In the second year two crosses out of the twenty possible were not made because of a shortage of two groups of pure strain females in one of the pens.) Two hatches, three weeks apart, were obtained each year, chicks from the first hatch always being assigned to Lethbridge, while those from the second hatch were sent to Charlottetown. The hatches were obtained at approximately the same date in each year. The chicks were sexed at hatching and proportional numbers of female chicks for the twenty-five subgroups (36 in year 1) were shipped to the test location after being allocated proportionately to the four sections of the shipping boxes.

At the two test locations all the chicks were intermingled and brooded as a single population for the first few weeks. The first year the chicks were randomly divided within strain into two groups at about six weeks of age, one receiving the all-mash rearing ration *ad libitum*, and the other group receiving only 70% of what the full-fed group ate the previous week. For the next three years the populations were divided at three weeks of age in the brooder house and the restricted feeding programme was started at this time with the restricted group receiving 90% of the amount the full-fed birds ate the previous week for one week, then 80% for the next week, and then 70% of what the full-fed birds ate for the period of five weeks to twenty-one weeks. Both groups were reared on equivalent poultry pastures until 147 days of age when they were housed in randomly allotted replicated pens. Both groups were put on the all-mash laying ration fed *ad libitum* to the end of the laying test when the birds were 500 days of age. The laying house management programme was standardized as far as possible between and within farms. The management programme and rations have been described in detail by Gowe *et al.* (1960).

Six traits were considered for this study. Individual body-weights to the nearest 10 g. were taken at 147 days of age and at 350 days of age. Age in days to first egg (sexual maturity) was estimated from the trap-nest records. Egg weight was estimated from the sample of eggs laid by each hen over a ten-day period when the birds were relatively mature (about 360 days of age) and the mean egg-weight for each hen considered as a trait. The egg production of hens surviving to the end of the test was estimated from the trap-nest records (birds trapped five days out of every seven). Laying house mortality calculations (period of 147 days to 500 days) were based on the number of birds housed per subclass at 147 days.

There were sufficient numbers of pullets per farm per treatment per strain or strain cross to permit randomly reducing the number of observations per subclass included in these analyses to twenty in the first two years and eighteen in the second two years. Data from 8320 birds were included in the analyses of the five traits with individual measurements. In a very few instances, where mortality had reduced groups below these numbers, the means of that subclass were substituted to keep

the numbers orthogonal and the degree of freedom adjusted for the analyses of variance. Since the percentage mortality (converted to angles) in each subclass was used in the analyses of variance of laying house mortality, there was no estimate of within subclass variation for this trait.

3. ANALYTICAL METHODS

A separate analysis of variance was performed for each of the six traits in each of the four years. The computations were programmed for an I.B.M. 650 digital computer.

The phenotype value (X_{ijklm}) for trait X of the mth individual of the jth strain of the ith class (pure strain or strain cross) at the kth farm and reared under the lth treatment was assumed to be made up of the following contributions:

$$X_{ijklm} = \mu + c_i + s:c_j + f_k + t_l + cf_{ik} + s:cf_{jk} + ct_{il} + s:ct_{jl} + ft_{kl} + cft_{ikl} + s:cft_{jkl} + e_{m(ijkl)}$$

where μ is the overall mean for strain X in the year considered;

c_i is the effect of class-of-strain i (pure or cross) measured over both farms and both treatments;

$s:c_j$ is the effect of strain j, within class, measured over both farms and both treatments;

f_k is the effect of farm k averaged over all strains in both treatments;

t_l is the effect of treatment l averaged over all strains at both farms;

cf_{ik} is the interaction of type of strain i with farm k;

$s:cf_{jk}$ is the interaction of strain j (within class) with farm k;

ct_{il} is the interaction of type of strain i with treatment l;

$s:ct_{jl}$ is the interaction of strain j (within class) with treatment t;

cft is the interaction of type of strain i with farm k and treatment l;

$s:cft_{jkl}$ is the interaction of strain j (within class) with farm k and treatment l;

$e_{m(ijkl)}$ is the deviation of individual m from the mean of the strain-farm-treatment subgroup.

