Synthesis and parameters of new populations of meat-type chickens*

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Summary. Sire and dam populations of meat-type chickens were developed at the Animal Research Centre, Ottawa to provide unselected control populations suitable for modern broiler research, estimate genetic parameters of broiler traits, and initiate selection experiments. The populations were synthesized from 16 commercial broiler parent stocks (nine sire and seven dam stocks) during two generations of cross-breeding and one generation of random mating. The estimated genetic contribution per stock to the respective population ranged from 8.3 to 16.7% for autosomal genes, from 5.5 to 17.8% for genes on Z chromosomes, and from 0 to 25.0% for genes on W chromosomes. Genetic differences among the original stocks had not been fully diffused among individuals within the populations at the time parameters were estimated. Consequently, genetic parameter estimates are probably slightly biased. Estimated heritabilities of broiler traits in these populations were generally high, 0.39 to 0.63. Hence, rapid genetic change of these traits is possible. The genetic correlation between 28 to 49 day feed efficiency and corresponding weight gain was 0.69 and between feed efficiency and abdominal fat percentage was -0.68. Increasing body weight gain, improving feed efficiency and reducing abdominal fatness of broilers by selection appears feasible.

Key words: Meat-type chickens – Synthetic populations – Parameters – Broiler traits

Introduction

The current goal of breeders of meat-type chickens is to produce rapidly growing, feed efficient broilers with

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lean carcasses. During past decades, major emphasis in selection programs for broiler body weight and rate of gain has been successful (Chambers et al. 1981). From a review of available literature (Chambers et al. 1983) it was obvious that, generally, breeders have relied on positive genetic correlations with growth rate to improve feed efficiency during selection for rapid growth. Excess fatness of some broiler carcasses which reflects the lack of direct selection against fatness by the breeder, reduces feed efficiency. Until recently labour and/or equipment costs have discouraged measurement of feed efficiency and carcass fatness. Further improvement in broiler efficiency and consumer acceptance might be obtained by including direct selection for feed efficiency and carcass leanness. Hence, research is needed to test effectiveness of such selection programs.

This research as well as that on meat-type chickens in general requires chickens representative of those used in the production of broiler meat. The purposes of the work reported in this paper were to develop sire and dam populations of meat-type chickens from broiler parent stocks provided by commercial breeders and to estimate parameters of relevant broiler traits in these populations as a basis for future selection.

Materials and methods

A reference population of meat-type chickens was developed earlier at Ottawa (Merritt and Gowe 1962). However, large genetic gains made by commercial breeders after this population was established (Chambers et al. 1981) have created the need for new control populations representative of current commercial stocks of broilers for research and measurement of genetic progress.

Commercial broiler growers use chicks produced by parent stocks from many commercial breeders. Hence, popu-

lations synthesized from several commercial parent stocks will be more representative of modern broilers than individual parent stocks. Starting in 1978, new sire and dam base populations of meat-type chickens were developed at the Animal Research Centre, Ottawa. Parent stocks instead of pure strains were used for synthesis due to the general reluctance of breeders to release pure strains. Moreover, parent stocks that are hybrid will represent two as opposed to one pure strain.

Stocks used and population synthesis

Fifty male and one hundred female day old chicks from broiler sire and dam stocks were requested from commercial broiler breeders in North America. Nine different companies responded by supplying chicks during the period Aug. 18 to Oct. 30, 1978. Four companies provided both sexes and five provided males only of broiler sire stocks. Both sexes of broiler dam stocks were received from five companies and females only were obtained from two companies. These stocks were considered representative of commercial broiler parents available at that time.

Sire (strain 20) and dam (strain 30) populations were developed in three generations using the above stocks. The genetic contributions of the stocks and sexes to the two populations are shown in Table 1.

Crossbreeding was practised for the first two generations. This allowed genetic recombination among gametes from different stocks thereby reducing genetic disequilibrium among loci caused by genetic differences among the original stocks.