The sources of variation considered in this analysis, and the expected composition of the mean square associated with each of these are shown in Table 1. These expected mean squares are based on the assumption that farm, treatment and class of strain are fixed effects, and that strains, within class, are random effects. It should be noted that the between strain mean square has been split into two parts, that due to the variation among pure strains ($S_{(p)}$), and that due to variation among strain crosses ($S_{(k)}$). The first-order interactions of strains within class, with farm and of strains, within class, with treatment and also the second-order interaction, of strains within class, with farm and with treatment have been similarly divided.

Variance components for each of the six traits were estimated for each year and the arithmetic mean of these four estimates is shown for all the components estimated. For the more important sources of variation the individual variance component estimates for each of the four experiments (years) is presented also. The variance components are symbolized as indicated in Table 1, using the method of Henderson (1959).

Table 1. *Expected mean squares for the analyses of variance of the pure strains and strain crosses on test at two farms and under two rearing treatments*

Source of variance		d.f.	Expectations of the mean squares
Pure vs. crosses	C	1	$\sigma_w^2 + 4n_w\,\sigma_{s.c}^2 + 4n_s n_w\,\sigma_c^2$
Strains within classes	S:C	$n_p + n_k - 2$	$\sigma_w^2 + 4n_w\,\sigma_{s:c}^2$
Pure strains	$S_{(p}$	$n_p - 1$	$\sigma_{w(p)}^2 + 4n_{w(p)}\,\sigma_{s(p)}^2$
Strain crosses	$S_{(k)}$	$n_k - 1$	$\sigma_{w(k)}^2 + 4n_{w(k)}\,\sigma_{s(k)}^2$
Farms	F	1	$\sigma_w^2 + 2n_w\,\sigma_{fs}^2 + 4n_s n_w\,\sigma_f^2$
Pure vs. crosses × farms	CF	1	$\sigma_w^2 + 2n_w\,\sigma_{fs:c}^2 + 2n_s n_w\,\sigma_c^2$
Farms × strains within classes	FS:C	$n_p + n_k - 2$	$\sigma_w^2 + 2n_w\,\sigma_{fs:c}^2$
Farms × pure strains	$FS_{(p)}$	$n_p - 1$	$\sigma_{w(p)}^2 + 2n_{w(p)}\,\sigma_{fs(p)}^2$
Farms × strain crosses	$FS_{(k)}$	$n_k - 1$	$\sigma_{w(k)}^2 + 2n_{w(k)}\,\sigma_{fs(k)}^2$
Rearing treatment	T	1	$\sigma_w^2 + 2n_w\,\sigma_{ts}^2 + 4n_s n_w\,\sigma_t^2$
Pure vs. crosses × treatment	CT	1	$\sigma_w^2 + 2n_w\,\sigma_{ts:c}^2 + 2n_s n_w\,\sigma_{ct}^2$
Treatment × strain within classes	TS:C	$n_p + n_k - 2$	$\sigma_w^2 + 2n_w\,\sigma_{ts:c}^2$
Treatment × pure strains	$TS_{(p)}$	$n_p - 1$	$\sigma_{w(p)}^2 + 2n_{w(p)}\,\sigma_{ts(p)}^2$
Treatment × strain crosses	$TS_{(k)}$	$n_k - 1$	$\sigma_{w(k)}^2 + 2n_{w(k)}\,\sigma_{ts(k)}^2$
Farms × treatments	FT	1	$\sigma_w^2 + n_w\,\sigma_{fts.c}^2 + 2n_s n_w\,\sigma_{ft}^2$
Pure vs. crosses × farms × treatments	CFT	1	$\sigma_w^2 + n_w\,\sigma_{fts.c}^2 + n_s n_w\,\sigma_{cft}^2$
Farms × treatments × strains within classes	FTS:C	$n_p + n_k - 2$	$\sigma_w^2 + n_w\,\sigma_{fts:c}^2$
Farms × treatments × pure strains	$FTS_{(p)}$	$n_p - 1$	$\sigma_{w(p)}^2 + n_{w(p)}\,\sigma_{fts(p)}^2$
Farms × treatments × strain crosses	$FTS_{(k)}$	$n_k - 1$	$\sigma_{w(k)}^2 + n_{w(k)}\,\sigma_{fts(k)}^2$
Within subclasses	W	$\frac{n_w - 1}{n_w} N$	σ_w^2
Within pure strains	$W_{(p}$	$\frac{n_{w(p)} - 1}{n_{w(p)}} N_p$	$\sigma_{w(p)}^2$
Within strain crosses	$W_{(k)}$	$\frac{n_{w(k)} - 1}{n_{w(k)}} N_k$	$\sigma_{w(k)}^2$

where n_p = number of pure strains;
n_k = number of strain crosses;
n_w = number of observations per subclass;
n_s = number of pure and strain crosses totally.

4. RESULTS

(i) *Effect of farm and rearing treatment*

Differences between farms were large for survivor egg production and laying house mortality in some years and small in others (Table 2), but they were significant in all four years (Table 3). Farm differences in egg size and body-weight at 147 days were significant in three years out of four, while farm differences for age at sexual maturity and mature body weight were significant two years out of four (Tables 2 and 3).

The rearing treatments had large effects on body-weight at housing and on age at sexual maturity and a small but still significant effect on final body-weight in all four years (Tables 2 and 3). The rearing treatment had little or no effect on survivor egg production or mature egg weight. However, the average delay in sexual maturity of the restricted-fed group was about 14 days, which meant these birds

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Table 2. *Mean performance of pure strains and strain crosses in the various environments for the six traits measured*

		Pure strains				Strain crosses			
		Farm 1		Farm 2		Farm 1		Farm 2	
Character	Year	Full fed	Restricted	Full fed	Restricted	Full fed	Restricted	Full fed	Restricted
Body-weight at housing in kg.	1	1·56	1·28	1·49	1·34	1·62	1·35	1·54	1·40
	2	1·47	1·07	1·43	1·24	1·52	1·14	1·47	1·28
	3	1·52	1·29	1·47	1·31	1·63	1·36	1·56	1·36
	4	1·56	1·24	1·52	1·14	1·63	1·29	1·59	1·17
Age at sexual maturity in days	1	179	196	178	181	175	189	173	178
	2	170	198	176	172	167	189	185	182
	3	169	190	172	184	166	181	167	178
	4	172	194	171	183	169	186	167	185
Body-weight in kg. at 365 days of age	1	1·95	1·90	2·04	2·00	2·01	1·96	2·07	2·08
	2	1·89	1·84	1·95	1·94	1·97	1·90	2·01	2·01
	3	1·98	1·95	2·04	2·00	2·11	2·04	2·12	2·06
	4	2·05	2·02	2·06	2·00	2·14	2·09	2·13	2·07
Mean weight of eggs produced at 350 days of age	1	59·1	59·4	59·4	58·9	59·5	59·6	59·8	59·4
	2	59·1	60·8	58·5	58·6	60·8	60·7	59·4	59·4
	3	58·9	58·6	60·2	60·2	60·1	59·3	61·4	60·9
	4	62·9	62·8	61·9	61·1	61·9	61·4	60·7	60·5
Egg production† of survivors to 500 days	1	170	166	170	172	181	179	183	184
	2	166	157	168	171	171	168	175	175
	3	161	157	172	188	178	172	175	186
	4	179	174	176	177	184	182	186	186
Laying house mortality in %	1	13·4	11·7	7·6	12·8	11·0	9·9	8·9	6·6
	2	18·9	11·5	12·0	10·6	14·2	12·7	11·4	9·6
	3	14·3	10·4	16·7	7·5	12·0	8·9	10·3	5·9
	4	6·4	2·6	11·2	9·5	5·2	5·5	8·9	6·0

† Based on trap-nesting populations 5 days a week.

had a two-week shorter laying period. Despite this the restricted-fed birds laid the same number of eggs on the average in the four years as the full-fed. Thus the rate of egg production from date of sexual maturity was higher for the restricted birds than for the full-fed birds which agrees with Gowe *et al.* (1960) and Hollands & Gowe (1961).