Table 1. Availability and expected genetic contribution of broiler parent stocks to synthetic sire and dam populations

Popula-tion	Source	Proportion[a]		Percentage contribution to		
		Sires : Dams		Auto-somes[b]	Sex chromosomes[c]	
		Sires	Dams		Z	W
Sire	1	0	0.250	12.5	8.3	25.0
	2	0	0.250	12.5	8.3	25.0
	6	0	0.250	12.5	8.3	25.0
	8	0	0.250	12.5	8.3	25.0
	3	0.200	–	10.0	13.3	0
	4	0.200	–	10.0	13.3	0
	7	0.200	–	10.0	13.3	0
	5	0.200	–	10.0	13.3	0
	9	0.200	–	10.0	13.3	0
Dam	1	0.200	0.133	16.7	17.8	13.3
	2	0.200	0.133	16.7	17.8	13.3
	6	0.200	0.133	16.7	17.8	13.3
	8	0.200	0.133	16.7	17.8	13.3
	3	0.200	0.133	16.7	17.8	13.3
	4	–	0.167	8.3	5.5	16.7
	7	–	0.167	8.3	5.5	16.7

[a] – = not available; 0 = available but not used; 0.133–0.250 = available and used. The numerical value is the proportion of parents of that sex represented by that stock
[b] The autosomal contribution per stock by sires (dams) = 0.50 × proportion of sires (dams) for that stock
[c] The Z chromosome contribution per stock by sires (dams) = 0.667 (0.333) × proportion of sires (dams) from that stock; the W chromosome contribution per stock = the proportion of dams from that stock

Crossbreeding can also disseminate the genetic variation existing among stocks uniformly among individuals within the population; however, several generations are required to complete the redistribution. The distribution pattern in the initial generations is illustrated in the Appendix. The two generations of crossbreeding substantially reduced genetic variation among crossbred groups. Additional crossbreeding would have eliminated the remaining variation among groups; however, this variation was not considered large enough to be important and further crossbreeding would have delayed use of these populations in research. The subsequent random mating in the G_2 generation at least partially reduced the remaining genetic variation among crossbred groups and virtually restored genetic equilibrium at individual, autosomal loci.

The mating plan attempted to make the contribution of each commercial stock to the respective base population as equal as possible (Table 2). Equalization of contribution of sex chromosomes was impossible when only one sex of the stock was available. Where chicks of both sexes were available but only those of one sex were to be used in the population synthesis, females were given preference in order to introduce samples of both Z and W sex chromosomes. During the first two generations of crossbreeding, non-productive parental candidates of both sexes were eliminated and replaced prior to mating to minimize reproductive failure among designated parents. This enhanced the similarity in number of progeny contributed per parent and per stock.

Within each broiler parent type, pullets of each commercial stock were mated to males of all other stocks contributing males to produce crossbred first generation progeny. The second generation of each population was produced using a modified diallel mating scheme by crossing the single crosses within the populations to produce four-way cross progeny. In the sire population, all 240 possible four-way crosses were made. Due to space limitations, 100 of the 400 possible four-way crosses in the dam population were systematically eliminated to avoid favouring specific stocks. The resulting G_2 generation was pedigreed and randomly mated avoiding sib matings to produce G_3 progeny (not shown in Table 2) used to estimate genetic parameters.

Feeding and management

Generations G_0, G_1 and G_2. Sexed chicks were wingbanded and brooded in pens in windowless, ventilated houses. Red light was used to illuminate pens 24 h/day for the first three days followed by either 6 h/day for the original stocks or 8 h/day for later generations until the chickens were housed. In all generations chicks were fed a starter mash, 2,809 kcal metabolizable energy (ME)/kg and 17.7% crude protein (CP) calculated analysis, ad libitum to 42 days of age. Thereafter they were fed a grower mash, 2,829 kcal ME/kg and 12.9% CP on a skip-a-day basis (access to feed for 6 h/day only on odd numbered Julian calendar days) until housing.

At or shortly before 138 days of age, the chickens were moved to a windowless laying house. Pullets were placed in individual cages 25.5 cm wide, cockerels in cages 30.5 cm wide. White light was used to illuminate the house for 8 h/day to 21 weeks of age. Thereafter the light period was increased by 0.5 h/week until 16 h/day was reached. Daily feeding of a restricted amount of laying mash, 2,680 kcal ME/kg and 15.0% CP commenced for pullets at 22 weeks of age. In the G_2 generation, restricted, daily feeding commenced at housing. All matings were by artificial insemination.

Generation G_3 used for genetic parameter estimation. Up to six pedigreed chicks per hen were wingbanded on the day of

Table 2. Mating designs for the syntheses of sire and dam populations

Generation	No. of			No. of			Mating procedure
	Genetic groups	Sires per group	Total sires	Genetic groups	Dams per group	Total dams	
Sire population (strain 20)							
G_0	5	32	160	4	80	320	All possible two-stock crosses
G_1	20	4	80	20	12	240	All 240 four-stock crosses
G_2	1	1/sire	80	1	1/dam[a]	240	Random mating excluding sibs
Dam population (strain 30)							
G_0	5	30	150	7 (5)[b] (2)	40 50	300	All possible two-stock crosses
G_1	30 (20) (10)	3 4	100	30 (20) (10)	9 12	300	300 of the 400 possible four-stock crosses
G_2	1	1/sire	80	1	1/dam[c]	240	Random mating excluding sibs

[a] Only 220 dams had live daughters at mating; hence full-sisters of 20 daughters also had to be included
[b] Bracketed values represent the number of genetic groups with the corresponding number of sires or dams per group
[c] Only 238 dams had live daughters at mating; hence full sisters of two daughters also had to be included

hatch and placed in battery cages (approximately 50/cage) for brooding to 25 days of age. From 25 days of age until slaughter, the broilers were confined individually in wire cages, 20.3 cm wide, normally used for laying hens. The cages were adapted for the broilers by inserting level wire mesh floors and water lines with drippers approximately 15 cm above the cage floor. Plastic feed containers were inserted in the feed trough to permit measurement of individual feed consumption.

To 28 days of age a crumbled broiler starter ration (3,155 kcal ME/kg and 23.5% CP) and thereafter a pelleted broiler grower ration (3,210 kcal ME/kg and 20.8% CP) were fed ad libitum. From hatch to slaughter 24 h of white light/day was provided for the broilers. After being fasted 16 to 22 h, the 50 day old broilers were stunned, bled, scalded, plucked and eviscerated.

Broiler trait measurements

Broiler traits measured included live body weights at 28, 42 and 49 days of age and feed consumption from 28 to 49 days of age. Weight gain and feed efficiency (gain/feed) from 28 to 49 days of age were calculated. Right and left abdominal wall thickness and fasted body weight were measured prior to slaughter at 50 days of age along with weights of the eviscerated carcass without leaf fat and of abdominal fat (leaf fat plus gizzard fat). Abdominal fat was also expressed as a percentage of the eviscerated carcass weight. Sex of the broilers was determined during evisceration by gonadal examination.

Abdominal wall thickness was measured using a modified procedure of Pym and Thompson (1980). One arm of a caliper was inserted four to five cm into the vent while the broiler was restrained on its back. The instrument was rotated laterally 45° from a horizontal position and the other arm allowed to close on the region between the pubis and sternum bones while avoiding feathers. After the meter reading stabilized, it was noted and the caliper was opened and rotated 90° and the other side similarly measured. If the two measures differed by two mm or more, the measurements were repeated. The average of the right and left measurements represented the abdominal wall thickness.

Parameter estimation

Nested analyses of variance and covariance were performed for all traits within each population-sex subclass. The model used was

$Y_{ijk} = \mu + s_i + d_{ij} + e_{ijk}$, where
Y_{ijk} = the trait value for the kth individual from the jth dam (d) mated to the ith sire (s),
μ = the subclass mean,
s_i = the random effect of the ith sire,
d_{ij} = the random effect of the jth dam mated to the ith sire,
e_{ijk} = the random residual effect of the kth bird of the ijth family.