(ii) *Comparison of the pure strains and strain crosses*

In each of the four years the strain crosses were significantly superior to the pure strains in survivor egg production (Tables 2, 3 and 4). The strain crosses were also heavier at the end of the restriction period (significant in one year) and at maturity than the pure strains. They were also characterized by earlier sexual maturity than pure strains (significant in two years).

Strains within the strain cross group differed significantly for all traits in all years except for laying house mortality where they differed significantly only two years out of four. Differences amongst the pure strains for the six traits in almost all instances were also significant (Table 3).

Table 3. *Arithmetic means of variance components from four analyses (years) for six traits for the pure strains and strain crosses tested at two farms under two rearing treatments each year. Superscripts indicate the number of 'F' tests that were significant at the 5% probability level or greater*

Variance component	Body-wt. at 147 days	Sexual maturity	Body-wt. at 365 days	Egg-wt. at 350 days	Survivor egg production	Laying house mortality
σ^2_c	$15{\cdot}2^1$	$9{\cdot}1^2$	$18{\cdot}3$	$0{\cdot}18^1$	$55{\cdot}5^4$	$0{\cdot}00$
$\sigma^2_{s:c}$	$33{\cdot}5^4$	$13{\cdot}3^4$	$68{\cdot}0^4$	$1{\cdot}33^4$	$26{\cdot}4^4$	$0{\cdot}67^2$
$\sigma^2_{s(p)}$	$58{\cdot}2^3$	$18{\cdot}0^3$	$107{\cdot}5^3$	$2{\cdot}06^4$	$26{\cdot}9^4$	$-0{\cdot}35$
$\sigma^2_{s(k)}$	$28{\cdot}7^4$	$12{\cdot}5^4$	$60{\cdot}9^4$	$1{\cdot}18^4$	$26{\cdot}6^4$	$0{\cdot}90^3$
σ^2_f	$11{\cdot}6^3$	$6{\cdot}4^2$	$17{\cdot}3^2$	$0{\cdot}65^3$	$25{\cdot}6^4$	$0{\cdot}17^4$
σ^2_{cf}	$-0{\cdot}2$	$1{\cdot}0$	$-1{\cdot}0$	$-0{\cdot}05$	$-1{\cdot}0$	$-0{\cdot}02$
$\sigma^2_{fs:c}$	$1{\cdot}1$	$2{\cdot}0^1$	$2{\cdot}9$	$0{\cdot}09^1$	$4{\cdot}4$	$0{\cdot}54^1$
$\sigma^2_{fs(p)}$	$-0{\cdot}8$	$0{\cdot}5$	$10{\cdot}1^1$	$0{\cdot}12$	$-1{\cdot}4$	$-0{\cdot}60$
$\sigma^2_{fs(k)}$	$1{\cdot}5$	$2{\cdot}4^1$	$1{\cdot}3$	$0{\cdot}08^1$	$6{\cdot}0^1$	$0{\cdot}78^1$
σ^2_t	$387{\cdot}5^4$	$109{\cdot}0^4$	$10{\cdot}3^4$	$0{\cdot}04^1$	$1{\cdot}2^1$	$0{\cdot}23^2$
σ^2_{ct}	$0{\cdot}1$	$0{\cdot}1$	$-0{\cdot}3$	$0{\cdot}01$	$-1{\cdot}6$	$0{\cdot}00$
$\sigma^2_{ts:c}$	$4{\cdot}9^2$	$4{\cdot}3^3$	$-1{\cdot}3$	$0{\cdot}08^1$	$1{\cdot}4$	$0{\cdot}06$
$\sigma^2_{ts(p)}$	$5{\cdot}8^2$	$9{\cdot}0^1$	$0{\cdot}7^1$	$-0{\cdot}02$	$10{\cdot}4$	$-0{\cdot}74$
$\sigma^2_{ts(k)}$	$4{\cdot}7^2$	$3{\cdot}2^3$	$-1{\cdot}9^1$	$0{\cdot}10$	$-0{\cdot}4$	$0{\cdot}25$
σ^2_{ft}	$41{\cdot}0^4$	$19{\cdot}8^3$	$3{\cdot}2^2$	$0{\cdot}00^1$	$2{\cdot}8^1$	$0{\cdot}02$
σ^2_{cft}	$-1{\cdot}4$	$4{\cdot}7^1$	$-2{\cdot}5$	$0{\cdot}04$	$-1{\cdot}9$	$0{\cdot}03$
$\sigma^2_{fts:c}$	$3{\cdot}0^2$	$1{\cdot}0^1$	$2{\cdot}6^1$	$0{\cdot}11$	$0{\cdot}0$	$37{\cdot}35$
$\sigma^2_{fts(p)}$	$4{\cdot}8$	$0{\cdot}1$	$-8{\cdot}5$	$-0{\cdot}17$	$0{\cdot}8$	$69{\cdot}61$
$\sigma^2_{fts(k)}$	$2{\cdot}6^2$	$1{\cdot}2^1$	$4{\cdot}8^1$	$-0{\cdot}10$	$0{\cdot}0$	$30{\cdot}42$
σ^2_w	$198{\cdot}1$	$214{\cdot}1$	$507{\cdot}1$	$15{\cdot}13$	$698{\cdot}0$	—
$\sigma^2_{w(p)}$	$178{\cdot}9$	$264{\cdot}0$	$475{\cdot}9$	$16{\cdot}08$	$803{\cdot}7$	—
$\sigma^2_{w(k)}$	$202{\cdot}7$	$201{\cdot}1$	$515{\cdot}3$	$14{\cdot}90$	$671{\cdot}9$	—