Due to the relatively small number of birds (< 250) per population-sex subclass, degrees of freedom, sums of squares and cross products and variance component coefficients (k values) were pooled before estimating the overall sire, dam and residual components of variance and covariance. Heritabilities (h^2) and genetic correlations (r_g) for traits x_1 and x_2 were estimated using the pooled variance and covariance components as follows:

$$h_1^2 = \frac{4 \, \sigma s_{x_1}^2}{\sigma s_{x_1}^2 + \sigma d_{x_1}^2 + \sigma e_{x_1}^2} \quad \text{and}$$

$$r_{g_{12}} = \frac{\sigma s_{x_1 x_2}}{(\sigma s_{x_1}^2 \cdot \sigma s_{x_2}^2)^{1/2}}$$

where $\sigma s_{x_1}^2$ = the sire component of variance,
$\sigma d_{x_1}^2$ = the dam component of variance,
$\sigma e_{x_1}^2$ = the residual component of variance and
$\sigma s_{x_1 x_2}$ = the sire component of covariance.

Phenotypic correlations were estimated as

$$r_{p_{12}} = \frac{\sigma s_{x_1 x_2} + \sigma d_{x_1 x_2} + \sigma e_{x_1 x_2}}{((\sigma s_{x_1}^2 + \sigma d_{x_1}^2 + \sigma e_{x_1}^2) \cdot (\sigma s_{x_2}^2 + \sigma d_{x_2}^2 + \sigma e_{x_2}^2))^{1/2}}$$

where $\sigma d_{x_1 x_2}$ and $\sigma e_{x_1 x_2}$ are the dam and residual components of covariance respectively.

Results

Genetic contributions of commercial stocks to the synthetic populations

Each stock obtained was included in the synthesis of one of the base populations. Respective contributions of the individual stocks to the synthetic sire and dam populations in terms of autosomes and Z and W chromosomes are shown in Table 1. For each sex, similar numbers of parents were selected from each original stock to contribute to the sire population. The number of females per stock chosen to contribute to the dam population differed. For the two stocks lacking males, more females (50 versus 40 in the initial generation) were selected to contribute to the gene pool. This action partially offset the reduction in genetic contribution caused by the lack of males in these stocks. Increasing the number of females from these two stocks increased the genetic contribution of each of these stocks: from 7.1 to 8.3% for autosomes; from 4.8 to 5.5% for Z chromosomes; from 14.3 to 16.7% for W chromosomes.

Population characteristics

Means for body weights and measurements of the commercial stocks, generation G_0, used to establish the synthetic populations are shown in Table 3 by sex and population to characterize their performance when reared as breeders. Stock means were not presented due to confounding of stock differences with sex and with differences in age of parental flocks, hatching dates and methods of hatching and shipping the stocks to Ottawa. Performance of generations G_1 and G_2 are not shown because they will be the subject of a separate publication dealing with sex-linked genetic and maternal effects.

The mean performance of generation G_3 broilers is presented in Table 4. Males and females of the sire populations were heavier, gained more, had better feed efficiency in spite of tendencies to eat more feed and had greater weights but similar proportions of abdominal fat compared to corresponding sexes of the dam population. In both populations males were larger, gained more weight and had better feed efficiencies and less abdominal fat than females.

Estimates of heritabilities, phenotypic variances and genetic and phenotypic correlations based on pooled sire components of variance and covariance within population and sex are shown in Table 5. The heritability estimates obtained were all above 0.38 and often differed from zero by two standard errors or more. Body weight at 28 days and feed consumption were moderately heritable.