Table 4. *Comparison of the pure strains and strain crosses pooled over both farms and the two rearing treatments for six traits*

	Pure strains	Strain crosses
Body-weight at housing (kg.)	1·37	1·43
Age at sexual maturity (days)	180	177
Body-weight at 365 days (kg.)	1·98	2·05
Egg-weight at 350 days (g.)	60·0	60·3
Egg production of survivors to 500 days†	170·2	179·1
Egg production of survivors to 500 days‡	238·3	250·7
Laying house mortality (%)	11·1	9·2

† Actual 5-day-a-week trap-nest production.
‡ Production converted to a 7-day week basis.

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(iii) *Interaction of farm and rearing treatment*

There was a highly significant amount of variation associated with the interaction of farm and rearing treatment for body-weight at 147 days (Table 3). To some extent this can be attributed to differences between farms in the quality and quantity of available food on the range area, other than that supplied in the all-mash diet. This also might be traced partly to slight variations in the total level of restriction of feed during the rearing period brought about by returning the birds to full-feed for short periods to treat them for minor coccidiosis outbreaks. There were similar interactions for the trait sexual maturity. The interaction of farm and treatment for sexual maturity was as large as that for the variation amongst pure strains or amongst strain crosses (Table 3). With the exception of laying house mortality, this interaction variance component was significant but small in one or two years out of four for all other traits.

(iv) *Interaction of genotype and environment*

Genotype-environment interactions may be real, that is they may be statistically significant, but still have little practical importance. For example, the interaction of strain (pure) × rearing treatment for housing body weight in year 1 was statistically significant (Table 5), yet the interaction component of variance only amounted to 6% of the total genetic variance (the sum of the components of variance for pure strains and the strain × rearing environment variance) and less than 1% of the total variance. On the average over all four years, only 0·7% of the total variance could be attributed to the interaction of strains (both pure and crosses) and rearing treatment for housing body weight (Table 6), and about 12% of the total genetic variance was found to be genotype-environment interaction, that is, the ratio of

$$\frac{\sigma^2_{ts:c}}{\sigma^2_{s:c}+\sigma^2_{ts:c}}$$

was smaller than 0·12. For the traits other than sexual maturity, the genotype-environment variance accounted for less than 10% of the genetic variance. When the interaction variance accounted for a very small proportion (less than 10%) of the genetic variance it would have little practical importance. This does not mean that selection of strains under a fixed environmental situation could not increase the relative magnitude of the interaction variance or decrease the genetic correlation as Falconer & Latyszewski (1952) have done, but rather that for strains selected under variable environmental (general commercial situation) conditions the genotype-environment interaction is not of great importance.

For sexual maturity the genetic variance was small and the interaction variance was on the average relatively large (Table 6), so the interaction variance accounted for about 24% of the genetic variance. This would be large enough to be of practical significance although it should be noted that there was considerable variation from year to year in the magnitude of this interaction component. This could be due to

Table 5. *Variance components for the pure strains, strain crosses, two environmental effects and the first-order interactions of genotype and environment for each of the 4 years*

Trait	Year	$\sigma^2_{s(p)}$	$\sigma^2_{s(k)}$	σ^2_f	$\sigma^2_{fs(p)}$	$\sigma^2_{fs(k)}$	σ^2_t	$\sigma^2_{ts(p)}$	$\sigma^2_{ts(k)}$	σ^2_w
Body-weight at housing	1	*123·2*†	*41·0*	0·4	−0·1	1·3	*202·3*	*7·6*	*7·1*	*185·1*
	2	*58·2*	*23·2*	*10·8*	−2·2	1·8	*409·1*	*9·5*	0·5	*186·9*
	3	*52·9*	*15·9*	*5·4*	−4·3	0·6	*253·3*	3·9	−0·9	*199·7*
	4	−1·5	*34·9*	*29·7*	3 3	2·3	*685·2*	2·1	*12·1*	*220·8*
Age at sexual maturity	1	*38·2*	*6·6*	*22·3*	3·4	0·9	*50·5*	4·9	2·9	*144·4*
	2	*21·5*	*22·8*	0·4	−2·0	*6·8*	*139·9*	*22·4*	*5·4*	*266·6*
	3	*13·5*	*7·9*	0·5	−4·5	−0·9	*93·9*	0·7	0·0	*214·0*
	4	−1·0	*13·0*	*2·3*	5·3	2·8	*151·8*	8·0	*4·7*	*231·3*
Body-weight at 365 days	1	*267·5*	*115·7*	*40·8*	10·3	3·2	*2·9*	−8·9	*5·9*	*459·1*
	2	*39·5*	*44·8*	*26·8*	*14·8*	−2·0	*4·8*	−0·2	−3·4	*472·9*
	3	*118·6*	*40·6*	1·7	7·6	1·6	*15·9*	*25·1*	−5·8	*528·9*
	4	4·3	*42·4*	0·0	7·9	2·5	*17·7*	−13·1	−4·3	*567·4*
Egg-weight at 350 days	1	*1·18*	*0·88*	−0·01	0·16	0·06	0·00	−0·22	0·00	*12·85*
	2	*3·98*	*2·02*	*0·89*	0·17	−0·03	−0·02	0·32	0·32	*13·44*
	3	*2·15*	*1·17*	*1·08*	0·06	*0·38*	*0·14*	0·12	0·04	*15·08*
	4	*0·94*	*0·63*	*0·64*	0·07	−0·07	0·05	−0·31	0·02	*19·15*
Egg production of survivors to 500 days	1	*35·9*	*13·2*	*6·0*	12·7	0·9	−0·3	8·5	0·8	*580·6*
	2	*18·8*	*29·7*	*17·7*	−8·9	*16·6*	1·3	22·5	1·6	*870·8*
	3	*31·6*	*30·4*	*76·1*	1·2	0·5	*3·9*	−1·1	−7·3	*698·3*
	4	*21·5*	*33·0*	*2·8*	−10·8	5·9	0·1	10·5	3·5	*642·2*
Laying house mortality	1	0·80	0·30	*0·14*	−0·05	0·19	0·11	1·77	0·09	*41·11*
	2	0·25	*0·90*	0·15	1·39	*1·52*	*0·08*	−0·04	0·30	*20·44*
	3	−0·52	*1·06*	*0·16*	0·59	0·34	*0·72*	−0·64	0·12	*28·20*
	4	−1·94	*1·32*	*0·24*	−4·35	1·07	0·02	−4·03	0·49	*59·66*