Genetic and phenotypic correlations indicated several important relationships. Larger broilers had greater body weight gains, appetites and feed efficiency. The correlations between body weights and feed efficiency tended to increase from 28 to 49 days of age. Faster gaining broilers had better 28 to 49 day feed efficiencies. Broilers with more abdominal fat ate more feed and had poorer feed efficiencies. This relationship was more pronounced for genetic than for phenotypic differences. The fatter broilers tended to be heavier but from 28 to 49 days of age the genetic relationship declined. Experimental error in measurements of body or carcass weight would contribute to a negative correlation between these traits and abdominal fat percentage. By definition, any increase (decrease) in carcass weight due to measurement error will cause a corresponding decrease (increase) in abdominal fat percentage. Hence the true biological correlations between these traits are expected to be slightly smaller, if negative, and slightly larger if positive.

Table 3. Means ± SE for body weights and measurements of the commercial broiler parent stocks (Generation G_0) obtained for population synthesis.

Trait	Sire stocks		Dam stocks	
	Males	Females	Males	Females
n	418	373	227	658
Body wt −42 d (g)	1,195 ±10	995 ± 6	1,086 ±10	1,013 ± 6
Breast angle (°)	90.6± 0.3	91.5± 0.3	87.0± 0.4	87.9± 0.3
Body depth (mm)	97.6± 0.3	90.2± 0.2	97.8± 0.5	· 92.0± 0.2
Keel length (mm)	89.7± 0.3	82.3± 0.2	88.8± 0.4	83.6± 0.2
Shank length (mm)	94.1± 0.3	86.5± 0.2	91.0± 0.3	87.5± 0.2
Shank circumference (mm)	43.8± 0.2	39.5± 0.1	43.4± 0.3	39.7± 0.1
n	303	314	˙170	492
Body wt −140 d (g)	2,949 ±30	2,323 ±14	2,756 ±26	2,246 ±12
Body wt −365 d (g)	4,941 ±37	3,691 ±25	4,918 ±47	3,560 ±19

Table 4. Means ± SE of broiler traits from the synthetic populations (Generation G_3)

Trait	Age (days)	Population							
		Sire (strain 20)				Dam (strain 30)			
		Males		Females		Males		Females	
n		232		224		215		233	
Body wt (g)	28	660	± 4	637	± 4	635	± 4	588	± 4
Body wt (g)	42	1,552	± 8	1,379	± 8	1,444	± 8	1,229	± 7
Body wt (g)	49	1,980	±10	1,735	±10	1,846	±10	1,547	± 8
Fasting wt (g)	50	1,860	±10	1,633	± 9	1,742	± 8	1,467	± 7
Carcass wt (g)	50	1,266	± 8	1,105	± 7	1,167	± 7	974	± 5
Weight gain (g)	28–49	1,320	± 7	1,099	± 7	1,211	± 8	960	± 6
Feed cons (g)	28–49	2,685	±14	2,433	±14	2,627	±14	2,294	±16
Feed efficiency	28–49	49.2	± 0.2	45.3	± 0.2	46.2	± 0.2	41.9	± 0.2
Abdominal fat wt (g)	50	19.5	± 1.0	23.1	± 0.6	18.1	± 0.6	20.1	± 0.6
Abdominal fat % (%)[a]	50	1.53	± 0.04	2.07	± 0.05	1.53	± 0.05	2.04	± 0.05
Abdominal wall thickness (mm)	50	5.90	± 0.06	6.38	± 0.06	5.07	± 0.06	5.45	± 0.06

[a] Abdominal fat as a percentage of the eviscerated carcass without leaf fat

Table 5. Heritabilities ± SE phenotypic variances, and genetic (above diagonal) and phenotypic (below diagonal) correlations for broiler traits of the synthetic populations

Trait	Heritabili- ties	Pheno- typic variances	Correlations										
			1	2	3	4	5	6	7	8	9	10	11
1 Body wt 28 d	0.39±0.26	6,268		1.03	0.80	0.79	0.76	0.57	0.89	−0.14	0.49	0.33	0.53
2 Body wt 42 d	0.63±0.26	20,849	0.77		1.00	1.01	1.00	0.83	0.93	0.21	0.30	0.10	0.30
3 Body wt 49 d	0.60±0.26	28,250	0.67	0.93		1.00	0.95	0.95	0.88	0.45	0.14	−0.05	0.26
4 Fasted wt 50 d	0.54±0.26	25,130	0.67	0.92	0.98		0.98	0.95	0.87	0.47	0.05	−0.14	0.29
5 Carcass wt[a] 50 d	0.46±0.25	13,564	0.65	0.88	0.94	0.95		0.91	0.81	0.48	0.02	−0.19	0.29
6 wt gain 28–49 d	0.54±0.26	16,747	0.26	0.74	0.89	0.86	0.82		0.73	0.69	−0.07	−0.24	0.09
7 Feed cons 28–49 d	0.39±0.24	62,036	0.54	0.79	0.80	0.78	0.76	0.71		0.00	0.42	0.24	0.19
8 Feed effic[b] 28–49 d	0.40±0.26	13.923	−0.31	0.06	0.25	0.24	0.21	0.52	−0.22		−0.62	−0.68	−0.11
9 Ab fat wt 50 d	0.55±0.23	101.81	0.43	0.44	0.41	0.41	0.39	0.27	0.45	−0.17		0.97	0.69
10 Ab fat %[c] 50 d	0.63±0.24	0.72044	0.33	0.28	0.25	0.24	0.21	0.12	0.32	−0.22	0.97		0.63
11 Ab wall thick 50 d	0.46±0.24	0.13800	0.37	0.36	0.34	0.35	0.33	0.21	0.32	−0.10	0.43	0.40	

[a] Carcass wt = weight of eviscerated carcass with leaf fat removed
[b] Feed effic = body weight gained/feed consumed
[c] Ab. fat % = (abdominal fat weight/carcass weight without leaf fat) × 100

Discussion

Contribution of original stocks to the synthetic populations

The synthetic parent populations have a broad genetic base and appear to be well suited as foundations for selected or control strains in genetic research related to broilers. The lack of both sexes for all stocks made equal genetic contributions to the synthetic populations by each stock impossible especially with regard to sex chromosomes. On the other hand, autosomal contributions per stock were similar, ranging from 8.3 to 16.7%.

Visual evidence confirmed the existance of genetic differences among the initial stocks. Some sire stocks were homozygous for the "gold" plumage (s) colour gene, some were segregating for the "pea" (P) comb type. Among dam stocks, some carried the "slow feathering" (K) and some the "silver" (S) sex-linked genes while some were segregating at the dominant white (I) and recessive white (c) plumage loci.

Population characteristics

It is generally recognized that specialized sire and dam lines developed by unique selection programs provide the greatest

net improvement in progeny performance (Smith 1964; Moav and Hill 1966; Dickerson 1969; Clayton 1974). Commercial breeding companies currently use this approach to produce meat-type chickens. Hence, separate sire and dam populations were synthesized.

Trait means of birds of the G_0 and G_3 generations indicated that the sire population grew faster and more efficiently and had better body conformation (greater breast angle) than the dam population. Means of birds of generation G_0 should be regarded cautiously due to confounding of stocks with sex and other environmental differences mentioned previously. However, population differences in body weights were consistent in the two generations in spite of differences in confinement and feeding methods. G_0 birds were confined in pens and fed as breeders; G_3 birds were confined in cages and fed as broilers. Confounding of environmental effects prevented accurate assessment of the effects of three generations of relaxed selection during population synthesis. Nevertheless, the differences between sire and dam populations and between sexes remained generally unchanged in the G_3 compared to the G_0 generation. In a separate study using birds from the G_0 generation, population differences were less effective than sex and stock differences in accounting for variation in 12 blood plasma traits of adult birds (Grunder et al. 1983).

In the sire population, generation G_3, there was a larger increase in weight gain than in feed consumption. Hence, this population had superior feed efficiency in spite of larger body size during test. Compared to the dam population, the sire population had

similar proportions but, due to greater body size, greater weights of abdominal fat. In a constant weight comparison, the dam population would have been older and may have become fatter because fatness tends to increase with age (Tzeng and Becker 1981).