† Italic type indicates the variances were significant ($P < 5\%$ point).

Table 6. *Components of variance averaged over 4 years for six traits as a percentage of the total variance*

Variance component	Body-wt. at 147 days	Sexual maturity	Body-wt. at 365 days	Egg-wt. at 350 days	Survivor egg production	Laying house mortality
σ^2_c	2·2	2·4	2·9	1·0	6·8	0·0
$\sigma^2_{s.c}$	4·8	3·4	10·9	7·6	3·2	1·7
σ^2_f	1·7	1·7	2·8	3·7	3·2	0·4
σ^2_{cf}	0·0	0·2	−0·2	−0·3	−0·1	0·0
$\sigma^2_{fs.c}$	0·2	0·5	0·5	0·5	0·5	1·4
σ^2_t	55·8	28·3	1·6	0·2	0·1	0·6
σ^2_{ct}	0·0	0·0	0·0	0·0	−0·2	0·0
$\sigma^2_{ts.c}$	0·7	1·1	−0·2	0·4	0·2	0·2
σ^2_{ft}	5·9	5·1	0·5	0·0	0·3	0·0
σ^2_{cft}	−0·2	1·2	−0·4	0·2	−0·2	0·1
$\sigma^2_{fts\ c}$	0·4	0·2	0·4	0·6	0·0	95·6
σ^2_w	28·5	55·6	81·2	85·9	86·1	—

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the strains used in any particular year or to environmental circumstances differing from year to year.

There were no significant interactions of the different classes of strains (pure strains versus strain crosses) with the farm environments or the rearing treatment (Table 3).

When the two traits, body-weight at 147 days and days to first egg, were considered it was found that a large proportion of the total variance (56% and 28% respectively) was associated with the rearing treatment effects (Table 6). The genetic effects ($\sigma^2_{s:c}$) were large and significant each year. These results are similar to those reported in earlier studies utilizing the same rearing treatment but different genotypes (Hull & Gowe, 1962, and Gowe, Lemay & Johnson, 1962). The farm effects were relatively small for these traits although significant some years. Under these circumstances (Tables 5 and 6) there was only one significant farm × strain interaction ($\sigma^2_{fs(p)}$ or $\sigma^2_{fs(k)}$) out of the sixteen possible, while there were eight significant rearing treatment × strain interactions ($\sigma^2_{ts(p)}$ and $\sigma^2_{ts(k)}$). For these two traits the variance among pure strains ($\sigma^2_{s(p)}$) was greater than that among strain crosses ($\sigma^2_{s(k)}$), except in year 4 where $\sigma^2_{s(k)}$ was greater than $\sigma^2_{s(p)}$, and also in year 2 in the case of age at sexual maturity, where there was little difference in the variances $\sigma^2_{s(p)}$ and $\sigma^2_{s(k)}$.

In the first three years there appeared to be a relationship between the relative size of the genetic variance and the magnitude of the interaction variances. For body weight at housing this generality held true in all cases. For sexual maturity there was general agreement with one exception (Table 5).