The influence of confinement on performance of the broilers in cages during test is not well known; however, performance based on trait means appeared similar to conventionally reared broilers. Abdominal fatness was low compared to other research (3.5% at 49 days-Leeson and Summers 1980; 3.1% at 55 days-Becker et al. 1981). The 1.8% in this study may reflect the influence of cage confinement similar to that reported by Friars et al. (1979).

Variances and covariances from the four population-sex subclasses were pooled producing only a single estimate of each parameter. This action was chosen to increase the reliability of the estimates. Parameter differences existing among the subclasses are lost in pooled estimates; however, only very large differences among the subclass estimates could have been significant due to the large standard errors of the subclass estimates.

Heritabilities of broiler traits are large enough to permit rapid improvement through selection. Values in the 0.55 to 0.63 range for body weight at 42 and at 49 days and for weight and percentage of abdominal fat were especially encouraging. The heritability estimates in this study were generally in good agreement with other reports (Table 6) in spite of large (0.23 to 0.26) standard errors. Unfortunately, these large standard

Table 6. Heritability estimates for broiler traits studied

Trait	This study	Other studies[a]			Other
		I	II	III	
Body wts	0.39–0.63	0.51–0.66	0.40, 0.79	0.63, 0.57 (males) 0.84, 1.30 (females)	0.41-median of 176 values Siegel 1962
Weight gain	0.54	0.42–0.67	0.81	0.52 (males) 1.35 (females)	– –
Feed consumption	0.39	0.60–0.85	0.69	0.40 (males) 1.01 (females)	–
Feed efficiency	0.40	0.03–0.48	–	–	–
Feed conversion	–	–	0.34	0.38 (males) 1.91 (females)	–
Abdominal fat wt	0.55	–	–	–	0.79 Ricard and Rouvier 1967 0.65 Ricard and Rouvier 1969 0.09–0.28 Leclercq et al. 1980
Abdominal fat percentage	0.63	–	–	–	0.72 Ricard and Rouvier 1969 0.39 Ricard 1974 0.24–0.81 Leclercq et al. 1980

[a]   I = Values at two to 6 week intervals between 4 and 10 weeks of age by Thomas et al. 1958
II = Values between 5 and 10 weeks of age by Wilson 1969
III = Values between 5 and 9 weeks of age by Pym and Nicholls 1979

errors for heritability and correlation estimates precluded formulation of a precise selection index for these three traits.

Due to the high positive correlations among body and carcass weights and weight gain, there is little to be gained by selecting for more than one of these traits. Stronger positive correlation with fatness, negative correlation with feed efficiency and lower heritability discourage use of 28 day body weight in favour of a later weight.

Some bias is associated with the genetic parameters estimated in this study. Due to the broad genetic bases of these populations, the genetic variances will tend to be larger than those found within specific strains. However, genetic variation among the initial stocks was not fully distributed among generation G_3 individuals within each population. Variation due to different crosses of more than four stocks will inflate variance among full-sib families whereas that due to differences among four-stock crosses will be expressed within full-sib families and will inflate variance within these families (see Appendix). It is difficult to quantify effects of the broad genetic base, of the incomplete diffusion of stock differences among all individuals, and the extent to which their influences cancel; however, their net influence is believed to be small.

Response to selection for improved growth rate, feed efficiency and carcass leanness would be expected to be greater when selection is against percentage rather than weight of abdominal fat. Abdominal fat percentage was more heritable than fat weight in agreement with Ricard and Rouvier (1969) and Leclercq et al. (1980). Abdominal fat percentage had larger negative correlations with feed efficiency and either smaller positive or larger negative correlations with body and carcass weights. Abdominal wall thickness increased with abdominal fatness; however, its use as a predictor of fatness in live broilers is limited because correlation coefficients were not large.

Feed efficiency improved with increases in body weights except at 28 days, in carcass weight and in weight gain after 28 days. Moreover, feed efficiency improved with reductions in abdominal fatness. Hence, simultaneous genetic improvement of body weight and feed efficiency and reduction of abdominal fatness is quite feasible. It may be possible to improve the three traits by selecting for only two of them. Further research is needed to compare expected and realized responses to selection for all three traits vs selection for body weight and either feed efficiency or reduced abdominal fatness.

Appendix

Redistribution of genetic differences among strains pooled to form a synthetic population

New synthetic populations of poultry may be developed for various purposes by combining two or more existing strains. Frequently breeders wish to determine the genetic properties, i.e. heritabilities and genetic correlations, of these new populations. Crossbreeding used to combine the strains causes genetic differences among strains to be redistributed according to a specific pattern if only crossbred matings are permitted. In the initial parental populations (G_0), the genetic differences

The redistribution of genetic variance due to strains when crossed to form a new population and its effect on heritability estimates

Generation	Genetic variation[a] re: families[b]		Estimated versus actual h^2
	Within	Between	
Two strains			
G_0	σ_w^2	$\sigma_b^2 + \sigma_s^2$	high
G_1	σ_w^2	σ_b^2	high if $h^2 > 0.5$; low if $h^2 < 0.5$
G_2	$\sigma_w^2 + \sigma_s^2$	σ_b^2	low
G_3	$\sigma_w^2 + \dfrac{\sigma_s^2}{2}$	$\sigma_b^2 + \dfrac{\sigma_s^2}{2}$	no bias
G_4	$\sigma_w^2 + \dfrac{\sigma_s^2}{2}$	$\sigma_b^2 + \dfrac{\sigma_s^2}{2}$	no bias
Four strains			
G_0	σ_w^2	$\sigma_b^2 + \sigma_{xw}^2 + \sigma_{xb}^2$	high
G_1	σ_w^2	$\sigma_b^2 + \sigma_{xb}^2$	high
G_2	$\sigma_w^2 + \sigma_{xw}^2$	σ_b^2	low
G_3	$\sigma_w^2 + \sigma_{xw}^2 + \dfrac{\sigma_{xb}^2}{2}$	$\sigma_b^2 + \dfrac{\sigma_{xw}^2}{2}$	low
G_4	$\sigma_w^2 + \dfrac{\sigma_{xw}^2}{2} + \dfrac{\sigma_{xb}^2}{2}$	$\sigma_b^2 + \dfrac{\sigma_{xw}^2}{2} + \dfrac{\sigma_{xb}^2}{2}$	no bias

[a] σ_w^2 = variation within families; σ_b^2 = variation among families within strains; σ_s^2 = added variation among families from different strains; σ_{xw}^2 = added variation among families from different strains of strain pairs, $\sigma_{xw}^2 = \sigma_s^2$ if there are only two strains; σ_{xb}^2 = added variation among families from different strain pairs, (or from different two strain crosses), $\sigma_{xw}^2 + \sigma_{xb}^2 = \sigma_s^2$ if there are four or fewer strains
[b] Full-sib families

among strains are confounded with and inflate estimates of genetic variation among families. The genetic variation due to strains is not expressed among progeny from crosses of two strains (G_1); however, it reappears as within family variation among grandprogeny (G_2) and is equally distributed within and among families in later generations.

If more than two strains are combined, the portion of the strain variance represented by differences between strains of a pair follows the pattern above; however, the appearance of differences among strain pairs within and among families is delayed one generation, or until the crosses are crossed. If more than four strains are combined, distribution of genetic differences among four strain combinations does not commence until the four-way cross grandprogeny are crossbred. Hence genetic parameters cannot be accurately estimated in newly developed populations until at least three generations (more if more than two strains are combined) after the original parents are crossed.

The redistribution of the genetic variance due to strains and its effect on heritability estimates for several generations is shown for populations developed from two and four strains. Due to uncertainty concerning the sign of the genetic covariance associated with various strain or strain combination differences it is not feasible to predict corresponding effects on genetic correlations.

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