In year 4 the variation among pure strains ($\sigma^2_{s(p)}$) was non-significant both in the case of housing body-weight and age to sexual maturity, while the variation among the strain crosses was significant. In just these two cases there was a significant interaction between strain crosses and rearing treatment, but not between pure strains and rearing treatment.

Turning to body-weight at 365 days of age, it is seen that the environmental effects, particularly rearing treatment, have a much smaller effect on performance. This is reflected in a great reduction in the size of genotype environment interaction components—six out of eight were essentially zero for the interaction of rearing treatment and body-weight at 365 days. However, the two largest interaction components are still those between pure strain and environment.

For the traits laying house mortality, egg weight and egg production, the treatment effects make up a small part of the total variation, not exceeding 0·6%. The genetic components of variance appear to be important for egg production and egg weight however, amounting to 10·0 and 8·6% of the total variation, respectively. The interaction components ($\sigma^2_{ts(p)}$ and $\sigma^2_{ts(k)}$) did not differ significantly from zero for all twenty-four estimates obtained for these three traits. The farm variance made up a larger proportion of the total variance for egg production and egg size, but only two out of sixteen components were significantly different from zero (Tables 5 and 6). For these three traits, the environmental differences did not appear to be sufficiently large to induce an important genotype-environment

interaction, even though the genetic components were large for egg-weight and moderate for egg production, therefore no comparison between the interaction with environment of pure strains with that of cross strains was possible.

There was one significant second-order interaction of class × farm × treatment for sexual maturity in year 4. It is not likely this has any general significance. In this year the pure strain birds on restricted feeding at farm 2 came into production twelve days later than the full-fed group at that farm, whereas the pure strain restricted group started to lay twenty-two days later at the other farm. Birds of the restricted strain crosses began to lay seventeen and eighteen days later than those of the full-fed crosses at the two farms. The reason for the early start of lay for the pure strains at one location in this year remains unexplained. The other second-order interaction components were small and insignificant.

It may be concluded that, in general, significant genotype-environment interactions of a large magnitude occurred only for those traits where environmental factors have a large effect on performance as demonstrated by the rearing treatment effect on the traits, age at sexual maturity and body-weight at housing (Table 5). Further than this it was found that where there was a greater between-group variance among pure strains than among cross strains (a number of more or less genetically dissimilar and homogeneous groups, when crossed, being expected to give a second set of groups which are less dissimilar), then the interaction of pure strains with environment was greater than that of cross strains with environment. Seven times out of eight for the two traits affected most by the environment—body-weight at housing, and age at sexual maturity—this held true (Table 5). It therefore seems likely that the importance of genotype-environment interaction variance in any given situation will be dependent to some degree on the total genetic variance, as well as the magnitude of the environmental effect. It seems probable that when a genotype-environmental interaction is detected, it may be associated not with some special class of genes, but rather with the same or similar genes which give rise to total genetic variation in any character. Thus it is not unreasonable to look for a relationship between interaction variance and total genetic variance.

5. SUMMARY

In these experiments comparisons were made between the magnitude of the interaction of 'pure' strains and strain crosses of poultry with two types of environments—location effects and a restricted-feed versus a full-feed rearing programme. The 'pure' strains were closed flocks of White Leghorns that had been selected for increased egg production, while the strain crosses were the reciprocal crosses of all combinations of these pure strains. Data from four separate experiments in four consecutive years used for this study involved 8320 laying birds. Six traits of the adult laying birds were used for these analyses.

It was expected that the 'pure' strains would differ in performance amongst themselves to a greater extent than the strain crosses, and for the two traits, body-weight at housing and sexual maturity, this was found to be the case in three

out of four years. These two traits were affected to the greatest extent by the rearing treatment. Also, the genotype-environment interaction variance was found to be significant and of important magnitude relative to the genetic variance for these two traits. Where the environmental effect was found to be smaller, the interaction variance made up a smaller proportion of the genetic variance.

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